POTENT AND SELECTIVE INHIBITORS OF $Na_V1.3$ AND $Na_V1.7$

[0001] Throughout this application various publications are referenced within parentheses or brackets. The disclosures of these publications in their entireties are hereby incorporated by reference in this application in order to more fully describe the state of the art to which this invention pertains.

BACKGROUND OF THE INVENTION

[0002] Field of the Invention

[0003] The present invention relates to the biochemical arts, in particular to therapeutic peptides and conjugates.

[0004] Discussion of the Related Art

[0005] Voltage-gated sodium channels (VGSC) are glycoprotein complexes responsible for initiation and propagation of action potentials in excitable cells such as central and peripheral neurons, cardiac and skeletal muscle myocytes, and neuroendocrine cells. Mammalian sodium channels are heterotrimers, composed of a central, pore-forming alpha (α) subunit and auxiliary beta (β) subunits. Mutations in alpha subunit genes have been linked to paroxysmal disorders such as epilepsy, long QT syndrome, and hyperkalemic periodic paralysis in humans, and motor endplate disease and cerebellar ataxia in mice. (Isom, Sodium channel beta subunits: anything but auxiliary, Neuroscientist 7(1):42-54 (2001)). The β-subunit modulates the localization, expression and functional properties of α-subunits in VGSCs.

[0006] Voltage gated sodium channels comprise a family consisting of 9 different subtypes ($Na_V1.1$-$Na_V1.9$). As shown in Table 1, these subtypes show tissue specific localization and functional differences (See, Goldin, A. L., Resurgence of sodium channel research, Annu Rev Physiol 63: 871-94 (2001); Wilson et al., Compositions useful as inhibitors of voltage-gated ion channels, US 2005/0187217 A1). Three members of the gene family ($Na_V1.8$, 1.9, 1.5) are resistant to block by the well-known sodium channel blocker tetrodotoxin (TTX), demonstrating subtype specificity within this gene family. Mutational analysis has identified glutamate 387 as a critical

residue for TTX binding (See, Noda, M., H. Suzuki, et al., A single point mutation confers tetrodotoxin and saxitoxin insensitivity on the sodium channel II" FEBS Lett 259(1): 213-6 (1989)).

Table 1. VGSC family with rat TTX IC_{50} values. Abbreviations: CNS = central nervous system, PNS = peripheral nervous system, DRG = dorsal root ganglion, TG = Trigeminal ganglion. (See, Wilson et al., Compositions useful as inhibitors of Voltage-gated ion channels, US 2005/0187217 A1; Goldin, Resurgence of Sodium Channel Research, Annu Rev Physiol 63:871-94 (2001)).

VGSC isoform	Tissue	TTX IC_{50} (nM)	Indication
$Na_V1.1$	CNS, PNS soma of neurons	10	Pain, Epilepsy, Neurodegeneration
$Na_V1.2$	CNS high in axons	10	Neurodegeneration, Epilepsy
$Na_V1.3$	CNS, embryonic, injured nerves	2-15	Pain, Epilepsy
$Na_V1.4$	Skeletal muscle	5	Myotonia
$Na_V1.5$	heart	2000	Arrhythmia, long QT
$Na_V1.6$	CNS widespread, most abundant	1	Pain, movement disorders
$Na_V1.7$	PNS, DRG, terminals neuroendocrine	4	Pain, Neuroendocrine disorders, prostate cancer
$Na_V1.8$	PNS, small neurons in DRG & TG	>50,000	Pain
$Na_V1.9$	PNS, small neurons in DRG & TG	1000	Pain

[0007] In general, voltage-gated sodium channels (Na_Vs) are responsible for initiating the rapid upstroke of action potentials in excitable tissue in the nervous system, which transmit the electrical signals that compose and encode normal and aberrant pain sensations. Antagonists of Na_V channels can attenuate these pain signals and are useful for treating a variety of pain conditions, including but not limited to acute, chronic, inflammatory, and neuropathic pain. Known Na_V antagonists, such as

TTX, lidocaine, bupivacaine, phenytoin, lamotrigine, and carbamazepine, have been shown to be useful for attenuating pain in humans and animal models. (See, Mao, J. and L. L. Chen, Systemic lidocaine for neuropathic pain relief, Pain 87(1): 7-17 (2000); Jensen, T. S., Anticonvulsants in neuropathic pain: rationale and clinical evidence, Eur J Pain 6 (Suppl A): 61-68 (2002); Rozen, T. D., Antiepileptic drugs in the management of cluster headache and trigeminal neuralgia, Headache 41 Suppl 1: S25-32 (2001); Backonja, M. M., Use of anticonvulsants for treatment of neuropathic pain, Neurology 59(5 Suppl 2): S14-7 (2002)).

[0008] The α-subunits of TTX-sensitive, voltage-gated $Na_V1.7$ channels are encoded by the *SCN9A* gene. The $Na_V1.7$ channels are preferentially expressed in peripheral sensory neurons of the dorsal root ganglia, some of which are involved in the perception of pain. In humans, mutations in the *SCN9A* gene have shown a critical role for this gene in pain pathways. For instance, a role for the $Na_V1.7$ channel in pain perception was established by recent clinical gene-linkage analyses that revealed gain-of-function mutations in the *SCN9A* gene as the etiological basis of inherited pain syndromes such as primary erythermalgia (PE), inherited erythromelalgia (IEM), and paroxysmal extreme pain disorder (PEPD). (See, e.g., Yang et al., Mutations in *SCN9A*, encoding a sodium channel alpha subunit, in patients with primary erythermalgia, J. Med. Genet. 41:171-174 (2004); Harty et al., $Na_V1.7$ mutant A863P in erythromelalgia: effects of altered activation and steady-state inactivation on excitability of nociceptive dorsal root ganglion neurons, J. Neurosci. 26(48):12566-75 (2006); Estacion et al., $Na_V1.7$ gain-of-function mutations as a continuum: A1632E displays physiological changes associated with erythromelalgia and paroxysmal extreme pain disorder mutations and produces symptoms of both disorders, J. Neurosci. 28(43):11079-88 (2008)). In addition, overexpression of $Na_V1.7$ has been detected in strongly metastatic prostate cancer cell lines. (Diss et al., A potential novel marker for human prostate cancer: voltage-gated sodium channel expression in vivo, Prostate Cancer and Prostatic Diseases 8:266-73 (2005); Uysal-Onganer et al., Epidermal growth factor potentiates in vitro metastatic behavior human prostate cancer PC-3M cells: involvement of voltage-gated sodium channel, Molec. Cancer 6:76 (2007)).

[0009] Loss-of-function mutations of the *SCN9A* gene result in a complete inability of an otherwise healthy individual to sense any form of pain. (e.g., Ahmad et

al., A stop codon mutation in *SCN9A* causes lack of pain sensation, Hum. Mol. Genet. 16(17):2114-21 (2007)).

[0010] A cell-specific deletion of the *SCN9A* gene in conditional knockout mice reduces their ability to perceive mechanical, thermal or inflammatory pain. (Nassar et al., Nociceptor-specific gene deletion reveals a major role for $Na_V1.7$ (PN1) in acute and inflammatory pain, Proc. Natl. Acad. Sci, U S A. 101(34): 12706–12711 (2004)).

[0011] Based on such evidence, decreasing $Na_V1.7$ channel activity or expression levels in peripheral sensory neurons of the dorsal root ganglia (DRG) has been proposed as an effective pain treatment, e.g. for chronic pain, neuropathic pain, and neuralgia. (E.g., Thakker et al., Suppression of SCN9A gene expression and/or function for the treatment of pain, WO 2009/033027 A2; Yeomans et al., Decrease in inflammatory hyperalgesia by herpes vector-mediated knockdown of $Na_V1.7$ sodium channels in primary afferents, Hum. Gene Ther. 16(2):271-7 (2005); Fraser et al., Potent and selective $Na_V1.7$ sodium channel blockers, WO 2007/109324 A2; Hoyt et al., Discovery of a novel class of benzazepinone Na(v)1.7 blockers: potential treatments for neuropathic pain, Bioorg. Med. Chem. Lett. 17(16):4630-34 (2007); Hoyt et al., Benzazepinone $Na_V1.7$ blockers: Potential treatments for neuropathic pain, Bioorg. Med. Chem. Lett. 17(22):6172-77 (2007)).

[0012] The α-subunits of TTX-sensitive, voltage-gated $Na_V1.3$ channels are encoded by the *SCN3A* gene. Four splice variants of human Nav1.3 were reported to have different biophysical properties. (Thimmapaya et al., Distribution and functional characterization of human $Na_V1.3$ splice variants, Eur. J. Neurosci. 22:1-9 (2005)). Expression of $Na_V1.3$ has been shown to be upregulated within DRG neurons following nerve injury and in thalamic neurons following spinal cord injury. (Hains et al., Changes in electrophysiological properties and sodium channel $Na_V1.3$ expression in thalamic neurons after spinal cord injury, Brain 128:2359-71 (2005)). A gain-in-function mutation in Nav1.3 (K354Q) was reportedly linked to epilepsy. (Estacion et al., A sodium channel mutation linked to epilepsy increases ramp and persistent current of $Na_V1.3$ and induces hyperexcitability in hippocampal neurons, Experimental Neurology 224(2):362-368 (2010)).

[0013] Toxin peptides produced by a variety of organisms have evolved to target ion channels. Snakes, scorpions, spiders, bees, snails and sea anemones are a few

examples of organisms that produce venom that can serve as a rich source of small bioactive toxin peptides or "toxins" that potently and selectively target ion channels and receptors. In most cases, these toxin peptides have evolved as potent antagonists or inhibitors of ion channels, by binding to the channel pore and physically blocking the ion conduction pathway. In some other cases, as with some of the tarantula toxin peptides, the peptide is found to antagonize channel function by binding to a region outside the pore (e.g., the voltage sensor domain).

[0014] Native toxin peptides are usually between about 20 and about 80 amino acids in length, contain 2-5 disulfide linkages and form a very compact structure. Toxin peptides (e.g., from the venom of scorpions, sea anemones and cone snails) have been isolated and characterized for their impact on ion channels. Such peptides appear to have evolved from a relatively small number of structural frameworks that are particularly well suited to addressing the critical issues of potency, stability, and selectivity. (See, e.g., Dauplais et al., On the convergent evolution of animal toxins: conservation of a diad of functional residues in potassium channel-blocking toxins with unrelated structures, J. Biol. Chem. 272(7):4302-09 (1997); Alessandri-Haber et al., Mapping the functional anatomy of BgK on Kv1.1, Kv1.2, and Kv1.3, J. Biol. Chem. 274(50):35653-61 (1999)). The majority of scorpion and Conus toxin peptides, for example, contain 10-40 amino acids and up to five disulfide bonds, forming extremely compact and constrained structures (microproteins) often resistant to proteolysis. The conotoxin and scorpion toxin peptides can be divided into a number of superfamilies based on their disulfide connections and peptide folds. The solution structure of many of these has been determined by Nuclear Magnetic Resonance (NMR) spectroscopy, illustrating their compact structure and verifying conservation of their family folding patterns. (E.g., Tudor et al., Ionisation behaviour and solution properties of the potassium-channel blocker ShK toxin, Eur. J. Biochem. 251(1-2):133-41(1998); Pennington et al., Role of disulfide bonds in the structure and potassium channel blocking activity of ShK toxin, Biochem. 38(44): 14549-58 (1999); Jaravine et al., Three-dimensional structure of toxin OSK1 from Orthochirus scrobiculosus scorpion venom, Biochem. 36(6):1223-32 (1997); del Rio-Portillo et al.; NMR solution structure of Cn12, a novel peptide from the Mexican scorpion Centruroides noxius with a typical beta-toxin sequence but with alpha-like physiological activity, Eur. J. Biochem.

271(12): 2504-16 (2004); Prochnicka-Chalufour et al., Solution structure of discrepin, a new K+-channel blocking peptide from the alpha-KTx15 subfamily, Biochem. 45(6):1795-1804 (2006)). Conserved disulfide structures can also reflect the individual pharmacological activity of the toxin family. (Nicke et al. (2004), Eur. J. Biochem. 271: 2305-19, Table 1; Adams (1999), Drug Develop. Res.46: 219-34). For example, α-conotoxins have well-defined four cysteine/two disulfide loop structures (Loughnan, 2004) and inhibit nicotinic acetylcholine receptors. In contrast, ω-conotoxins have six cysteine/three disulfide loop consensus structures (Nielsen, 2000) and block calcium channels. Structural subsets of toxins have evolved to inhibit either voltage-gated or calcium-activated potassium channels.

[0015] Spider venoms contain many peptide toxins that target voltage-gated ion channels, including Kv, Cav, and Nav channels. A number of these peptides are gating modifiers that conform to the inhibitory cystine knot (ICK) structural motif. (See, Norton et al., The cystine knot structure of ion channel toxins and related polypeptides, Toxicon 36(11):1573-1583 (1998); Pallaghy et al., A common structural motif incorporating a cystine knot and a triple-stranded β-sheet in toxic and inhibitory polypeptides, Prot. Sci. 3(10):1833-6, (1994)). In contrast to some scorpion and sea anemone toxins, many spider toxins do not affect the rate of inactivation but inhibit channel activity by restricting the movement of the voltage sensor into the open channel conformation, shifting their voltage dependence of activation to a more positive potential. Many of these spider toxins are promiscuous within and across voltage-gated ion channel families.

[0016] A variety of toxin peptides that target VGSCs, in particular, have been reported. (See, Billen et al., Animal peptides targeting voltage-activated sodium channels, Cur. Pharm. Des. 14:2492-2502, (2008)). Three classes of peptide toxins have been described: 1) site 1 toxins, the μ-conotoxins, bind to the pore of the channel and physically occlude the conduction pathway; 2) site 3 toxins, including the α-scorpion toxins, some sea anemone toxins and δ-conotoxins, bind to the S3-S4 linker of domain IV and slow channel inactivation; and 3) site 4 toxins, including the β-scorpion toxins, bind to the S3-S4 linker in domain II and facilitate channel activation. Both site 3 and site 4 families of peptides alter the open probability of Na_V channels and affect gating transitions and are therefore called "gating modifiers."

[0017] μ-Conotoxin KIIIA (SEQ ID NO:530), a site 1 toxin originally isolated from *Conus kinoshitai*, is a C-terminally amidated peptide 16 amino acids in length that contains 6 cysteine residues engaged in 3 intramolecular disulfide bonds. It was initially characterized as an inhibitor of tetrodotoxin (TTX)-resistant sodium channels in amphibian dorsal root ganglion (DRG) neurons. (See, Bulaj et al., Novel conotoxins from *Conus striatus* and *Conus kinoshitai* selectively block TTX-resistant sodium channels, Biochem. 44(19):7259-7265, (2005)). Later it was found to more effectively inhibit TTX-sensitive than TTX-resistant sodium current in mouse DRG neurons. (See, Zhang et al., Structure/function characterization of μ-conotoxin KIIIA , an analgesic, nearly irreversible blocker of mammalian neuronal sodium channels, J. Biol. Chem. 282(42):30699-30706, (2007)). KIIIA has been found to block cloned mammalian (rodent) channels expressed in *Xenopus laevis* oocytes with the following rank order potency: $Na_V1.2 > Na_V1.4 > Na_V1.6 > Na_V1.7 > Na_V1.3 > Na_V1.5$. Intraperitoneal injection of KIIIA has demonstrated analgesic activity in a formalin-induced pain assay in mice with an ED_{50} of 1.6 nmol/mouse (0.1 mg/kg) without observed motor impairment; some motor impairment but not paralytic acitity was observed at a higher dose (10 nmol). (See, Zhang et al., 2007). Substitution of alanine for Lys7 and Arg10 modified maximal block, while substituion of His12 and Arg14 altered Nav isoform specificity. (See, McArthur et al., Interactions of key charged residues contributing to selective block of neuronal sodium channels by μ-conotoxin KIIIA, Mol. Pharm. 80(4): 573-584, (2011)). "Alanine scan" analogs of KIIIA have identified Lys7, Trp8, Arg10, Asp11, His12, and Arg14 as being important for activity against $rNa_V1.4$. (See Zhang et al., 2007). The NMR solution structure of KIIIA places these residues within or adjacent to an α-helix near the C-terminus of the molecule. (See, Khoo et al., Structure of the analgesic μ-conotoxin KIIIA and effects on the structure and function of disulfide deletion, Biochem. 48(6):1210-1219, (2009)). The disulfide bond between Cys1 and Cys9 may be removed by substitution of alanine (KIIIA[C1A,C9A]) without greatly reducing the activity of the compound. (See, Khoo et al., 2009; Han et al., Structurally minimized μ-conotoxin analogs as sodium channel blockers: implications for designing conopeptide-based therapeutics, ChemMedChem 4(3):406-414, (2009)). Replacing a second disulfide bond between Cys2 and Cys16 with a diselenide bond between selenocysteine residues has given rise to the disulfide-depleted selenoconopeptide

analogs of KIIIA. These compounds have retained the activity of KIIIA but are more synthetically accessible. (See, Han et al., Disulfide-depleted selenoconopeptides: simplified oxidative folding of cysteine-rich peptides, ACS Med. Chem. Lett.1(4):140-144, (2010)). The native structure has been further minimized to a lactam-stabilized helical peptide scaffold with Nav inhibitory activity. (See, Khoo et al., Lactam-stabilized helical analogues of the analgesic μ-conotoxin KIIIA, J. Med. Chem. 54:7558-7566 (2011)). KIIIA binds to the neurotoxin receptor site 1 in the outer vestibule of the conducting pore of the VGSCs and blocks the channel in an all-or-none manner. Recent studies have shown that some analogs of KIIIA only partially inhibit the sodium current and may be able to bind simultaneously with TTX and saxitoxin (STX). (See, Zhang et al., Cooccupancy of the outer vestibule of voltage-gated sodium channels by μ-conotoxin KIIIA and saxitoxin or tetrodotoxin, J. Neurophys. 104(1):88-97, (2010); French et al., The tetrodotoxin receptor of voltage-gated sodium channels - perspectives from interactions with μ-conotoxins, Marine Drugs 8:2153-2161, (2010); Zhang et al., μ-Conotoxin KIIIA derivatives with divergent affinities versus efficacies in blocking voltage-gated sodium channels. Biochem. 49(23):4804-4812, (2010); Zhang et al., Synergistic and antagonistic interactions between tetrodotoxin and μ-conotoxin in blocking voltage-gated sodium channels, Channels 3(1):32-38, (2009)).

[0018] OD1 (SEQ ID NO:589) is an α-like toxin isolated from the venom of the Iranian yellow scorpion *Odonthobuthus doriae*. (See, Jalali et al., OD1, the first toxin isolated from the venom of the scorpion *Odonthobuthus doriae* active on voltage-gated Na+ channels, FEBS Lett. 579(19):4181-4186, (2005)). This peptide is 65 amino acids in length with an amidated C-terminus containing 6 cysteine residues that form 3 disulfide bonds. OD1 has been characterized as an $Na_V1.7$ modulator that impairs fast inactivation (EC_{50} = 4.5 nM), increases the peak current at all voltages, and induces a persistent current, with selectivity against $Na_V1.8$ and $Na_V1.3$. (See Maertens et al., Potent modulation of the voltage-gated sodium channel Nav1.7 by OD1, a toxin from the scorpion *Odonthobuthus doriae*, Mol. Pharm. 70(1):405-414, (2006)).

[0019] Huwentoxin-IV(HWTX-IV; SEQ ID NO:528) is a 35 residue C-terminal peptide amide with 3 disulfide bridges between 6 cysteine residues isolated from the venom of the Chinese bird spider, *Selenocosmia huwena*. (See, Peng et al., Function and solution structure of huwentoxin - IV , a potent neuronal tetrodotoxin

(TTX)-sensitive sodium channel antagonist from chinese bird spider *Selenocosmia huwena*, J. Biol. Chem. 277(49):47564-47571, (2002)). The disulfide bonding pattern (C1—C4, C2—C5, C3—C6) and NMR solution structure place HWTX-IV in the ICK structural family since the C3—C6 disulfide bond passes through the 16-residue ring formed by the other two disulfide bridges (C1—C4 and C2—C5). HWTX-IV inhibits TTX-sensitive sodium currents in adult rat DRG neurons with an IC_{50} value of 30 nM but has no effect on TTX-resistant VGSCs at up to a 100 nM concentration. (See, Peng et al., 2002). HWTX-IV was also 12-fold less potent against central neuronal sodium channels in rat hippocampus neurons, suggesting that it may be selective toward $Na_V1.7$. (See, Xiao et al., Synthesis and characterization of huwentoxin-IV, a neurotoxin inhibiting central neuronal sodium channels, Toxicon 51(2):230-239, (2008)). Testing HWTX-IV against VGSC sub-types determined the relative sensitivity to be hNav1.7 (IC_{50} = 26 nM) > rNav1.2 >> rNav1.3 > rNav1.4 ≥ hNav1.5. (See Xiao et al., Tarantula huwentoxin-IV inhibits neuronal sodium channels by binding to receptor site 4 and trapping the domain II voltage sensor in the closed configuration, J. Biol. Chem. 283(40):27300-27313, (2008)). Site directed protein mutagenesis mapped the binding of HWTX-IV to neurotoxin site 4, the extracellular S3-S4 linker betweendomain II, and its behavior in response to changes in voltage and channel activation is consistent with binding to the voltage sensor of Nav1.7 and trapping it in the resting configuration. (See, Xiao et al., 2008). Huwentoxin-I (HWTX-I; SEQ ID NO:529), a related family member is less potent against VGSCs but is active against N-Type Ca_V channels. (See, Wang et al., The cross channel activities of spider neurotoxin huwentoxin I on rat dorsal root ganglion neurons, Biochem. Biophys. Res. Comm. 357(3):579-583, (2007); Chen et al., Antinociceptive effects of intrathecally administered huwentoxin-I, a selective N-type calcium channel blocker, in the formalin test in conscious rats, Toxicon 45(1):15-20, (2005); Liang et al., Properties and amino acid sequence of huwentoxin-I, a neurotoxin purified from the venom of the Chinese bird spider *Selenocosmia huwena*, Toxicon 31(8):969-78, (1993)).

[0020] ProTx-II (SEQ ID NO:531), isolated from the venom of the tarantula *Thixopelma pruriens*, is a 30 amino acid polypeptide with a C-terminal free acid and 6 cysteine residues that form 3 disulfide bonds. It differs from other members of the ICK family because it contains only three residues between the fifth and sixth cysteine

residues instead of the normal 4-11. ProTx-II is a potent inhibitor of several Na_V channel sub-types including $Na_V1.2$, $Na_V1.7$ (IC_{50} < 1 nM), $Na_V1.5$, and $Na_V1.8$, as well as Cav3.1 channels but not K_V channels. (See, Middleton et al., Two tarantula peptides inhibit activation of multiple sodium channels, Biochem. 41(50):14734-14747, (2002); Priest et al., ProTx-I and ProTx-II: gating modifiers of voltage-gated sodium channels, Toxicon 49(2):194-201, (2007); Edgerton et al., Inhibition of the activation pathway of the T-type calcium channel CaV3.1 by ProTxII, Toxicon 56(4):624-636, (2010)). The "alanine scan" analogs of ProTx-II were tested against Nav1.5, identifying Met6, Trp7, Arg13, Met19, Val20, Arg22, Leu23, Trp24, Lys27, Leu29, and Trp30 as being important for activity. (See, Smith et al., Molecular interactions of the gating modifier toxin ProTx-II with Nav1.5: implied existence of a novel toxin binding site coupled to activation, J. Biol. Chem. 282(17):12687-12697, (2007)). Biophysical characterization showed that ProTx-II differs from HwTx-IV in its ability to interact with lipid membranes. (See, Smith et al., Differential phospholipid binding by site 3 and site 4 toxins: implications for structural variability between voltage-sensitive sodium channel comains, J. Biol. Chem. 280(12):11127-11133, (2005). Doses of 0.01 and 0.1 mg/kg i.v. of ProTx-II were well tolerated in rats, but 1 mg/kg doses were lethal. ProTx-II was not efficacious in a mechanical hyperalgesia study. (See, Schmalhofer et al., ProTx-II, a selective inhibitor of NaV1.7 sodium channels, blocks action potential propagation in nociceptors, Mol. Pharm. 74(5):1476-1484, (2008)). Intrathecal administration was lethal at 0.1 mg/kg and not effective in the hyperalgesia study at lower doses. ProTx-II application to desheathed cutaneous nerves completely blocked the C-fiber compound action potential but had little effect on action potential propagation of the intact nerve. (See, Schmalhofer et al., 2008). ProTx-II is believed to bind to the S3-S4 linker of domain II of $Na_V1.7$ to inhibit channel activation but may also interact with the domain IV voltage sensor and affect sodium channel activation at higher concentrations. (See, Xiao et al., The tarantula toxins ProTx-II and huwentoxin-IV differentially interact with human Nav1.7 voltage sensors to inhibit channel activation and inactivation, Mol. Pharm. 78(6):1124-1134, (2010); Sokolov et al., Inhibition of sodium channel gating by trapping the domain II voltage sensor with protoxin II, Mol. Pharm. 73(3):1020-1028, (2008); Edgerton et al., Evidence for multiple effects of ProTxII on activation gating in NaV1.5, Toxicon 52(3):489-500, (2008)).

[0021] Production of toxin peptides is a complex process in venomous organisms, and is an even more complex process synthetically. Due to their conserved disulfide structures and need for efficient oxidative refolding, toxin peptides present challenges to synthesis. (See, Steiner and Bulaj, Optimization of oxidative folding methods for cysteine-rich peptides: a study of conotoxins containing three disulfide bridges, J. Pept. Sci. 17(1): 1-7, (2011); Góngora-Benítez et al., Optimized Fmoc solid-phase synthesis of the cysteine-rich peptide Linaclotide, Biopolymers Pept. Sci. 96(1):69-80, (2011)). Although toxin peptides have been used for years as highly selective pharmacological inhibitors of ion channels, the high cost of synthesis and refolding of the toxin peptides and their short half-life in vivo have impeded the pursuit of these peptides as a therapeutic modality. Far more effort has been expended to identify small molecule inhibitors as therapeutic antagonists of ion channels, than has been given the toxin peptides themselves. One exception is the approval of the small ω-conotoxin MVIIA peptide (Prialt®, ziconotide), an inhibitor of neuron-specific N-type voltage-sensitive calcium channels, for treatment of intractable pain. The synthetic and refolding production process for ziconotide, however, is costly and only results in a small peptide product with a very short half-life in vivo (about 4 hours).

[0022] A small clinical trial in humans showed that local, non-systemic injection of the non-peptide tetrodotoxin produced pain relief in patients suffering from pain due to cancer and / or to chemotherapy (Hagen et al., J Pain Symp Manag 34:171-182 (2007)). Tetrodotoxin is a non-CNS-penetrant inhibitor of sodium channels including $Na_V1.3$ and $Na_V1.7$; although it cannot be used systemically due to lack of selectivity among sodium channel subtypes, its efficacy provides further validation for treating chronic pain syndromes with inhibitors of $Na_V1.7$ and / or $Na_V1.3$ in peripheral neurons.

[0023] Polypeptides typically exhibit the advantage of greater target selectivity than is characteristic of small molecules. Non-CNS penetrant toxin peptides and peptide analogs selective for Nav1.7 and/or Nav1.3 are desired, and are provided by the present invention.

SUMMARY

[0024] The present disclosure includes a composition of matter comprising an isolated polypeptide, which is a peripherally-restricted $Na_V1.7$ inhibitor.

[0024a] In one aspect, there is provided an isolated polypeptide comprising the amino acid sequence of the formula:

$X_{aa}{}^{1}X_{aa}{}^{2}$ $Cys^{3}X_{aa}{}^{4}X_{aa}{}^{5}X_{aa}{}^{6}X_{aa}{}^{7}X_{aa}{}^{8}X_{aa}{}^{9}Cys^{10}X_{aa}{}^{11}X_{aa}{}^{12}X_{aa}{}^{13}X_{aa}{}^{14}Asp^{15}X_{aa}{}^{16}Cys^{17}$

$Cys^{18}X_{aa}{}^{19}X_{aa}{}^{20}X_{aa}{}^{21}X_{aa}{}^{22}X_{aa}{}^{23}Cys^{24}X_{aa}{}^{25}X_{aa}{}^{26}X_{aa}{}^{27}X_{aa}{}^{28}X_{aa}{}^{29}Trp^{30}$

$Cys^{31}Lys^{32}Tyr^{33}X_{aa}{}^{34}Phe^{35}X_{aa}{}^{36}X_{aa}{}^{37}X_{aa}{}^{38}$

or a pharmaceutically acceptable salt thereof,

wherein:

$X_{aa}{}^{1}$ is absent and $X_{aa}{}^{2}$ is any amino acid residue;

$X_{aa}{}^{4}$ is an acidic, hydrophobic, basic, or neutral hydrophilic amino acid residue;

$X_{aa}{}^{5}$ is a Gly, Ala, hydrophobic, or basic amino acid residue;

$X_{aa}{}^{6}$ is a Gly, Ala, 2-Abu, 2-Aib, Ile, Leu, Val, Nle, or Nva;

$X_{aa}{}^{7}$ is a Gly, Ala, aromatic, or hydrophobic amino acid residue;

$X_{aa}{}^{8}$ is a basic, acidic, or neutral hydrophilic amino acid residue, or an Ala residue;

$X_{aa}{}^{9}$ is a basic or neutral hydrophilic amino acid residue;

$X_{aa}{}^{11}$ is any amino acid residue;

$X_{aa}{}^{12}$ is a Pro, acidic, neutral, or hydrophobic amino acid residue;

$X_{aa}{}^{13}$ is any amino acid residue;

$X_{aa}{}^{14}$ is any amino acid residue;

$X_{aa}{}^{16}$ is a basic, neutral hydrophilic, or acidic amino acid residue, or an Ala residue;

$X_{aa}{}^{19}$ is any amino acid residue;

$X_{aa}{}^{20}$ is a Pro, Gly, basic, or neutral hydrophilic residue;

$X_{aa}{}^{21}$ is a basic, hydrophobic, or neutral hydrophilic amino acid residue;

$X_{aa}{}^{22}$ is a hydrophobic or basic amino acid residue;

$X_{aa}{}^{23}$ is a hydrophobic, basic, or neutral hydrophilic amino acid residue;

$X_{aa}{}^{25}$ is a Ser, Ala, or a neutral hydrophilic amino acid residue;

$X_{aa}{}^{26}$ is an Ala, acidic, basic, or neutral hydrophilic amino acid residue;

$X_{aa}{}^{27}$ is an acidic, basic, neutral hydrophilic or hydrophobic residue;

$X_{aa}{}^{28}$ is an aromatic or basic amino acid residue;

X_{aa}^{29} is an acidic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{34} is any amino acid residue;

each of X_{aa}^{36} , X_{aa}^{37} , and X_{aa}^{38} is independently absent or is independently a neutral, basic, or hydrophobic amino acid residue;

and wherein the isolated polypeptide selectively inhibits Nav1.7 sodium channels relative to Nav1.4 and Nav1.5 sodium channels.

[0024b] In one example, the isolated polypeptide is a dual inhibitor of $Na_V1.7$ and $Na_V1.3$ having the amino acid sequence DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-NH_2 (SEQ ID NO:1), which is a peptide we have designated "GpTx-1", and which was isolated from the venom of the tarantula *Grammostola porteri*, as described herein. Other examples of the present disclosure comprise a peptide analog of GpTx-1. In other examples, the present disclosure is directed to a composition of matter comprising an isolated polypeptide comprising the amino acid sequence of the formula:

$X_{aa}^{1}X_{aa}^{2}X_{aa}^{3}X_{aa}^{4}X_{aa}^{5}X_{aa}^{6}X_{aa}^{7}X_{aa}^{8}X_{aa}^{9}X_{aa}^{10}X_{aa}^{11}X_{aa}^{12}X_{aa}^{13}X_{aa}^{14}Asp^{15}$

$X_{aa}^{16}X_{aa}^{17}X_{aa}^{18}X_{aa}^{19}X_{aa}^{20}X_{aa}^{21}X_{aa}^{22}X_{aa}^{23}X_{aa}^{24}X_{aa}^{25}X_{aa}^{26}X_{aa}^{27}X_{aa}^{28}X_{aa}^{29}$

$X_{aa}^{30}X_{aa}^{31}Lys^{32}X_{aa}^{33}X_{aa}^{34}X_{aa}^{35}X_{aa}^{36}X_{aa}^{37}X_{aa}^{38}$// SEQ ID NO:475

or a pharmaceutically acceptable salt thereof,

wherein:

$X_{aa}^{1}X_{aa}^{2}$ is absent; or X_{aa}^{1} is any amino acid residue and X_{aa}^{2} is any amino acid residue; or X_{aa}^{1} is absent and X_{aa}^{2} is any amino acid residue;

X_{aa}^{3} is Cys, if X_{aa}^{18} is Cys; or X_{aa}^{3} is SeCys, if X_{aa}^{18} is SeCys; or X_{aa}^{3} is an alkyl amino acid residue, if X_{aa}^{18} is an alkyl amino acid residue;

X_{aa}^{4} is an acidic, hydrophobic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{5} is a Gly, Ala, hydrophobic, or basic amino acid residue;

X_{aa}^{6} is a Gly, Ala, 2-Abu, Nle, Nva, or hydrophobic amino acid residue;

X_{aa}^{7} is a Gly, Ala, aromatic, or hydrophobic amino acid residue;

X_{aa}^{8} is a basic, acidic, or neutral hydrophilic amino acid residue, or an Ala residue;

X_{aa}^{9} is a basic or neutral hydrophilic amino acid residue;

X_{aa}^{10} is Cys if X_{aa}^{24} is Cys; or X_{aa}^{10} is SeCys if X_{aa}^{24} is SeCys;

X_{aa}^{11} is any amino acid residue;

X_{aa}^{12} is a Pro, acidic, neutral, or hydrophobic amino acid residue;

X_{aa}^{13} is any amino acid residue;

X_{aa}^{14} is any amino acid residue;

X_{aa}^{16} is a basic, neutral hydrophilic, or acidic amino acid residue, or an Ala residue;

X_{aa}^{17} is a Cys if X_{aa}^{31} is Cys; or X_{aa}^{17} is a SeCys if X_{aa}^{31} is SeCys;

X_{aa}^{18} is a Cys, SeCys, or an alkyl amino acid residue;

X_{aa}^{19} is any amino acid residue;

X_{aa}^{20} is a Pro, Gly, basic, or neutral hydrophilic residue;

X_{aa}^{21} is a basic, hydrophobic, or neutral hydrophilic amino acid residue;

X_{aa}^{22} is a hydrophobic or basic amino acid residue;

X_{aa}^{23} is a hydrophobic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{24} is a Cys or SeCys residue;

X_{aa}^{25} is a Ser, Ala, or a neutral hydrophilic amino acid residue;

X_{aa}^{26} is an Ala, acidic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{27} is an acidic, basic, neutral hydrophilic or hydrophobic residue;

X_{aa}^{28} is an aromatic or basic amino acid residue;

X_{aa}^{29} is acidic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{30} is a Trp, 5-bromoTrp, 6-bromoTrp, 5-chloroTrp, 6-chloroTrp, 1-Nal, 2-Nal, or thioTrp residue;

X_{aa}^{31} is a Cys or SeCys;

X_{aa}^{33} is a hydrophobic or aromatic amino acid residue;

X_{aa}^{34} is any amino acid residue;

X_{aa}^{35} is a hydrophobic amino acid residue;

each of X_{aa}^{36}, X_{aa}^{37}, and X_{aa}^{38} is independently absent or is independently a neutral, basic, or hydrophobic amino acid residue;

and wherein:

if X_{aa}^{3} and X_{aa}^{18} are both Cys residues, there is a disulfide bond between residue X_{aa}^{3} and residue X_{aa}^{18}; or if X_{aa}^{3} and X_{aa}^{18} are both SeCys residues, there is a diselenide bond between residue X_{aa}^{3} and residue X_{aa}^{18};

if X_{aa}^{10} and X_{aa}^{24} are both Cys residues, there is a disulfide bond between residue X_{aa}^{10} and residue X_{aa}^{24}; or if X_{aa}^{10} and X_{aa}^{24} are both SeCys residues, there is a diselenide bond between residue X_{aa}^{10} and residue X_{aa}^{24};

if X_{aa}^{17} and X_{aa}^{31} are both Cys residues, there is a disulfide bond between residue X_{aa}^{17} and residue X_{aa}^{31}; or if X_{aa}^{17} and X_{aa}^{31} are both SeCys residues, there is a diselenide bond between residue X_{aa}^{17} and residue X_{aa}^{31};

the amino-terminal residue is optionally acetylated, biotinylated, 4-pentynoylated, or PEGylated; and

the carboxy-terminal residue is optionally amidated.

In some examples the composition of matter comprises an amino acid sequence selected from SEQ ID NOS: 3-30, 32-72, 74-134, 136-178, 180-211, 218-239, 241-305, 307-363, 366-386, 388-432, 434-474, 515-527, 532-588, 590, 591, 593-775, 777, 778, 780-788, 790-1049, and 1062-3086.

[0025] The present disclosure includes a composition of matter, comprising an amino acid sequence selected from SEQ ID NOS: 3-134, 136-305, 307-386, 388-474, 515-527, 532-588, 590, 591, 593-1049, and 1062-3086.

[0026] The present disclosure also encompasses a nucleic acid (e.g., DNA or RNA) encoding any of SEQ ID NOS: 3-134, 136-305, 307-386, 388-474, 515-527, 532-588, 590, 591, 593-1049, and 1062-3086 that does not include a non-canonical amino acid; an expression vector comprising the nucleic acid; and a recombinant host cell comprising the expression vector. In one aspect, there is provided the use of a prophylactically effective amount of the isolated polypeptide of the present invention in the manufacture of a medicament for preventing pain. In another aspect, there is provided the use of a therapeutically effective amount of the isolated polypeptide of the present invention in the manufacture of a medicament for treating pain. The compositions of the disclosure provide an effective method of treating, or preventing, pain, for example acute, persistent, or chronic pain. For example, a dual inhibitor of Nav1.7 and Nav1.3 can be effective in some forms of chronic pain, particularly in cases where Nav1.7 inhibition alone is insufficient. Selectivity against off-target sodium channels, particularly those governing cardiac excitability (Nav1.5) and skeletal muscle excitability (NaV1.4), is cardinal for any systemically delivered therapeutic. This selectivity is a particularly high hurdle for a dual inhibitor. Compositions of the present disclosure provide such selectivity against Nav1.5 and Nav1.4. For example, the GpTx-1 peptide (SEQ ID NO:1) is a weak inhibitor of Nav1.4. Moreover, the inhibition of Nav1.4 is strongly state dependent, such that GpTx-1 exerts negligible

effects on the physiological, non-inactivated states of Nav1.4. (This is a key distinction between GpTx-1 and tetrodotoxin, which has little selectivity against Nav1.4, and which inhibits equally the inactivated and non-inactivated states of Nav1.4).

[0027] In one aspect, there is provided a pharmaceutical composition, comprising the isolated polypeptide of the present invention, and a pharmaceutically acceptable carrier. The present disclosure also includes a pharmaceutical composition or a medicament containing the composition of matter as described herein, and a pharmaceutically acceptable carrier.

[0028] GpTx-1 and GpTx-1 peptide analogs are also useful as research tools. Heretofore, there have not been available specific biochemical probes for Nav1.7 or for Nav1.3, and particularly no probes for correctly folded, functional Nav1.7 in the plasma membrane of live cells. As GpTx-1 and its congeners inhibit Nav1.7 / Nav1.3, they clearly bind to the channel molecule with high potency and selectivity. Labeling with fluorescent or other tracer groups at the non-active sites of GpTx-1 as defined by NMR and by residue substitution can provide research tools suitable for, but not limited to, localizing sodium channels, sorting cells that express sodium channels, and screening or panning for peptides that bind to Nav1.7 or Nav1.3.

BRIEF DESCRIPTION OF THE DRAWINGS

[0029] Figure 1 (top panel) shows the reversed phase (RP) HPLC separation of crude venom extracted from *Grammostola porteri*. The tick marks along the x-axis represent time slices of fractionation. Figure 1 (bottom panel) shows the activity of the isolated venom fraction (percent of control, POC) in the $Na_V1.7$ IonWorks® Quatrro (IWQ) assay. Fraction 31 (indicated with rectangular box) contained a major peak in the RP-HPLC chromatogram, exhibited > 80% inhibition in the ion channel assay, and was later deconvoluted to yield GpTx-1 (SEQ ID NO:1).

[0030] Figure 2 (inset) shows the high resolution electrospray ionization-mass spectrometry (ESI-MS) analysis of the indicated fraction (31) from the initial separation of *Grammostola porteri* venom. The arrows indicate the (m/z) ratios observed for the different ionization states of a peptide with a molecular weight of 4071 Da that was eventually identifed as GpTx-1. Additional peaks in the mass spectrum indicate that the venom fraction is a mixture of at least four distinct peptides.

[0031] Figure 3 shows the matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) analysis of fraction 31 from the separation of *Grammostola porteri* venom. The inset shows the low and mid mass ranges. The peak with an m/z ratio of 4074.9 was eventually identified as GpTx-1, but the fraction is a mixture of at least four distinct peptides.

[0032] Figure 4 (top panel) shows the RP-HPLC separation (sub-fractionation) of the material in fraction 31 from the intial separation of *Grammostola porteri* venom. The tick marks along the x-axis represent time slices of the sub-fractionation. Figure 4 (bottom panel) shows the activity of the isolated sub-fractions (POC) in the $Na_V1.7$ IonWorks® Quatrro (IWQ) assay. The major peak in the RP-HPLC chromatogram was the most active in the $Na_V1.7$ assay and was deconvoluted to identify GpTx-1.

[0033] Figure 5 shows LC-MS analysis of synthetic GpTx-1. The top panel shows the RP-HPLC chromatogram of UV absorbance at 214 nm. The bottom panel shows the total ion count (TIC) of the ESI-MS detector.

[0034] Figure 6 shows the ESI-MS analysis of the peak with the retention time (r_t) of 6.75 minutes in Figure 5. The peaks with m/z ratios of 1358.8 and 1019.4

represent the $[M+3H]^{3+}$ and $[M+3H]^{4+}$ charge states, resepctively, of GpTx-1, which has a monoisotopic molecular weight of 4071.9 Da.

[0035] Figure 7 shows the overlay of the peptide backbone for the 20 lowest energy conformations (RMSD = 0.1±0.05Å) from the structural determination of GpTx-1 by NMR spectroscopy.

[0036] Figure 8 shows the overlay of the peptide heavy atoms for the 20 lowest energy conformations (RMSD = 0.74±0.12Å) from the structural determination of GpTx-1 by NMR spectroscopy.

[0037] Figure 9 shows a ribbon representation of the peptide backbone and disulfide bonds (with the numbers corresponding to the cysteine residues) from the structural determination of GpTx-1 by NMR spectroscopy.

[0038] Figure 10 shows GpTx-1 oriented with the hydrophobic and putative binding face formed by the C-terminal β-strand and residues Phe5 and Met6 oriented toward the reader. On the right, is a ribbon representation of the peptide backbone with the side chains of key residues depicted, and the left shows a partially transparent surface rendering of the molecule.

[0039] Figure 11 (left) shows the hydrophobic and putative binding face of GpTx-1 with an opaque surface. On the right, the molecule has been rotated clockwise by 90° to show the topological contrast between the flat hydrophobic face and the hydrophilic (solvent-exposed) face of the peptide.

[0040] Figure 12A-N shows schematic structures of some embodiments of a composition of the invention that include one or more units of a pharmacologically active toxin, e.g., GpTx-1, or toxin (e.g., GpTx-1) peptide analog (squiggle) fused, via an optional peptidyl linker moiety such as but not limited to L5 or L10 described herein, with one or more domains of an immunoglobulin. These schematics show a more typical IgG1, although they are intended to apply as well to IgG2s, which will have 4 disulfide bonds in the hinge and a different arrangement of the disulfide bond linking the heavy and light chain, and IgG3s and IgG4s. Figure 12A represents a monovalent heterodimeric Fc-toxin peptide analog fusion or conjugate with the toxin peptide analog fused or conjugated to the C-terminal end of one of the immunoglobulin Fc domain monomers. Figure 12B represents a bivalent homodimeric Fc-toxin peptide analog fusion or conjugate, with toxin peptide analogs fused to the C-terminal ends of both of

the immunoglobulin Fc domain monomers. Figure 12C represents a monovalent heterodimeric toxin peptide analog-Fc fusion or conjugate with the toxin peptide analog fused or chemically conjugated to the N-terminal end of one of the immunoglobulin Fc domain monomers. Figure 12D represents a bivalent homodimeric toxin peptide analog-Fc fusion or conjugate, with toxin peptide analogs fused to the N-terminal ends of both of the immunoglobulin Fc domain monomers. Figure 12E represents a monovalent heterotrimeric Fc-toxin peptide analog/Ab comprising an immunoglobulin heavy chain (HC) + immunoglobulin light chain (LC) + an immunoglobulin Fc monomer with a toxin peptide analog fused to its C-terminal end. Figure 12 F represents a monovalent heterotetrameric (HT) antibody HC-toxin peptide analog fusion or conjugate, with a toxin peptide analog fused to the C-terminal end of one of the HC monomers. Figure 12G represents a bivalent HT antibody Ab HC-toxin peptide analog fusion or conjugate having toxin peptide analogs on the C-terminal ends of both HC monomers. Figure 12H represents a monovalent HT toxin peptide analog-LC Ab, with the toxin peptide analog fused to the N-terminal end of one of the LC monomers. Figure 12I represents a monovalent HT toxin peptide analog-HC Ab, with the toxin peptide analog fused to the N-terminal end of one of the HC monomers. Figure 12J represents a monovalent HT Ab LC-toxin peptide analog fusion or conjugate (i.e., LC-toxin peptide analog fusion or conjugate + LC + 2(HC)), with the toxin peptide analog fused to the C-terminal end of one of the LC monomers. Figure 12K represents a bivalent HT Ab LC-toxin peptide analog fusion or conjugate (i.e., 2(LC-toxin peptide analog fusion or conjugate) + 2(HC)), with toxin peptide analogs fused to the C-terminal end of both of the LC monomers. Figure 12 L represents a trivalent HT Ab LC-toxin peptide analog/HC-toxin peptide analog (i.e., 2(LC-toxin peptide analog fusion or conjugate) + HC-toxin peptide analog fusion or conjugate + HC), with the toxin peptide analogs fused to the C-terminal ends of both of the LC monomers and one of the HC monomers. Figure 12M represents a bivalent antibody with a toxin peptide analog moiety inserted into an internal loop of the immunoglobulin Fc domain of each HC monomer. Figure 12N represents a monovalent antibody with a toxin peptide analog moiety inserted into an internal loop of the immunoglobulin Fc domain of one of the HC monomers. Dimers or trimers will form spontaneously in certain host cells upon expression of a deoxyribonucleic acid (DNA) construct encoding a single chain.

In other host cells, the cells can be placed in conditions favoring formation of dimers/trimers or the dimers/trimers can be formed in vitro. If more than one HC monomer, LC monomer, or immunoglobulin Fc domain monomer is part of a single embodiment, the individual monomers can be, if desired, identical or different from each other.

[0041] Figure 13A-F illustrates in situ hybridization studies detecting expression of $Na_V1.7$ message RNA in human trigeminal ganglia (Figure 13 A-B) and in human dorsal root ganglia (Figure 13C-F). Figure 13A, Figure 13C, Figure 13E show Hematoxylin and Eosin (H & E) stained cells; Figure 13B, Figure 13D, and Figure 13F show expression of Nav1.7 via hybridization of ^{33}P-labeled antisense probe as blue dots. $Na_V1.7$-specific staining also was detected in myenteric plexes of stomach and small intestine. No $Na_V1.7$-specific staining was detected in human cerebellum, cerebral cortex, adrenal medulla, or pituitary, and only light staining was detected in hypothalamic nuclei. Staining from spinal cord was restricted to light staining in ventral motor areas and to spinal ependyma (epithelial cells lining the central canal). All staining was done under RNAse-free conditions on formalin-fixed, paraffin-embedded tissue. Probe was verified specific for $Na_V1.7$ by verifying a positive signal on HEK-293T cell lines expressing cloned human $Na_V1.7$ and a lack of signal on cell lines expressing any of the following sodium channels: $hNa_V1.1$ (HEK-293T), $hNa_V1.2$ (CHO), $hNa_V1.3$ (CHO), $hNa_V1.4$ (HEK-293T), $hNa_V1.5$ (HEK-293T), $hNa_V1.6$ (HEK-293T), $rNa_V1.3$ (HEK-293T), and on the parental 293T cell lines.

[0042] Figure 14A-E shows that individual neurons acutely isolated from rat sensory ganglia express a heterogeneous population of sodium currents. Individual neurons expressed either fast, tetrodotoxin-sensitive sodium currents (likely $Na_V1.7$ and $Na_V1.3$), slow, tetrodotoxin-resistant sodium currents (likely $Na_V1.8$), or a mixed population (no one current type encodes > 90% of the total sodium current). Figure 14A-C show examples of a neuron expressing fast TTX-S (Figure 14A), mixed (Figure 14B), or slow TTX-R (Figure 14C) sodium currents. Figure 14D-E illustrate that neurons isolated from sensory ganglia of rats that have undergone spinal nerve ligation ("SNL") surgery (Figure 14E) express a far greater proportion of fast TTX-S currents than control rats (Figure 14D).

[0043] Figure 15A-B shows sequence alignments of KIIIA (SEQ ID NO:530), GpTx-1(1-34) (SEQ ID NO:1), Huwentoxin-IV(SEQ ID NO:528), Huwentoxin-I (SEQ ID NO:529), and ProTx II (SEQ ID NO:531).

[0044] Figure 16 shows the concentration–time profile of GpTx-1 in mouse plasma following a 1 mg/kg subcutaneous ("s.c.") administration.. The GpTx-1 concentration was below the lower limit of quantitation in two of the three animals, and the profile could not be obtained.

[0045] Figure 17A shows the concentration–time profile of [Ala5]GpTx-1 (SEQ ID NO:22) in plasma from two mice following a 1 mg/kg intravenous ("i.v.") administration. (Exposures from a third mouse were lower than the quantitation limit, and the profile could not be obtained.)

[0046] Figure 17B shows the average plasma concentration-time profiles of [Ala5]GpTx-1 (SEQ ID NO:22) in plasma from mice following a 5 mg/kg s.c. dose (n = 3), a 1 mg/kg s.c. dose (n=2), and a 1 mg/kg intravenous (i.v.) dose (n=2). For the 5 mg/kg dose, peptide concentrations in the plasma were sustained at about 0.6 μM, approximately 40-fold over the in vitro Nav1.7 IC_{50} by PatchXpress® (PX), for 3 h.

[0047] Figure 18 shows the dose response relationship for GpTx-1 (SEQ ID NO:1; n=7), [Ala5]GpTx-1 (SEQ ID NO:22; n=8), and BSA control tested against hERG. The IC_{50} value for both compounds was > 10 μM.

[0048] Figure 19A shows the dose response relationship for GpTx-1 (SEQ ID NO:1; n=7) tested against hNav1.5. The IC_{50} value for GpTx-1 was 9.8 μM.

[0049] Figure 19B shows the dose response relationship for [Ala5]GpTx-1 (SEQ ID NO:22, n=9) tested against hNav1.5. The IC_{50} value for [Ala5]GpTx-1 was > 30 μM.

[0050] Figure 20 shows the effect of GpTx-1 (SEQ ID NO:1) on hNav1.7 channels. Cells were held at -140 mV and peak inward hNav1.7 currents were measured at -10 mV. "Baseline" trace shows hNav1.7 current before GpTx-1, and '100 nM GpTx-1' trace shows hNav1.7 current after GpTx-1 addition.

[0051] Figure 21 shows a dose-response curve of GpTx-1 (SEQ ID NO:1) against hNav1.7 channels. Peak inward hNav1.7 currents were measured at -10 mV in the presence of increasing concentrations of GpTx-1; cells were held at -140 mV. Currents were normalized with 100 representing Nav1.7 current with no peptide

addition and 0 representing Nav1.7 current following complete block. The IC_{50} of GpTx-1 against hNav1.7 channels was 7.40 nM.

[0052] Figure 22 shows a time course of increasing concentrations of GpTx-1 (SEQ ID NO:1) against hNav1.7 channels. Peak inward hNav1.7 currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of GpTx-1; cells were held at a -140 mV. "Baseline" indicates hNav1.7 current in the absence of GpTx-1 and "Wash" indicates hNav1.7 current following removal of GpTx-1.

[0053] Figure 23 shows the effect of GpTx-1 (SEQ ID NO:1) on hNav1.3 channels. Cells were held at -140 mV and peak inward hNav1.3 currents were measured at -10 mV. "Baseline" trace shows hNav1.3 current before GpTx-1, and '300 nM GpTx-1' trace shows hNav1.3 current after GpTx-1 addition.

[0054] Figure 24 shows a dose-response curve of GpTx-1 (SEQ ID NO:1) against hNav1.3 channels. Peak inward hNav1.3 currents were measured at -10 mV in the presence of increasing concentrations of GpTx-1; cells were held at -140 mV. Currents were normalized with 100 representing Nav1.3 current with no peptide addition and 0 representing Nav1.3 current following complete block. The IC_{50} of GpTx-1 against hNav1.3 channels was 16.8 nM.

[0055] Figure 25 shows a time course of increasing concentrations of GpTx-1 (SEQ ID NO:1) against hNav1.3 channels. Peak inward hNav1.3 currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of GpTx-1; cells were held at a -140 mV. "Baseline" indicates hNav1.3 current in the absence of GpTx-1 and "Wash" indicates hNav1.3 current following removal of GpTx-1.

[0056] Figure 26 shows the effect of GpTx-1 (SEQ ID NO:1) on hNav1.4 channels. Cells were held at -140 mV and peak inward hNav1.4 currents were measured at -10 mV. "Baseline" trace shows hNav1.4 current before GpTx-1, and '3 μM GpTx-1' trace shows hNav1.4 current after GpTx-1 addition.

[0057] Figure 27 shows a dose-response curve of GpTx-1 (SEQ ID NO:1) against hNav1.4 channels. Peak inward hNav1.4 currents were measured at -10 mV in the presence of increasing concentrations of GpTx-1; cells were held at -140 mV. Currents were normalized with 100 representing Nav1.4 current with no peptide

addition and 0 representing Nav1.4 current following complete block. The IC_{50} of GpTx-1 against hNav1.4 channels was 2.9 μM.

[0058] Figure 28 shows a dose-response curve of GpTx-1 (SEQ ID NO:1) against hNav1.4 channels. Peak inward hNav1.4 currents were measured at -10 mV in the presence of increasing concentrations of GpTx-1; cells were held at a potential yielding approximately 20% inactivation. Note that GpTx-1 is more potent against hNav1.4 when channels are partially inactivated. Currents were normalized with 100 representing Nav1.4 current with no peptide addition and 0 representing Nav1.4 current following complete block. The IC_{50} of GpTx-1 against partially inactivated hNav1.4 channels was 0.26 μM.

[0059] Figure 29 shows a time course of increasing concentrations of GpTx-1 (SEQ ID NO:1) against hNav1.4 channels. Peak inward hNav1.4 currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of GpTx-1; cells were held at a -140 mV. "Baseline" indicates hNav1.4 current in the absence of GpTx-1 and "Wash" indicates hNav1.4 current following removal of GpTx-1.

[0060] Figure 30 shows a time course of increasing concentrations of GpTx-1 (SEQ ID NO:1) against hNav1.4 channels. Peak inward hNav1.4 currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of GpTx-1; cells were held at -140 mV (squares) or a potential yielding approximately 20% inactivation (circles). "Baseline" indicates hNav1.4 current in the absence of GpTx-1 and "Wash" indicates hNav1.4 current following removal of GpTx-1. Note that GpTx-1 is more potent against hNav1.4 when channels are partially inactivated.

[0061] Figure 31 shows the effect of GpTx-1 (SEQ ID NO:1) on hNav1.5 channels. Cells were held at -140 mV and peak inward hNav1.5 currents were measured at -10 mV. "Baseline" trace shows hNav1.5 current before GpTx-1, and '3 μM GpTx-1' trace shows hNav1.5 current after GpTx-1 addition.

[0062] Figure 32 shows a dose-response curve of GpTx-1 (SEQ ID NO:1) against hNav1.5 channels. Peak inward hNav1.5 currents were measured at -10 mV in the presence of increasing concentrations of GpTx-1; cells were held at -140 mV. Currents were normalized with 100 representing Nav1.5 current with no peptide

addition and 0 representing Nav1.5 current following complete block. The IC_{50} of GpTx-1 against hNav1.5 channels was 8.9 μM.

[0063] Figure 33 shows a time course of increasing concentrations of GpTx-1 (SEQ ID NO:1) against hNav1.5 channels. Peak inward hNav1.5 currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of GpTx-1; cells were held at a -140 mV. "Baseline" indicates hNav1.5 current in the absence of GpTx-1 and "Wash" indicates hNav1.5 current following removal of GpTx-1.

[0064] Figure 34 shows the effect of [Ala5]GpTx-1 (SEQ ID NO:22) on hNav1.7 channels. Cells were held at -140 mV and peak inward hNav1.7 currents were measured at -10 mV. 'Baseline" trace shows hNav1.7 current before [Ala5]GpTx-1 addition, and "300 nM [Ala5]GpTx-1" trace shows hNav1.7 current after [Ala5]GpTx-1 addition. Cells were held at a potential yielding approximately 20% inactivation.

[0065] Figure 35 shows a dose-response curve of [Ala5]GpTx-1 (SEQ ID NO:22) against hNav1.7 channels. Peak inward hNav1.7 currents were measured at -10 mV in the presence of increasing concentrations of [Ala5]GpTx-1; cells were held at a potential yielding approximately 20% inactivation. Currents were normalized with 100 representing Nav1.7 current with no peptide addition and 0 representing Nav1.7 current following complete block. The IC_{50} of [Ala5]GpTx-1 against partially inactivated hNav1.7 channels was 13.2 nM.

[0066] Figure 36 shows a time course of increasing concentrations of [Ala5]GpTx-1 (SEQ ID NO:22) against hNav1.7 channels. Peak inward hNav1.7 currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of [Ala5]GpTx-1; cells were held at -140 mV (squares) or a potential yielding approximately 20% inactivation (circles). "Baseline" indicates hNav1.7 current in the absence of [Ala5]GpTx-1 and "Wash" indicates hNav1.7 current following removal of [Ala5]GpTx-1.

[0067] Figure 37 shows a time course of increasing concentrations of GpTx-1 (SEQ ID NO:1) against TTX-sensitive Nav channels in mouse dorsal root ganglion (DRG) neurons. Peak inward Nav currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of GpTx-1; cells were held at -140 mV. "Control" indicates Nav current in the absence of GpTx-1, 'TTX' indicates Nav current

in the presence of 300 nM TTX, and "Wash" indicates Nav current following removal of GpTx-1 and TTX. Note that GpTx-1 blocked nearly all TTX-sensitive Nav current. Currents measured in this study were almost all TTX-sensitive currents, identified at the start of the record on the basis of fast kinetics of inactivation.

[0068] Figure 38 shows a representative dose-response curve of GpTx-1 (SEQ ID NO:1) against TTX-sensitive Nav channels in mouse DRG neurons. Peak inward Nav currents were measured at -10 mV in the presence of increasing concentrations of GpTx-1; cells were held at -140 mV. The IC_{50} value of GpTx-1 against TTX-sensitive sodium channels in mDRG neurons was measured to be 7.1 nM. Currents were normalized with 100 representing TTX-sensitive current with no peptide addition and 0 representing TTX-sensitive current following complete block.

[0069] Figure 39 shows the effect of a single concentration of GpTx-1 (SEQ ID NO:1) on TTX-sensitive Nav channels in mouse DRG neurons. Cells were held at -140 mV and peak inward Nav currents were measured at -10 mV. "Baseline" trace shows Nav current before GpTx-1 addition, and "200 nM GpTx-1" trace shows Nav current after GpTx-1 addition. Note that inactivation of control currents was complete in a couple milliseconds, which distinguishes TTX-sensitive current from TTX-resistant current.

[0070] Figure 40 shows the time course of increasing concentrations of GpTx-1 (SEQ ID NO:1) against TTX-sensitive Nav channels in mouse DRG neurons. Peak inward Nav currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of GpTx-1; cells were held at a potential yielding approximately 20% inactivation. "Control" indicates Nav current in the absence of GpTx-1, "TTX" indicates Nav current in the presence of 300 nM TTX, and "Wash" indicates Nav current following removal of GpTx-1 and TTX. Note that GpTx-1 blocked all TTX-sensitive Nav current, since 300 nM TTX gave no additional current block.

[0071] Figure 41 shows a representative dose-response curve of GpTx-1 (SEQ ID NO:1) against TTX-sensitive Nav channels in mouse DRG neurons, as defined by fast inactivation kinetics. Peak inward Nav currents were measured at -10 mV in the presence of increasing concentrations of GpTx-1; cells were held at a potential yielding approximately 20% inactivation. The IC_{50} value of GpTx-1 against TTX-sensitive

sodium channels in mDRG neurons was measured to be 4.7 nM. Currents were normalized with 100 representing TTX-sensitive current with no peptide addition and 0 representing TTX-sensitive current following complete block.

[0072] Figure 42 shows the effect of GpTx-1 (SEQ ID NO:1) on TTX-sensitive Nav channels in mouse DRG neurons. Cells were held at a potential yielding approximately 20% inactivation and peak inward Nav currents were measured at -10 mV. "Baseline" trace shows Nav current before GpTx-1 addition, and "200 nM GpTx-1" trace shows Nav current after GpTx-1 addition.

[0073] Figure 43 shows the time course of increasing concentrations of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) against TTX-sensitive Nav channels in mouse DRG neurons. Peak inward Nav currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of [Ala5]GpTx-1(1-34) (SEQ ID NO:22); cells were held at -140 mV. "Control" indicates Nav current in the absence of [Ala5]GpTx-1(1-34) (SEQ ID NO:22), "TTX"' indicates Nav current in the presence of 300 nM TTX, and "Wash" indicates Nav current following removal of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) and TTX. Note that [Ala5]GpTx-1(1-34) (SEQ ID NO:22) blocked nearly all TTX-sensitive Nav current.

[0074] Figure 44 shows a representative dose-response curve of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) against TTX-sensitive Nav channels in mouse DRG neurons. Peak inward Nav currents were measured at -10 mV in the presence of increasing concentrations of [Ala5]GpTx-1(1-34); cells were held at -140 mV. The IC_{50} value of [Ala5]GpTx-1(1-34) against TTX-sensitive sodium channels in mDRG neurons was measured to be 17.0 nM. Currents were normalized with 100 representing TTX-sensitive current with no peptide addition and 0 representing TTX-sensitive current following complete block.

[0075] Figure 45 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) on TTX-sensitive Nav channels in mouse DRG neurons. Cells were held at -140 mV and peak inward Nav currents were measured at -10 mV. "Baseline" trace shows Nav current before addition of [Ala5]GpTx-1(1-34) (SEQ ID NO:22), "300 nM SEQ ID NO:22" trace shows Nav current after SEQ ID NO:22 addition, and "300 nM SEQ ID NO:22 + 300 nM TTX" trace shows Nav current after SEQ ID NO:22 and TTX

addition. Note that [Ala5]GpTx-1(1-34) selectively blocked TTX-sensitive Nav current but not TTX-resistant Nav current.

[0076] Figure 46 shows a time course of increasing concentrations of a homodimeric conjugate (Homodimeric Conjugate 1) of peptide monomer [Phe6,Atz13]GpTx-1(1-34) (SEQ ID NO:591) against hNav1.7 channels. Peak inward hNav1.7 currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of Homodimeric Conjugate 1; cells were held at -140 mV. "Control" indicates human Nav1.7 (hNav1.7) current in the absence of Homodimeric Conjugate 1and "Wash" indicates hNav1.7 current following removal of Homodimeric Conjugate 1.

[0077] Figure 47 shows a representative dose-response curve of Homodimeric Conjugate 1 against human Nav1.7 channels. Peak inward hNav1.7 currents were measured at -10 mV in the presence of increasing concentrations of Homodimeric Conjugate 1; cells were held at -140 mV. The IC_{50} value of Homodimeric Conjugate 1 against hNav1.7 sodium channels was measured to be 1.2 nM. Currents were normalized with 100 representing Nav1.7 current with no peptide addition and 0 representing Nav1.7 current following complete block.

[0078] Figure 48 shows the recovery of hNav1.7 currents following washout of Homodimeric Conjugate 1. Peak inward hNav1.7 currents were measured at -10 mV every 10 seconds in the presence of 3 nM or 300 nM Homodimeric Conjugate 1; cells were held at a -140 mV. "Control" indicates hNav1.7 current in the absence of Homodimeric Conjugate 1 and "Wash" indicates hNav1.7 current following removal of Homodimeric Conjugate 1. Note that hNav1.7 currents partially recover following washout of 3 nM Homodimeric Conjugate 1 but do not recover following washout of 300 nM of Homodimeric Conjugate 1.

[0079] Figure 49 shows the effect of Homodimeric Conjugate 1 on hNav1.7 channels. Cells were held at -140 mV and peak inward hNav1.7 currents were measured at -10 mV. "Baseline" trace shows hNav1.7 current before Homodimeric Conjugate 1 addition, and '10 nM Homodimeric Conjugate 1' trace shows hNav1.7 current after Homodimeric Conjugate 1 addition.

[0080] Figure 50 shows a time course of increasing concentrations of Homodimeric Conjugate 1 against hNav1.7 channels. Peak inward hNav1.7 currents

were measured at -10 mV every 10 seconds in the presence of increasing concentrations of Homodimeric Conjugate 1; cells were held at a potential yielding approximately 20% inactivation. "Control" indicates hNav1.7 current in the absence of Homodimeric Conjugate 1 and "Wash" indicates hNav1.7 current following removal of Homodimeric Conjugate 1.

[0081] Figure 51 shows a representative dose-response curve of Homodimeric Conjugate 1 against hNav1.7 channels. Peak inward hNav1.7 currents were measured at -10 mV in the presence of increasing concentrations of Homodimeric Conjugate 1; cells were held at a potential yielding approximately 20% inactivation. The IC_{50} value of Homodimeric Conjugate 1 against TTX-sensitive sodium channels in mDRG neurons was measured to be 0.66 nM. Currents were normalized with 100 representing Nav1.7 current with no peptide addition and 0 representing Nav1.7 current following complete block.

[0082] Figure 52 shows the effect of Homodimeric Conjugate 1 on hNav1.7 channels. Cells were held at a potential yielding approximately 20% inactivation and peak inward hNav1.7 currents were measured at -10 mV. "Baseline" trace shows hNav1.7 current before Homodimeric Conjugate 1 addition, and "3 nM Homodimeric Conjugate 1" trace shows hNav1.7 current after Homodimeric Conjugate 1 addition.

[0083] Figure 53 shows a time course of increasing concentrations of Homodimeric Conjugate 1 against hNav1.5 channels. Peak inward hNav1.5 currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of Homodimeric Conjugate 1; cells were held at a -140 mV. "Control" indicates hNav1.5 current in the absence of Homodimeric Conjugate 1 and "Wash" indicates hNav1.5 current following removal of Homodimeric Conjugate 1. Note that hNav1.5 currents partially recover following washout of Homodimeric Conjugate 1.

[0084] Figure 54 shows a representative dose-response curve of Homodimeric Conjugate 1 against hNav1.5 channels. Peak inward hNav1.5 currents were measured at -10 mV in the presence of increasing concentrations of Homodimeric Conjugate 1; cells were held at -140 mV. The IC_{50} value of Homodimeric Conjugate 1 against hNav1.5 sodium channels was measured to be 75.5 nM. Currents were normalized with 100 representing Nav1.5 current with no peptide addition and 0 representing Nav1.5 current following complete block.

[0085] Figure 55 shows the effect of Homodimeric Conjugate 1 on hNav1.5 channels. Cells were held at -140 mV and peak inward hNav1.5 currents were measured at -10 mV. "Baseline" trace shows hNav1.5 current before Homodimeric Conjugate 1 addition, and "2 μM Homodimeric Conjugate 1" trace shows hNav1.5 current after Homodimeric Conjugate 1 addition.

[0086] Figure 56 shows the time course of increasing concentrations of Homodimeric Conjugate 1 against hNav1.5 channels. Peak inward hNav1.5 currents were measured at -10 mV every 10 seconds in the presence of increasing concentrations of Homodimeric Conjugate 1; cells were held at a potential yielding approximately 20% inactivation. "Control" indicates hNav1.5 current in the absence of Homodimeric Conjugate 1 and "Wash" indicates hNav1.5 current following removal of Homodimeric Conjugate 1.

[0087] Figure 57 shows a representative dose-response curve of Homodimeric Conjugate 1 against hNav1.5 channels. Peak inward hNav1.5 currents were measured at -10 mV in the presence of increasing concentrations of Homodimeric Conjugate 1; cells were held at a potential yielding approximately 20% inactivation. The IC_{50} value of Homodimeric Conjugate 1 against hNav1.5 sodium channels was measured to be 57 nM. Currents were normalized with 100 representing Nav1.5 current with no peptide addition and 0 representing Nav1.5 current following complete block.

[0088] Figure 58 shows the effect of Homodimeric Conjugate 1 on hNav1.5 channels. Cells were held at a potential yielding approximately 20% inactivation and peak inward hNav1.5 currents were measured at -10 mV. "Baseline" trace shows hNav1.5 current before Homodimeric Conjugate 1 addition, and "2 uM Homodimeric Conjugate 1" trace shows hNav1.5 current after Homodimeric Conjugate 1 addition.

[0089] Figure 59 shows the timecourse of the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) in the formalin pain model in male CD-1 mice with a 1-hour pre-treatment dose of 5 mg/kg s.c. The peptide had no effect in the first or acute phase (0-5 minutes post formalin injection). The peptide significantly reduced the time spent lifting and/or licking the affected paw during the second phase (5-40 minutes post formalin injection, associated with spinal sensitization) compared to vehicle (PBS). In this experiment the 1 mg/kg s.c. dose of morphine used as a positive control was insufficient to significantly reduce pain response in the animals, and it was increased to

3 mg/kg in the following studies. The terminal plasma exposure (peptide plasma concentrations at 45 min post formalin injection) for the peptide was 0.80 ± 0.21 μM.

[0090] Figure 60 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) in the formalin pain model in male CD-1 mice with a 1-hour pre-treatment dose of 5 mg/kg s.c. during the first phase (0-5 minutes post formalin injection). Neither the peptide nor the morphine positive control significantly reduced the time spent lifting and/or licking the affected paw during the first phase. Pharmacological reductions in flinching during this first phase generally reflect nonspecific effects on animal movement, consciousness, or health rather than an actual reduction in pain.

[0091] Figure 61 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) in the formalin pain model in male CD-1 mice with a 1-hour pre-treatment dose of 5 mg/kg s.c. during the second phase (5-40 minutes post formalin injection). The peptide but not the morphine control significantly reduced the time spent lifting and/or licking the affected paw during the second phase. Again, the lack of effect of the morphine positive control does not reflect a "failed" assay, but the variability of mouse responses to this concentration of morphine. Morphine doses for future experiments were increased to 3 mg/kg.

[0092] Figure 62 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) on paw edema in the formalin pain model in male CD-1 mice with a 1-hour pre-treatment dose of 5 mg/kg s.c. Neither the peptide nor the morphine positive control significantly reduced the paw edema caused by formalin injection relative to the vehicle (PBS).

[0093] Figure 63 shows the timecourse of the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) in a repeat of the formalin pain model in male CD-1 mice with 1-hour pre-treatment doses of 5, 1.67, and 0.5 mg/kg s.c. The peptide had no effect at any dose in the first phase (0-5 minutes post formalin injection). The positive control, a 3 mg/kg s.c. dose of morphine, did significantly reduce the time spent lifting/licking the affected paw in the first phase. The 5 mg/kg s.c. dose of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) demonstrated a significant reduction of the time spent lifting/licking in the second phase of the study, as did the morphine positive control. The lower peptide doses (1.67 and 0.5 mg/ kg s.c.) had no effect relative to the vehicle in the second phase. Terminal exposures (peptide plasma concentrations at 45 min post formalin injection) were 0.58

± 0.26 μM, 0.15 ± 0.05 μM, and 0.04 ± 0.2 μM for the 5.0, 1.67, and 0.5 mg/kg doses, respectively.

[0094] Figure 64 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) in the first phase of the formalin pain model in male CD-1 mice with 1-hour pre-treatment doses of 5, 1.67, and 0.5 mg/kg s.c. The peptide had no effect at any dose in the first phase (0-5 minutes post formalin injection) relative to the vehicle, but the positive control, a 3 mg/kg s.c. dose of morphine, did significantly reduce the time spent lifting/licking the affected paw in the first phase.

[0095] Figure 65 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) in the second phase of the formalin pain model in male CD-1 mice with 1-hour pre-treatment doses of 5, 1.67, and 0.5 mg/kg s.c. The 5 mg/kg s.c. dose of peptide demonstrated a significant reduction of the time spent lifting/licking in the second phase of the study, as did the morphine positive control. The lower peptide doses (1.67 and 0.5 mg/ kg s.c.) had no effect relative to the vehicle in the second phase.

[0096] Figure 66 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) on paw edema in the formalin pain model in male CD-1 mice with a 1-hour pre-treatment doses of 5, 1.67, and 0.5 mg/kg s.c. Neither the peptide nor the morphine control significantly reduced the paw edema caused by formalin injection relative to the vehicle (PBS).

[0097] Figure 67 shows the timecourse of the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) in a third repetition of the formalin pain model in male CD-1 mice with 1-hour pre-treatment doses of 5, 3, and 1 mg/kg s.c. The 5 mg/kg peptide dose and the 3 mg/kg s.c. dose of morphine (30 minutes pretreatment) had no effect in the first phase (0-5 minutes post formalin injection). However, the lower peptide doses (1 and 3 mg/kg s.c.) appeared to increase the time spent lifting/licking relative to the vehicle control. The 5 mg/kg s.c. dose of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) demonstrated a significant reduction of the time spent lifting/licking in the second phase of the study, as did the morphine positive control. However, the lower peptide doses did not show a reduction in lifting/licking behavior relative to the vehicle control in the second phase. The 1 mg/kg s.c. group was not significantly different from the vehicle control, whereas the 3 mg/ kg s.c. group appeared to significantly increase time spent lifting/licking in the second phase. Terminal exposures (peptide plasma concentrations at 45 min post

formalin injection) were 1.84 ± 0.18 μM, 0.53 ± 0.23 μM, and 0.20 ± 0.05 μM for the 5.0, 3, and 1 mg/kg doses, respectively.

[0098] Figure 68 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) in the first phase of the formalin pain model in male CD-1 mice with 1-hour pre-treatment doses of 5, 3, and 1 mg/kg s.c. The 5 mg/kg peptide dose and the 3 mg/kg s.c. dose of morphine had no effect in the first phase (0-5 minutes post formalin injection). However, the lower peptide doses (1 and 3 mg/kg s.c.) appeared to increase the time spent lifting/licking relative to the control.

[0099] Figure 69 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) in the second phase of the formalin pain model in male CD-1 mice with 1 hour pre-treatment doses of 5, 3, and 1 mg/kg s.c. The 5 mg/kg s.c. dose of peptide demonstrated a significant reduction of the time spent lifting/licking in the second phase of the study, as did the morphine positive control. However, the lower peptide doses did not show a reduction in lifting/licking behavior relative to the vehicle control in the second phase. The 1 mg/kg s.c. group was not significantly different from the vehicle control, whereas the 3 mg/kg s.c. group appeared to significantly increase the time spent lifting/licking in the second phase.

[00100] Figure 70 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) on paw edema in the formalin pain model in male CD-1 mice with a 1-hour pre-treatment doses of 5, 3, and 1 mg/kg s.c. Neither the peptide nor the morphine control significantly reduced the paw edema caused by formalin injection relative to the vehicle (PBS).

[00101] Figure 71 shows the effects of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at 3 and 5 mg/kg s.c. doses with a 1-hour pre-treatment time on the total basic movement component of locomotor activity in male CD-1 mice. No doses of peptide significantly decreased exploratory behavior in relation to the vehicle control. Terminal exposures (peptide plasma concentrations at 2 h post peptide injection) were 1.79 ± 0.38 and 0.89 ± 0.33 μM for the 5 and 3 mg/kg s.c. doses, respectively.

[00102] Figure 72 shows the effects of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at 3 and 5 mg/kg s.c. doses with a 1-hour pre-treatment time on fine movement component of locomotor activity in male CD-1 mice. At the 3 mg/kg dose, fine movement was not

significantly affected. At the 5mg/kg dose, peptide significantly reduced the total fine movement relative to the vehicle.

[00103] Figure 73 shows the effects of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at 3 and 5 mg/kg s.c. doses with a 1-hour pre-treatment time on the total rearing component of locomotor activity in male CD-1 mice. No doses of peptide significantly decreased exploratory behavior in relation to the vehicle control.

[00104] Figure 74 shows the effects of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at 3 and 5 mg/kg s.c. doses with a 1-hour pre-treatment time on the total time rearing component of locomotor activity in male CD-1 mice. At the 3 mg/kg dose, total time rearing was not significantly affected. At the 5 mg/kg dose, peptide significantly reduced the total time rearing relative to the vehicle.

[00105] Figure 75 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time and mexiletine at a 30 mg/kg intraperitoneal ("i.p.") dose with a 30 minute pre-treatment time on the veratridine-induced (1 μg injection in the dorsal paw) spontaneous nociceptive behaviors in male CD-1 mice measured for 20 minutes after veratridine injection. Overall there was a good paw lifting response from the vehicle group that was significantly reversed with mexiletine. At 5 mg/kg, [Ala5]GpTx-1(1-34) (SEQ ID NO:22) did not significantly reduce the lifting behavior. There is no reduction of paw edema across all groups.

[00106] Figure 76 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time and mexiletine at a 30 mg/kg i.p. dose with a 30 minute pre-treatment time on the veratridine-induced (1 μg injection in the dorsal paw) paw edema in male CD-1 mice. There is no reduction of paw edema across all groups.

[00107] Figure 77 shows the time course of the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time and mexiletine at a 30 mg/kg i.p. dose with a 30 minute pre-treatment time on the veratridine-induced (1 μg injection in the dorsal paw) spontaneous nociceptive behaviors in male CD-1 mice. Overall there was a good paw lifting response from the vehicle group that was significantly reversed with mexiletine throughout the course of the experiment. At 5 mg/kg, [Ala5]GpTx-1(1-34) (SEQ ID NO:22) was unable to significantly reduce the lifting behavior during the course of the entire experiment, though it did trend toward a

reduction in paw lifting and licking during the 10-15 and 15-20 minute time bins. Terminal exposure (peptide plasma concentration at 1.5 h post peptide injection) was 0.70 ± 0.10 μM for the 5 mg/kg dose.

[00108] Figure 78 shows repeat testing of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at a 1 and 5 mg/kg s.c. doses with a 1-hour pre-treatment time (n = 9-10) and mexiletine at a 30 mg/kg i.p. dose with a 30 minute pre-treatment time (n = 10) on veratridine-induced (1 μg injection in the dorsal paw) spontaneous nociceptive behaviors in male CD-1 mice. Overall there was a good paw lifting response from the vehicle group that was significantly reversed with mexiletine. At 1 and 5 mg/kg, [Ala5]GpTx-1(1-34) (SEQ ID NO:22) did not significantly reduce the lifting behavior.

[00109] Figure 79 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at 1 and 5 mg/kg s.c. doses with a 1-hour pre-treatment time and mexiletine at a 30 mg/kg i.p. dose with a 30 minute pre-treatment time on the veratridine-induced (1 μg injection in the dorsal paw) paw edema in male CD-1 mice. There was no reduction of paw edema in any group.

[00110] Figure 80 shows the time course of the effects of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at 1 and 5 mg/kg s.c. doses with a 1 hour pre-treatment time and mexiletine at a 30 mg/kg i.p. dose with a 30 minute pre-treatment time on the veratridine-induced (1 μg injection in the dorsal paw) spontaneous nociceptive behaviors in male CD-1 mice. Overall there was a good paw lifting response from the vehicle group that was significantly reversed with mexiletine throughout the course of the experiment. At 1 and 5 mg/kg, [Ala5]GpTx-1(1-34) (SEQ ID NO:22) did not significantly reduce the lifting behavior at any point during the course of the experiment. Terminal exposures (peptide plasma concentration at 1.5 h post peptide injection) were 0.72 ± 0.13 and 0.09 ± 0.05 μM for the 5 and 1 mg/kg doses, respectively.

[00111] Figure 81A shows the reaction of alkyne-containing peptide [Phe6; Pra13]GpTx-1(1-34) (SEQ ID NO:1049) with a 2 kDa PEG bis-azide via a copper catalyzed 1,3-dipolar cycloaddition reaction to obtain the site-specific homodimeric peptide with two triazole linkages by converting the propargylglycine or Pra residues in the sequences to 3-(1,2,3-triazol-4-yl)alanine or Atz residues.

[00112] Figure 81B shows the two step sequence of first reacting an alkyne-containing peptide [Ala5,Phe6,Pra13,Leu26,Arg28]GpTx-1(1-34) (SEQ ID NO:640) with an azido-PEG11-bromoacetamide linker via a copper catalyzed 1,3-dipolar cycloaddition reaction to obtain the site-specifically PEGylated peptide-linker construct (SEQ ID NO:1062) with a triazole linkage by converting the propargylglycine or Pra residue in the peptide sequence to a 3-(1,2,3-triazol-4-yl)alanine or Atz residue. Second, the engineered free cysteines in the anti-DNP mAb (E273C) hIgG1 (comprising immunoglobulin monomers SEQ ID NO:3087; SEQ ID NO:3088; SEQ ID NO:3087; SEQ ID NO:3088) react with the bromoacetamide functionality in peptide-linker to form a site-specific immunoglobulin-peptide conjugate with a stable thioacetamide linkage (Immunoglobulin-peptide Conjugate 1). If one cysteine reacts, then the result is a monovalent immunoglobulin-peptide conjugate as represented, but if both cysteines react, then the result is a bivalent immunoglobulin-peptide conjugate.

[00113] Figure 82 shows a reducing SDS-PAGE gel of the site specific conjugation reaction mixture of peptide-linker construct (SEQ ID NO:1062) with anti-DNP mAb (E273C) hIgG1 (comprising immunoglobulin monomers SEQ ID NO:3087; SEQ ID NO:3088; SEQ ID NO:3087; SEQ ID NO:3088) prior to purification on the SP-column. Approximately 75% of mAb heavy chain (HC) shows a 5-kD shift, indicating conjugation of a single GpTX-1 peptide analog. The higher molecular weight band indicates higher order conjugate due to over reduction.

[00114] Figure 83 shows the results from the purification of the site specific conjugation reaction mixture of peptide-linker construct (SEQ ID NO:1062) with anti-DNP mAb (E273C) hIgG1 (comprising immunoglobulin monomers SEQ ID NO:3087; SEQ ID NO:3088; SEQ ID NO:3087; SEQ ID NO:3088). The left panel shows the cation exchange chromatogram of UV absorbance at 280 nm of the conjugation reaction using a 5-mL HiTrap SP-HP column. The right panel shows the non-reducing SDS-PAGE gel (left) of the peaks from the cation exchange chromatogram indicating that the internal disulfide bonds of the antibody-peptide conjugates are intact and the reducing SDS-PAGE gel (right) of the peaks from the cation exchange chromatogram. Peak 1 shows the heavy chain (HC) of the non-reacted antibody. Peak 2 shows approximately 50% of the HC shifted indicating a monovalent antibody- GpTx-1 peptide analog

conjugate. Peak 3 shows nearly 100% HC shifted indicating bivalent antibody- GpTx-1 peptide analog conjugate.

[00115] Figure 84 shows the results from the purification of the site specific conjugation reaction mixture of peptide-linker construct (SEQ ID NO:1062) with anti-DNP mAb (E273C) hIgG1 Fc domain (homodimer of SEQ ID NO:3089). The left panel shows the cation exchange chromatogram of UV absorbance at 280 nm of the conjugation reaction using a 5 mL HiTrap SP-HP column. The right panel shows the non-reducing SDS-PAGE gel (left) of the peaks from the cation exchange chromatogram indicating that the internal disulfide bonds of the antibody-peptide conjugates are intact and the reducing SDS-PAGE gel (right) of the peaks from the cation exchange chromatogram. Peak 1 shows approximately 50% of the HC shifted indicating a monovalent antibody-peptide conjugate. Peak 2 shows near 100% HC shifted indicating bivalent antibody-peptide conjugate.

[00116] Figure 85 shows the analytical size exclusion chromatogram of UV absorbance at 280 nm for the (top panel) unmodified anti-DNP mAb (E273C) hIgG1 (comprising SEQ ID NO:3087; SEQ ID NO:3088; SEQ ID NO:3087; SEQ ID NO:3088) and the (bottom panel) bivalent antibody- GpTx-1 peptide analog conjugate (Immunoglobulin-peptide Conjugate 2) run on a Tosoh Bioscience Super SW3000, 4 μM, 250A, 4.6 mm x 30 cm column in 100 mM sodium phosphate, 250 mM NaCl, pH 6.8 with isocratic elution of 0.35 mL/min for 20 min. The chromatogram indicates no aggregation in the peptide conjugate sample.

[00117] Figure 86 shows the results from the deconvoluted LC-MS TOF of the bivalent peptide conjugate of peptide-linker construct (SEQ ID NO:1062) with anti-DNP mAb (E273C) hIgG1 (comprising immunoglobulin monomers SEQ ID NO:3087; SEQ ID NO:3088; SEQ ID NO:3087; SEQ ID NO:3088), which is Immunoglobulin-peptide Conjugate 2. The presence of multiple peaks indicates different glycosylation isoforms.

[00118] Figure 87 shows the results from the deconvoluted LC-MS TOF of the bivalent peptide conjugate of peptide-linker construct (SEQ ID NO:1062) with anti-DNP mAb (E52C) hIgG1 Fc domain (homodimer of SEQ ID NO:3089), which is Fc-peptide Conjugate 2. The presence of multiple peaks indicates different glycosylation isoforms.

[00119] Figure 88 shows a schematic representation of Fc-peptide Conjugate 1 for illustrative purposes only. A homology model of the immunoglobulin anti-DNP mAb (E52C) hIgG1 Fc domain (homodimer of SEQ ID NO:3089) was constructed from an immunoglobulin crystal structure (1HZH.pdb) and is depicted as a solid ribbon. Cys52 of SEQ ID 3089, the site of conjugation, is rendered in CPK format. The PEG11 linker is depicted as a solid tube, in an arbitrary conformation in this embodiment, connecting the C52 residue in the immunoglobulin Fc domain to the Atz13 residue in the peptide. A homology model of the peptide (SEQ ID NO:1046) was constructed from the NMR structure of GpTx-1 and is displayed as a solid ribbon and shown in this embodiment in an arbitrary relative orientation to the immunoglobulin Fc domain.

[00120] Figure 89 shows a schematic representation of Fc-peptide Conjugate 2 for illustrative purposes only. A homology model of the anti-DNP mAb (E52C) hIgG1 Fc domain (homodimer of SEQ ID NO:3089) was constructed from an immunoglobulin crystal structure (1HZH.pdb) and is depicted as a solid ribbon. Cys52 residues of both Fc domain monomers (SEQ ID 3089), were the sites of conjugation, and are rendered in CPK format. The PEG11 linkers are depicted as solid tubes in this embodiment in an arbitrary conformation connecting the C52 residues in the immunoglobulin Fc domain to the Atz13 residues in the peptides. Homology models of the peptide (SEQ ID NO:1046) were constructed from the NMR structure of GpTx-1 and are displayed as a solid ribbon and shown in arbitrary relative orientations to the immunoglobulin Fc domain. Two peptides are shown to reflect the bivalent nature of Fc-peptide Conjugate 2.

[00121] Figure 90 shows a schematic representation of Immunoglobulin-peptide Conjugate 1 for illustrative purposes only. A homology model of the anti-DNP mAb (E273C) hIgG1 (comprising immunoglobulin monomers SEQ ID NO:3087; SEQ ID NO:3088; SEQ ID NO:3087; SEQ ID NO:3088) was constructed from an immunoglobulin crystal structure (1HZH.pdb) and is depicted as a solid ribbon. Cys273, the site of conjugation, is rendered in CPK format. In this embodiment, the PEG11 linker is depicted as a solid tube in an arbitrary conformation connecting the C273 residue in the immunoglobulin to the Atz13 residue in the peptide. A homology model of the peptide (SEQ ID NO:1046) was constructed from the NMR structure of

GpTx-1 and is displayed as a solid ribbon and shown in an arbitrary relative orientation to the immunoglobulin in this embodiment.

[00122] Figure 91 shows a schematic representation of Immunoglobulin-peptide Conjugate 2 for illustrative purposes only. A homology model of the anti-DNP mAb (E273C) hIgG1 (comprising immunoglobulin monomers SEQ ID NO:3087; SEQ ID NO:3088; SEQ ID NO:3087; SEQ ID NO:3088) was constructed from an immunoglobulin crystal structure (1HZH.pdb) and is depicted as a solid ribbon. Both Cys273 residues, the sites of conjugation, are rendered in CPK format. In this embodiment, the PEG11 linkers are depicted as solid tubes in an arbitrary conformation connecting the C273 residues in the immunoglobulin to the Atz13 residues in the peptides. Homology models of the peptide (SEQ ID NO:1046) were constructed from the NMR structure of GpTx-1 and are displayed as a solid ribbon and shown in arbitrary relative orientations to the immunoglobulin in this embodiment. Two peptides are shown to reflect the bivalent nature of Immunoglobulin-peptide Conjugate 2.

[00123] Figure 92 shows the mean plasma concentration – time profiles of GpTx-1 peptide analog-Fc conjugate (Fc-Peptide Conjugate 2) and control Fc (homodimer of SEQ ID NO:3089) following a 1 and 10 mg/kg s.c. dose to mice (n=3).

[00124] Figure 93 shows the mean plasma concentration – time profiles of peptide-IgG conjugate (Immunoglobulin-Peptide Conjugate 2) and control IgG (hIgG1 mAb comprising SEQ ID NO:3087; SEQ ID NO:3088; SEQ ID NO:3087; SEQ ID NO:3088) following a 1 and 10 mg/kg s.c. dose to mice (n=3).

[00125] Figure 94 shows the effects of peptide [Ala5]GpTx-1 (SEQ ID NO:22) at 500 nM on fast sodium current and voltage-gated potassium currents. Traces are voltage-clamp recordings from a neuron enzymatically isolated from rat dorsal root ganglia. Inward sodium and outward potassium currents combined were evoked simultaneously by a 20 ms step to 0 mV from a holding voltage of -90 mV. Trace at right was taken approximately 160 seconds after addition of 500 nM peptide. [Ala5]GpTx-1 (SEQ ID NO:22) at 500 nM blocked fast sodium current but not voltage-gated potassium currents.

[00126] Figure 95 shows the timecourse of the effect of [Glu29]GpTx-1(1-34) (SEQ ID NO:30) in the formalin pain model in male CD-1 mice with a 1-hour pre-treatment dose of 5 mg/kg s.c. The 5 mg/kg peptide dose and the 3 mg/kg s.c. dose of

the positive control morphine (30 minutes pretreatment) had no significant effect in the first phase (0-5 minutes post formalin injection). The 5 mg/kg s.c. dose of [Glu29]GpTx-1(1-34) (SEQ ID NO:30) did not demonstrate a significant reduction of the time spent lifting/licking in the second phase of the study (5-40 minutes post formalin injection), but the morphine positive control did significantly reduce the time spent lifting/licking in the second phase. Terminal exposure (peptide plasma concentration at 45 min post formalin injection) was 0.502 ± 0.271 μM for the 5 mg/kg peptide dose.

[00127] Figure 96 shows the effect of [Glu29]GpTx-1(1-34) (SEQ ID NO:30) in the first phase of the formalin pain model in male CD-1 mice with a 1-hour pre-treatment dose of 5 mg/kg s.c. The 5 mg/kg peptide dose and the 3 mg/kg s.c. dose of morphine had no effect in the first phase (0-5 minutes post formalin injection).

[00128] Figure 97 shows the effect of [Glu29]GpTx-1(1-34) (SEQ ID NO:30) in the second phase of the formalin pain model (5-40 minutes post formalin injection) in male CD-1 mice with a 1 hour pre-treatment dose of 5 mg/kg s.c. The 5 mg/kg s.c. dose of peptide did not demonstrate a significant reduction of the time spent lifting/licking in the second phase of the study relative to the vehicle control. The morphine positive control did significantly reduce the time spent lifting/licking in the second phase.

[00129] Figure 98 shows the effect of [Glu29]GpTx-1(1-34) (SEQ ID NO:30) on paw edema in the formalin pain model in male CD-1 mice with a 1-hour pre-treatment dose 5 mg/kg s.c. Neither the peptide nor the morphine control significantly reduced the paw edema caused by formalin injection relative to the vehicle (PBS).

[00130] Figure 99 shows a repeat of the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the total basic movement component of locomotor activity in male CD-1 mice. Total basic movement was significantly reduced by the 5 mg/kg peptide dose. Terminal exposure (peptide plasma concentration at 2 h post peptide injection) was 2.1 ± 0.47 μM.

[00131] Figure 100 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the fine movement component of locomotor activity in male CD-1 mice. At the 5mg/kg dose, peptide significantly reduced the total fine movement relative to the vehicle.

[00132] Figure 101 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the total rearing component of locomotor activity in male CD-1 mice. At the 5mg/kg dose, peptide significantly reduced total rearing relative to the vehicle control.

[00133] Figure 102 shows the effect of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the total time rearing component of locomotor activity in male CD-1 mice. At the 5 mg/kg dose, peptide significantly reduced the total time rearing relative to the vehicle control.

[00134] Figure 103 shows the effect of [Glu29]GpTx-1(1-34) (SEQ ID NO:30) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the total basic movement component of locomotor activity in male CD-1 mice. The peptide dose did not significantly decrease exploratory behavior or total basic movement relative to the vehicle control. Terminal exposure (peptide plasma concentration at 2 h post peptide injection) was 0.771 ± 0.272 μM for the 5 mg/kg s.c. peptide dose.

[00135] Figure 104 shows the effect of [Glu29]GpTx-1(1-34) (SEQ ID NO:30) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the fine movement component of locomotor activity in male CD-1 mice. At the 5 mg/kg dose, fine movement was not significantly affected relative to the vehicle control.

[00136] Figure 105 shows the effect of [Glu29]GpTx-1(1-34) (SEQ ID NO:30) at 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the total rearing component of locomotor activity in male CD-1 mice. The peptide dose did not significantly decrease exploratory behavior or total rearing in relation to the vehicle control.

[00137] Figure 106 shows the effect of [Glu29]GpTx-1(1-34) (SEQ ID NO:30) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the total time rearing component of locomotor activity in male CD-1 mice. At the 5 mg/kg dose, total time rearing was not significantly affected relative to the vehicle control.

[00138] Figure 107 shows the effect of [Glu28]GpTx-1(1-34) (SEQ ID NO:153) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the total basic movement component of locomotor activity in male CD-1 mice. Total basic movement was significantly reduced by the 5 mg/kg peptide dose. Terminal exposure (peptide plasma concentration at 2 h post peptide injection) was 1.28 ± 0.403 μM.

[00139] Figure 108 shows the effect of [Glu28]GpTx-1(1-34) (SEQ ID NO:153) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the fine movement component of locomotor activity in male CD-1 mice. At the 5mg/kg dose, peptide significantly reduced the total fine movement relative to the vehicle.

[00140] Figure 109 shows the effect of [Glu28]GpTx-1(1-34) (SEQ ID NO:153) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the total rearing component of locomotor activity in male CD-1 mice. At the 5mg/kg dose, peptide significantly reduced total rearing relative to the vehicle control.

[00141] Figure 110 shows the effect of [Glu28]GpTx-1(1-34) (SEQ ID NO:153) at a 5 mg/kg s.c. dose with a 1-hour pre-treatment time on the total time rearing component of locomotor activity in male CD-1 mice. At the 5 mg/kg dose, peptide significantly reduced the total time rearing relative to the vehicle control.

[00142] Figure 111 shows the effects of 10 mg/kg s.c. doses of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2 with a 1-hour pre-treatment time on the total basic movement component of locomotor activity in male CD-1 mice. The peptide conjugate doses did not significantly decrease exploratory behavior or total basic movement relative to the vehicle control. Terminal exposures (peptide conjugate plasma concentrations at 24.5 h post peptide conjugate injection) were 0.034 ± 0.009 μM and 0.051 ± 0.007 μM for the 10 mg/kg s.c. doses of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2, respectively.

[00143] Figure 112 shows the effects of 10 mg/kg s.c. doses of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2 with a 1-hour pre-treatment time on the fine movement component of locomotor activity in male CD-1 mice. At the 10 mg/kg doses, fine movement was not significantly affected by either peptide conjugate relative to the vehicle control.

[00144] Figure 113 shows the effects of 10 mg/kg s.c. doses of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2 with a 1-hour pre-treatment time on the total rearing component of locomotor activity in male CD-1 mice. The peptide conjugate doses did not significantly decrease exploratory behavior or total rearing in relation to the vehicle control.

[00145] Figure 114 shows the effects of 10 mg/kg s.c. doses of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2 with a 1-hour pre-treatment time

on the total time rearing component of locomotor activity in male CD-1 mice. At the 10 mg/kg doses, total time rearing was not significantly affected by either peptide conjugate relative to the vehicle control.

[00146] Figure 115 shows the timecourse of the effects of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2 in the formalin pain model in male CD-1 mice with 1-hour pre-treatment doses of 10 mg/kg s.c. The 10 mg/kg peptide doses and the 3 mg/kg s.c. dose of the positive control morphine (30 minutes pretreatment) had no significant effect in the first phase (0-5 minutes post formalin injection). The 10 mg/kg s.c. doses of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2 did not demonstrate a significant reduction of the time spent lifting/licking in the second phase of the study (5-40 minutes post formalin injection), but the morphine positive control did significantly reduce the time spent lifting/licking in the second phase. Terminal exposures (peptide conjugate plasma concentrations at 45 min post formalin injection) were 0.035 ± 0.011 μM and 0.040 ± 0.011 μM for the 10 mg/kg doses of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2, respectively.

[00147] Figure 116 shows the effects of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2 in the first phase of the formalin pain model in male CD-1 mice with 1-hour pre-treatment doses of 10 mg/kg s.c. The 10 mg/kg s.c. doses of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2 and the 3 mg/kg s.c. dose of morphine had no effect in the first phase (0-5 minutes post formalin injection).

[00148] Figure 117 shows the effects of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2 in the second phase of the formalin pain model (5-40 minutes post formalin injection) in male CD-1 mice with 1 hour pre-treatment doses of 10 mg/kg s.c. The 10 mg/kg s.c. doses of Fc-peptide Conjugate 2 and Immunoglobulin-peptide Conjugate 2 did not demonstrate a significant reduction of the time spent lifting/licking in the second phase of the study relative to the vehicle control. The morphine positive control did significantly reduce the time spent lifting/licking in the second phase.

DETAILED DESCRIPTION OF EMBODIMENTS

[00149] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[00150] Definitions

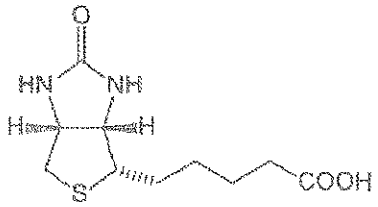
[00151] Unless otherwise defined herein, scientific and technical terms used in connection with the present application shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. Thus, as used in this specification and the appended claims, the singular forms "a", "an" and "the" include plural referents unless the context clearly indicates otherwise. For example, reference to "a protein" includes a plurality of proteins; reference to "a cell" includes populations of a plurality of cells.

[00152] "Polypeptide" and "protein" are used interchangeably herein and include a molecular chain of two or more amino acids linked covalently through peptide bonds. The terms do not refer to a specific length of the product. Thus, "peptides," and "oligopeptides," are included within the definition of polypeptide. The terms include post-translational modifications of the polypeptide, for example, glycosylations, acetylations, biotinylations, 4-pentynoylations, PEGylations, phosphorylations and the like. In addition, protein fragments, analogs, mutated or variant proteins, fusion proteins and the like are included within the meaning of polypeptide. The terms also include molecules in which one or more amino acid analogs or non-canonical or unnatural amino acids are included as can be expressed recombinantly using known protein engineering techniques. In addition, fusion proteins can be derivatized as described herein by well-known organic chemistry techniques.

[00153] A composition of the present invention that includes a peptide or polypeptide of the invention covalently linked, attached, or bound, either directly or indirectly through a linker moiety, to another peptide or polypeptide of the invention or to a half-life extending moiety is a "conjugate" or "conjugated" molecule, whether conjugated by chemical means (e.g., post-translationally or post-synthetically) or by recombinant fusion.

[00154] "Biotin" is a water-soluble B-complex vitamin, i.e., vitamin B7, that is composed of an ureido (tetrahydroimidizalone) ring fused with a tetrahydrothiophene ring (See, Formula I).

Formula I:



A valeric acid substituent is attached to one of the carbon atoms of the tetrahydrothiophene ring. In nature, biotin is a coenzyme in the metabolism of fatty acids and leucine, and it plays a role in vivo in gluconeogenesis. Biotin binds very tightly to the tetrameric protein avidin (e.g., Chicken avidin, bacterial streptavidin, and neutravidin), with a dissociation equilibrium constant K_D in the order of 10^{-14} M to 10^{-16} M, which is one of the strongest known protein-ligand interactions, approaching the covalent bond in strength. (Laitinen et al.. *Genetically engineered avidins and streptavidins*, Cell Mol Life Sci. 63 (24): 2992–30177 (2006)). The biotin-avidin non-covalent interaction is often used in different biotechnological applications. (See, Laitinen et al., *Genetically engineered avidins and streptavidins*, Cell Mol Life Sci. 63 (24): 2992–30177 (2006)).

[00155] "Biotinylated" means that a substance is covalently conjugated to one or more biotin moieties. Biotinylated peptides useful in practicing the invention can be purchased commercially (e.g., Midwest Bio-Tech Inc.) or can be readily synthesized and biotinylated. Biotinylation of compounds, such as peptides, can be by any known chemical technique. These include primary amine biotinylation, sulfhydryl biotinylation, and carboxyl biotinylation. For example, amine groups on the peptide, which are present as lysine side chain epsilon-amines and N-terminal α-amines, are common targets for primary amine biotinylation biotinylation. Amine-reactive biotinylation reagents can be divided into two groups based on water solubility.

1) N-hydroxysuccinimide (NHS)-esters of biotin have poor solubility in aqueous solutions. For reactions in aqueous solution, they must first be dissolved in an organic solvent, then diluted into the aqueous reaction mixture. The most

commonly used organic solvents for this purpose are dimethyl sulfoxide (DMSO) and dimethyl formamide (DMF), which are compatible with most proteins at low concentrations.

2) Sulfo-NHS-esters of biotin are more soluble in water, and are dissolved in water just before use because they hydrolyze easily. The water solubility of sulfo-NHS-esters stems from their sulfonate group on the N-hydroxysuccinimide ring and eliminates the need to dissolve the reagent in an organic solvent.

Chemical reactions of NHS- and sulfo-NHS-esters are essentially the same: an amide bond is formed and NHS or sulfo-NHS become leaving groups. Because the targets for the ester are deprotonated primary amines, the reaction is prevalent above pH 7. Hydrolysis of the NHS-ester is a major competing reaction, and the rate of hydrolysis increases with increasing pH. NHS- and sulfo-NHS-esters have a half-life of several hours at pH 7, but only a few minutes at pH 9. The conditions for conjugating NHS-esters to primary amines of peptides include incubation temperatures in the range 4-37°C, reaction pH values in the range 7-9, and incubation times from a few minutes to about 12 hours. Buffers containing amines (such as Tris or glycine) must be avoided because they compete with the reaction. The HABA dye (2-(4-hydroxyazobenzene) benzoic acid) method can be used to determine the extent of biotinylation. Briefly, HABA dye is bound to avidin and yields a characteristic absorbance. When biotin, in the form of biotinylated protein or other molecule, is introduced, it displaces the dye, resulting in a change in absorbance at 500 nm. The absorbance change is directly proportional to the level of biotin in the sample.

[00156] "4-pentynoylation" of an amino acid residue is typically by coupling 4-pentynoic acid via a standard amide bond reaction via the N-terminal or at a side chain. When appropriate for additional PEGylations, 4-pentynoylation can alternatively employ an alkyne in the copper-catalyzed 1,3-dipolar cycloaddition reaction (the so-called "Click" reaction) to react with the azide in the azido-PEG molecule to link the peptide and the PEG via a triazole.

[00157] An "isolated polypeptide" is a polypeptide molecule that is purified or separated from at least one contaminant polypeptide molecule with which it is ordinarily associated in the natural source of the polypeptide. An isolated polypeptide molecule is other than in the form or setting in which it is found in nature.

[00158] "Toxin peptides" include peptides and polypeptides having the same amino acid sequence of a naturally occurring pharmacologically active peptide or polypeptide that can be isolated from a venom, and also include modified peptide analogs of such naturally occurring molecules. (See, e.g., Kalman et al., ShK-Dap22, a potent Kv1.3-specific immunosuppressive polypeptide, J. Biol. Chem. 273(49):32697-707 (1998); Kem et al., US Patent No. 6,077,680; Mouhat et al., OsK1 derivatives, WO 2006/002850 A2; Chandy et al., Analogs of SHK toxin and their uses in selective inhibition of Kv1.3 potassium channels, WO 2006/042151; Sullivan et al., Toxin Peptide therapeutic agents, WO 2006/116156 A2, all of which are incorporated herein by reference in their entirety). Snakes, scorpions, spiders, bees, snails and sea anemone are a few examples of organisms that produce venom that can serve as a rich source of small bioactive toxin peptides or "toxins" that potently and selectively target ion channels and receptors. GpTx-1 (SEQ ID NO:1); GpTx-2 (SEQ ID NO:467); GpTx-3 (SEQ ID NO:468); GpTx-4 (SEQ ID NO:469); GpTx-5 (SEQ ID NO:470); GpTx-6(1-35) (SEQ ID NO:471); and GpTx-7(1-35) (SEQ ID NO:473) are examples of toxin peptides. Some other examples of toxins that inhibit voltage-gated sodium channels include Huwentoxin-IV (ECLEI FKACN PSNDQ CCKSS KLVCS RKTRW CKYQI-NH_2// SEQ ID NO:528) and Huwentoxin-I (ACKGV FDACT PGKNE CCPNR VCSDK HKWCK WKL //SEQ ID NO:529), isolated from the venom of tarantula *Ornithoctonus huwena*; KIIIA (CCNCS SKWCR DHSRC C-NH_2//SEQ ID NO:530) isolated from the venom of marine cone snail *Conus kinoshitai*; and ProTxII (YCQKW MWTCD SERKC CEGMV CRLWC KKKLW //SEQ ID NO:531) isolated from the venom of tarantula *Thrixopelma pruriens*. Another example is the alpha toxin OD1 (GVRDAYIADD KNCVYTCASN GYCNTECTKN GAESGYCQWI GRYGNACWCI KLPDEVPIRIPGKCR-NH_2//SEQ ID NO:589), a toxin isolated from the venom of the scorpion *Odonthobuthus doriae*. Another example of a toxin peptide is OSK1 (also known as OsK1), a toxin peptide isolated from *Orthochirus scrobiculosus* scorpion venom. (e.g., Mouhat et al., K+ channel types targeted by synthetic OSK1, a toxin from *Orthochirus scrobiculosus* scorpion venom, Biochem. J. 385:95-104 (2005); Mouhat et al., Pharmacological profiling of Orthochirus scrobiculosus toxin 1 analogs with a trimmed N-terminal domain, Molec. Pharmacol. 69:354- 62 (2006); Mouhat et al., OsK1 derivatives, WO 2006/002850 A2). Another example is ShK, isolated from the

venom of the sea anemone *Stichodactyla helianthus*, and its peptide analogs. (E.g., Tudor et al., Ionisation behaviour and solution properties of the potassium-channel blocker ShK toxin, Eur. J. Biochem. 251(1-2):133-41(1998); Pennington et al., Role of disulfide bonds in the structure and potassium channel blocking activity of ShK toxin, Biochem. 38(44): 14549-58 (1999); Kem et al., ShK toxin compositions and methods of use, US Patent No. 6,077,680; Lebrun et al., Neuropeptides originating in scorpion, US Patent No. 6,689,749; Beeton et al., Targeting effector memory T cells with a selective peptide inhibitor of Kv1.3 channnels for therapy of autoimmune diseases, Molec. Pharmacol. 67(4):1369-81 (2005); and Sullivan et al., Selective and potent peptide inhibitors of $K_V1.3$, WO 2010/108154 A2).

[00159] The toxin peptides are usually between about 20 and about 80 amino acids in length, contain 2-5 disulfide linkages and form a very compact structure. Toxin peptides (e.g., from the venom of scorpions, sea anemones and cone snails) have been isolated and characterized for their impact on ion channels. Such peptides appear to have evolved from a relatively small number of structural frameworks that are particularly well suited to addressing the critical issues of potency and stability. The majority of scorpion and *Conus* toxin peptides, for example, contain 10-40 amino acids and up to five disulfide bonds, forming extremely compact and constrained structure (microproteins) often resistant to proteolysis. The conotoxin and scorpion toxin peptides can be divided into a number of superfamilies based on their disulfide connections and peptide folds. The solution structure of many toxin peptides has been determined by NMR spectroscopy, illustrating their compact structure and verifying conservation of family folding patterns. (E.g., Tudor et al., Ionisation behaviour and solution properties of the potassium-channel blocker ShK toxin, Eur. J. Biochem. 251(1-2):133-41(1998); Pennington et al., Role of disulfide bonds in the structure and potassium channel blocking activity of ShK toxin, Biochem. 38(44): 14549-58 (1999); Jaravine et al., Three-dimensional structure of toxin OSK1 from *Orthochirus scrobiculosus* scorpion venom, Biochem. 36(6):1223-32 (1997); del Rio-Portillo et al.; NMR solution structure of Cn12, a novel peptide from the Mexican scorpion *Centruroides noxius* with a typical beta-toxin sequence but with alpha-like physiological activity, Eur. J. Biochem. 271(12): 2504-16 (2004); Prochnicka-Chalufour et al., Solution structure of discrepin, a new K+-channel blocking peptide

from the alpha-KTx15 subfamily, Biochem. 45(6):1795-1804 (2006)). Other examples are known in the art, or can be found in Sullivan et al., Toxin Peptide Therapeutic Agents, WO06116156 A2 or U.S. Patent No. 7,833,979; Sullivan et al., Selective and potent peptide inhibitors of $K_V1.3$, WO 2010/108154 A2; Mouhat et al., OsK1 derivatives, WO 2006/002850 A2; Sullivan et al., U.S. Patent Application No. 11/978,076 (titled: , filed 25 October 2007), Lebrun et al., U.S. Patent No. 6,689,749, which are each incorporated by reference in their entireties.

[00160] The term "peptide analog" refers to a peptide having a sequence that differs from a peptide sequence existing in nature by at least one amino acid residue substitution, internal addition, or internal deletion of at least one amino acid, and/or amino- or carboxy- terminal end truncations or additions, and/or carboxy-terminal amidation. An "internal deletion" refers to absence of an amino acid from a sequence existing in nature at a position other than the N- or C-terminus. Likewise, an "internal addition" refers to presence of an amino acid in a sequence existing in nature at a position other than the N- or C-terminus.

[00161] Embodiments of the inventive composition of matter includes a toxin peptide analog, or a pharmaceutically acceptable salt thereof. "Toxin peptide analogs" contain modifications of a native toxin peptide sequence of interest (e.g., amino acid residue substitutions, internal additions or insertions, internal deletions, and/or amino- or carboxy- terminal end truncations, or additions as previously described above) relative to a native toxin peptide sequence of interest, such as GpTx-1 (DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-NH_2 //SEQ ID NO:1). Toxin peptide analogs of the present invention are 20 to about 80 amino acid residues long and, in relation to SEQ ID NO:1, have C^1-C^4, C^2-C^5 and C^3-C^6 disulfide (or diselenide) bonding in which, C^1, C^2, C^3, C^4, C^5 and C^6 represent the order of cysteine (or selenocysteine) residues appearing in the primary sequence of the toxin peptide stated conventionally with the N-terminus of the peptide(s) on the left, with the first and sixth cysteines (or selenocysteines) in the amino acid sequence forming a disulfide bond (or diselenide bond, if SeCys), the second and fourth cysteines (or selenocysteines) forming a disulfide bond (or diselenide bond, if SeCys), and the third and fifth cysteines (or selenocysteines) forming a disulfide bond (or diselenide bond, if SeCys). As described herein, the toxin peptide analogs of the present invention can also have

additional amino acid residues at the N-terminal and/or C-terminal ends, in relation to SEQ ID NO:1.

[00162] By "physiologically acceptable salt" of the composition of matter, for example a salt of the toxin peptide analog, is meant any salt or salts that are known or later discovered to be pharmaceutically acceptable. Some non-limiting examples of pharmaceutically acceptable salts are: acetate; trifluoroacetate; hydrohalides, such as hydrochloride and hydrobromide; sulfate; citrate; maleate; tartrate; glycolate; gluconate; succinate; mesylate; besylate; salts of gallic acid esters (gallic acid is also known as 3,4, 5 trihydroxybenzoic acid) such as PentaGalloylGlucose (PGG) and epigallocatechin gallate (EGCG), salts of cholesteryl sulfate, pamoate, tannate and oxalate salts.

[00163] The term "fusion protein" indicates that the protein includes polypeptide components derived from more than one parental protein or polypeptide. Typically, a fusion protein is expressed from a fusion gene in which a nucleotide sequence encoding a polypeptide sequence from one protein is appended in frame with, and optionally separated by a linker from, a nucleotide sequence encoding a polypeptide sequence from a different protein. The fusion gene can then be expressed by a recombinant host cell as a single protein.

[00164] The terms "-mimetic peptide," "peptide mimetic," and "-agonist peptide" refer to a peptide or protein having biological activity comparable to a naturally occurring protein of interest, for example, but not limited to, a toxin peptide molecule. These terms further include peptides that indirectly mimic the activity of a naturally occurring peptide molecule, such as by potentiating the effects of the naturally occurring molecule.

[00165] The term "-antagonist peptide," "peptide antagonist," and "inhibitor peptide" refer to a peptide that blocks or in some way interferes with the biological activity of a receptor of interest, or has biological activity comparable to a known antagonist or inhibitor of a receptor of interest, such as, but not limited to, an ion channel (e.g., Kv1.3) or a G-Protein Coupled Receptor (GPCR).

[00166] A "domain" of a protein is any portion of the entire protein, up to and including the complete protein, but typically comprising less than the complete protein. A domain can, but need not, fold independently of the rest of the protein chain and/or be

correlated with a particular biological, biochemical, or structural function or location (e.g., a ligand binding domain, or a cytosolic, transmembrane or extracellular domain).

[00167] As used herein "soluble" when in reference to a protein produced by recombinant DNA technology in a host cell is a protein that exists in aqueous solution; if the protein contains a twin-arginine signal amino acid sequence the soluble protein is exported to the periplasmic space in gram negative bacterial hosts, or is secreted into the culture medium by eukaryotic host cells capable of secretion, or by bacterial host possessing the appropriate genes (e.g., the *kil* gene). Thus, a soluble protein is a protein which is not found in an inclusion body inside the host cell. Alternatively, depending on the context, a soluble protein is a protein which is not found integrated in cellular membranes. In contrast, an insoluble protein is one which exists in denatured form inside cytoplasmic granules (called an inclusion body) in the host cell, or again depending on the context, an insoluble protein is one which is present in cell membranes, including but not limited to, cytoplasmic membranes, mitochondrial membranes, chloroplast membranes, endoplasmic reticulum membranes, etc.

[00168] A distinction is also drawn between proteins which are "soluble" (i.e., dissolved or capable of being dissolved) in an aqueous solution devoid of significant amounts of ionic detergents (e.g., SDS) or denaturants (e.g., urea, guanidine hydrochloride) and proteins which exist as a suspension of insoluble protein molecules dispersed within the solution. A "soluble" protein will not be removed from a solution containing the protein by centrifugation using conditions sufficient to remove cells present in a liquid medium (e.g., centrifugation at 5,000×g for 4-5 minutes). In some embodiments of the inventive composition, the toxin peptide analog is synthesized by the host cell and segregated in an insoluble form within cellular inclusion bodies, which can then be purified from other cellular components in a cell extract with relative ease, and the toxin peptide analog can in turn be solubilized, refolded and/or further purified.

[00169] A distinction is drawn between a "soluble" protein (i.e., a protein which when expressed in a host cell is produced in a soluble form) and a "solubilized" protein. An insoluble recombinant protein found inside an inclusion body or found integrated in a cell membrane may be solubilized (i.e., rendered into a soluble form) by treating purified inclusion bodies or cell membranes with denaturants such as guanidine hydrochloride, urea or sodium dodecyl sulfate (SDS). These denaturants must then be

removed from the solubilized protein preparation to allow the recovered protein to renature (refold). Although the inventive compositions can be refolded in active form, not all proteins will refold into an active conformation after solubilization in a denaturant and removal of the denaturant. Many proteins precipitate upon removal of the denaturant. SDS may be used to solubilize inclusion bodies and cell membranes and will maintain the proteins in solution at low concentration. However, dialysis will not always remove all of the SDS (SDS can form micelles which do not dialyze out); therefore, SDS-solubilized inclusion body protein and SDS-solubilized cell membrane protein is soluble but not refolded.

[00170] A "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a secretory signal peptide sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage. In some other embodiments of the inventive composition, the toxin peptide analog can be synthesized by the host cell as a secreted protein, which can then be further purified from the extracellular space and/or medium.

[00171] The term "recombinant" indicates that the material (e.g., a nucleic acid or a polypeptide) has been artificially or synthetically (i.e., non-naturally) altered by human intervention. The alteration can be performed on the material within, or removed from, its natural environment or state. For example, a "recombinant nucleic acid" is one that is made by recombining nucleic acids, e.g., during cloning, DNA shuffling or other well known molecular biological procedures. Examples of such molecular biological procedures are found in Maniatis et al., Molecular Cloning. A Laboratory Manual. Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y. (1982). A "recombinant DNA molecule," is comprised of segments of DNA joined together by means of such molecular biological techniques. The term "recombinant protein" or "recombinant polypeptide" as used herein refers to a protein molecule which is expressed using a recombinant DNA molecule. A "recombinant host cell" is a cell that contains and/or expresses a recombinant nucleic acid.

[00172] The term "polynucleotide" or "nucleic acid" includes both single-stranded and double-stranded nucleotide polymers containing two or more nucleotide residues. The nucleotide residues comprising the polynucleotide can be ribonucleotides or deoxyribonucleotides or a modified form of either type of nucleotide. Said modifications include base modifications such as bromouridine and inosine derivatives, ribose modifications such as 2',3'-dideoxyribose, and internucleotide linkage modifications such as phosphorothioate, phosphorodithioate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phosphoraniladate and phosphoroamidate.

[00173] The term "oligonucleotide" means a polynucleotide comprising 200 or fewer nucleotide residues. In some embodiments, oligonucleotides are 10 to 60 bases in length. In other embodiments, oligonucleotides are 12, 13, 14, 15, 16, 17, 18, 19, or 20 to 40 nucleotides in length. Oligonucleotides may be single stranded or double stranded, e.g., for use in the construction of a mutant gene. Oligonucleotides may be sense or antisense oligonucleotides. An oligonucleotide can include a label, including an isotopic label (e.g., ^{125}I, ^{14}C, ^{13}C, ^{35}S, ^{3}H, ^{2}H, ^{13}N, ^{15}N, ^{18}O, ^{17}O, etc.), for ease of quantification or detection, a fluorescent label, a hapten or an antigenic label, for detection assays. Oligonucleotides may be used, for example, as PCR primers, cloning primers or hybridization probes.

[00174] A "polynucleotide sequence" or "nucleotide sequence" or "nucleic acid sequence," as used interchangeably herein, is the primary sequence of nucleotide residues in a polynucleotide, including of an oligonucleotide, a DNA, and RNA, a nucleic acid, or a character string representing the primary sequence of nucleotide residues, depending on context. From any specified polynucleotide sequence, either the given nucleic acid or the complementary polynucleotide sequence can be determined. Included are DNA or RNA of genomic or synthetic origin which may be single- or double-stranded, and represent the sense or antisense strand. Unless specified otherwise, the left-hand end of any single-stranded polynucleotide sequence discussed herein is the 5' end; the left-hand direction of double-stranded polynucleotide sequences is referred to as the 5' direction. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA transcript that are 5' to the 5' end of the

RNA transcript are referred to as "upstream sequences;" sequence regions on the DNA strand having the same sequence as the RNA transcript that are 3' to the 3' end of the RNA transcript are referred to as "downstream sequences."

[00175] As used herein, an "isolated nucleic acid molecule" or "isolated nucleic acid sequence" is a nucleic acid molecule that is either (1) identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the nucleic acid or (2) cloned, amplified, tagged, or otherwise distinguished from background nucleic acids such that the sequence of the nucleic acid of interest can be determined. An isolated nucleic acid molecule is other than in the form or setting in which it is found in nature. However, an isolated nucleic acid molecule includes a nucleic acid molecule contained in cells that ordinarily express a polypeptide (e.g., an oligopeptide or antibody) where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

[00176] As used herein, the terms "nucleic acid molecule encoding," "DNA sequence encoding," and "DNA encoding" refer to the order or sequence of deoxyribonucleotides along a strand of deoxyribonucleic acid. The order of these deoxyribonucleotides determines the order of ribonucleotides along the mRNA chain, and also determines the order of amino acids along the polypeptide (protein) chain. The DNA sequence thus codes for the RNA sequence and for the amino acid sequence.

[00177] The term "gene" is used broadly to refer to any nucleic acid associated with a biological function. Genes typically include coding sequences and/or the regulatory sequences required for expression of such coding sequences. The term "gene" applies to a specific genomic or recombinant sequence, as well as to a cDNA or mRNA encoded by that sequence. A "fusion gene" contains a coding region that encodes a polypeptide with portions from different proteins that are not naturally found together, or not found naturally together in the same sequence as present in the encoded fusion protein (i.e., a chimeric protein). Genes also include non-expressed nucleic acid segments that, for example, form recognition sequences for other proteins. Non-expressed regulatory sequences including transcriptional control elements to which regulatory proteins, such as transcription factors, bind, resulting in transcription of adjacent or nearby sequences.

[00178] "Expression of a gene" or "expression of a nucleic acid" means transcription of DNA into RNA (optionally including modification of the RNA, e.g., splicing), translation of RNA into a polypeptide (possibly including subsequent post-translational modification of the polypeptide), or both transcription and translation, as indicated by the context.

[00179] As used herein the term "coding region" or "coding sequence" when used in reference to a structural gene refers to the nucleotide sequences which encode the amino acids found in the nascent polypeptide as a result of translation of an mRNA molecule. The coding region is bounded, in eukaryotes, on the 5' side by the nucleotide triplet "ATG" which encodes the initiator methionine and on the 3' side by one of the three triplets which specify stop codons (i.e., TAA, TAG, TGA).

[00180] The term "control sequence" or "control signal" refers to a polynucleotide sequence that can, in a particular host cell, affect the expression and processing of coding sequences to which it is ligated. The nature of such control sequences may depend upon the host organism. In particular embodiments, control sequences for prokaryotes may include a promoter, a ribosomal binding site, and a transcription termination sequence. Control sequences for eukaryotes may include promoters comprising one or a plurality of recognition sites for transcription factors, transcription enhancer sequences or elements, polyadenylation sites, and transcription termination sequences. Control sequences can include leader sequences and/or fusion partner sequences. Promoters and enhancers consist of short arrays of DNA that interact specifically with cellular proteins involved in transcription (Maniatis, et al., Science 236:1237 (1987)). Promoter and enhancer elements have been isolated from a variety of eukaryotic sources including genes in yeast, insect and mammalian cells and viruses (analogous control elements, i.e., promoters, are also found in prokaryotes). The selection of a particular promoter and enhancer depends on what cell type is to be used to express the protein of interest. Some eukaryotic promoters and enhancers have a broad host range while others are functional in a limited subset of cell types (for review see Voss, et al., Trends Biochem. Sci., 11:287 (1986) and Maniatis, et al., Science 236:1237 (1987)).

[00181] The term "vector" means any molecule or entity (e.g., nucleic acid, plasmid, bacteriophage or virus) used to transfer protein coding information into a host cell.

[00182] The term "expression vector" or "expression construct" as used herein refers to a recombinant DNA molecule containing a desired coding sequence and appropriate nucleic acid control sequences necessary for the expression of the operably linked coding sequence in a particular host cell. An expression vector can include, but is not limited to, sequences that affect or control transcription, translation, and, if introns are present, affect RNA splicing of a coding region operably linked thereto. Nucleic acid sequences necessary for expression in prokaryotes include a promoter, optionally an operator sequence, a ribosome binding site and possibly other sequences. Eukaryotic cells are known to utilize promoters, enhancers, and termination and polyadenylation signals. A secretory signal peptide sequence can also, optionally, be encoded by the expression vector, operably linked to the coding sequence of interest, so that the expressed polypeptide can be secreted by the recombinant host cell, for more facile isolation of the polypeptide of interest from the cell, if desired. Such techniques are well known in the art. (E.g., Goodey, Andrew R.; et al., Peptide and DNA sequences, U.S. Patent No. 5,302,697; Weiner et al., Compositions and methods for protein secretion, U.S. Patent No. 6,022,952 and U.S. Patent No. 6,335,178; Uemura et al., Protein expression vector and utilization thereof, U.S. Patent No. 7,029,909; Ruben et al., 27 human secreted proteins, US 2003/0104400 A1).

[00183] The terms "in operable combination", "in operable order" and "operably linked" as used herein refer to the linkage of nucleic acid sequences in such a manner that a nucleic acid molecule capable of directing the transcription of a given gene and/or the synthesis of a desired protein molecule is produced. The term also refers to the linkage of amino acid sequences in such a manner so that a functional protein is produced. For example, a control sequence in a vector that is "operably linked" to a protein coding sequence is ligated thereto so that expression of the protein coding sequence is achieved under conditions compatible with the transcriptional activity of the control sequences.

[00184] The term "host cell" means a cell that has been transformed, or is capable of being transformed, with a nucleic acid and thereby expresses a gene of

interest. The term includes the progeny of the parent cell, whether or not the progeny is identical in morphology or in genetic make-up to the original parent cell, so long as the gene of interest is present. Any of a large number of available and well-known host cells may be used in the practice of this invention. The selection of a particular host is dependent upon a number of factors recognized by the art. These include, for example, compatibility with the chosen expression vector, toxicity of the peptides encoded by the DNA molecule, rate of transformation, ease of recovery of the peptides, expression characteristics, bio-safety and costs. A balance of these factors must be struck with the understanding that not all hosts may be equally effective for the expression of a particular DNA sequence. Within these general guidelines, useful microbial host cells in culture include bacteria (such as *Escherichia coli* sp.), yeast (such as *Saccharomyces* sp.) and other fungal cells, insect cells, plant cells, mammalian (including human) cells, e.g., CHO cells and HEK-293 cells. Modifications can be made at the DNA level, as well. The peptide-encoding DNA sequence may be changed to codons more compatible with the chosen host cell. For *E. coli*, optimized codons are known in the art. Codons can be substituted to eliminate restriction sites or to include silent restriction sites, which may aid in processing of the DNA in the selected host cell. Next, the transformed host is cultured and purified. Host cells may be cultured under conventional fermentation conditions so that the desired compounds are expressed. Such fermentation conditions are well known in the art.

[00185] The term "transfection" means the uptake of foreign or exogenous DNA by a cell, and a cell has been "transfected" when the exogenous DNA has been introduced inside the cell membrane. A number of transfection techniques are well known in the art and are disclosed herein. See, e.g., Graham et al., 1973, Virology 52:456; Sambrook et al., 2001, Molecular Cloning: A Laboratory Manual, supra; Davis et al., 1986, Basic Methods in Molecular Biology, Elsevier; Chu et al., 1981, Gene 13:197. Such techniques can be used to introduce one or more exogenous DNA moieties into suitable host cells.

[00186] The term "transformation" refers to a change in a cell's genetic characteristics, and a cell has been transformed when it has been modified to contain new DNA or RNA. For example, a cell is transformed where it is genetically modified from its native state by introducing new genetic material via transfection, transduction,

or other techniques. Following transfection or transduction, the transforming DNA may recombine with that of the cell by physically integrating into a chromosome of the cell, or may be maintained transiently as an episomal element without being replicated, or may replicate independently as a plasmid. A cell is considered to have been "stably transformed" when the transforming DNA is replicated with the division of the cell.

[00187] The term "transgene" refers to an isolated nucleotide sequence, originating in a different species from the host, that may be inserted into one or more cells of a mammal or mammalian embryo. The transgene optionally may be operably linked to other genetic elements (such as a promoter, poly A sequence and the like) that may serve to modulate, either directly, or indirectly in conjunction with the cellular machinery, the transcription and/or expression of the transgene. Alternatively or additionally, the transgene may be linked to nucleotide sequences that aid in integration of the transgene into the chromosomal DNA of the mammalian cell or embryo nucleus (as for example, in homologous recombination). The transgene may be comprised of a nucleotide sequence that is either homologous or heterologous to a particular nucleotide sequence in the mammal's endogenous genetic material, or is a hybrid sequence (i.e. one or more portions of the transgene are homologous, and one or more portions are heterologous to the mammal's genetic material). The transgene nucleotide sequence may encode a polypeptide or a variant of a polypeptide, found endogenously in the mammal, it may encode a polypeptide not naturally occurring in the mammal (i.e. an exogenous polypeptide), or it may encode a hybrid of endogenous and exogenous polypeptides. Where the transgene is operably linked to a promoter, the promoter may be homologous or heterologous to the mammal and/or to the transgene. Alternatively, the promoter may be a hybrid of endogenous and exogenous promoter elements (enhancers, silencers, suppressors, and the like).

[00188] Peptides. Recombinant DNA- and/or RNA-mediated protein expression and protein engineering techniques, or any other methods of preparing peptides, are applicable to the making of the inventive polypeptides, e.g., toxin peptide analogs and fusion protein conjugates thereof (e.g., fusion proteins containing a toxin peptide analog and an immunoglobulin Fc domain, transthyretin, or human serum albumin). For example, the peptides can be made in transformed host cells. Briefly, a recombinant DNA molecule, or construct, coding for the peptide is prepared. Methods of preparing

such DNA molecules are well known in the art. For instance, sequences encoding the peptides can be excised from DNA using suitable restriction enzymes. Any of a large number of available and well-known host cells may be used in the practice of this invention. The selection of a particular host is dependent upon a number of factors recognized by the art. These include, for example, compatibility with the chosen expression vector, toxicity of the peptides encoded by the DNA molecule, rate of transformation, ease of recovery of the peptides, expression characteristics, bio-safety and costs. A balance of these factors must be struck with the understanding that not all hosts may be equally effective for the expression of a particular DNA sequence. Within these general guidelines, useful microbial host cells in culture include bacteria (such as *Escherichia coli* sp.), yeast (such as *Saccharomyces* sp.) and other fungal cells, insect cells, plant cells, mammalian (including human) cells, e.g., CHO cells and HEK293 cells. Modifications can be made at the DNA level, as well. The peptide-encoding DNA sequence may be changed to codons more compatible with the chosen host cell. For E. coli, optimized codons are known in the art. Codons can be substituted to eliminate restriction sites or to include silent restriction sites, which may aid in processing of the DNA in the selected host cell. Next, the transformed host is cultured and purified. Host cells may be cultured under conventional fermentation conditions so that the desired compounds are expressed. Such fermentation conditions are well known in the art. In addition, the DNA optionally further encodes, 5' to the coding region of a fusion protein, a signal peptide sequence (e.g., a secretory signal peptide) operably linked to the expressed toxin peptide analog. For further examples of appropriate recombinant methods and exemplary DNA constructs useful for recombinant expression of the inventive compositions by mammalian cells, including dimeric Fc fusion proteins ("peptibodies") or chimeric immunoglobulin(light chain + heavy chain)-Fc heterotrimers ("hemibodies"), conjugated to pharmacologically active toxin peptide analogs of the invention, see, e.g., Sullivan et al., Toxin Peptide Therapeutic Agents, US2007/0071764 and Sullivan et al., Toxin Peptide Therapeutic Agents, PCT/US2007/022831, published as WO 2008/088422, which are both incorporated herein by reference in their entireties.

[00189] Peptide compositions of the present invention can also be made by synthetic methods. Solid phase synthesis is the preferred technique of making

individual peptides since it is the most cost-effective method of making small peptides. For example, well known solid phase synthesis techniques include the use of protecting groups, linkers, and solid phase supports, as well as specific protection and deprotection reaction conditions, linker cleavage conditions, use of scavengers, and other aspects of solid phase peptide synthesis. Suitable techniques are well known in the art. (E.g., Merrifield (1973), Chem. Polypeptides, pp. 335-61 (Katsoyannis and Panayotis eds.); Merrifield (1963), J. Am. Chem. Soc. 85: 2149; Davis et al. (1985), Biochem. Intl. 10: 394-414; Stewart and Young (1969), Solid Phase Peptide Synthesis; U.S. Pat. No. 3,941,763; Finn et al. (1976), The Proteins (3rd ed.) 2: 105-253; and Erickson et al. (1976), The Proteins (3rd ed.) 2: 257-527; "Protecting Groups in Organic Synthesis," 3rd Edition, T. W. Greene and P. G. M. Wuts, Eds., John Wiley & Sons, Inc., 1999; NovaBiochem Catalog, 2000; "Synthetic Peptides, A User's Guide," G. A. Grant, Ed., W.H. Freeman & Company, New York, N.Y., 1992; "Advanced Chemtech Handbook of Combinatorial & Solid Phase Organic Chemistry," W. D. Bennet, J. W. Christensen, L. K. Hamaker, M. L. Peterson, M. R. Rhodes, and H. H. Saneii, Eds., Advanced Chemtech, 1998; "Principles of Peptide Synthesis, 2nd ed.," M. Bodanszky, Ed., Springer-Verlag, 1993; "The Practice of Peptide Synthesis, 2nd ed.," M. Bodanszky and A. Bodanszky, Eds., Springer-Verlag, 1994; "Protecting Groups," P. J. Kocienski, Ed., Georg Thieme Verlag, Stuttgart, Germany, 1994; "Fmoc Solid Phase Peptide Synthesis, A Practical Approach," W. C. Chan and P. D. White, Eds., Oxford Press, 2000, G. B. Fields et al., Synthetic Peptides: A User's Guide, 1990, 77-183). For further examples of synthetic and purification methods known in the art, which are applicable to making the inventive compositions of matter, see, e.g., Sullivan et al., Toxin Peptide Therapeutic Agents, US2007/0071764 and Sullivan et al., Toxin Peptide Therapeutic Agents, PCT/US2007/022831, published as WO 2008/088422 A2, which are both incorporated herein by reference in their entireties.

[00190] In further describing the toxin peptide analogs herein, a one-letter abbreviation system is frequently applied to designate the identities of the twenty "canonical" amino acid residues generally incorporated into naturally occurring peptides and proteins (Table 2). Such one-letter abbreviations are entirely interchangeable in meaning with three-letter abbreviations, or non-abbreviated amino acid names. Within the one-letter abbreviation system used herein, an upper case letter

indicates a L-amino acid, and a lower case letter indicates a D-amino acid. For example, the abbreviation "R" designates L-arginine and the abbreviation "r" designates D-arginine.

Table 2. One-letter abbreviations for the canonical amino acids.
Three-letter abbreviations are in parentheses.

Alanine (Ala)	A
Glutamine (Gln)	Q
Leucine (Leu)	L
Serine (Ser)	S
Arginine (Arg)	R
Glutamic Acid (Glu)	E
Lysine (Lys)	K
Threonine (Thr)	T
Asparagine (Asn)	N
Glycine (Gly)	G
Methionine (Met)	M
Tryptophan (Trp)	W
Aspartic Acid (Asp)	D
Histidine (His)	H
Phenylalanine (Phe)	F
Tyrosine (Tyr)	Y
Cysteine (Cys)	C
Isoleucine (Ile)	I
Proline (Pro)	P
Valine (Val)	V

[00191] An amino acid substitution in an amino acid sequence is typically designated herein with a one-letter abbreviation for the amino acid residue in a particular position, followed by the numerical amino acid position relative to a native sequence of interest, which is then followed by the one-letter symbol for the amino acid residue substituted in. For example, "T30D" symbolizes a substitution of a threonine

residue by an aspartate residue at amino acid position 30, relative to the native sequence of interest.

[00192] Non-canonical amino acid residues can be incorporated into a peptide within the scope of the invention by employing known techniques of protein engineering that use recombinantly expressing cells. (See, e.g., Link et al., Non-canonical amino acids in protein engineering, Current Opinion in Biotechnology, 14(6):603-609 (2003)). The term "non-canonical amino acid residue" refers to amino acid residues in D- or L-form that are not among the 20 canonical amino acids generally incorporated into naturally occurring proteins, for example, β-amino acids, homoamino acids, cyclic amino acids and amino acids with derivatized side chains. Examples include (in the L-form or D-form) β-alanine, β-aminopropionic acid, piperidinic acid, aminocaprioic acid, aminoheptanoic acid, aminopimelic acid, desmosine, diaminopimelic acid, N^{α}-ethylglycine, N^{α}-ethylaspargine, hydroxylysine, allo-hydroxylysine, isodesmosine, allo-isoleucine, ω-methylarginine, N^{α}-methylglycine, N^{α}-methylisoleucine, N^{α}-methylvaline, , γ-carboxyglutamate, ε-N,N,N-trimethyllysine, ε-N-acetyllysine, O-phosphoserine, N^{α}-acetylserine, N^{α}-formylmethionine, 3-methylhistidine, 5-hydroxylysine, and other similar amino acids, and those listed in Table 3 below, and derivatized forms of any of these as described herein. Table 3 contains some exemplary non-canonical amino acid residues that are useful in accordance with the present invention and associated abbreviations as typically used herein, although the skilled practitioner will understand that different abbreviations and nomenclatures may be applicable to the same substance and appear interchangeably herein. Some amino acid sequences, as recited herein may include "{H}-" at the N-terminal, which represents an N-terminal amino group, and/or may include "-{Free Acid}" at the C-terminal, which represents a C-terminal carboxy group.

Table 3. Useful non-canonical amino acids for amino acid addition, insertion, or substitution into peptide sequences in accordance with the present invention. In the event an abbreviation listed in Table 3 differs from another abbreviation for the same substance disclosed elsewhere herein, both abbreviations are understood to be applicable. The amino acids listed in Table 3 can be in the L-form or D-form, unless otherwise noted.

Amino Acid	Abbreviation(s)
Acetamidomethyl	Acm
Acetylarginine	acetylarg
α-aminoadipic acid	Aad
aminobutyric acid	Abu
2-aminobutyric acid	2-Abu
6-aminohexanoic acid	Ahx; εAhx
3-amino-6-hydroxy-2-piperidone	Ahp
2-aminoindane-2-carboxylic acid	Aic
α-amino-isobutyric acid	Aib
3-amino-2-naphthoic acid	Anc
2-aminotetraline-2-carboxylic acid	Atc
Aminophenylalanine	Aminophe; Amino-Phe
4-amino-phenylalanine (also known as para-aminophenylalanine)	4AmP; 4-AminoF; 4-Amino-Phe
4-amidino-phenylalanine	4AmPhe
2-amino-2-(1-carbamimidoylpiperidin-4-yl)acetic acid	4AmPig
ω-N-methylarginine	R(Me)
Arg ψ(CH_2NH) -reduced amide bond	rArg
3-(1,2,3-triazol-4-yl)Alanine	Atz
(S)-2-amino-3-(1-(1-bromo-2-oxo-6,9,12-trioxa-3-azatetradecan-14-yl)-1H-1,2,3-triazol-4-yl)propanoic acid	Atz(PEG3-bromoacetamide)
3-(1-(O-(aminoethyl)-O'-(ethylene)-decaethyleneglycol)-1,2,3-triazol-4-	Atz(amino-PEG10)

yl)Alanine	
3-(1-(O-(aminoethyl)-O'-(ethylene)-ethyleneglycol450avg)-1,2,3-triazol-4-yl)Alanine	Atz(20kDa PEG)
(S)-2-amino-3-(1-(2-oxo-6,9,12,15,18,21,24,27,30,33,36-undecaoxa-3-azaoctatriacontan-38-yl)-1H-1,2,3-triazol-4-yl)propanoic acid	Atz(PEG11-(acetamidomethyl)
(S)-2-amino-3-(1-(1-hydroxy-5-oxo-9,12,15,18,21,24,27,30,33,36,39-undecaoxa-3-thia-6-azahentetracontan-41-yl)-1H-1,2,3-triazol-4-yl)propanoic acid	Atz(PEG11-((2-hydroxyethyl)thio)acetamide)
(S)-2-amino-3-(1-(1-bromo-2-oxo-6,9,12,15,18,21,24,27,30,33,36-undecaoxa-3-azaoctatriacontan-38-yl)-1H-1,2,3-triazol-4-yl)propanoic acid	Atz(PEG11-bromoacetamide)
(S)-2-amino-6-(3-(1-(1-bromo-2-oxo-6,9,12,15,18,21,24,27,30,33,36-undecaoxa-3-azaoctatriacontan-38-yl)-1H-1,2,3-triazol-4-yl)propanamido)hexanoic acid	K(ethyl-triazole-PEG11-bromoacetamide)
β-alanine	bA
β-homoarginine	bhArg
β-homolysine	bhomoK
β-homo Tic	BhTic
β-homophenylalanine	BhPhe
β-homoproline	BhPro
β-homotryptophan	BhTrp
4,4'-biphenylalanine; 4-phenyl-phenylalanine ; or biphenylalanine	Bip; 4Bip

β, β-diphenyl-alanine	BiPhA
β-phenylalanine	BPhe
p-carboxyl-phenylalanine	Cpa
Citrulline	Cit
Cyclohexylalanine	Cha
Cyclohexylglycine	Chg
Cyclopentylglycine	Cpg
4-tert-butyl-L-phenylalanine	4tBu-F
4-benzoyl-L-phenylalanine	4-Bz-F
2-chloro-L-phenylalanine	2-Cl-F
4-trifluoromethyl-L-phenylalanine	4CF3-F
4-fluoro-L-phenylalanine	4-F-F
4-methyl-L-phenylalanine	4-Me-F
2-amino-3-guanidinopropanoic acid	3G-Dpr
α, γ-diaminobutyric acid	Dab
2,4-diaminobutyric acid	Dbu
diaminopropionic acid	Dap
3,4-dichloro-L-phenylalanine	DiCl-F
3,4-dimethoxy-L-phenylalanine	DiMeO-F
α, β-diaminopropionoic acid (or 2,3-diaminopropionic acid	Dpr
3,3-diphenylalanine	Dip
4-guanidino phenylalanine	Guf
4-guanidino proline	4GuaPr
Homoarginine	hArg; hR
Homocitrulline	hCit
Homoglutamine	hQ
Homoleucine	hLeu; hL
Homolysine	hLys; hK; homoLys
Homophenylalanine	hPhe; homoPhe
4-hydroxyproline (or hydroxyproline)	Hyp
2-indanylglycine (or indanylglycine)	Igl
indoline-2-carboxylic acid	Idc
Iodotyrosine	I-Tyr

Lys ψ(CH_2NH)-reduced amide bond	rLys
(S)-6-((S)-2-acetamidopent-4-ynamido)-2-aminohexanoic acid	K(Ac-Pra)
N-ε-biotinyl-L-lysine	K(Biotin)
(S)-2,2',2''-(10-(2-((5-amino-5-carboxypentyl)amino)-2-oxoethyl)-1,4,7,10-tetraazacyclododecane-1,4,7-triyl)triacetic acid	K(DOTA)
(S)-2-amino-6-(pent-4-ynamido)hexanoic acid	K(4-Pen)
methionine oxide	Met[O]
methionine sulfone	Met[$O]_2$
N^{α}-methylarginine	NMeR
Nα-[$(CH_2)_3NHCH(NH)NH_2$] substituted glycine	N-Arg
N^{α}-methylcitrulline	NMeCit
N^{α}-methylglutamine	NMeQ
N^{α}-methylhomocitrulline	N $^{\alpha}$-MeHoCit
N^{α}-methylhomolysine	NMeHoK
N^{α}-methylleucine	N$^{\alpha}$-MeL; NMeL; NMeLeu; NMe-Leu
N^{α}-methyllysine	NMe-Lys
Nε-methyl-lysine	N-eMe-K
Nε-ethyl-lysine	N-eEt-K
Nε-isopropyl-lysine	N-eIPr-K
N^{α}-methylnorleucine	NMeNle; NMe-Nle
N^{α}-methylornithine	N $^{\alpha}$-MeOrn; NMeOrn
N^{α}-methylphenylalanine	NMe-Phe
1'N-methyltryptophan	1'NMeW
4-methyl-phenylalanine	MePhe
α-methylphenyalanine	AMeF
N^{α}-methylthreonine	NMe-Thr; NMeThr

N^{α}-methylvaline	NMeVal; NMe-Val
Nε-(O-(aminoethyl)-O'-(2-propanoyl)-undecaethyleneglycol)-Lysine	K(NPeg11)
Nε-(O-(aminoethyl)-O'-(2-propanoyl)-(ethyleneglycol)27-Lysine	K(NPeg27)
3-(1-naphthyl)alanine	1-Nal; 1Nal
3-(2-naphthyl)alanine	2-Nal; 2Nal
nipecotic acid	Nip
Nitrophenylalanine	nitrophe
norleucine	Nle
norvaline	Nva or Nvl
O-methyltyrosine	Ome-Tyr
(S)-octylglycine	OctylG
octahydroindole-2-carboxylic acid	Oic
Ornithine	Orn
Orn ψ(CH2NH)-reduced amide bond	rOrn
pyroglutamic acid	pGlu; PE; pE
L-phosphoserine	pS
4-piperidinylalanine	4PipA
4-pyridinylalanine	4Pal
3-pyridinylalanine	3Pal
2-pyridinylalanine	2Pal
para-iodophenylalanine (or 4-iodophenylalanine)	pI-Phe
Phenylglycine	Phg
Propargylglycine	Pra
pipecolic acid	Pip
4-amino-1-piperidine-4-carboxylic acid	4Pip
Sarcosine	Sar
1,2,3,4-tetrahydroisoquinoline	Tic
1,2,3,4-tetrahydroisoquinoline-1-carboxylic acid	Tiq
1,2,3,4-tetrahydroisoquinoline-7-	Hydroxyl-Tic

hydroxy-3-carboxylic acid	
1,2,3,4-tetrahydronorharman-3-carboxylic acid	Tpi
thiazolidine-4-carboxylic acid	Thz
3-thienylalanine	Thi
(S)-tert-butylglycine	Tlc
symmetrical N'-ω-dimethyl arginine	SDMA
N-ε-dimethyl lysine	K(Me2)
4-carboxyphenylalanine	4CO2-F

[00193] Nomenclature and Symbolism for Amino Acids and Peptides by the UPAC-IUB Joint Commission on Biochemical Nomenclature (JCBN) have been published in the following documents: Biochem. J., 1984, 219, 345-373; Eur. J. Biochem., 1984, 138, 9-37; 1985, 152, 1; 1993, 213, 2; Internat. J. Pept. Prot. Res., 1984, 24, following p 84; J. Biol. Chem., 1985, 260, 14-42; Pure Appl. Chem., 1984, 56, 595-624; Amino Acids and Peptides, 1985, 16, 387-410; Biochemical Nomenclature and Related Documents, 2nd edition, Portland Press, 1992, pages 39-69.

[00194] The one or more useful modifications to peptide domains of the inventive compositions can include amino acid additions or insertions, amino acid deletions, peptide truncations, amino acid substitutions, and/or chemical derivatization of amino acid residues, accomplished by known chemical techniques. For example, the thusly modified amino acid sequence includes at least one amino acid residue inserted or substituted therein, relative to the amino acid sequence of the native sequence of interest, in which the inserted or substituted amino acid residue has a side chain comprising a nucleophilic or electrophilic reactive functional group by which the peptide is covalently conjugated to a linker and/or half-life extending moiety. In accordance with the invention, useful examples of such a nucleophilic or electrophilic reactive functional group include, but are not limited to, a thiol, a primary amine, a seleno, a hydrazide, an aldehyde, a carboxylic acid, a ketone, an aminooxy, a masked (protected) aldehyde, or a masked (protected) keto functional group. Examples of amino acid residues having a side chain comprising a nucleophilic reactive functional group include, but are not limited to, a lysine residue, a homolysine, an α,β-

diaminopropionic acid residue, an α,γ-diaminobutyric acid residue, an ornithine residue, a cysteine, a homocysteine, a glutamic acid residue, an aspartic acid residue, or a selenocysteine ("SeCys") residue.

[00195] Amino acid residues are commonly categorized according to different chemical and/or physical characteristics. The term "acidic amino acid residue" refers to amino acid residues in D- or L-form having side chains comprising acidic groups. Exemplary acidic residues include aspartic acid and glutamic acid residues. The term "alkyl amino acid residue" refers to amino acid residues in D- or L-form having C_{1-6}alkyl side chains which may be linear, branched, or cyclized, including to the amino acid amine as in proline, wherein the C_{1-6}alkyl is substituted by 0, 1, 2 or 3 substituents selected from C_{1-4}haloalkyl, halo, cyano, nitro, $-C(=O)R^b$, $-C(=O)OR^a$, $-C(=O)NR^aR^a$, $-C(=NR^a)NR^aR^a$, $-NR^aC(=NR^a)NR^aR^a$, $-OR^a$, $-OC(=O)R^b$, $-OC(=O)NR^aR^a$, $-OC_{2-6}$alkylNR^aR^a, $-OC_{2-6}$alkylOR^a, $-SR^a$, $-S(=O)R^b$, $-S(=O)_2R^b$, $-S(=O)_2NR^aR^a$, $-NR^aR^a$, $-N(R^a)C(=O)R^b$, $-N(R^a)C(=O)OR^b$, $-N(R^a)C(=O)NR^aR^a$, $-N(R^a)C(=NR^a)NR^aR^a$, $-N(R^a)S(=O)_2R^b$, $-N(R^a)S(=O)_2NR^aR^a$, $-NR^aC_{2-6}$alkylNR^aR^a and $-NR^aC_{2-6}$alkylOR^a; wherein R^a is independently, at each instance, H or R^b; and R^b is independently, at each instance C_{1-6}alkyl substituted by 0, 1, 2 or 3 substituents selected from halo, C_{1-4}alk, C_{1-3}haloalk, $-OC_{1-4}$alk, $-NH_2$, $-NHC_{1-4}$alk, and $-N(C_{1-4}alk)C_{1-4}$alk; or any protonated form thereof, including alanine, valine, leucine, isoleucine, proline, serine, threonine, lysine, arginine, histidine, aspartate, glutamate, asparagine, glutamine, cysteine, methionine, hydroxyproline, cyclohexylalanine, norleucine, norvaline, 2-aminobutyric acid, but which residues do not contain an aryl or aromatic group. The term "aromatic amino acid residue" refers to amino acid residues in D- or L-form having side chains comprising aromatic groups. Exemplary aromatic residues include tryptophan, tyrosine, 3-(1-naphthyl)alanine, histidine, or phenylalanine residues. The term "basic amino acid residue" refers to amino acid residues in D- or L-form having side chains comprising basic groups. Exemplary basic amino acid residues include histidine, lysine, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, and homoarginine (hR) residues. The term "hydrophilic amino acid residue" refers to amino acid residues in D- or L-form having side chains comprising polar groups. Exemplary hydrophilic residues include cysteine, serine, threonine, histidine, lysine, asparagine, aspartate, glutamate,

glutamine, and citrulline (Cit) residues. The terms "lipophilic amino acid residue" refers to amino acid residues in D- or L-form having sidechains comprising uncharged, aliphatic or aromatic groups. Exemplary lipophilic sidechains include phenylalanine, isoleucine, leucine, methionine, valine, tryptophan, and tyrosine. Alanine (A) is amphiphilic—it is capable of acting as a hydrophilic, or lipophilic (i.e., hydrophobic), residue. Alanine, therefore, is included within the definition of both "lipophilic" (i.e., "hydrophobic") residue and "hydrophilic" residue. The term "nonfunctional" or "neutral" amino acid residue refers to amino acid residues in D- or L-form having side chains that lack acidic, basic, or aromatic groups. Exemplary neutral amino acid residues include methionine, glycine, alanine, valine, isoleucine, leucine, and norleucine (Nle) residues.

[00196] Additional useful embodiments of toxin peptide analogs can result from conservative modifications of the amino acid sequences of the toxin polypeptides disclosed herein. Conservative modifications will produce half-life extending moiety-conjugated peptides having functional, physical, and chemical characteristics similar to those of the conjugated (e.g., PEG-conjugated) peptide from which such modifications are made. Such conservatively modified forms of the conjugated toxin peptide analogs disclosed herein are also contemplated as being an embodiment of the present invention.

[00197] In contrast, substantial modifications in the functional and/or chemical characteristics of peptides may be accomplished by selecting substitutions in the amino acid sequence that differ significantly in their effect on maintaining (a) the structure of the molecular backbone in the region of the substitution, for example, as an α-helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the size of the molecule.

[00198] For example, a "conservative amino acid substitution" may involve a substitution of a native amino acid residue with a nonnative residue such that there is little or no effect on the polarity or charge of the amino acid residue at that position. Furthermore, any native residue in the polypeptide may also be substituted with alanine, as has been previously described for "alanine scanning mutagenesis" (see, for example, MacLennan et al., Acta Physiol. Scand. Suppl., 643:55-67 (1998); Sasaki et al., 1998, Adv. Biophys. 35:1-24 (1998), which discuss alanine scanning mutagenesis).

[00199] In some useful embodiments of the compositions of the invention, the amino acid sequence of the toxin peptide is modified in one or more ways relative to a native toxin peptide sequence of interest, such as, but not limited to, a native GpTx-1 sequence (SEQ ID NO:1), a peptide analog of GpTx-1, or any other toxin peptides having amino acid sequences as set for in Table 5A, Table 5B, and Table 31, or elsewhere herein. The one or more useful modifications can include amino acid additions or insertions, amino acid deletions, peptide truncations, amino acid substitutions, and/or chemical derivatization of amino acid residues, accomplished by known chemical techniques. Such modifications can be, for example, for the purpose of enhanced potency, selectivity, and/or proteolytic stability, or the like. Those skilled in the art are aware of techniques for designing peptide analogs with such enhanced properties, such as alanine scanning, rational design based on alignment mediated mutagenesis using known toxin peptide sequences and/or molecular modeling.

[00200] The term "protease" is synonymous with "peptidase". Proteases comprise two groups of enzymes: the endopeptidases which cleave peptide bonds at points within the protein, and the exopeptidases, which remove one or more amino acids from either N- or C-terminus respectively. The term "proteinase" is also used as a synonym for endopeptidase. The four mechanistic classes of proteinases are: serine proteinases, cysteine proteinases, aspartic proteinases, and metallo-proteinases. In addition to these four mechanistic classes, there is a section of the enzyme nomenclature which is allocated for proteases of unidentified catalytic mechanism. This indicates that the catalytic mechanism has not been identified.

[00201] Cleavage subsite nomenclature is commonly adopted from a scheme created by Schechter and Berger (Schechter I. & Berger A., On the size of the active site in proteases. I. Papain, Biochemical and Biophysical Research Communication, 27:157 (1967); Schechter I. & Berger A., On the active site of proteases. 3. Mapping the active site of papain; specific inhibitor peptides of papain, Biochemical and Biophysical Research Communication, 32:898 (1968)). According to this model, amino acid residues in a substrate undergoing cleavage are designated P1, P2, P3, P4 etc. in the N-terminal direction from the cleaved bond. Likewise, the residues in the C-terminal direction are designated P1', P2', P3', P4', etc.

[00202] The skilled artisan is aware of a variety of tools for identifying protease binding or protease cleavage sites of interest. For example, the PeptideCutter software tool is available through the ExPASy (Expert Protein Analysis System) proteomics server of the Swiss Institute of Bioinformatics (SIB; www.expasy.org/tools/peptidecutter). PeptideCutter searches a protein sequence from the SWISS-PROT and/or TrEMBL databases or a user-entered protein sequence for protease cleavage sites. Single proteases and chemicals, a selection or the whole list of proteases and chemicals can be used. Different forms of output of the results are available: tables of cleavage sites either grouped alphabetically according to enzyme names or sequentially according to the amino acid number. A third option for output is a map of cleavage sites. The sequence and the cleavage sites mapped onto it are grouped in blocks, the size of which can be chosen by the user. Other tools are also known for determining protease cleavage sites. (E.g., Turk, B. et al., Determination of protease cleavage site motifs using mixture-based oriented peptide libraries, Nature Biotechnology, 19:661-667 (2001); Barrett A. et al., Handbook of proteolytic enzymes, Academic Press (1998)).

[00203] The serine proteinases include the chymotrypsin family, which includes mammalian protease enzymes such as chymotrypsin, trypsin or elastase or kallikrein. The serine proteinases exhibit different substrate specificities, which are related to amino acid substitutions in the various enzyme subsites interacting with the substrate residues. Some enzymes have an extended interaction site with the substrate whereas others have a specificity restricted to the P1 substrate residue.

[00204] Trypsin preferentially cleaves at R or K in position P1. A statistical study carried out by Keil (1992) described the negative influences of residues surrounding the Arg- and Lys- bonds (i.e. the positions P2 and P1', respectively) during trypsin cleavage. (Keil, B., Specificity of proteolysis, Springer-Verlag Berlin-Heidelberg-NewYork, 335 (1992)). A proline residue in position P1' normally exerts a strong negative influence on trypsin cleavage. Similarly, the positioning of R and K in P1' results in an inhibition, as well as negatively charged residues in positions P2 and P1'.

[00205] Chymotrypsin preferentially cleaves at a W, Y or F in position P1 (high specificity) and to a lesser extent at L, M or H residue in position P1. (Keil, 1992).

Exceptions to these rules are the following: When W is found in position P1, the cleavage is blocked when M or P are found in position P1' at the same time. Furthermore, a proline residue in position P1' nearly fully blocks the cleavage independent of the amino acids found in position P1. When an M residue is found in position P1, the cleavage is blocked by the presence of a Y residue in position P1'. Finally, when H is located in position P1, the presence of a D, M or W residue also blocks the cleavage.

[00206] Membrane metallo-endopeptidase (NEP; neutral endopeptidase, kidney-brush-border neutral proteinase, enkephalinase, EC 3.4.24.11) cleaves peptides at the amino side of hydrophobic amino acid residues. (Connelly, JC et al., Neutral Endopeptidase 24.11 in Human Neutrophils: Cleavage of Chemotactic Peptide, PNAS, 82(24):8737-8741 (1985)).

[00207] Thrombin preferentially cleaves at an R residue in position P1. (Keil, 1992). The natural substrate of thrombin is fibrinogen. Optimum cleavage sites are when an R residue is in position P1 and Gly is in position P2 and position P1'. Likewise, when hydrophobic amino acid residues are found in position P4 and position P3, a proline residue in position P2, an R residue in position P1, and non-acidic amino acid residues in position P1' and position P2'. A very important residue for its natural substrate fibrinogen is a D residue in P10.

[00208] Caspases are a family of cysteine proteases bearing an active site with a conserved amino acid sequence and which cleave peptides specifically following D residues. (Earnshaw WC et al., Mammalian caspases: Structure, activation, substrates, and functions during apoptosis, Annual Review of Biochemistry, 68:383-424 (1999)).

[00209] The Arg-C proteinase preferentially cleaves at an R residue in position P1. The cleavage behavior seems to be only moderately affected by residues in position P1'. (Keil, 1992). The Asp-N endopeptidase cleaves specifically bonds with a D residue in position P1'. (Keil, 1992).

[00210] The foregoing is merely exemplary and by no means an exhaustive treatment of knowledge available to the skilled artisan concerning protease binding and/or cleavage sites that the skilled artisan may be interested in eliminating in practicing the invention.

[00211] Desired amino acid substitutions (whether conservative or non-conservative) can be determined by those skilled in the art at the time such substitutions are desired. For example, amino acid substitutions can be used to identify important residues of the peptide sequence, or to increase or decrease the affinity of the peptide or vehicle-conjugated peptide molecules described herein.

[00212] Naturally occurring residues may be divided into classes based on common side chain properties:

1) hydrophobic: norleucine (Nor or Nle), Met, Ala, Val, Leu, Ile;
2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln;
3) acidic: Asp, Glu;
4) basic: His, Lys, Arg;
5) residues that influence chain orientation: Gly, Pro; and
6) aromatic: Trp, Tyr, Phe.

[00213] Conservative amino acid substitutions may involve exchange of a member of one of these classes with another member of the same class. Conservative amino acid substitutions may encompass non-naturally occurring amino acid residues, which are typically incorporated by chemical peptide synthesis rather than by synthesis in biological systems. These include peptidomimetics and other reversed or inverted forms of amino acid moieties.

[00214] Non-conservative substitutions may involve the exchange of a member of one of these classes for a member from another class. Such substituted residues may be introduced into regions of the toxin peptide analog.

[00215] In making such changes, according to certain embodiments, the hydropathic index of amino acids may be considered. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics. They are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

[00216] The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is understood in the art (see, *for example*,

Kyte *et al.*, 1982, *J. Mol. Biol.* 157:105-131). It is known that certain amino acids may be substituted for other amino acids having a similar hydropathic index or score and still retain a similar biological activity. In making changes based upon the hydropathic index, in certain embodiments, the substitution of amino acids whose hydropathic indices are within ±2 is included. In certain embodiments, those that are within ±1 are included, and in certain embodiments, those within ±0.5 are included.

[00217] It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity, particularly where the biologically functional protein or peptide thereby created is intended for use in immunological embodiments, as disclosed herein. In certain embodiments, the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, *i.e.*, with a biological property of the protein.

[00218] The following hydrophilicity values have been assigned to these amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 ± 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5) and tryptophan (-3.4). In making changes based upon similar hydrophilicity values, in certain embodiments, the substitution of amino acids whose hydrophilicity values are within ±2 is included, in certain embodiments, those that are within ±1 are included, and in certain embodiments, those within ±0.5 are included. One may also identify epitopes from primary amino acid sequences on the basis of hydrophilicity. These regions are also referred to as "epitopic core regions."

[00219] Examples of conservative substitutions include the substitution of one non-polar (hydrophobic) amino acid residue such as isoleucine, valine, leucine norleucine, alanine, or methionine for another, the substitution of one polar (hydrophilic) amino acid residue for another such as between arginine and lysine, between glutamine and asparagine, between glycine and serine, the substitution of one basic amino acid residue such as lysine, arginine or histidine for another, or the substitution of one acidic residue, such as aspartic acid or glutamic acid for another. The phrase "conservative amino acid substitution" also includes the use of a chemically

derivatized residue in place of a non-derivatized residue, provided that such polypeptide displays the requisite bioactivity. Other exemplary amino acid substitutions that can be useful in accordance with the present invention are set forth in Table 4 below.

Table 4. Some Useful Amino Acid Substitutions.

Original Residues	Exemplary Substitutions
Ala	Val, Leu, Ile, Gly
Arg	Lys, Gln, Asn, His
Asn	Gln
Asp	Glu
Cys	Ser, Ala
Gln	Asn
Glu	Asp
Gly	Pro, Ala
His	Asn, Gln, Lys, Arg
Ile	Leu, Val, Met, Ala, Phe, Norleucine
Leu	Norleucine, Ile, Val, Met, Ala, Phe
Lys	Arg, 1,4-Diamino-butyric Acid, Gln, Asn, His
Met	Leu, Phe, Ile
Phe	Leu, Val, Ile, Ala, Tyr
Pro	Ala
Ser	Thr, Ala, Cys
Thr	Ser
Trp	Tyr, Phe
Tyr	Trp, Phe, Thr, Ser

Val	Ile, Met, Leu, Phe, Ala, Norleucine

[00220] By way of illustration, in embodiments of the present invention directed to a composition of matter comprising an isolated polypeptide comprising the amino acid sequence of the formula:

$X_{aa}^{1}X_{aa}^{2}X_{aa}^{3}X_{aa}^{4}X_{aa}^{5}X_{aa}^{6}X_{aa}^{7}X_{aa}^{8}X_{aa}^{9}X_{aa}^{10}X_{aa}^{11}X_{aa}^{12}X_{aa}^{13}X_{aa}^{14}Asp^{15}X_{aa}^{16}X_{aa}^{17}$
$X_{aa}^{18}X_{aa}^{19}X_{aa}^{20}X_{aa}^{21}X_{aa}^{22}X_{aa}^{23}X_{aa}^{24}X_{aa}^{25}X_{aa}^{26}X_{aa}^{27}X_{aa}^{28}X_{aa}^{29}X_{aa}^{30}X_{aa}^{31}Lys^{32}$
$X_{aa}^{33}X_{aa}^{34}X_{aa}^{35}X_{aa}^{36}X_{aa}^{37}X_{aa}^{38}$ // SEQ ID NO:475

or a pharmaceutically acceptable salt thereof,

wherein:

[00221] $X_{aa}^{1}X_{aa}^{2}$ is absent; or X_{aa}^{1} is any amino acid residue and X_{aa}^{2} is any amino acid residue; or X_{aa}^{1} is absent and X_{aa}^{2} is any amino acid residue;

X_{aa}^{3} is Cys, if X_{aa}^{18} is Cys; or X_{aa}^{3} is SeCys, if X_{aa}^{18} is SeCys; or X_{aa}^{3} is an alkyl amino acid residue, if X_{aa}^{18} is an alkyl amino acid residue (for example, $X_{aa}^{3}$and X_{aa}^{18} can be, independently, Ala or 2-Abu residues);

X_{aa}^{4} is an acidic, hydrophobic, basic, or neutral hydrophilic amino acid residue (e.g., X_{aa}^{4} can be selected from Ala, Glu, Asp, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, Phe, Pro, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, cyclohexylglycine (Chg), cyclohexylalanine (Cha), glycine, norleucine, norvaline, 1-Nal, 2-Nal, 4-phenyl-phenylalanine (Bip), Gln, Asn, Ser, Thr, and Cit residues);

X_{aa}^{5} is a Gly, Ala, hydrophobic, or basic amino acid residue (e.g., X_{aa}^{5} can be selected from Ala, Phe, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, glycine, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues);

X_{aa}^{6} is a Gly, Ala, 2-Abu, norleucine (Nle), norvaline (Nva), or hydrophobic amino acid residue (e.g., X_{aa}^{6} can be selected from Ala, Phe, Ile, Leu, Met, Val, Trp, Tyr, proline,

thiaproline, methionine, glycine, 1-Nal, 2-Nal, 1'NMe-Trp, cyclopentylglycine (Cpg), phenylglycine, N-methylleucine, N-methylphenylalanine, N-methylvaline, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, and 4-phenyl-phenylalanine (Bip) residues);

X_{aa}^{7} is a Gly, Ala, aromatic, or hydrophobic amino acid residue (e.g., X_{aa}^{7} can be selected from Gly, Ala, Phe, Ile, Leu, Met, Val, Trp, Tyr, Pro, 2-pyridinylalanine, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, and 4-phenyl-phenylalanine (Bip) residues);

X_{aa}^{8} is a basic, acidic, or neutral hydrophilic amino acid residue, or an Ala residue (e.g., X_{aa}^{8} can be selected from Ala, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Ser, Thr, Asn, Gln, Cit, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, Asp, and Glu residues);

X_{aa}^{9} is a basic or neutral hydrophilic amino acid residue (e.g., X_{aa}^{9} can be selected from Ala, Pro, Met, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Gln, Asn, Ser, Thr, and Cit residues);

X_{aa}^{10} is Cys if X_{aa}^{24} is Cys; or X_{aa}^{10} is SeCys if X_{aa}^{24} is SeCys;

X_{aa}^{11} is any amino acid residue (e.g., X_{aa}^{11} can be selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues);

X_{aa}^{12} is a Pro, acidic, neutral, or hydrophobic amino acid residue (e.g., X_{aa}^{12} can be selected from alanine, valine, leucine, isoleucine, proline, serine, threonine, aspartic acid, glutamatic acid, glycine, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, Cha,

and 4-phenyl-phenylalanine (Bip), cyclohexylglycine (Chg), cyclohexylalanine (Cha), asparagine, glutamine, methionine, hydroxyproline, phenylalanine, tryptophan, and tyrosine);

X_{aa}^{13} is any amino acid residue (e.g., X_{aa}^{13} can be selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues);

X_{aa}^{14} is any amino acid residue (e.g., X_{aa}^{14} can be selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues);

X_{aa}^{16} is a basic, neutral hydrophilic, or acidic amino acid residue, or an Ala residue (e.g., X_{aa}^{16} can be selected from Ala, Pro, Met, Arg, Lys, His, Pra, Atz, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Gln, Asn, Ser, Thr, Cit, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, Asp, and Glu residues);

X_{aa}^{17} is a Cys if X_{aa}^{31} is Cys; or X_{aa}^{17} is a SeCys if X_{aa}^{31} is SeCys;

X_{aa}^{18} is a Cys, SeCys, or an alkyl amino acid residue;

X_{aa}^{19} is any amino acid residue (e.g., X_{aa}^{19} can be selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues);

X_{aa}^{20} is a Pro, Gly, basic, or neutral hydrophilic residue (e.g., X_{aa}^{20} can be selected from Ala, Pro, Met, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine,

homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Gln, Asn, Ser, Thr, and Cit residues);

X_{aa}^{21} is a basic, hydrophobic, or neutral hydrophilic amino acid residue (e.g., X_{aa}^{21} can be selected from Ala, Phe, Pro, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, cyclohexylglycine (Chg), cyclohexylalanine (Cha), glycine, norleucine, norvaline, 1-Nal, 2-Nal, 4-phenyl-phenylalanine (Bip), Gln, Asn, Ser, Thr, and Cit residues);

X_{aa}^{22} is a hydrophobic or basic amino acid residue (e.g., X_{aa}^{22} can be selected from Ala, Phe, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, glycine, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues);

X_{aa}^{23} is a hydrophobic, basic, or neutral hydrophilic amino acid residue (e.g., X_{aa}^{23} can be selected from Ala, Phe, Pro, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, Pra, Atz, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, cyclohexylglycine (Chg), cyclohexylalanine (Cha), glycine, norleucine, norvaline, 1-Nal, 2-Nal, 4-phenyl-phenylalanine (Bip), Gln, Asn, Ser, Thr, and Cit residues);

X_{aa}^{24} is a Cys or SeCys residue;

X_{aa}^{25} is a Ser, Ala, or a neutral hydrophilic amino acid residue (e.g., X_{aa}^{25} is selected from Ala, Gly, Pro, Met, glycine, Gln, Asn, Ser, Thr, and Cit residues);

X_{aa}^{26} is an Ala, acidic, basic, or neutral hydrophilic amino acid residue (e.g., X_{aa}^{26} can be selected from Ala, Pro, Met, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, glycine, Asp, Glu, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, Gln, Asn, Ser, Thr, and Cit residues);

X_{aa}^{27} is an acidic, basic, neutral hydrophilic, or hydrophobic residue (e.g., X_{aa}^{27} can be selected from Thr, Leu, Ile, Val, Ser, Met, Gln, Asn, Phe, Tyr, Trp, Arg, Lys, His,

homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Asp, Glu, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, cyclohexylglycine (Chg), cyclohexylalanine (Cha), norleucine, norvaline, 1-Nal, 2-Nal, 4-phenyl-phenylalanine (Bip), Glu, Asp, and Gly residues);

X_{aa}^{28} is an aromatic or basic amino acid residue (e.g., X_{aa}^{28} can be selected fromPhe, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, 1-Nal, 2-Nal, 2-pyridyl-alanine, 3-pyridyl-alanine, 4-pyridyl-alanine, 4-piperidinyl-alanine, and 4-phenyl-phenylalanine (Bip) residues);

X_{aa}^{29} is an acidic, basic, or neutral hydrophilic amino acid residue (e.g., X_{aa}^{29} can be selected from Ala, Asp, Glu, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, Phe, Gly, His, Lys, Asn, Pro, Gln, Arg, Ser, Thr, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, and Dab residues). In some useful embodiment X_{aa}^{29} is an acidic or neutral hydrophilic residue (e.g., an Ala, Asp, Glu, Gly, Asn, Gln, Ser, Thr, phosphoserine, phosphotyrosine, or gamma-carboxyglutamic acid residue [e.g., SEQ ID NOS: 1071-2798]);

X_{aa}^{30} is a Trp, 5-bromoTrp, 6-bromoTrp, 5-chloroTrp, 6-chloroTrp, 1-Nal, 2-Nal, or thioTrp residue;

X_{aa}^{31} is a Cys or SeCys;

X_{aa}^{33} is a hydrophobic or aromatic amino acid residue (e.g., X_{aa}^{33} can be selected from Phe, Ile, Leu, Met, Val, Trp, Tyr, norleucine, norvaline, 1-Nal, 2-Nal, 2-pyridyl-alanine, 3-pyridyl-alanine, 4-pyridyl-alanine, 4-piperidinyl-alanine, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, and 4-phenyl-phenylalanine (Bip) residues);

X_{aa}^{34} is any amino acid residue (e.g., X_{aa}^{34} can be selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine,

Dab, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, 2-pyridyl-alanine, 3-pyridyl-alanine, 4-carboxy-phenylalanine, and 4-phenyl-phenylalanine (Bip) residues);

X_{aa}^{35} is a hydrophobic amino acid residue (e.g., X_{aa}^{35} can be selected from Phe, Ile, Leu, Met, Val, Trp, Tyr, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, and 4-phenyl-phenylalanine (Bip) residues);

each of X_{aa}^{36}, X_{aa}^{37}, and X_{aa}^{38} is independently absent or is independently a neutral, basic, or hydrophobic amino acid residue (e.g., each of X_{aa}^{36}, X_{aa}^{37}, and X_{aa}^{38} can be independently absent or independently selected from Ala, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues);

and wherein:

if X_{aa}^{3} and X_{aa}^{18} are both Cys residues, there is a disulfide bond between residue X_{aa}^{3} and residue X_{aa}^{18}; or if X_{aa}^{3} and X_{aa}^{18} are both SeCys residues, there is a diselenide bond between residue X_{aa}^{3} and residue X_{aa}^{18};

if X_{aa}^{10} and X_{aa}^{24} are both Cys residues, there is a disulfide bond between residue X_{aa}^{10} and residue X_{aa}^{24}; or if X_{aa}^{10} and X_{aa}^{24} are both SeCys residues, there is a diselenide bond between residue X_{aa}^{10} and residue X_{aa}^{24};

if X_{aa}^{17} and X_{aa}^{31} are both Cys residues, there is a disulfide bond between residue X_{aa}^{17} and residue X_{aa}^{31}; or if X_{aa}^{17} and X_{aa}^{31} are both SeCys residues, there is a diselenide bond between residue X_{aa}^{17} and residue X_{aa}^{31};

the amino-terminal residue is optionally acetylated, biotinylated, 4-pentynoylated, or PEGylated; and

the carboxy-terminal residue is optionally amidated. Many particular examples of such C-terminally amidated appear in Table 5A and Table 5B.

Another example of the inventive composition described immediately above (SEQ ID NO:475) is the composition of matter wherein theisolated polypeptide comprises the amino acid sequence of the formula:

[00222] $X_{aa}^{1}X_{aa}^{2}$ Cys$^{3}X_{aa}^{4}X_{aa}^{5}$Ala$^{6}X_{aa}^{7}X_{aa}^{8}X_{aa}^{9}Cys^{10}X_{aa}^{11}X_{aa}^{12}X_{aa}^{13}X_{aa}^{14}$Asp^{15} X_{aa}^{16} Cys^{17}Cys$^{18}X_{aa}^{19}$ $X_{aa}^{20}X_{aa}^{21}X_{aa}^{22}X_{aa}^{23}$ Cys$^{24}X_{aa}^{25}$ $X_{aa}^{26}X_{aa}^{27}X_{aa}^{28}X_{aa}^{29}X_{aa}^{30}$ Cys^{31}Lys$^{32}X_{aa}^{33}X_{aa}^{34}X_{aa}^{35}$ $X_{aa}^{36}X_{aa}^{37}X_{aa}^{38}$// SEQ ID NO:476, and the variable positions of SEQ ID NO:476 are exemplified as in the immediately preceding paragraphs concerning the variable positions of SEQ ID NO:475. Particularly useful embodiments of the composition of matter comprise an Ala, Gly, 2-Abu, Nle, or Nva residue at position $X_{aa}^{6}$of SEQ ID NO:475, with some of these embodiments also having a Glu residue at position $X_{aa}^{27}$of SEQ ID NO:475, for example, [Ala5, Glu26]GpTx-1, [Gly5, Glu26]GpTx-1, [2-Abu5, Glu26]GpTx-1, [Nle5, Glu26]GpTx-1, or [Nva5, Glu26]GpTx-1 peptide analogs, which, optionally, can also have additional substituted amino acid residues at other amino acid positions and/or additional residues at the N-terminal and/or C-terminal end. Other useful examples comprise an Asp, Glu, or Gln residue at position X_{aa}^{29} of SEQ ID NO: 475 or X_{aa}^{29} of SEQ ID NO:476, with or without a Glu residue at position $X_{aa}^{27}$of SEQ ID NO:475, e.g., [Ala5, Asp28]GpTx-1, [Ala5, Glu28]GpTx-1, [Ala5, Gln28]GpTx-1, [Ala5, Glu26, Asp28]GpTx-1, [Ala5, Glu26, Glu28]GpTx-1, [Ala5, Glu26, Gln28]GpTx-1, [Gly5, Asp28]GpTx-1, [Gly5, Glu28]GpTx-1, [Gly5, Gln28]GpTx-1, [Gly5, Glu26, Asp28]GpTx-1, [Gly5, Glu26, Glu28]GpTx-1, [Gly5, Glu26, Gln28]GpTx-1, [2-Abu5, Asp28]GpTx-1, [2-Abu5, Glu28]GpTx-1, [2-Abu5, Gln28]GpTx-1, [2-Abu5, Glu26, Asp28]GpTx-1, [2-Abu5, Glu26, Glu28]GpTx-1, [2-Abu5, Glu26, Gln28]GpTx-1, [Nle5, Asp28]GpTx-1, [Nle5, Glu28]GpTx-1, [Nle5, Gln28]GpTx-1, [Nle5, Glu26, Asp28]GpTx-1, [Nle5, Glu26, Glu28]GpTx-1, and [Nle5, Glu26, Gln28]GpTx-1, [Nva5, Asp28]GpTx-1, [Nva5, Glu28]GpTx-1, [Nva5, Gln28]GpTx-1, [Nva5, Glu26, Asp28]GpTx-1, [Nva5, Glu26, Glu28]GpTx-1, and [Nva5, Glu26, Gln28]GpTx-1.

[00223] Some examples of the composition of matter comprising an amino acid sequence that comprises an Ala residue at position $X_{aa}^{6}$of SEQ ID NO:475 include: SEQ ID NOS: 22, 252-263, 419-439, 518-521, 524, 525, 562-580, 602, 691, 692, 696-703, 715, 721-735, 737-749, 756, 757, 761, 762, 764-771, 787-796, 798, 800, 802, 803, 809-812, 1028, 1030-1040, 1043-1047, 1062-1065, 1068-1070, 1082, 1096, 1110,

1124, 1135, 1146, 1157, 1165, 1173, 1181, 1192, 1203, 1214, 1222, 1230, 1238, 1249, 1260, 1271, 1279, 1287, 1295, 1306, 1317, 1328, 1336, 1344, 1352, 1360, 1368, 1376, 1384, 1392, 1400, 1408, 1416, 1424, 1432, 1440, 1448, 1456, 1464, 1472, 1480, 1488, 1496, 1504, 1512, 1520, 1528, 1536, 1544, 1552, 1560, 1568, 1576, 1584, 1592, 1600, 1608, 1616, 1624, 1632, 1640, 1658, 1672, 1686, 1700, 1711, 1722, 1733, 1741, 1749, 1757, 1768, 1779, 1790, 1798, 1806, 1814, 1825, 1836, 1847, 1855, 1863, 1871, 1882, 1893, 1904, 1912, 1920, 1928, 1936, 1944, 1952, 1960, 1968, 1976, 1984, 1992, 2000, 2008, 2016, 2024, 2032, 2040, 2048, 2056, 2064, 2072, 2080, 2088, 2096, 2104, 2112, 2120, 2128, 2136, 2144, 2152, 2160, 2168, 2176, 2184, 2192, 2200, 2208, 2216, 2234, 2248, 2262, 2276, 2287, 2298, 2309, 2317, 2325, 2333, 2344, 2355, 2366, 2374, 2382, 2390, 2401, 2412, 2423, 2431, 2439, 2447, 2458, 2469, 2480, 2488, 2496, 2504, 2512, 2520, 2528, 2536, 2544, 2552, 2560, 2568, 2576, 2584, 2592, 2600, 2608, 2616, 2624, 2632, 2640, 2648, 2656, 2664, 2672, 2680, 2688, 2696, 2704, 2712, 2720, 2728, 2736, 2744, 2752, 2760, 2768, 2776, 2784, 2792, 2808, 2822, 2833, 2844, 2855, 2863, 2871, 2879, 2890, 2901, 2912, 2920, 2928, 2936, 2944, 2952, 2960, 2968, 2976, 2984, 2992, 3000, 3008, 3016, 3024, 3032, 3040, 3048, 3056, 3064, 3072, and 3080, as set forth in Table 5A and Table 5B. Other examples comprise a free acid at the C-terminal (rather than an amidated C-terminal residue) of any of the foregoing, such as SEQ ID NOS: 597-601 and 813-1027, as set forth in Table 5A and Table 5B.

[00224] Some examples of the composition of matter comprising an amino acid sequence that comprises a Gly residue at position X_{aa}^{6} of SEQ ID NO:475 include: SEQ ID NOS: 265, 751, 752, 754, 755, 1081, 1095, 1109, 1123, 1134, 1145, 1156, 1164, 1172, 1180, 1191, 1202, 1213, 1221, 1229, 1237, 1248, 1259, 1270, 1278, 1286, 1294, 1305, 1316, 1327, 1335, 1343, 1351, 1359, 1367, 1375, 1383, 1391, 1399, 1407, 1415, 1423, 1431, 1439, 1447, 1455, 1463, 1471, 1479, 1487, 1495, 1503, 1511, 1519, 1527, 1535, 1543, 1551, 1559, 1567, 1575, 1583, 1591, 1599, 1607, 1615, 1623, 1631, 1639, 1657, 1671, 1685, 1699, 1710, 1721, 1732, 1740, 1748, 1756, 1767, 1778, 1789, 1797, 1805, 1813, 1824, 1835, 1846, 1854, 1862, 1870, 1881, 1892, 1903, 1911, 1919, 1927, 1935, 1943, 1951, 1959, 1967, 1975, 1983, 1991, 1999, 2007, 2015, 2023, 2031, 2039, 2047, 2055, 2063, 2071, 2079, 2087, 2095, 2103, 2111, 2119, 2127, 2135, 2143, 2151, 2159, 2167, 2175, 2183, 2191, 2199, 2207, 2215, 2233, 2247, 2261, 2275, 2286, 2297, 2308, 2316, 2324, 2332, 2343, 2354, 2365, 2373, 2381, 2389, 2400, 2411, 2422, 2430,

2438, 2446, 2457, 2468, 2479, 2487, 2495, 2503, 2511, 2519, 2527, 2535, 2543, 2551, 2559, 2567, 2575, 2583, 2591, 2599, 2607, 2615, 2623, 2631, 2639, 2647, 2655, 2663, 2671, 2679, 2687, 2695, 2703, 2711, 2719, 2727, 2735, 2743, 2751, 2759, 2767, 2775, 2783, 2791, 2807, 2821, 2832, 2843, 2854, 2862, 2870, 2878, 2889, 2900, 2911, 2919, 2927, 2935, 2943, 2951, 2959, 2967, 2975, 2983, 2991, 2999, 3007, 3015, 3023, 3031, 3039, 3047, 3055, 3063, 3071, and 3079, as set forth in Table 5A and Table 5B.

[00225] Some examples of the composition of matter comprising an amino acid sequence that comprises a 2-Abu residue at position X_{aa}^{6} of SEQ ID NO:475 include: SEQ ID NOS: 605, 636, 649, 706, 707, 718, 753, 758, 797, 799, 801, 804, 807, 808, 1029, 1041, 1042, 1048, 1066, 1067, 1083, 1097, 1111, 1125, 1136, 1147, 1158, 1166, 1174, 1182, 1193, 1204, 1215, 1223, 1231, 1239, 1250, 1261, 1272, 1280, 1288, 1296, 1307, 1318, 1329, 1337, 1345, 1353, 1361, 1369, 1377, 1385, 1393, 1401, 1409, 1417, 1425, 1433, 1441, 1449, 1457, 1465, 1473, 1481, 1489, 1497, 1505, 1513, 1521, 1529, 1537, 1545, 1553, 1561, 1569, 1577, 1585, 1593, 1601, 1609, 1617, 1625, 1633, 1641, 1659, 1673, 1687, 1701, 1712, 1723, 1734, 1742, 1750, 1758, 1769, 1780, 1791, 1799, 1807, 1815, 1826, 1837, 1848, 1856, 1864, 1872, 1883, 1894, 1905, 1913, 1921, 1929, 1937, 1945, 1953, 1961, 1969, 1977, 1985, 1993, 2001, 2009, 2017, 2025, 2033, 2041, 2049, 2057, 2065, 2073, 2081, 2089, 2097, 2105, 2113, 2121, 2129, 2137, 2145, 2153, 2161, 2169, 2177, 2185, 2193, 2201, 2209, 2217, 2235, 2249, 2263, 2277, 2288, 2299, 2310, 2318, 2326, 2334, 2345, 2356, 2367, 2375, 2383, 2391, 2402, 2413, 2424, 2432, 2440, 2448, 2459, 2470, 2481, 2489, 2497, 2505, 2513, 2521, 2529, 2537, 2545, 2553, 2561, 2569, 2577, 2585, 2593, 2601, 2609, 2617, 2625, 2633, 2641, 2649, 2657, 2665, 2673, 2681, 2689, 2697, 2705, 2713, 2721, 2729, 2737, 2745, 2753, 2761, 2769, 2777, 2785, 2793, 2809, 2823, 2834, 2845, 2856, 2864, 2872, 2880, 2891, 2902, 2913, 2921, 2929, 2937, 2945, 2953, 2961, 2969, 2977, 2985, 2993, 3001, 3009, 3017, 3025, 3033, 3041, 3049, 3057, 3065, 3073, and 3081, as set forth in Table 5A and Table 5B.

[00226] Some examples of the composition of matter comprising an amino acid sequence that comprises a Nle residue at position X_{aa}^{6} of SEQ ID NO:475 include: SEQ ID NOS: 607, 638, 651, 1085, 1099, 1113, 1127, 1138, 1149, 1160, 1168, 1176, 1184, 1195, 1206, 1217, 1225, 1233, 1241, 1252, 1263, 1274, 1282, 1290, 1298, 1309, 1320, 1331, 1339, 1347, 1355, 1363, 1371, 1379, 1387, 1395, 1403, 1411, 1419, 1427, 1435, 1443, 1451, 1459, 1467, 1475, 1483, 1491, 1499, 1507, 1515, 1523, 1531, 1539, 1547,

1555, 1563, 1571, 1579, 1587, 1595, 1603, 1611, 1619, 1627, 1635, 1643, 1661, 1675, 1689, 1703, 1714, 1725, 1736, 1744, 1752, 1760, 1771, 1782, 1793, 1801, 1809, 1817, 1828, 1839, 1850, 1858, 1866, 1874, 1885, 1896, 1907, 1915, 1923, 1931, 1939, 1947, 1955, 1963, 1971, 1979, 1987, 1995, 2003, 2011, 2019, 2027, 2035, 2043, 2051, 2059, 2067, 2075, 2083, 2091, 2099, 2107, 2115, 2123, 2131, 2139, 2147, 2155, 2163, 2171, 2179, 2187, 2195, 2203, 2211, 2219, 2237, 2251, 2265, 2279, 2290, 2301, 2312, 2320, 2328, 2336, 2347, 2358, 2369, 2377, 2385, 2393, 2404, 2415, 2426, 2434, 2442, 2450, 2461, 2472, 2483, 2491, 2499, 2507, 2515, 2523, 2531, 2539, 2547, 2555, 2563, 2571, 2579, 2587, 2595, 2603, 2611, 2619, 2627, 2635, 2643, 2651, 2659, 2667, 2675, 2683, 2691, 2699, 2707, 2715, 2723, 2731, 2739, 2747, 2755, 2763, 2771, 2779, 2787, 2795, 2811, 2825, 2836, 2847, 2858, 2866, 2874, 2882, 2893, 2904, 2915, 2923, 2931, 2939, 2947, 2955, 2963, 2971, 2979, 2987, 2995, 3003, 3011, 3019, 3027, 3035, 3043, 3051, 3059, 3067, 3075, and 3083, as set forth in Table 5A and Table 5B.

[00227] Some examples of the composition of matter comprising an amino acid sequence that comprises a Nva residue at position X_{aa}^{6} of SEQ ID NO:475 include: SEQ ID NOS: 606, 637, 650, 705, 708, 717, 759, 760, 805, 806, 1084, 1098, 1112, 1126, 1137, 1148, 1159, 1167, 1175, 1183, 1194, 1205, 1216, 1224, 1232, 1240, 1251, 1262, 1273, 1281, 1289, 1297, 1308, 1319, 1330, 1338, 1346, 1354, 1362, 1370, 1378, 1386, 1394, 1402, 1410, 1418, 1426, 1434, 1442, 1450, 1458, 1466, 1474, 1482, 1490, 1498, 1506, 1514, 1522, 1530, 1538, 1546, 1554, 1562, 1570, 1578, 1586, 1594, 1602, 1610, 1618, 1626, 1634, 1642, 1660, 1674, 1688, 1702, 1713, 1724, 1735, 1743, 1751, 1759, 1770, 1781, 1792, 1800, 1808, 1816, 1827, 1838, 1849, 1857, 1865, 1873, 1884, 1895, 1906, 1914, 1922, 1930, 1938, 1946, 1954, 1962, 1970, 1978, 1986, 1994, 2002, 2010, 2018, 2026, 2034, 2042, 2050, 2058, 2066, 2074, 2082, 2090, 2098, 2106, 2114, 2122, 2130, 2138, 2146, 2154, 2162, 2170, 2178, 2186, 2194, 2202, 2210, 2218, 2236, 2250, 2264, 2278, 2289, 2300, 2311, 2319, 2327, 2335, 2346, 2357, 2368, 2376, 2384, 2392, 2403, 2414, 2425, 2433, 2441, 2449, 2460, 2471, 2482, 2490, 2498, 2506, 2514, 2522, 2530, 2538, 2546, 2554, 2562, 2570, 2578, 2586, 2594, 2602, 2610, 2618, 2626, 2634, 2642, 2650, 2658, 2666, 2674, 2682, 2690, 2698, 2706, 2714, 2722, 2730, 2738, 2746, 2754, 2762, 2770, 2778, 2786, 2794, 2810, 2824, 2835, 2846, 2857, 2865, 2873, 2881, 2892, 2903, 2914, 2922, 2930, 2938, 2946, 2954, 2962, 2970, 2978, 2986, 2994, 3002,

3010, 3018, 3026, 3034, 3042, 3050, 3058, 3066, 3074, and 3082, as set forth in Table 5A and Table 5B.

[00228] Other exemplary embodiments of the inventive composition are unconjugated and conjugated peptide analogs of GpTx-1 having one of the amino acid sequences as set forth in Table 5A, Table 5B, and Table 31. Particular embodiments of the inventive isolated polypeptides include those having an amino acid sequence selected from SEQ ID NOS: 3-134, 136-305, 307-386, 388-474, 515-527, 532-588, 590, 591, 593-1049, and 1062-3086, and more particularly an amino acid sequence selected from SEQ ID NOS: 3-30, 32-72, 74-134, 136-178, 180-211, 218-239, 241-305, 307-363, 366-386, 388-432, 434-474, 515-527, 532-588, 590, 591, 593-775, 777, 778, 780-788, 790-1049, and 1062-3086. Any of these further comprising an optional linker moiety and a pharmaceutically acceptable, covalently linked half-life extending moiety, as described herein, are also encompassed within the present invention. A pharmaceutical composition comprising any of these polypeptides (with or without a covalently linked half-life extending moiety) and a pharmaceutically acceptable carrier is also encompassed within the present invention.

Table 5A. Amino acid sequences of GpTx-1 and GpTx-1 peptide analogs. {H}- = amino group of N-terminal; -{Amide} = amidated C-terminal; Ac- = acetylated N-terminal; -{Free Acid} = carboxylated C-terminal; {biotin}- = biotinylated N-terminal; {4-Pen}- = 4-pentynoylated N-terminal; {bromoacetamide-PEG11-triazole}- = 3-(1-(1-bromo-2-oxo-6,9,12,15,18,21,24,27,30,33,36-undecaoxa-3-azaoctatriacontan-38-yl)-1H-1,2,3-triazol-4-yl)propanoyl covalently conjugated to N-terminal.

Designation	Amino Acid Sequence	SEQ ID NO:
GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	1
[All D-isomer]GpTx-1(1-34)	{H}-dclgfmrkcipdndkccrpnlvcsrthkwckyvf-{Amide}	2
[SeMet6]GpTx-1(1-34)	{H}-DCLGF[SeMet]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-	3

	{Amide}	
[Ala12]GpTx-1(1-34)	{H}-DCLGFMRKCIPANDKCCRPNLVCSRTHKWCKYVF-{Amide}	4
[Ala13]GpTx-1(1-34)	{H}-DCLGFMRKCIPDADKCCRPNLVCSRTHKWCKYVF-{Amide}	5
[Ala15]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDACCRPNLVCSRTHKWCKYVF-{Amide}	6
[Ala20]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPALVCSRTHKWCKYVF-{Amide}	7
[Ala22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLACSRTHKWCKYVF-{Amide}	8
[Ala25]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSATHKWCKYVF-{Amide}	9
[Ala26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRAHKWCKYVF-{Amide}	10
[Ala27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTAKWCKYVF-{Amide}	11
[Ala28]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHAWCKYVF-{Amide}	12
[Ala31]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCAYVF-{Amide}	13
[Ala32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKAVF-{Amide}	14
[Ala33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYAF-{Amide}	15
GpTx-1(1-34)-Ala	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFA-{Amide}	16
Glu-GpTx-1(1-34)	{H}-EDCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	17
[Glu1]GpTx-1(1-34)	{H}-ECLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	18
[Glu3]GpTx-1(1-34)	{H}-DCEGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	19
[Ala1]GpTx-1(1-34)	{H}-ACLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	20
[Ala3]GpTx-1(1-34)	{H}-DCAGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	21
[Ala5]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	22
[Ala6]GpTx-1(1-34)	{H}-DCLGFARKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	23
[Glu4]GpTx-1(1-34)	{H}-DCLEFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	24
[Glu8]GpTx-1(1-34)	{H}-DCLGFMRECIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	25
[Glu12]GpTx-1(1-34)	{H}-DCLGFMRKCIPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	26
[Glu13]GpTx-1(1-34)	{H}-DCLGFMRKCIPDEDKCCRPNLVCSRTHKWCKYVF-{Amide}	27
[Glu15]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDECCRPNLVCSRTHKWCKYVF-{Amide}	28
[Glu27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTEKWCKYVF-{Amide}	29
[Glu29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKECKYVF-{Amide}	30
[Glu31]GpTx-1(1-	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCEYVF-	31

34)	{Amide}	
[Glu32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKEVF-{Amide}	32
[Glu33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYEF-{Amide}	33
[Glu34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVE-{Amide}	34
GpTx-1(1-34)-Glu	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFE-{Amide}	35
Lys-GpTx-1(1-34)	{H}-KDCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	36
[Lys1]GpTx-1(1-34)	{H}-KCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	37
[Lys3]GpTx-1(1-34)	{H}-DCKGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	38
[Lys4]GpTx-1(1-34)	{H}-DCLKFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	39
[Lys7]GpTx-1(1-34)	{H}-DCLGFMKKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	40
[Lys10]GpTx-1(1-34)	{H}-DCLGFMRKCKPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	41
[Lys12]GpTx-1(1-34)	{H}-DCLGFMRKCIPKNDKCCRPNLVCSRTHKWCKYVF-{Amide}	42
[Ala7]GpTx-1(1-34)	{H}-DCLGFMAKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	43
[Ala8]GpTx-1(1-34)	{H}-DCLGFMRACIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	44
[Ala10]GpTx-1(1-34)	{H}-DCLGFMRKCAPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	45
[Ala11]GpTx-1(1-34)	{H}-DCLGFMRKCIADNDKCCRPNLVCSRTHKWCKYVF-{Amide}	46
[Ala29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKACKYVF-{Amide}	47
[Lys13]GpTx-1(1-34)	{H}-DCLGFMRKCIPDKDKCCRPNLVCSRTHKWCKYVF-{Amide}	48
[Lys18]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCKPNLVCSRTHKWCKYVF-{Amide}	49
[Lys19]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRKNLVCSRTHKWCKYVF-{Amide}	50
[Lys20]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPKLVCSRTHKWCKYVF-{Amide}	51
[Lys22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLKCSRTHKWCKYVF-{Amide}	52
[Lys25]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSKTHKWCKYVF-{Amide}	53
[Lys26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRKHKWCKYVF-{Amide}	54
[Lys27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTKKWCKYVF-{Amide}	55
[Lys29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKKCKYVF-{Amide}	56
[Lys32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKKVF-{Amide}	57
[Lys33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYKF-{Amide}	58
[Lys34]GpTx-1(1-	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVK-	59

34)	{Amide}	
GpTx-1(1-34)-Lys	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFK-{Amide}	60
Arg-GpTx-1(1-34)	{H}-RDCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	61
[Arg1]GpTx-1(1-34)	{H}-RCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	62
[Arg4]GpTx-1(1-34)	{H}-DCLRFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	63
[Arg6]GpTx-1(1-34)	{H}-DCLGFRRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	64
[Arg8]GpTx-1(1-34)	{H}-DCLGFMRRCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	65
[Arg10]GpTx-1(1-34)	{H}-DCLGFMRKCRPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	66
[Arg12]GpTx-1(1-34)	{H}-DCLGFMRKCIPRNDKCCRPNLVCSRTHKWCKYVF-{Amide}	67
[Arg15]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDRCCRPNLVCSRTHKWCKYVF-{Amide}	68
[Arg20]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPRLVCSRTHKWCKYVF-{Amide}	69
[Arg26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRRHKWCKYVF-{Amide}	70
[Arg27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTRKWCKYVF-{Amide}	71
[Arg28]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	72
[Arg31]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCRYVF-{Amide}	73
[Arg33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYRF-{Amide}	74
[Arg34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVR-{Amide}	75
GpTx-1(1-34)-Arg	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFR-{Amide}	76
[1-Nal1]GpTx-1(1-34)	{H}-[1-Nal]CLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	77
[1-Nal10]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	78
[1-Nal29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[1-Nal]CKYVF-{Amide}	79
[1-Nal34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[1-Nal]-{Amide}	80
[Trp1]GpTx-1(1-34)	{H}-WCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	81
[Trp5]GpTx-1(1-34)	{H}-DCLGWMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	82
[Trp10]GpTx-1(1-34)	{H}-DCLGFMRKCWPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	83
[Trp27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTWKWCKYVF-{Amide}	84
[Trp32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKWVF-{Amide}	85
[Trp34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVW-{Amide}	86

GpTx-1(1-34)-Trp	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFW-{Amide}	87
[Ile5]GpTx-1(1-34)	{H}-DCLGIMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	88
[Phe6]GpTx-1(1-34)	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	89
[Asn10]GpTx-1(1-34)	{H}-DCLGFMRKCNPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	90
[Ser12]GpTx-1(1-34)	{H}-DCLGFMRKCIPSNDKCCRPNLVCSRTHKWCKYVF-{Amide}	91
[Gln15]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDQCCRPNLVCSRTHKWCKYVF-{Amide}	92
[Ser-Ser19]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRSSNLVCSRTHKWCKYVF-{Amide}	93
[Lys26;Thr27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRKTKWCKYVF-{Amide}	94
[Gln33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYQF-{Amide}	95
[Ile34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVI-{Amide}	96
[Tyr1]GpTx-1(1-34)	{H}-YCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	97
[Gln3]GpTx-1(1-34)	{H}-DCQGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	98
[Lys32;1-Nal34]GpTx-1(1-34)-Trp	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKKV[1-Nal]W-{Amide}	99
Ala-GpTx-1(1-34)	{H}-ADCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	100
[Ala34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVA-{Amide}	101
[Glu22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLECSRTHKWCKYVF-{Amide}	102
[Arg13]GpTx-1(1-34)	{H}-DCLGFMRKCIPDRDKCCRPNLVCSRTHKWCKYVF-{Amide}	103
[Arg29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKRCKYVF-{Amide}	104
[1-Nal5]GpTx-1(1-34)	{H}-DCLG[1-Nal]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	105
Trp-GpTx-1(1-34)	{H}-WDCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	106
GpTx-1(1-34)-FreeAcid	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{FreeAcid}	107
GpTx-1(2-34)	{H}-CLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	108
[Phe27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTFKWCKYVF-{Amide}	109
[Tyr27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTYKWCKYVF-{Amide}	110
[Leu27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTLKWCKYVF-{Amide}	111
[Phe29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKFCKYVF-{Amide}	112
[Tyr29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKYCKYVF-{Amide}	113
[Leu29]GpTx-1(1-	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKLCKYVF-	114

34)	{Amide}	
[Cit7]GpTx-1(1-34)	{H}-DCLGFM[Cit]KCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	115
[Cit18]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCC[Cit]PNLVCSRTHKWCKYVF-{Amide}	116
[Cit25]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCS[Cit]THKWCKYVF-{Amide}	117
[Thr8]GpTx-1(1-34)	{H}-DCLGFMRTCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	118
[Asp10]GpTx-1(1-34)	{H}-DCLGFMRKCDPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	119
[Met21]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNMVCSRTHKWCKYVF-{Amide}	120
[Leu26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	121
[Leu34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVL-{Amide}	122
[Nle6]GpTx-1(1-34)	{H}-DCLGF[Nle]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	123
[2-Abu6]GpTx-1(1-34)	{H}-DCLGF[2-Abu]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	124
[2-Abu2,17]GpTx-1(1-34)	{H}-D[2-Abu]LGFMRKCIPDNDKC[2-Abu]RPNLVCSRTHKWCKYVF-{Amide}	125
[Gly19]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRGNLVCSRTHKWCKYVF-{Amide}	126
[Lys32]GpTx-1(1-34)-Trp	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKKVFW-{Amide}	127
[2-Nal5]GpTx-1(1-34)	{H}-DCLG[2-Nal]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	128
[2-Nal29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[2-Nal]CKYVF-{Amide}	129
[2-Nal34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[2-Nal]-{Amide}	130
GpTx-1(1-34)-2-Nal	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF[2-Nal]-{Amide}	131
Ac-GpTx-1(1-34)	{Acetyl}DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	132
GpTx-1(1-34)-Trp-FreeAcid	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFW{Free Acid}	133
[Glu18;desAsn20]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCEGLVCSRTHKWCKYVF-{Amide}	134
[2-Abu9,23]GpTx-1(1-34)	{H}-DCLGFMRK[2-Abu]IPDNDKCCRPNLV[2-Abu]SRTHKWCKYVF-{Amide}	135
[2-Nal5,34]GpTx-1(1-34)	{H}-DCLG[2-Nal]MRKCIPDNDKCCRPNLVCSRTHKWCKYV[2-Nal]-{Amide}	136
[2-Nal5;1-Nal34]GpTx-1(1-34)	{H}-DCLG[2-Nal]MRKCIPDNDKCCRPNLVCSRTHKWCKYV[1-Nal]-{Amide}	137
[1-Nal34]GpTx-1(1-34)-Trp	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[1-Nal]W-{Amide}	138
[2-Nal34]GpTx-1(1-34)-Trp	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[2-Nal]W-{Amide}	139
[Ala2,17]GpTx-1(1-34)	{H}-DALGFMRKCIPDNDKCARPNLVCSRTHKWCKYVF-{Amide}	140

[Ala4]GpTx-1(1-34)	{H}-DCLAFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	141
[Ala24]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCARTHKWCKYVF-{Amide}	142
[Glu5]GpTx-1(1-34)	{H}-DCLGEMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	143
[Glu6]GpTx-1(1-34)	{H}-DCLGFERKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	144
[Glu7]GpTx-1(1-34)	{H}-DCLGFMEKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	145
[Glu10]GpTx-1(1-34)	{H}-DCLGFMRKCEPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	146
[Glu11]GpTx-1(1-34)	{H}-DCLGFMRKCIEDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	147
[Glu18]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCEPNLVCSRTHKWCKYVF-{Amide}	148
[Glu20]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPELVCSRTHKWCKYVF-{Amide}	149
[Glu24]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCERTHKWCKYVF-{Amide}	150
[Glu25]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSETHKWCKYVF-{Amide}	151
[Glu26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSREHKWCKYVF-{Amide}	152
[Glu28]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	153
[Lys6]GpTx-1(1-34)	{H}-DCLGFKRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	154
[Arg3]GpTx-1(1-34)	{H}-DCRGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	155
[Arg5]GpTx-1(1-34)	{H}-DCLGRMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	156
[Arg19]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRRNLVCSRTHKWCKYVF-{Amide}	157
[Arg22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLRCSRTHKWCKYVF-{Amide}	158
[Arg32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKRVF-{Amide}	159
[1-Nal4]GpTx-1(1-34)	{H}-DCL[1-Nal]FMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	160
[1-Nal6]GpTx-1(1-34)	{H}-DCLGF[1-Nal]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	161
[1-Nal12]GpTx-1(1-34)	{H}-DCLGFMRKCIP[1-Nal]NDKCCRPNLVCSRTHKWCKYVF-{Amide}	162
[1-Nal13]GpTx-1(1-34)	{H}-DCLGFMRKCIPD[1-Nal]DKCCRPNLVCSRTHKWCKYVF-{Amide}	163
[1-Nal20]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRP[1-Nal]LVCSRTHKWCKYVF-{Amide}	164
[1-Nal21]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPN[1-Nal]VCSRTHKWCKYVF-{Amide}	165
[1-Nal27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRT[1-Nal]KWCKYVF-{Amide}	166
[1-Nal32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[1-Nal]VF-{Amide}	167
[1-Nal33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[1-Nal]F-{Amide}	168

[Trp4]GpTx-1(1-34)	{H}-DCLWFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	169
[Trp6]GpTx-1(1-34)	{H}-DCLGFWRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	170
[Trp11]GpTx-1(1-34)	{H}-DCLGFMRKCIWDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	171
[Trp12]GpTx-1(1-34)	{H}-DCLGFMRKCIPWNDKCCRPNLVCSRTHKWCKYVF-{Amide}	172
[Trp13]GpTx-1(1-34)	{H}-DCLGFMRKCIPDWDKCCRPNLVCSRTHKWCKYVF-{Amide}	173
[Trp18]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCWPNLVCSRTHKWCKYVF-{Amide}	174
[Trp20]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPWLVCSRTHKWCKYVF-{Amide}	175
[Trp21]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNWVCSRTHKWCKYVF-{Amide}	176
[Trp22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLWCSRTHKWCKYVF-{Amide}	177
[Trp26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRWHKWCKYVF-{Amide}	178
[Trp31]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCWYVF-{Amide}	179
[Trp33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYWF-{Amide}	180
[Ser19]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRSNLVCSRTHKWCKYVF-{Amide}	181
[Gln33;1-Nal34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYQ[1-Nal]-{Amide}	182
[Arg28;Gln33;1-Nal34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHRWCKYQ[1-Nal]-{Amide}	183
[Arg20;Gln33;1-Nal34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPRLVCSRTHKWCKYQ[1-Nal]-{Amide}	184
[Arg20,28;Gln33;1-Nal34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPRLVCSRTHRWCKYQ[1-Nal]-{Amide}	185
[Arg15;Gln33;1-Nal34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDRCCRPNLVCSRTHKWCKYQ[1-Nal]-{Amide}	186
Arg-GpTx-1(1-34)-Trp	{H}-RDCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFW-{Amide}	187
[PE1]GpTx-1(1-34)	{H}-[PE]CLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	188
[Ile1]GpTx-1(1-34)	{H}-ICLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	189
[Pro1]GpTx-1(1-34)	{H}-PCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	190
[Ser1]GpTx-1(1-34)	{H}-SCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	191
[Thr1]GpTx-1(1-34)	{H}-TCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	192
[Leu12]GpTx-1(1-34)	{H}-DCLGFMRKCIPLNDKCCRPNLVCSRTHKWCKYVF-{Amide}	193

[Gly12]GpTx-1(1-34)	{H}-DCLGFMRKCIPGNDKCCRPNLVCSRTHKWCKYVF-{Amide}	194
[Ile12]GpTx-1(1-34)	{H}-DCLGFMRKCIPINDKCCRPNLVCSRTHKWCKYVF-{Amide}	195
[Thr12]GpTx-1(1-34)	{H}-DCLGFMRKCIPTNDKCCRPNLVCSRTHKWCKYVF-{Amide}	196
[Tyr12]GpTx-1(1-34)	{H}-DCLGFMRKCIPYNDKCCRPNLVCSRTHKWCKYVF-{Amide}	197
[Gly20]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPGLVCSRTHKWCKYVF-{Amide}	198
[Phe20]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPFLVCSRTHKWCKYVF-{Amide}	199
[Tyr20]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPYLVCSRTHKWCKYVF-{Amide}	200
1-Nal-GpTx-1(1-34)	{H}-[1-Nal]DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	201
[Trp3]GpTx-1(1-34)	{H}-DCWGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	202
[1-Nal3]GpTx-1(1-34)	{H}-DC[1-Nal]GFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	203
[Lys5]GpTx-1(1-34)	{H}-DCLGKMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	204
[Trp7]GpTx-1(1-34)	{H}-DCLGFMWKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	205
[1-Nal7]GpTx-1(1-34)	{H}-DCLGFM[1-Nal]KCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	206
[Trp8]GpTx-1(1-34)	{H}-DCLGFMRWCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	207
[1-Nal8]GpTx-1(1-34)	{H}-DCLGFMR[1-Nal]CIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	208
[Lys11]GpTx-1(1-34)	{H}-DCLGFMRKCIKDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	209
[Arg11]GpTx-1(1-34)	{H}-DCLGFMRKCIRDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	210
[1-Nal11]GpTx-1(1-34)	{H}-DCLGFMRKCI[1-Nal]DNDKCCRPNLVCSRTHKWCKYVF-{Amide}	211
[Ala14]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNAKCCRPNLVCSRTHKWCKYVF-{Amide}	212
[Glu14]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNEKCCRPNLVCSRTHKWCKYVF-{Amide}	213
[Lys14]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNKKCCRPNLVCSRTHKWCKYVF-{Amide}	214
[Arg14]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNRKCCRPNLVCSRTHKWCKYVF-{Amide}	215
[Trp14]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNWKCCRPNLVCSRTHKWCKYVF-{Amide}	216
[1-Nal14]GpTx-1(1-34)	{H}-DCLGFMRKCIPDN[1-Nal]KCCRPNLVCSRTHKWCKYVF-{Amide}	217
[Trp15]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDWCCRPNLVCSRTHKWCKYVF-{Amide}	218
[1-Nal15]GpTx-1(1-34)	{H}-DCLGFMRKCIPDND[1-Nal]CCRPNLVCSRTHKWCKYVF-{Amide}	219
[Ala18]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCAPNLVCSRTHKWCKYVF-{Amide}	220

[1-Nal18]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCC[1-Nal]PNLVCSRTHKWCKYVF-{Amide}	221
[Ala19]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRANLVCSRTHKWCKYVF-{Amide}	222
[Glu19]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRENLVCSRTHKWCKYVF-{Amide}	223
[Trp19]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRWNLVCSRTHKWCKYVF-{Amide}	224
[1-Nal19]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCR[1-Nal]NLVCSRTHKWCKYVF-{Amide}	225
[Ala21]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNAVCSRTHKWCKYVF-{Amide}	226
[Glu21]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNEVCSRTHKWCKYVF-{Amide}	227
[Lys21]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNKVCSRTHKWCKYVF-{Amide}	228
[Arg21]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNRVCSRTHKWCKYVF-{Amide}	229
[1-Nal22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNL[1-Nal]CSRTHKWCKYVF-{Amide}	230
[Lys24]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCKRTHKWCKYVF-{Amide}	231
[Arg24]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCRRTHKWCKYVF-{Amide}	232
[Trp24]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCWRTHKWCKYVF-{Amide}	233
[1-Nal24]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVC[1-Nal]RTHKWCKYVF-{Amide}	234
[Trp25]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSWTHKWCKYVF-{Amide}	235
[1-Nal25]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCS[1-Nal]THKWCKYVF-{Amide}	236
[1-Nal26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSR[1-Nal]HKWCKYVF-{Amide}	237
[Trp28]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHWWCKYVF-{Amide}	238
[1-Nal28]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTH[1-Nal]WCKYVF-{Amide}	239
[1-Nal31]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWC[1-Nal]YVF-{Amide}	240
GpTx-1(1-34)-1-Nal	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF[1Nal]-{Amide}	241
[Bip5]GpTx-1(1-34)	{H}-DCLG[Bip]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	242
[Cha5]GpTx-1(1-34)	{H}-DCLG[Cha]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	243
[Leu6]GpTx-1(1-34)	{H}-DCLGFLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	244
[Cha6]GpTx-1(1-34)	{H}-DCLGF[Cha]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	245
[1'NMeW32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[1'NMeW]VF-{Amide}	246

[pI-Phe5]GpTx-1(1-34)	{H}-DCLG[pI-Phe]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	247
[Ile33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYIF-{Amide}	248
[pI-Phe33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[pI-Phe]F-{Amide}	249
[1'NMeW33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[1'NMeW]F-{Amide}	250
[Arg28;1-Nal32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHRWCK[1-Nal]VF-{Amide}	251
[Ala5;Trp33]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYWF-{Amide}	252
[Ala5;Trp32]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKWVF-{Amide}	253
[Ala5;1-Nal32]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCK[1-Nal]VF-{Amide}	254
[Ala5;Leu26]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	255
[Ala5;1-Nal6]GpTx-1(1-34)	{H}-DCLGA[1-Nal]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	256
[Ala5;Phe6]GpTx-1(1-34)	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	257
[Ala5;1-Nal33]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKY[1-Nal]F-{Amide}	258
[Ala5;1-Nal10]GpTx-1(1-34)	{H}-DCLGAMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	259
[Ala5;Arg28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	260
[Ala5;Trp6]GpTx-1(1-34)	{H}-DCLGAWRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	261
[Ala5;Phe6;Leu26;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRLHRWCKYVF-{Amide}	262
[Ala5;Phe6;Leu26]GpTx-1(1-34)	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	263
[1'NMeW5]GpTx-1(1-34)	{H}-DCLG[1'NMeW]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	264
[Gly5]GpTx-1(1-34)	{H}-DCLGGMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	265

[His5]GpTx-1(1-34)	{H}-DCLGHMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	266
[Leu5]GpTx-1(1-34)	{H}-DCLGLMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	267
[Met5]GpTx-1(1-34)	{H}-DCLGMMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	268
[Pro5]GpTx-1(1-34)	{H}-DCLGPMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	269
[Thr5]GpTx-1(1-34)	{H}-DCLGTMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	270
[Tyr5]GpTx-1(1-34)	{H}-DCLGYMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	271
[Val5]GpTx-1(1-34)	{H}-DCLGVMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	272
[D-Phe5]GpTx-1(1-34)	{H}-DCLGfMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	273
[NMeTrp5]GpTx-1(1-34)	{H}-DCLG[NMeTrp]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	274
[Phg5]GpTx-1(1-34)	{H}-DCLG[Phg]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	275
[4CO2-F5]GpTx-1(1-34)	{H}-DCLG[4CO2-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	276
[2PAL5]GpTx-1(1-34)	{H}-DCLG[2PAL]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	277
[Asn6]GpTx-1(1-34)	{H}-DCLGFNRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	278
[Gln6]GpTx-1(1-34)	{H}-DCLGFQRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	279
[Gly6]GpTx-1(1-34)	{H}-DCLGFGRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	280
[His6]GpTx-1(1-34)	{H}-DCLGFHRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	281
[Ile6]GpTx-1(1-34)	{H}-DCLGFIRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	282
[Pro6]GpTx-1(1-34)	{H}-DCLGFPRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	283
[Ser6]GpTx-1(1-34)	{H}-DCLGFSRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	284
[Thr6]GpTx-1(1-34)	{H}-DCLGFTRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	285
[Tyr6]GpTx-1(1-34)	{H}-DCLGFYRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	286
[Val6]GpTx-1(1-34)	{H}-DCLGFVRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	287
[Phg6]GpTx-1(1-34)	{H}-DCLGF[Phg]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	288
[NMeTrp6]GpTx-1(1-34)	{H}-DCLGF[NMeTrp]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	289
[NMePhe6]GpTx-1(1-34)	{H}-DCLGF[NMePhe]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	290

[pI-Phe6]GpTx-1(1-34)	{H}-DCLGF[pI-Phe]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	291
[1'NMeW6]GpTx-1(1-34)	{H}-DCLGF[1'NMeW]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	292
[4CO2-F6]GpTx-1(1-34)	{H}-DCLGF[4CO2-F]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	293
[2PAL6]GpTx-1(1-34)	{H}-DCLGF[2PAL]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	294
[K(Me2)7]GpTx-1(1-34)	{H}-DCLGFM[K(Me2)]KCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	295
[SDMA7]GpTx-1(1-34)	{H}-DCLGFM[SDMA]KCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	296
[SDMA8]GpTx-1(1-34)	{H}-DCLGFMR[SDMA]CIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	297
[K(Me2)8]GpTx-1(1-34)	{H}-DCLGFMR[K(Me2)]CIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	298
[Tyr10]GpTx-1(1-34)	{H}-DCLGFMRKCYPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	299
[NMeTrp10]GpTx-1(1-34)	{H}-DCLGFMRKC[NMeTrp]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	300
[Val10]GpTx-1(1-34)	{H}-DCLGFMRKCVPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	301
[Phe10]GpTx-1(1-34)	{H}-DCLGFMRKCFPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	302
[Leu10]GpTx-1(1-34)	{H}-DCLGFMRKCLPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	303
[His10]GpTx-1(1-34)	{H}-DCLGFMRKCHPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	304
[Ser10]GpTx-1(1-34)	{H}-DCLGFMRKCSPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	305
[Met10]GpTx-1(1-34)	{H}-DCLGFMRKCMPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	307
[Pro10]GpTx-1(1-34)	{H}-DCLGFMRKCPPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	308
[Thr10]GpTx-1(1-34)	{H}-DCLGFMRKCTPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	309
[4CO2-F10]GpTx-1(1-34)	{H}-DCLGFMRKC[4CO2-F]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	310
[2PAL10]GpTx-1(1-34)	{H}-DCLGFMRKC[2PAL]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	311
[SDMA15]GpTx-1(1-34)	{H}-DCLGFMRKCIPDND[SDMA]CCRPNLVCSRTHKWCKYVF-{Amide}	312
[K(Me2)15]GpTx-1(1-34)	{H}-DCLGFMRKCIPDND[K(Me2)]CCRPNLVCSRTHKWCKYVF-{Amide}	313
[K(Me2)18]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCC[K(Me2)]PNLVCSRTHKWCKYVF-	314

	{Amide}	
[SDMA18]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCC[SDMA]PNLVCSRTHKWCKYVF-{Amide}	315
[2PAL18]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCC[2PAL]PNLVCSRTHKWCKYVF-{Amide}	316
[4CO2-F21]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPN[4CO2-F]VCSRTHKWCKYVF-{Amide}	317
[2PAL21]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPN[2PAL]VCSRTHKWCKYVF-{Amide}	318
[Phe22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLFCSRTHKWCKYVF-{Amide}	319
[Pro22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLPCSRTHKWCKYVF-{Amide}	320
[Ile22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLICSRTHKWCKYVF-{Amide}	321
[Leu22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLLCSRTHKWCKYVF-{Amide}	322
[Ser22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLSCSRTHKWCKYVF-{Amide}	323
[Gly22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLGCSRTHKWCKYVF-{Amide}	324
[Asn22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLNCSRTHKWCKYVF-{Amide}	325
[His22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLHCSRTHKWCKYVF-{Amide}	326
[Asp22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLDCSRTHKWCKYVF-{Amide}	327
[NMePhe22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNL[NMePhe]CSRTHKWCKYVF-{Amide}	328
[Thr22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLTCSRTHKWCKYVF-{Amide}	329
[Phg22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNL[Phg]CSRTHKWCKYVF-{Amide}	330
[Tyr22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLYCSRTHKWCKYVF-{Amide}	331
[Met22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLMCSRTHKWCKYVF-{Amide}	332
[4CO2-F22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNL[4CO2-F]CSRTHKWCKYVF-{Amide}	333
[2PAL22]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNL[2PAL]CSRTHKWCKYVF-{Amide}	334
[K(Me2)25]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCS[K(Me2)]THKWCKYVF-{Amide}	335
[SDMA25]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCS[SDMA]THKWCKYVF-{Amide}	336
[His26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRHHKWCKYVF-{Amide}	337
[Ser26]GpTx-1(1-	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRSHKWCKYVF-	338

34)	{Amide}	
[Gln26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRQHKWCKYVF-{Amide}	339
[Tyr26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRYHKWCKYVF-{Amide}	340
[Phe26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRFHKWCKYVF-{Amide}	341
[Asn26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRNHKWCKYVF-{Amide}	342
[Gly26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRGHKWCKYVF-{Amide}	343
[Val26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRVHKWCKYVF-{Amide}	344
[Pro26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRPHKWCKYVF-{Amide}	345
[Met26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRMHKWCKYVF-{Amide}	346
[Asp26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRDHKWCKYVF-{Amide}	347
[Ile26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRIHKWCKYVF-{Amide}	348
[2PAL26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSR[2PAL]HKWCKYVF-{Amide}	349
[4CO2-F26]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSR[4CO2-F]HKWCKYVF-{Amide}	350
[4CO2-F27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRT[4CO2-F]KWCKYVF-{Amide}	351
[2PAL27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRT[2PAL]KWCKYVF-{Amide}	352
[SDMA27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRT[SDMA]KWCKYVF-{Amide}	353
[K(Me2)27]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRT[K(Me2)]KWCKYVF-{Amide}	354
[K(Me2)28]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTH[K(Me2)]WCKYVF-{Amide}	355
[SDMA28]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTH[SDMA]WCKYVF-{Amide}	356
[NMeTrp29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[NMeTrp]CKYVF-{Amide}	357
[pI-Phe29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[pI-Phe]CKYVF-{Amide}	358
[NMePhe29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[NMePhe]CKYVF-{Amide}	359
[Bip29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[Bip]CKYVF-{Amide}	360
[1'NMeW29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[1'NMeW]CKYVF-{Amide}	361

[Phg29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[Phg]CKYVF-{Amide}	362
[4CO2-F29]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[4CO2-F]CKYVF-{Amide}	363
[2PAL31]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWC[2PAL]YVF-{Amide}	364
[SDMA31]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWC[SDMA]YVF-{Amide}	365
[Gln32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKQVF-{Amide}	366
[Ile32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKIVF-{Amide}	367
[Met32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKMVF-{Amide}	368
[Thr32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKTVF-{Amide}	369
[NMePhe32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[NMePhe]VF-{Amide}	370
[NMeTrp32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[NMeTrp]VF-{Amide}	371
[Val32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKVVF-{Amide}	372
[Leu32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKLVF-{Amide}	373
[Phg32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[Phg]VF-{Amide}	374
[Cha32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[Cha]VF-{Amide}	375
[Bip32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[Bip]VF-{Amide}	376
[Phe32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKFVF-{Amide}	377
[Gly32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKGVF-{Amide}	378
[Asn32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKNVF-{Amide}	379
[His32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKHVF-{Amide}	380
[pI-Phe32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[pI-Phe]VF-{Amide}	381
[Ser32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKSVF-{Amide}	382
[Pro32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKPVF-{Amide}	383
[2PAL32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[2PAL]VF-{Amide}	384
[4CO2-F32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[4CO2-F]VF-{Amide}	385
[Cha33]GpTx-1(1-	{H}-	386

34)	DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[Cha]F-{Amide}	
[NMePhe33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[NMePhe]F-{Amide}	388
[NMeTrp33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[NMeTrp]F-{Amide}	389
[Phe33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYFF-{Amide}	390
[Met33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYMF-{Amide}	391
[His33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYHF-{Amide}	392
[Phg33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[Phg]F-{Amide}	393
[Asn33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYNF-{Amide}	394
[Asp33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYDF-{Amide}	395
[Thr33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYTF-{Amide}	396
[Ser33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYSF-{Amide}	397
[Pro33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYPF-{Amide}	398
[Tyr33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYYF-{Amide}	399
[Leu33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYLF-{Amide}	400
[Gly33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYGF-{Amide}	401
[2PAL33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[2PAL]F-{Amide}	402
[4CO2-F33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[4CO2-F]F-{Amide}	403
[D-Phe34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVf-{Amide}	404
[Cha34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[Cha]-{Amide}	405
[Phg34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[Phg]-{Amide}	406
[NMeTrp34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[NMeTrp]-{Amide}	407
[NMePhe34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[NMePhe]-{Amide}	408
[1'NMeW34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[1'NMeW]-{Amide}	409

[4CO2-F34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[4CO2-F]-{Amide}	410
[2PAL34]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[2PAL]-{Amide}	411
GpTx-1(1-34)-2-Nal	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF[2-Nal]-{Amide}	412
GpTx-1(1-34)-4CO2-F	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF[4CO2-F]-{Amide}	413
GpTx-1(1-34)-2PAL	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF[2PAL]-{Amide}	414
GpTx-1(1-33)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV-{Amide}	415
GpTx-1(1-32)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY-{Amide}	416
GpTx-1(1-31)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK-{Amide}	417
GpTx-1(1-30)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWC-{Amide}	418
[Ala5;Glu33]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYEF-{Amide}	419
[Ala5;Arg28;1-Nal33]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHRWCKY[1-Nal]F-{Amide}	420
[Ala5;1-Nal20]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRP[1-Nal]LVCSRTHKWCKYVF-{Amide}	421
[Ala5;Trp20]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPWLVCSRTHKWCKYVF-{Amide}	422
[Ala5;Trp12]GpTx-1(1-34)	{H}-DCLGAMRKCIPWNDKCCRPNLVCSRTHKWCKYVF-{Amide}	423
[Trp4;Ala5]GpTx-1(1-34)	{H}-DCLWAMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	424
[1-Nal1;Ala5]GpTx-1(1-34)	{H}-[1-Nal]CLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	425
[Ala5,33]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYAF-{Amide}	426
[Ala5;1-Nal13]GpTx-1(1-34)	{H}-DCLGAMRKCIPD[1-Nal]DKCCRPNLVCSRTHKWCKYVF-{Amide}	427
[Ala5;Trp13]GpTx-1(1-34)	{H}-DCLGAMRKCIPDWDKCCRPNLVCSRTHKWCKYVF-{Amide}	428
[Glu4;Ala5]GpTx-1(1-34)	{H}-DCLEAMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	429
[Ala5;Glu34]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYVE-{Amide}	430
[Ala5,34]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYVA-{Amide}	431
[Ala5,32]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKAVF-{Amide}	432
[Ala5,31]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCAYVF-{Amide}	433
[Ala5,29]GpTx-	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKACKYVF-	434

1(1-34)	{Amide}	
[Ala5;Glu28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	435
[Ala5;Glu7]GpTx-1(1-34)	{H}-DCLGAMEKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	436
[Ala5;Glu29]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKECKYVF-{Amide}	437
[Ala5;Glu25]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSETHKWCKYVF-{Amide}	438
[Ala5;Glu15]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDECCRPNLVCSRTHKWCKYVF-{Amide}	439
[1-Nal10;Trp32]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKWVF-{Amide}	440
[1-Nal10;Arg28]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	441
[Arg28;1-Nal33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHRWCKY[1-Nal]F-{Amide}	442
[Arg28;Trp32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHRWCKWVF-{Amide}	443
[Arg28;Trp33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHRWCKYWF-{Amide}	444
[Leu26;Arg28]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHRWCKYVF-{Amide}	445
[Leu26;Trp32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHKWCKWVF-{Amide}	446
[Leu26;Trp33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHKWCKYWF-{Amide}	447
[Trp6;Arg28]GpTx-1(1-34)	{H}-DCLGFWRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	448
[Trp6,32]GpTx-1(1-34)	{H}-DCLGFWRKCIPDNDKCCRPNLVCSRTHKWCKWVF-{Amide}	449
[Trp32,33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKWWF-{Amide}	450
[1-Nal6;Trp32]GpTx-1(1-34)	{H}-DCLGF[1-Nal]RKCIPDNDKCCRPNLVCSRTHKWCKWVF-{Amide}	451
[1-Nal10,32]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCK[1-Nal]VF-{Amide}	452
[Leu26;1-Nal32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHKWCK[1-Nal]VF-{Amide}	453
[1-Nal6;Arg28]GpTx-1(1-34)	{H}-DCLGF[1-Nal]RKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	454
[Trp32;1-Nal33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKW[1-Nal]F-{Amide}	455
[Trp6;Leu26]GpTx-1(1-34)	{H}-DCLGFWRKCIPDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	456
[1-Nal10;Leu26]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	457
[Trp6;1-	{H}-DCLGFWRKC[1-	458

Nal10]GpTx-1(1-34)	Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	
[1-Nal10;Trp12]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PWNDKCCRPNLVCSRTHKWCKYVF-{Amide}	459
[1-Nal32;Trp33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[1-Nal]WF-{Amide}	460
[Trp6;1-Nal33]GpTx-1(1-34)	{H}-DCLGFWRKCIPDNDKCCRPNLVCSRTHKWCKY[1-Nal]F-{Amide}	461
[1-Nal10,33]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKY[1-Nal]F-{Amide}	462
[Leu26;1-Nal33]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHKWCKY[1-Nal]F-{Amide}	463
Trp-[1-Nal10]GpTx-1(1-34)	{H}-WDCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	464
[Trp1;1-Nal10]GpTx-1(1-34)	{H}-WCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	465
[1-Nal1,10]GpTx-1(1-34)	{H}-[1-Nal]CLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	466
GpTx-2	{H}-DCLGFMRKCSPDNDKCCRPNLVCSRKHKWCKYEI-{Amide}	467
GpTx-3	{H}-DCLGWFKGCDPDNDKCCEGYKCNRRDKWCKYKL-{Amide}	468
GpTx-4	{H}-DCLGWFKGCDPDNDKCCENYKCNRREQWCKYKL-{Amide}	469
GpTx-5(1-35)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFK-{FreeAcid}	470
GpTx-6(1-35)	{H}-DCLGWFKGCDPDNDKCCEGYKCNRRDKWCKYKLWK-{FreeAcid}	471
GpTx-6(1-34)	{H}-DCLGWFKGCDPDNDKCCEGYKCNRRDKWCKYKLW-{FreeAcid}	472
GpTx-7(1-35)	{H}-DCLGWFKGCDPDNDKCCENYKCNRRDKWCKYKLWK-{FreeAcid}	473
GpTx-7(1-34)	{H}-DCLGWFKGCDPDNDKCCENYKCNRRDKWCKYKLW-{FreeAcid}	474
[Phe6;Atz(20kDa PEG)13]GpTx-1(1-34)	{H}-DCLGFFRKCIPD[Atz(20kDa PEG)]DKCCRPNLVCSRTHKWCKYVF-{Amide}	590
[Phe6;Atz13]GpTx-1(1-34)	DCLGFFRKCIPD[Atz]DKCCRPNLVCSRTHKWCKYVF{Amide}	591
[Phe6,Atz(20kDa Peg)28]GpTx-1(1-34)	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTH[Atz(20kDa PEG)]WCKYVF-{Amide}	593
[Phe6,Atz(20kDa Peg)22]GpTx-1(1-34)	{H}-DCLGFFRKCIPDNDKCCRPNL[Atz(20kDa PEG)]CSRTHKWCKYVF-{Amide}	594
[1-Nal10;Glu29]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKECKYVF-{Amide}	595

[3Pal5]GpTx-1(1-34)	{H}-DCLG[3Pal]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	596
[Ala5;Phe6;Tyr13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDYDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	597
[Ala5;Leu6;Gly28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHGWCKYVF-{FreeAcid}	598
[Ala5;Leu6;His28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHHWCKYVF-{FreeAcid}	599
[Ala5;Leu6]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{FreeAcid}	600
[Ala5;Leu6;Asn28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHNWCKYVF-{FreeAcid}	601
[D-Ala5;Phe6]GpTx-1(1-34)	{H}-DCLGaFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	602
[bAla5;Phe6]GpTx-1(1-34)	{H}-DCLG[bAla]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	603
[Aib5;Phe6]GpTx-1(1-34)	{H}-DCLG[Aib]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	604
[2-Abu5;Phe6]GpTx-1(1-34)	{H}-DCLG[2-Abu]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	605
[Nva5;Phe6]GpTx-1(1-34)	{H}-DCLG[Nva]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	606
[Nle5;Phe6]GpTx-1(1-34)	{H}-DCLG[Nle]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	607
[OctylG5;Phe6]GpTx-1(1-34)	{H}-DCLG[OctylG]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	608
[Tle5;Phe6]GpTx-1(1-34)	{H}-DCLG[Tle]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	609
[hLeu5;Phe6]GpTx-1(1-34)	{H}-DCLG[hLeu]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	610
[Met5;Phe6]GpTx-1(1-34)	{H}-DCLGMFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	611
[Leu5;Phe6]GpTx-1(1-34)	{H}-DCLGLFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	612
[3Pal5;Phe6]GpTx-1(1-34)	{H}-DCLG[3Pal]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	613
[Thi5;Phe6]GpTx-1(1-34)	{H}-DCLG[Thi]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	614
[Cpg5;Phe6]GpTx-1(1-34)	{H}-DCLG[Cpg]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	615
[Chg5;Phe6]GpTx-1(1-34)	{H}-DCLG[Chg]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	616

[Ser5;Phe6]GpTx-1(1-34)	{H}-DCLGSFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	617
[Val5;Phe6]GpTx-1(1-34)	{H}-DCLGVFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	618
[4-Bz-F5;Phe6]GpTx-1(1-34)	{H}-DCLG[4-Bz-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	619
[DiMeO-F5;Phe6]GpTx-1(1-34)	{H}-DCLG[DiMeO-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	620
[DiCl-F5;Phe6]GpTx-1(1-34)	{H}-DCLG[DiCl-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	621
[pI-Phe5;Phe6]GpTx-1(1-34)	{H}-DCLG[pI-Phe]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	622
[4CF3-F5;Phe6]GpTx-1(1-34)	{H}-DCLG[4CF3-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	623
[4-F-F5;Phe6]GpTx-1(1-34)	{H}-DCLG[4-F-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	624
[4-Me-F5;Phe6]GpTx-1(1-34)	{H}-DCLG[4-Me-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	625
[4tBu-F5;Phe6]GpTx-1(1-34)	{H}-DCLG[4tBu-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	626
[NMeVal5;Phe6]GpTx-1(1-34)	{H}-DCLG[NMeVal]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	627
[NMeLeu5;Phe6]GpTx-1(1-34)	{H}-DCLG[NMeLeu]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	628
[NMePhe5;Phe6]GpTx-1(1-34)	{H}-DCLG[NMePhe]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	629
[2-Cl-F5;Phe6]GpTx-1(1-34)	{H}-DCLG[2-Cl-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	630
[hPhe5;Phe6]GpTx-1(1-34)	{H}-DCLG[hPhe]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	631
[Sar5;Phe6]GpTx-1(1-34)	{H}-DCLG[Sar]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	632
[D-Ala5;Leu6]GpTx-1(1-34)	{H}-DCLGaLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	633
[bAla5;Leu6]GpTx-1(1-34)	{H}-DCLG[bAla]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	634
[Aib5;Leu6]GpTx-1(1-34)	{H}-DCLG[Aib]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	635
[2-Abu5;Leu6]GpTx-1(1-34)	{H}-DCLG[2-Abu]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	636

[Nva5;Leu6]GpTx-1(1-34)	{H}-DCLG[Nva]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	637
[Nle5;Leu6]GpTx-1(1-34)	{H}-DCLG[Nle]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	638
[OctylG5;Leu6]GpTx-1(1-34)	{H}-DCLG[OctylG]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	639
[Ala5,Phe6,Pra13,Leu26,Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCIPD[Pra]DKCCRPNLVCSRLHRWCKYVF-{Amide}	640
[Met5;Leu6]GpTx-1(1-34)	{H}-DCLGMLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	641
[3Pal5;Leu6]GpTx-1(1-34)	{H}-DCLG[3Pal]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	642
[Ser5;Leu6]GpTx-1(1-34)	{H}-DCLGSLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	643
[Val5;Leu6]GpTx-1(1-34)	{H}-DCLGVLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	644
[DiMeO-F5;Leu6]GpTx-1(1-34)	{H}-DCLG[DiMeO-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	645
[Sar5;Leu6]GpTx-1(1-34)	{H}-DCLG[Sar]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	646
[D-Ala5]GpTx-1(1-34)	{H}-DCLGaMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	647
[bAla5]GpTx-1(1-34)	{H}-DCLG[bAla]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	648
[2-Abu5]GpTx-1(1-34)	{H}-DCLG[2-Abu]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	649
[Nva5]GpTx-1(1-34)	{H}-DCLG[Nva]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	650
[Nle5]GpTx-1(1-34)	{H}-DCLG[Nle]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	651
[DiMeO-F5]GpTx-1(1-34)	{H}-DCLG[DiMeO-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	652
[DiCl-F5]GpTx-1(1-34)	{H}-DCLG[DiCl-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	653
[4CF3-F5]GpTx-1(1-34)	{H}-DCLG[4CF3-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	654
[4-F-F5]GpTx-1(1-34)	{H}-DCLG[4-F-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	655
[NMeVal5]GpTx-1(1-34)	{H}-DCLG[NMeVal]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	656
[NMePhe5]GpTx-1(1-34)	{H}-DCLG[NMePhe]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	657
[Sar5]GpTx-1(1-34)	{H}-DCLG[Sar]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	658
[Tle5;Leu6]GpTx-1(1-34)	{H}-DCLG[Tle]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	659
[hLeu5;Leu6]GpTx	{H}-	660

-1(1-34)	DCLG[hLeu]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	
[Leu5,6]GpTx-1(1-34)	{H}-DCLGLLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	661
[Thi5;Leu6]GpTx-1(1-34)	{H}-DCLG[Thi]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	662
[Cpg5;Leu6]GpTx-1(1-34)	{H}-DCLG[Cpg]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	663
[Chg5;Leu6]GpTx-1(1-34)	{H}-DCLG[Chg]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	664
[4-Bz-F5;Leu6]GpTx-1(1-34)	{H}-DCLG[4-Bz-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	665
[DiCl-F5;Leu6]GpTx-1(1-34)	{H}-DCLG[DiCl-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	666
[pI-Phe5;Leu6]GpTx-1(1-34)	{H}-DCLG[pI-Phe]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	667
[4CF3-F5;Leu6]GpTx-1(1-34)	{H}-DCLG[4CF3-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	668
[4-F-F5;Leu6]GpTx-1(1-34)	{H}-DCLG[4-F-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	669
[4-Me-F5;Leu6]GpTx-1(1-34)	{H}-DCLG[4-Me-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	670
[4tBu-F5;Leu6]GpTx-1(1-34)	{H}-DCLG[4tBu-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	671
[NMeVal5;Leu6]GpTx-1(1-34)	{H}-DCLG[NMeVal]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	672
[NMeLeu5;Leu6]GpTx-1(1-34)	{H}-DCLG[NMeLeu]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	673
[NMePhe5;Leu6]GpTx-1(1-34)	{H}-DCLG[NMePhe]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	674
[2-Cl-F5;Leu6]GpTx-1(1-34)	{H}-DCLG[2-Cl-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	675
[hPhe5;Leu6]GpTx-1(1-34)	{H}-DCLG[hPhe]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	676
[OctylG5]GpTx-1(1-34)	{H}-DCLG[OctylG]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	677
[Tle5]GpTx-1(1-34)	{H}-DCLG[Tle]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	678
[hLeu5]GpTx-1(1-34)	{H}-DCLG[hLeu]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	679

[Cha5;Phe6]GpTx-1(1-34)	{H}-DCLG[Cha]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	680
[Cha5;Leu6]GpTx-1(1-34)	{H}-DCLG[Cha]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	681
[Thi5]GpTx-1(1-34)	{H}-DCLG[Thi]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	682
[Cpg5]GpTx-1(1-34)	{H}-DCLG[Cpg]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	683
[Chg5]GpTx-1(1-34)	{H}-DCLG[Chg]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	684
[4-Bz-F5]GpTx-1(1-34)	{H}-DCLG[4-Bz-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	685
[4-Me-F5]GpTx-1(1-34)	{H}-DCLG[4-Me-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	686
[4tBu-F5]GpTx-1(1-34)	{H}-DCLG[4tBu-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	687
[NMeLeu5]GpTx-1(1-34)	{H}-DCLG[NMeLeu]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	688
[2-Cl-F5]GpTx-1(1-34)	{H}-DCLG[2-Cl-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	689
[hPhe5]GpTx-1(1-34)	{H}-DCLG[hPhe]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	690
[Ala5;Glu28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	691
[Ala5;1'NMeW32]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCK[1'NMeW]VF-{Amide}	692
[Met5;1'NMeW32]GpTx-1(1-34)	{H}-DCLGMMRKCIPDNDKCCRPNLVCSRTHKWCK[1'NMeW]VF-{Amide}	693
[Arg4;Met5]GpTx-1(1-34)	{H}-DCLRMMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	694
[Ser19;1'NMeW32]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRSNLVCSRTHKWCK[1'NMeW]VF-{Amide}	695
[Ala5;Leu6]GpTx-1(1-34)	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	696
[Ala5;Gly6]GpTx-1(1-34)	{H}-DCLGAGRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	697
[Ala5;Tyr6]GpTx-1(1-34)	{H}-DCLGAYRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	698
[Ala5;1'NMeW6]GpTx-1(1-34)	{H}-DCLGA[1'NMeW]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	699
[Ala5;Asp10]GpTx-1(1-34)	{H}-DCLGAMRKCDPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	700
[Ala5;Asp10;Glu12]GpTx-1(1-34)	{H}-DCLGAMRKCDPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	701
[Ala5;Phe6;Asp10]GpTx-1(1-34)	{H}-DCLGAFRKCDPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	702

[Ala5;Phe6;Glu12] GpTx-1(1-34)	{H}-DCLGAFRKCIPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	703
[Val5;Glu28]GpTx-1(1-34)	{H}-DCLGVMRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	704
[Nva5;Glu28]GpTx-1(1-34)	{H}-DCLG[Nva]MRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	705
[2-Abu5;Glu28]GpTx-1(1-34)	{H}-DCLG[2-Abu]MRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	706
[2-Abu5;Leu6;Glu28] GpTx-1(1-34)	{H}-DCLG[2-Abu]LRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	707
[Nva5;Leu6;Glu28] GpTx-1(1-34)	{H}-DCLG[Nva]LRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	708
[Val5;Leu6;Glu28] GpTx-1(1-34)	{H}-DCLGVLRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	709
[Val5;Asp10]GpTx-1(1-34)	{H}-DCLGVMRKCDPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	710
[Val5;Glu12]GpTx-1(1-34)	{H}-DCLGVMRKCIPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	711
[Val5;Asp10;Glu12]GpTx-1(1-34)	{H}-DCLGVMRKCDPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	712
[Val5;Cit25]GpTx-1(1-34)	{H}-DCLGVMRKCIPDNDKCCRPNLVCS[Cit]THKWCKYVF-{Amide}	713
[Thr5;Asp10]GpTx-1(1-34)	{H}-DCLGTMRKCDPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	714
[Ala5;Gly28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHGWCKYVF-{Amide}	715
[2-Abu2,17;Ala5;Asp 10]GpTx-1(1-34)	{H}-D[2-Abu]LGAMRKCDPDNDKC[2-Abu]RPNLVCSRTHKWCKYVF-{Amide}	716
[2-Abu2,17;Nva5;Leu 6;Glu28]GpTx-1(1-34)	{H}-D[2-Abu]LG[Nva]LRKCIPDNDKC[2-Abu]RPNLVCSRTHEWCKYVF-{Amide}	717
[2-Abu2,5,17;Leu6;Gl u28]GpTx-1(1-34)	{H}-D[2-Abu]LG[2-Abu]LRKCIPDNDKC[2-Abu]RPNLVCSRTHEWCKYVF-{Amide}	718
[2-Abu2,17;Ala5;Leu 6;Glu28]GpTx-1(1-34)	{H}-D[2-Abu]LGALRKCIPDNDKC[2-Abu]RPNLVCSRTHEWCKYVF-{Amide}	719
[2-Abu2,17;Val5;Leu 6;Glu28]GpTx-1(1-34)	{H}-D[2-Abu]LGVLRKCIPDNDKC[2-Abu]RPNLVCSRTHEWCKYVF-{Amide}	720
[Ala5;Nle6]GpTx-1(1-34)	{H}-DCLGA[Nle]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	721
[Ala5;Nle6;Glu10] GpTx-1(1-34)	{H}-DCLGA[Nle]RKCEPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	722
[Ala5;Leu6;Glu10] GpTx-1(1-34)	{H}-DCLGALRKCEPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	723
[Ala5;Phe6;Glu10] GpTx-1(1-34)	{H}-DCLGAFRKCEPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	724

[Ala5;Nle6;Glu12] GpTx-1(1-34)	{H}-DCLGA[Nle]RKCIPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	725
[Ala5;Leu6;Glu12] GpTx-1(1-34)	{H}-DCLGALRKCIPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	726
[Ala5;Nle6;Glu28] GpTx-1(1-34)	{H}-DCLGA[Nle]RKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	727
[Ala5;Leu6;Glu28] GpTx-1(1-34)	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	728
[Ala5;Phe6;Glu28] GpTx-1(1-34)	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	729
[Ala5,25;Nle6]GpTx-1(1-34)	{H}-DCLGA[Nle]RKCIPDNDKCCRPNLVCSATHKWCKYVF-{Amide}	730
[Ala5,25;Leu6]GpTx-1(1-34)	{H}-DCLGALRKCIPDNDKCCRPNLVCSATHKWCKYVF-{Amide}	731
[Ala5,25;Phe6]GpTx-1(1-34)	{H}-DCLGAFRKCIPDNDKCCRPNLVCSATHKWCKYVF-{Amide}	732
[Ala5;Nle6;Glu25] GpTx-1(1-34)	{H}-DCLGA[Nle]RKCIPDNDKCCRPNLVCSETHKWCKYVF-{Amide}	733
[Ala5;Leu6;Glu25] GpTx-1(1-34)	{H}-DCLGALRKCIPDNDKCCRPNLVCSETHKWCKYVF-{Amide}	734
[Ala5;Phe6;Glu25] GpTx-1(1-34)	{H}-DCLGAFRKCIPDNDKCCRPNLVCSETHKWCKYVF-{Amide}	735
[Phe6,Pra15]GpTx-1(1-34)	{H}-DCLGFFRKCIPDND[Pra]CCRPNLVCSRTHKWCKYVF-{Amide}	736
[Ala5;His28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHHWCKYVF-{Amide}	737
[Ala5;Ser28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHSWCKYVF-{Amide}	738
[Ala5;Gln28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHQWCKYVF-{Amide}	739
[Ala5;3Pal28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[3Pal]WCKYVF-{Amide}	740
[Ala5;4-aminoF28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[4-aminoF]WCKYVF-{Amide}	741
[Ala5;K(Ac)28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[K(Ac)]WCKYVF-{Amide}	742
[Ala5;SDMA28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[SDMA]WCKYVF-{Amide}	743
[Ala5;hArg28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[hArg]WCKYVF-{Amide}	744
[Ala5;R(Me)28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[R(Me)]WCKYVF-{Amide}	745
[Ala5;Orn28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[Orn]WCKYVF-{Amide}	746
[Ala5;Dap28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[Dap]WCKYVF-{Amide}	747
[Ala5;Cit28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[Cit]WCKYVF-{Amide}	748

[Ala5;HCit28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[HCit]WCKYVF-{Amide}	749
[Asp28]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHDWCKYVF-{Amide}	750
[Gly5;Val6]GpTx-1(1-34)	{H}-DCLGGVRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	751
[Gly5;Ile6]GpTx-1(1-34)	{H}-DCLGGIRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	752
[2-Abu5;Nle6]GpTx-1(1-34)	{H}-DCLG[2-Abu][Nle]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	753
[Gly5;Phe6;Glu10]GpTx-1(1-34)	{H}-DCLGGFRKCEPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	754
[Gly5;Phe6;Glu28]GpTx-1(1-34)	{H}-DCLGGFRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	755
4-Pen-[Ala5;Phe6;2-Abu13;Arg28]GpTx-1(1-34)	{4-Pen}-DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	756
4-Pen-[Ala5;Phe6;2-Abu13]GpTx-1(1-34)	{4-Pen}-DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRTHKWCKYVF-{Amide}	757
4-Pen-[2-Abu5,13;Leu6]GpTx-1(1-34)	{4-Pen}-DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRTHKWCKYVF-{Amide}	758
4-Pen-[Nva5;Leu6;2-Abu13;Arg28]GpTx-1(1-34)	{4-Pen}-DCLG[Nva]LRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	759
4-Pen-[Nva5;Leu6;2-Abu13]GpTx-1(1-34)	{4-Pen}-DCLG[Nva]LRKCIPD[2-Abu]DKCCRPNLVCSRTHKWCKYVF-{Amide}	760
[Ala5;Guf28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[Guf]WCKYVF-{Amide}	761
[Ala5;Dab28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[Dab]WCKYVF-{Amide}	762
[Gln28]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHQWCKYVF-{Amide}	763
[Ala5;Phe28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHFWCKYVF-{Amide}	764
[Ala5;Tyr28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHYWCKYVF-{Amide}	765
[Ala5;Leu28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHLWCKYVF-{Amide}	766
[Ala5;Asn28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHNWCKYVF-{Amide}	767
[Ala5;Cit25]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCS[Cit]THKWCKYVF-{Amide}	768
[Ala5;Asp28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHDWCKYVF-{Amide}	769
[Ala5;Met28]GpTx-	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHMWCKYVF-	770

1(1-34)	{Amide}	
[Ala5;K(Me)28]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[K(Me)]WCKYVF-{Amide}	771
[pS28]GpTx-1(1-34)	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTH[pS]WCKYVF-{Amide}	772
[Thr5;Asp10;Glu12]GpTx-1(1-34)	{H}-DCLGTMRKCDPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	773
[1-Nal10;Glu33]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYEF-{Amide}	774
[1-Nal10;Glu32]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKEVF-{Amide}	775
[1-Nal10;Glu31]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCEYVF-{Amide}	776
[1-Nal10;Ala33]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYAF-{Amide}	777
[1-Nal10;Ala32]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKAVF-{Amide}	778
[1-Nal10;Ala31]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCAYVF-{Amide}	779
[1-Nal10;Glu28]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	780
[1-Nal10;Glu15]GpTx-1(1-34)	{H}-DCLGFMRKC[1-Nal]PDNDECCRPNLVCSRTHKWCKYVF-{Amide}	781
[Glu8;1-Nal10]GpTx-1(1-34)	{H}-DCLGFMREC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	782
[Glu4;1-Nal10]GpTx-1(1-34)	{H}-DCLEFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	783
[1-Nal1;Glu8]GpTx-1(1-34)	{H}-[1-Nal]CLGFMRECIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	784
[1-Nal1;Glu7]GpTx-1(1-34)	{H}-[1-Nal]CLGFMEKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	785
[1-Nal1;Glu6]GpTx-1(1-34)	{H}-[1-Nal]CLGFERKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	786
[Ala5;Glu26]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSREHKWCKYVF-{Amide}	787
[Ala5;Glu27]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTEKWCKYVF-{Amide}	788
[Ala5;Glu31]GpTx-1(1-34)	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCEYVF-{Amide}	789
[Ala5]GpTx-1(1-34)-Glu	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYVFE-{Amide}	790
[Ala5,Met(O)6]GpT	{H}-	791

x-1 isomer1	DCLGA[METO1]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	
[Ala5,Met(O)6]GpTx-1 isomer2	{H}-DCLGA[METO1]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	792
[Ala5;Phe6;Pra13]GpTx-1(1-34)	{H}-DCLGAFRKCIPD[Pra]DKCCRPNLVCSRTHKWCKYVF-{Amide}	793
[Ala5;Phe6;K(Ac-Pra)13]GpTx-1(1-34)	{H}-DCLGAFRKCIPD[K(Ac-Pra)]DKCCRPNLVCSRTHKWCKYVF-{Amide}	794
[Ala5;Phe6;K(Ac-Pra)13;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCIPD[K(Ac-Pra)]DKCCRPNLVCSRTHRWCKYVF-{Amide}	795
[Ala5;Leu6,26;Pra13;Arg28]GpTx-1(1-34)	{H}-DCLGALRKCIPD[Pra]DKCCRPNLVCSRLHRWCKYVF-{Amide}	796
[2-Abu5;Leu6;Pra13]GpTx-1(1-34)	{H}-DCLG[2-Abu]LRKCIPD[Pra]DKCCRPNLVCSRTHKWCKYVF-{Amide}	797
[Ala5;Phe6;Glu10;Pra13;Leu26;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCEPD[Pra]DKCCRPNLVCSRLHRWCKYVF-{Amide}	798
[2-Abu5;Leu6;K(Ac-Pra)13]GpTx-1(1-34)	{H}-DCLG[2-Abu]LRKCIPD[K(Ac-Pra)]DKCCRPNLVCSRTHKWCKYVF-{Amide}	799
[Ala5;Leu6,26;Glu10;Pra13;Arg28]GpTx-1(1-34)	{H}-DCLGALRKCEPD[Pra]DKCCRPNLVCSRLHRWCKYVF-{Amide}	800
[2-Abu5;Leu6;K(4-Pen)13;Arg28]GpTx-1(1-34)	{H}-DCLG[2-Abu]LRKCIPD[K(4-Pen)]DKCCRPNLVCSRTHRWCKYVF-{Amide}	801
[Ala5;Leu6,26;Pra12;Arg28]GpTx-1(1-34)	{H}-DCLGALRKCIP[Pra]NDKCCRPNLVCSRLHRWCKYVF-{Amide}	802
[Ala5;Phe6;Pra12;Leu26;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCIP[Pra]NDKCCRPNLVCSRLHRWCKYVF-{Amide}	803
[2-Abu5;Phe6;K(4-Pen)13]GpTx-1(1-34)	{H}-DCLG[2-Abu]FRKCIPD[K(4-Pen)]DKCCRPNLVCSRTHKWCKYVF-{Amide}	804
[Nva5;Leu6;K(4-Pen)13;Arg28]GpTx-1(1-34)	{H}-DCLG[Nva]LRKCIPD[K(4-Pen)]DKCCRPNLVCSRTHRWCKYVF-{Amide}	805
[Nva5;Leu6;K(4-Pen)13]GpTx-1(1-34)	{H}-DCLG[Nva]LRKCIPD[K(4-Pen)]DKCCRPNLVCSRTHKWCKYVF-{Amide}	806
4-Pen-[2-Abu5,13;Leu6;Arg28]GpTx-1(1-34)	{4-Pen}-DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	807
[2-Abu5;Leu6;K(4-Pen)13;Glu28]GpTx-1(1-34)	{H}-DCLG[2-Abu]LRKCIPD[K(4-Pen)]DKCCRPNLVCSRTHEWCKYVF-{Amide}	808
[Ala5;Phe6;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	809
[Ala5;Leu6;Arg28]	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVF-	810

GpTx-1(1-34)	{Amide}	
Gly-Ser-[Ala5;Phe6;Arg28] GpTx-1(1-34)	{H}-GSDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	811
Gly-Ser-[Ala5;Leu6;Arg28] GpTx-1(1-34)	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	812
[Ala5;Phe6;Arg28] GpTx-1(1-34)-Trp-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFW-{FreeAcid}	813
[Ala5;Leu6;Arg28] GpTx-1(1-34)-Trp-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFW-{FreeAcid}	814
Gly-Ser-[Ala5;Phe6;Arg28] GpTx-1(1-34)-Trp-FreeAcid	{H}-GSDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFW-{FreeAcid}	815
Gly-Ser-[Ala5;Leu6;Arg28] GpTx-1(1-34)-Trp-FreeAcid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFW-{FreeAcid}	816
[Ala5;Phe6;Arg28] GpTx-1(1-34)-Phe-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	817
[Ala5;Leu6;Arg28] GpTx-1(1-34)-Phe-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	818
Gly-Ser-[Ala5;Phe6;Arg28] GpTx-1(1-34)-Phe-FreeAcid	{H}-GSDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	819
Gly-Ser-[Ala5;Leu6;Arg28] GpTx-1(1-34)-Phe-FreeAcid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	820
Gly-Ser-[Ala5;Phe6;Arg28] GpTx-1(1-34)-FreeAcid	{H}-GSDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	821
Gly-Ser-[Ala5;Leu6;Arg28] GpTx-1(1-34)-FreeAcid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	822
[Ala5;Phe6;Arg28] GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	823
[Ala5,28;Phe6]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHAWCKYVF-{FreeAcid}	824
[Ala5;Phe6;Asp28] GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHDWCKYVF-{FreeAcid}	825
[Ala5;Phe6;Glu28] GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{FreeAcid}	826
[Ala5;Phe6;Gly28]	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHGWCKYVF-	827

GpTx-1(1-34)-FreeAcid	{FreeAcid}	
[Ala5;Phe6;His28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHHWCKYVF-{FreeAcid}	828
[Ala5;Phe6]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{FreeAcid}	829
[Ala5;Phe6;Leu28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHLWCKYVF-{FreeAcid}	830
[Ala5;Phe6;Met28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHMWCKYVF-{FreeAcid}	831
[Ala5;Phe6;Asn28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHNWCKYVF-{FreeAcid}	832
[Ala5;Phe6;Pro28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHPWCKYVF-{FreeAcid}	833
[Ala5;Phe6;Gln28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHQWCKYVF-{FreeAcid}	834
[Ala5;Phe6;Ser28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHSWCKYVF-{FreeAcid}	835
[Ala5,13;Phe6;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDADKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	836
[Ala5;Phe6;Asp13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDDDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	837
[Ala5;Phe6;Glu13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDEDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	838
[Ala5;Phe6,13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDFDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	839
[Ala5;Phe6;Gly13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDGDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	840
[Ala5;Phe6;His13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDHDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	841
[Ala5;Phe6;Ile13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDIDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	842
[Ala5;Phe6;Lys13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDKDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	843
[Ala5;Phe6;Leu13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDLDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	844
[Ala5;Phe6;Met13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDMDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	845
[Ala5;Phe6;Pro13;	{H}-DCLGAFRKCIPDPDKCCRPNLVCSRTHRWCKYVF-	846

Arg28]GpTx-1(1-34)-FreeAcid	{FreeAcid}	
[Ala5;Phe6;Gln13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDQDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	847
[Ala5;Phe6;Arg13,28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDRDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	848
[Ala5;Phe6;Ser13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDSDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	849
[Ala5;Phe6;Thr13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDTDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	850
[Ala5;Phe6;Val13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDVDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	851
[Ala5;Phe6;Trp13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGAFRKCIPDWDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	852
[Ala5;Leu6;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	853
[Ala5;Leu6;Asp28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHDWCKYVF-{FreeAcid}	854
[Ala5;Leu6;Glu28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{FreeAcid}	855
[Ala5;Leu6,28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHLWCKYVF-{FreeAcid}	856
[Ala5;Leu6;Met28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHMWCKYVF-{FreeAcid}	857
[Ala5;Leu6;Gln28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHQWCKYVF-{FreeAcid}	858
[Ala5;Leu6;Ser28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHSWCKYVF-{FreeAcid}	859
[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	860
[Ala5;Leu6;Asp13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDDDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	861
[Ala5;Leu6;Glu13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDEDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	862
[Ala5;Leu6;Phe13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDFDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	863
[Ala5;Leu6;His13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDHDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	864
[Ala5;Leu6;Ile13;A	{H}-DCLGALRKCIPDIDKCCRPNLVCSRTHRWCKYVF-	865

rg28]GpTx-1(1-34)-FreeAcid	{FreeAcid}	
[Ala5;Leu6;Lys13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDKDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	866
[Ala5;Leu6,13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDLDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	867
[Ala5;Leu6;Met13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDMDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	868
[Ala5;Leu6;Gln13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDQDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	869
[Ala5;Leu6;Arg13,28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDRDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	870
[Ala5;Leu6;Ser13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDSDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	871
[Ala5;Leu6;Val13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDVDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	872
[Ala5;Leu6;Tyr13;Arg28]GpTx-1(1-34)-FreeAcid	{H}-DCLGALRKCIPDYDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	873
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Gly-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFG -{FreeAcid}	874
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Gly-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFG -{FreeAcid}	875
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Gly-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFG -{FreeAcid}	876
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Ile-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFI -{FreeAcid}	877
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Ile-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFI -{FreeAcid}	878
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Ile-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFI -{FreeAcid}	879
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Ile-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFI -{FreeAcid}	880
Gly-Ser-[Ala5;Leu6;Arg28]	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFL -	881

GpTx-1(1-34)-Leu-Free Acid	{FreeAcid}	
Gly-Ser-[Ala5;Leu6;Arg28] GpTx-1(1-34)-Phe-Leu-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFL-{FreeAcid}	882
Gly-Ser-[Ala5,13;Leu6;Arg 28]GpTx-1(1-34)-Leu-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFL-{FreeAcid}	883
Gly-Ser-[Ala5,13;Leu6;Arg 28]GpTx-1(1-34)-Phe-Leu-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFL-{FreeAcid}	884
Gly-Ser-[Ala5;Leu6;Arg28] GpTx-1(1-34)-Ser-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFS-{FreeAcid}	885
Gly-Ser-[Ala5;Leu6;Arg28] GpTx-1(1-34)-Phe-Ser-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFS-{FreeAcid}	886
Gly-Ser-[Ala5,13;Leu6;Arg 28]GpTx-1(1-34)-Ser-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFS-{FreeAcid}	887
Gly-Ser-[Ala5,13;Leu6;Arg 28]GpTx-1(1-34)-Phe-Ser-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFS-{FreeAcid}	888
Gly-Ser-[Ala5;Leu6;Arg28] GpTx-1(1-34)-Thr-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFT-{FreeAcid}	889
Gly-Ser-[Ala5;Leu6;Arg28] GpTx-1(1-34)-Phe-Thr-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFT-{FreeAcid}	890
Gly-Ser-[Ala5,13;Leu6;Arg 28]GpTx-1(1-34)-Thr-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFT-{FreeAcid}	891
Gly-Ser-[Ala5,13;Leu6;Arg 28]GpTx-1(1-34)-Phe-Thr-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFT-{FreeAcid}	892
Gly-Ser-[Ala5;Leu6;Arg28] GpTx-1(1-34)-Tyr-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFY-{FreeAcid}	893
Gly-Ser-[Ala5;Leu6;Arg28] GpTx-1(1-34)-Phe-Tyr-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFY-{FreeAcid}	894
Gly-Ser-[Ala5,13;Leu6;Arg 28]GpTx-1(1-34)-	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFY-{FreeAcid}	895

Tyr-Free Acid		
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Tyr-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFY-{FreeAcid}	896
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFA-{FreeAcid}	897
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFA-{FreeAcid}	898
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Phe-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFFA-{FreeAcid}	899
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Tyr-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFYA-{FreeAcid}	900
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Leu-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFLA-{FreeAcid}	901
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Ile-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFIA-{FreeAcid}	902
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Ala-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFAA-{FreeAcid}	903
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Ser-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFSA-{FreeAcid}	904
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Thr-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFTA-{FreeAcid}	905
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Ala-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFAA-{FreeAcid}	906
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Gly-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFGA-{FreeAcid}	907
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Ala-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFA-{FreeAcid}	908
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFA-{FreeAcid}	909

Phe-Ala-Free Acid		
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Phe-Ala-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFFA-{FreeAcid}	910
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Tyr-Ala-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFYA-{FreeAcid}	911
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Leu-Ala-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFLA-{FreeAcid}	912
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Ile-Ala-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFIA-{FreeAcid}	913
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Ala-Ala-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFAA-{FreeAcid}	914
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Ser-Ala-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFSA-{FreeAcid}	915
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Thr-Ala-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFTA-{FreeAcid}	916
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Ala-Ala-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFAA-{FreeAcid}	917
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Gly-Ala-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFGA-{FreeAcid}	918
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFA-{FreeAcid}	919
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Ala-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFA-{FreeAcid}	920
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFA-{FreeAcid}	921

Ala-Free Acid		
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Ala-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFFA-{FreeAcid}	922
Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Phe-Free Acid	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFFF-{FreeAcid}	923
Gly-Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	924
Gly-Gly-Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	925
Gly-Gly-Gly-Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	926
Ser-Gly-Gly-Gly-Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-SGGGGSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	927
Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSGGGGSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	928
Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSGGGGSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	929
Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGSGGGGSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	930
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	931
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	932
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-	{H}-GGGGSGGGGSDCLGAFRKCIPDADKCCRPNLVCSRTHR	933

Gly-Ser-[Ala5,13;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	WCKYVFF-{FreeAcid}	
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	934
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Gly-Phe-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFGF-{FreeAcid}	935
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	936
Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	937
Gly-Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	938
Gly-Gly-Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	939
Gly-Gly-Gly-Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	940
Ser-Gly-Gly-Gly-Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-SGGGGSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	941
Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSGGGGSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	942
Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSGGGGSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	943
Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGSGGGGSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	944
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-	{H}-GGGGSGGGGSDCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	945

[Ala5,13;Leu6;Arg 28]GpTx-1(1-34)-Phe-Free Acid		
Gly-Ser-[Ala5;Leu6;Gly13; Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDGDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	946
Gly-Ser-[Ala5;Leu6;Ser13; Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDSDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	947
Gly-Ser-[Ala5;Leu6;Ile13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDIDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	948
Gly-Ser-[Ala5;Leu6;Pro13; Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDPDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	949
Gly-Ser-[Ala5;Leu6;Met13; Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDMDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	950
Gly-Ser-[Ala5;Leu6;Val13; Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDVDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	951
Gly-Ser-[Ala5;Leu6;Thr13; Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDTDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	952
Gly-Ser-[Ala5;Leu6;Phe13; Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDFDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	953
Gly-Ser-[Ala5;Leu6;Tyr13; Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGALRKCIPDYDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	954
Gly-Ser-[Ala5;Phe6;Gly13; Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGAFRKCIPDGDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	955
Gly-Ser-[Ala5;Phe6;Ser13; Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGAFRKCIPDSDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	956
Gly-Ser-[Ala5;Phe6;Ile13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGAFRKCIPDIDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	957
Gly-Ser-[Ala5;Phe6;Leu13; Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGAFRKCIPDLDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	958
Gly-Ser-[Ala5;Phe6;Met13;	{H}-GSDCLGAFRKCIPDMDKCCRPNLVCSRTHRWCKYVFF-	959

Arg28]GpTx-1(1-34)-Phe-Free Acid	{FreeAcid}	
Gly-Ser-[Ala5;Phe6;Val13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGAFRKCIPDVDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	960
Gly-Ser-[Ala5;Phe6;Thr13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGAFRKCIPDTDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	961
Gly-Ser-[Ala5;Phe6,13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGAFRKCIPDFDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	962
Gly-Ser-[Ala5;Phe6;Tyr13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GSDCLGAFRKCIPDYDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	963
Gly-Ile-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GIDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	964
Gly-Ala-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	965
Gly-Thr-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GTDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	966
Gly-Ala-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	967
Gly-Gly-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	968
Gly-Phe-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GFDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	969
Gly-Tyr-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GYDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	970
Gly-Leu-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GLDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	971
Gly-Val-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GVDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	972
Gly-Ile-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-	{H}-GIDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	973

Free Acid		
Gly-Ala-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	974
Gly-Thr-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GTDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	975
Gly-Ala-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	976
Gly-Gly-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	977
Gly-Phe-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GFDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	978
Gly-Tyr-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GYDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	979
Gly-Leu-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GLDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	980
Gly-Val-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GVDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	981
Gly-Ala-[Ala5;Phe6;Gly13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGAFRKCIPDGDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	982
Gly-Ala-[Ala5;Phe6;Ser13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGAFRKCIPDSDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	983
Gly-Ala-[Ala5;Phe6;Ile13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGAFRKCIPDIDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	984
Gly-Ala-[Ala5;Phe6;Leu13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGAFRKCIPDLDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	985
Gly-Ala-[Ala5;Phe6;Met13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGAFRKCIPDMDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	986
Gly-Ala-[Ala5;Phe6;Val13;Arg28]GpTx-1(1-	{H}-GADCLGAFRKCIPDVDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	987

34)-Phe-Free Acid		
Gly-Ala-[Ala5;Phe6;Thr13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGAFRKCIPDTDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	988
Gly-Ala-[Ala5;Phe6,13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGAFRKCIPDFDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	989
Gly-Ala-[Ala5;Phe6;Tyr13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGAFRKCIPDYDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	990
Gly-Ala-[Ala5;Leu6;Gly13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGALRKCIPDGDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	991
Gly-Ala-[Ala5;Leu6;Ser13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGALRKCIPDSDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	992
Gly-Ala-[Ala5;Leu6;Ile13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGALRKCIPDIDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	993
Gly-Ala-[Ala5;Leu6,13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGALRKCIPDLDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	994
Gly-Ala-[Ala5;Leu6;Met13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGALRKCIPDMDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	995
Gly-Ala-[Ala5;Leu6;Val13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGALRKCIPDVDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	996
Gly-Ala-[Ala5;Leu6;Thr13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGALRKCIPDTDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	997
Gly-Ala-[Ala5;Leu6;Phe13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGALRKCIPDFDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	998
Gly-Ala-[Ala5;Leu6;Tyr13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GADCLGALRKCIPDYDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	999
Gly-Gly-[Ser1;Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1000
Gly-Gly-[Trp1;Ala5;Leu6;Arg28]GpTx-1(1-34)-	{H}-GGWCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1001

Phe-Free Acid		
Gly-Gly-[Phe1;Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGFCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1002
Gly-Gly-[Ile1;Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGICLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1003
Gly-Gly-Ser-[Ser1;Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSSCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1004
Gly-Gly-Ser-[Trp1;Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSWCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1005
Gly-Gly-Ser-[Phe1;Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSFCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1006
Gly-Gly-Ser-[Ile1;Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSICLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1007
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Ile1;Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSICLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1008
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Phe1;Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSFCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1009
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Trp1;Ala5,13;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSWCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1010
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Ile1;Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSICLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1011
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Phe1;Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSFCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1012
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-	{H}-GGGGSGGGGSWCLGALRKCIPDNDKCCRPNLVCSRTHR	1013

Gly-Ser-[Trp1;Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-Free Acid	WCKYVFF-{FreeAcid}	
Gly-Gly-[Ser1;Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1014
Gly-Gly-[Trp1;Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGWCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1015
Gly-Gly-[Phe1,6;Ala5;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGFCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1016
Gly-Gly-[Ile1;Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGICLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1017
Gly-Gly-Ser-[Ser1;Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSSCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1018
Gly-Gly-Ser-[Trp1;Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSWCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1019
Gly-Gly-Ser-[Phe1,6;Ala5;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSFCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1020
Gly-Gly-Ser-[Ile1;Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGSICLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1021
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Ile1;Ala5,13;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSICLGAFRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1022
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Phe1,6;Ala5,13;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSFCLGAFRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1023
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Trp1;Ala5,13;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSWCLGAFRKCIPDADKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1024
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-	{H}-GGGGSGGGGSICLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1025

[Ile1;Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid		
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Phe1,6;Ala5;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSFCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1026
Gly-Gly-Gly-Gly-Ser-Gly-Gly-Gly-Gly-Ser-[Trp1;Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-Free Acid	{H}-GGGGSGGGGSWCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFF-{FreeAcid}	1027
[Ala5;Phe6;Atz13]GpTx-1(1-34)	DCLGAFRKCIPD[Atz]DKCCRPNLVCSRTHKWCKYVF-{Amide}	1028
Biotin-Ahx-[2-Abu5,13;Leu6;Arg28]GpTx-1(1-34)	{Biotin}-[Ahx]DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	1029
[Ala5;Phe6;Glu10;K(Biotin)13;Leu26;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCEPD[K(Biotin)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1030
Biotin-Ahx--[Ala5,Phe6,Atz13,Leu26,Arg28]GpTx-1(1-34)}	{Biotin}[Ahx]DCLGAFRKCIPD[Atz]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1031
DOTA-[Ala5]GpTx-1(1-34)	{DOTA}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	1032
[Ala5;Phe6;K(DOTA)13;Leu26;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCIPDK(DOTA)DKCCRPNLVCSRLHRWCKYVF-{Amide}	1033
[Ala5,Phe6,2-Abu13,Leu26,Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1034
[Ala5,Phe6,Glu10,2-Abu13,Leu26,Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCEPD[2-Abu]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1035
[Ala5,Leu6,2-Abu13,Leu26,Arg28]GpTx-1(1-34)	{H}-DCLGALRKCIPD[2-Abu]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1036
[Ala5,Phe6,Atz(PEG11-((2-hydroxyethyl)thio)acetamide)13,Leu26,Arg28]GpTx-1	{H}-DCLGAFRKCIPD[Atz(PEG11-((2-hydroxyethyl)thio)acetamide)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1037
[Ala5,Phe6,Atz(PEG3-(2-hydroxyethyl)thioacetamide)13,Leu26,Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCIPD[Atz(PEG3-((2-hydroxyethyl)thio)acetamide)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1038
[Ala5;Phe6;Glu10;Atz(PEG11-((2-	{H}-DCLGAFRKCEPD[Atz(PEG11-((2-hydroxyethyl)thio)acetamide)]DKCCRPNLVCSRLHRWCKY	1039

hydroxyethyl)thio)acetamide)13;Leu26;Arg28]GpTx-1(1-34)	VF-{Amide}	
[Ala5;Phe6;**Glu10**;Atz(**PEG3**-((2-hydroxyethyl)thio)acetamide)13;Leu26;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCEPD[Atz(PEG3-((2-hydroxyethyl)thio)acetamide)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1040
((2-Hydroxyethyl)thio)acetamide-NPEG11-triazole-[2-Abu5,13;Leu6;Arg28]GpTx-1(1-34)	{((2-Hydroxyethyl)thio)acetamide-NPEG11-triazole}-DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	1041
[2-Abu5,Leu6,K(ethyl-triazole-PEG11-((2-hydroxyethyl)thio)acetamide)13,Arg28]GpTx-1(1-34)	{H}-DCLG[2-Abu]LRKCIPDK(ethyl-triazole-PEG11-((2-hydroxyethyl)thio)acetamide)DKCCRPNLVCSRTHRWCKYVF-{Amide}	1042
[Ala5;**Leu6**,26;Atz(PEG11-((2-hydroxyethyl)thio)acetamide)13;Arg28]GpTx-1(1-34)	{H}-DCLGALRKCIPD[Atz(PEG3-((2-hydroxyethyl)thio)acetamide)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1043
[Ala5;**Leu6**,26;**Glu10**;Atz(PEG11-((2-hydroxyethyl)thio)acetamide)13;Arg28]GpTx-1(1-34)	{H}-DCLGALRKCEPD[Atz(PEG11-((2-hydroxyethyl)thio)acetamide)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1044
((2-hydroxyethyl)thio)acetamide-NPEG11-triazole-[Ala5,Phe6,2-Abu13,Arg28]GpTx-1(1-34)	{((2-Hydroxyethyl)thio)acetamide-NPEG11-triazole}-DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	1045
[Ala5;Phe6;Atz13;Leu26;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCIPD[Atz]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1046
[Ala5;Phe6;Glu10;Atz13;Leu26;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCEPD[Atz]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1047
[2-Abu5,13;Leu6;Arg28]GpTx-1(1-34	{H}-DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	1048
[Ala5,Phe6,Atz(PEG11-bromoacetamide)13,Leu26,Arg28]GpTx-1	{H}-DCLGAFRKCIPD[Atz(PEG11-bromoacetamide)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1062
[Ala5,Phe6,Atz(PE	{H}-DCLGAFRKCIPD[Atz(PEG3-	1063

G3-bromoacetamide)13,Leu26,Arg28]GpTx-1(1-34)	bromoacetamide)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	
[Ala5;Phe6;Glu10;Atz(PEG11-bromoacetamide)13;Leu26;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCEPD[Atz(PEG11-bromoacetamide)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1064
[Ala5;Phe6;Glu10;Atz(PEG3-bromoacetamide)13;Leu26;Arg28]GpTx-1(1-34)	{H}-DCLGAFRKCEPD[Atz(PEG3-bromoacetamide)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1065
bromoacetamide-PEG11-triazole-[2-Abu5,13;Leu6;Arg28]GpTx-1(1-34)	{bromoacetamide-PEG11-triazole}-DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	1066
[2-Abu5,Leu6,K(ethyl-triazole-PEG11-bromoacetamide)13,Arg28]GpTx-1(1-34)	{H}-DCLG[2-Abu]LRKCIPDK(ethyl-triazole-PEG11-bromoacetamide)DKCCRPNLVCSRTHRWCKYVF-{Amide}	1067
[Ala5;Leu6,26;Atz(PEG11-bromoacetamide)13;Arg28]GpTx-1(1-34)	{H}-DCLGALRKCIPD[Atz(PEG3-bromoacetamide)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1068
[Ala5;Leu6,26;Glu10;Atz(PEG11-bromoacetamide)13;Arg28]GpTx-1(1-34)	{H}-DCLGALRKCEPD[Atz(PEG11-bromoacetamide)]DKCCRPNLVCSRLHRWCKYVF-{Amide}	1069
bromoacetamide-PEG11-triazole-[Ala5,Phe6,2-Abu13,Arg28]GpTx-1(1-34)	{bromoacetamide-PEG11-triazole}-DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	1070

Table 5B. Amino acid sequences of GpTx-1 and GpTx-1 peptide analogs. -{Amide} = amidated C-terminal.

Amino Acid Sequence	Designation	SEQ ID NO.
DCLGFMRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu13;Glu28]GpTx-1(1-34)	1071
DCLGFMRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Pra13;Glu28]GpTx-1(1-34)	1072
DCLGFMRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1073
DCLGFMRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Pra13;Leu26;Glu28]GpTx-1(1-34)	1074
DCLGFMRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Glu11,28;2-Abu13]GpTx-1(1-34)	1075
DCLGFMRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Glu10,28;2-Abu13]GpTx-1(1-34)	1076
DCLGFMRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1077
DCLGFFRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Phe6;2-Abu13;Glu28]GpTx-1(1-34)	1078
DCLGFLRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu6;2-Abu13;Glu28]GpTx-1(1-34)	1079
DCLGF[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle6;2-Abu13;Glu28]GpTx-1(1-34)	1080
DCLGGMRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;2-Abu13;Glu28]GpTx-1(1-34)	1081
DCLGAMRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;2-Abu13;Glu28]GpTx-1(1-34)	1082
DCLG[2-Abu]MRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Glu28]GpTx-1(1-34)	1083
DCLG[Nva]MRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;2-Abu13;Glu28]GpTx-1(1-34)	1084
DCLG[Nle]MRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;2-Abu13;Glu28]GpTx-1(1-34)	1085
DCLGVMRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;2-Abu13;Glu28]GpTx-1(1-34)	1086

DCLGLMRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;2-Abu13;Glu28]GpTx-1(1-34)	1087
DCLGIMRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;2-Abu13;Glu28]GpTx-1(1-34)	1088
DCLGFMRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Glu11,28;Pra13]GpTx-1(1-34)	1089
DCLGFMRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Glu10,28;Pra13]GpTx-1(1-34)	1090
DCLGFMRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Asp10;Pra13;Glu28]GpTx-1(1-34)	1091
DCLGFFRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Phe6;Pra13;Glu28]GpTx-1(1-34)	1092
DCLGFLRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu6;Pra13;Glu28]GpTx-1(1-34)	1093
DCLGF[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle6;Pra13;Glu28]GpTx-1(1-34)	1094
DCLGGMRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Pra13;Glu28]GpTx-1(1-34)	1095
DCLGAMRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Pra13;Glu28]GpTx-1(1-34)	1096
DCLG[2-Abu]MRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Pra13;Glu28]GpTx-1(1-34)	1097
DCLG[Nva]MRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Pra13;Glu28]GpTx-1(1-34)	1098
DCLG[Nle]MRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Pra13;Glu28]GpTx-1(1-34)	1099
DCLGVMRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Pra13;Glu28]GpTx-1(1-34)	1100
DCLGLMRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Pra13;Glu28]GpTx-1(1-34)	1101
DCLGIMRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Pra13;Glu28]GpTx-1(1-34)	1102
DCLGFMRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1103
DCLGFMRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1104
DCLGFMRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1105
DCLGFFRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Phe6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1106

DCLGFLRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu6,26;2-Abu13;Glu28]GpTx-1(1-34)	1107
DCLGF[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1108
DCLGGMRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1109
DCLGAMRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1110
DCLG[2-Abu]MRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Leu26;Glu28]GpTx-1(1-34)	1111
DCLG[Nva]MRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1112
DCLG[Nle]MRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1113
DCLGVMRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1114
DCLGLMRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;2-Abu13;Glu28]GpTx-1(1-34)	1115
DCLGIMRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1116
DCLGFMRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1117
DCLGFMRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1118
DCLGFMRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1119
DCLGFFRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Phe6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1120
DCLGFLRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu6,26;Pra13;Glu28]GpTx-1(1-34)	1121
DCLGF[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1122
DCLGGMRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Pra13;Leu26;Glu28]GpTx-1(1-34)	1123
DCLGAMRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Pra13;Leu26;Glu28]GpTx-1(1-34)	1124
DCLG[2-Abu]MRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Pra13;Leu26;Glu28]GpTx-1(1-34)	1125
DCLG[Nva]MRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Pra13;Leu26;Glu28]GpTx-1(1-34)	1126

DCLG[Nle]MRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Pra13;Leu26;Glu28]GpTx-1(1-34)	1127
DCLGVMRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Pra13;Leu26;Glu28]GpTx-1(1-34)	1128
DCLGLMRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Pra13;Glu28]GpTx-1(1-34)	1129
DCLGIMRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Pra13;Leu26;Glu28]GpTx-1(1-34)	1130
DCLGFFRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Phe6;Glu11,28;2-Abu13]GpTx-1(1-34)	1131
DCLGFLRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu6;Glu11,28;2-Abu13]GpTx-1(1-34)	1132
DCLGF[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle6;Glu11,28;2-Abu13]GpTx-1(1-34)	1133
DCLGGMRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Glu11,28;2-Abu13]GpTx-1(1-34)	1134
DCLGAMRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Glu11,28;2-Abu13]GpTx-1(1-34)	1135
DCLG[2-Abu]MRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Glu11,28]GpTx-1(1-34)	1136
DCLG[Nva]MRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Glu11,28;2-Abu13]GpTx-1(1-34)	1137
DCLG[Nle]MRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Glu11,28;2-Abu13]GpTx-1(1-34)	1138
DCLGVMRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Glu11,28;2-Abu13]GpTx-1(1-34)	1139
DCLGLMRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Glu11,28;2-Abu13]GpTx-1(1-34)	1140
DCLGIMRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Glu11,28;2-Abu13]GpTx-1(1-34)	1141
DCLGFFRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Phe6;Glu10,28;2-Abu13]GpTx-1(1-34)	1142
DCLGFLRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu6;Glu10,28;2-Abu13]GpTx-1(1-34)	1143
DCLGF[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle6;Glu10,28;2-Abu13]GpTx-1(1-34)	1144
DCLGGMRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Glu10,28;2-Abu13]GpTx-1(1-34)	1145
DCLGAMRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Glu10,28;2-Abu13]GpTx-1(1-34)	1146

DCLG[2-Abu]MRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Glu10,28]GpTx-1(1-34)	1147
DCLG[Nva]MRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Glu10,28;2-Abu13]GpTx-1(1-34)	1148
DCLG[Nle]MRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Glu10,28;2-Abu13]GpTx-1(1-34)	1149
DCLGVMRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Glu10,28;2-Abu13]GpTx-1(1-34)	1150
DCLGLMRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Glu10,28;2-Abu13]GpTx-1(1-34)	1151
DCLGIMRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Glu10,28;2-Abu13]GpTx-1(1-34)	1152
DCLGFFRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Phe6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1153
DCLGFLRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1154
DCLGF[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1155
DCLGGMRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1156
DCLGAMRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1157
DCLG[2-Abu]MRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Asp10;Glu28]GpTx-1(1-34)	1158
DCLG[Nva]MRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1159
DCLG[Nle]MRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1160
DCLGVMRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1161
DCLGLMRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1162
DCLGIMRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1163
DCLGGFRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Phe6;2-Abu13;Glu28]GpTx-1(1-34)	1164
DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Phe6;2-Abu13;Glu28]GpTx-1(1-34)	1165
DCLG[2-Abu]FRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu28]GpTx-1(1-34)	1166

DCLG[Nva]FRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Phe6;2-Abu13;Glu28]GpTx-1(1-34)	1167
DCLG[Nle]FRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Phe6;2-Abu13;Glu28]GpTx-1(1-34)	1168
DCLGVFRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Phe6;2-Abu13;Glu28]GpTx-1(1-34)	1169
DCLGLFRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Phe6;2-Abu13;Glu28]GpTx-1(1-34)	1170
DCLGIFRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Phe6;2-Abu13;Glu28]GpTx-1(1-34)	1171
DCLGGLRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Leu6;2-Abu13;Glu28]GpTx-1(1-34)	1172
DCLGALRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Leu6;2-Abu13;Glu28]GpTx-1(1-34)	1173
DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Leu6;Glu28]GpTx-1(1-34)	1174
DCLG[Nva]LRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Leu6;2-Abu13;Glu28]GpTx-1(1-34)	1175
DCLG[Nle]LRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Leu6;2-Abu13;Glu28]GpTx-1(1-34)	1176
DCLGVLRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Leu6;2-Abu13;Glu28]GpTx-1(1-34)	1177
DCLGLLRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5,6;2-Abu13;Glu28]GpTx-1(1-34)	1178
DCLGILRKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Leu6;2-Abu13;Glu28]GpTx-1(1-34)	1179
DCLGG[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Nle6;2-Abu13;Glu28]GpTx-1(1-34)	1180
DCLGA[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Nle6;2-Abu13;Glu28]GpTx-1(1-34)	1181
DCLG[2-Abu][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu28]GpTx-1(1-34)	1182
DCLG[Nva][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Nle6;2-Abu13;Glu28]GpTx-1(1-34)	1183
DCLG[Nle][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5,6;2-Abu13;Glu28]GpTx-1(1-34)	1184
DCLGV[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Nle6;2-Abu13;Glu28]GpTx-1(1-34)	1185
DCLGL[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Nle6;2-Abu13;Glu28]GpTx-1(1-34)	1186

DCLGI[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Nle6;2-Abu13;Glu28]GpTx-1(1-34)	1187
DCLGFFRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Phe6;Glu11,28;Pra13]GpTx-1(1-34)	1188
DCLGFLRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu6;Glu11,28;Pra13]GpTx-1(1-34)	1189
DCLGF[Nle]RKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle6;Glu11,28;Pra13]GpTx-1(1-34)	1190
DCLGGMRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Glu11,28;Pra13]GpTx-1(1-34)	1191
DCLGAMRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Glu11,28;Pra13]GpTx-1(1-34)	1192
DCLG[2-Abu]MRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Glu11,28;Pra13]GpTx-1(1-34)	1193
DCLG[Nva]MRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Glu11,28;Pra13]GpTx-1(1-34)	1194
DCLG[Nle]MRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Glu11,28;Pra13]GpTx-1(1-34)	1195
DCLGVMRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Glu11,28;Pra13]GpTx-1(1-34)	1196
DCLGLMRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Glu11,28;Pra13]GpTx-1(1-34)	1197
DCLGIMRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Glu11,28;Pra13]GpTx-1(1-34)	1198
DCLGFFRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Phe6;Glu10,28;Pra13]GpTx-1(1-34)	1199
DCLGFLRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu6;Glu10,28;Pra13]GpTx-1(1-34)	1200
DCLGF[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle6;Glu10,28;Pra13]GpTx-1(1-34)	1201
DCLGGMRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Glu10,28;Pra13]GpTx-1(1-34)	1202
DCLGAMRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Glu10,28;Pra13]GpTx-1(1-34)	1203
DCLG[2-Abu]MRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Glu10,28;Pra13]GpTx-1(1-34)	1204
DCLG[Nva]MRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Glu10,28;Pra13]GpTx-1(1-34)	1205
DCLG[Nle]MRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Glu10,28;Pra13]GpTx-1(1-34)	1206

DCLGVMRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Glu10,28;Pra13]GpTx-1(1-34)	1207
DCLGLMRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Glu10,28;Pra13]GpTx-1(1-34)	1208
DCLGIMRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Glu10,28;Pra13]GpTx-1(1-34)	1209
DCLGFFRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Phe6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1210
DCLGFLRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1211
DCLGF[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1212
DCLGGMRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Asp10;Pra13;Glu28]GpTx-1(1-34)	1213
DCLGAMRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Asp10;Pra13;Glu28]GpTx-1(1-34)	1214
DCLG[2-Abu]MRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Asp10;Pra13;Glu28]GpTx-1(1-34)	1215
DCLG[Nva]MRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Asp10;Pra13;Glu28]GpTx-1(1-34)	1216
DCLG[Nle]MRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Asp10;Pra13;Glu28]GpTx-1(1-34)	1217
DCLGVMRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Asp10;Pra13;Glu28]GpTx-1(1-34)	1218
DCLGLMRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Asp10;Pra13;Glu28]GpTx-1(1-34)	1219
DCLGIMRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Asp10;Pra13;Glu28]GpTx-1(1-34)	1220
DCLGGFRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Phe6;Pra13;Glu28]GpTx-1(1-34)	1221
DCLGAFRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Phe6;Pra13;Glu28]GpTx-1(1-34)	1222
DCLG[2-Abu]FRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Phe6;Pra13;Glu28]GpTx-1(1-34)	1223
DCLG[Nva]FRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Phe6;Pra13;Glu28]GpTx-1(1-34)	1224
DCLG[Nle]FRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Phe6;Pra13;Glu28]GpTx-1(1-34)	1225
DCLGVFRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Phe6;Pra13;Glu28]GpTx-1(1-34)	1226

DCLGLFRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Phe6;Pra13;Glu28]GpTx-1(1-34)	1227
DCLGIFRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Phe6;Pra13;Glu28]GpTx-1(1-34)	1228
DCLGGLRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Leu6;Pra13;Glu28]GpTx-1(1-34)	1229
DCLGALRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Leu6;Pra13;Glu28]GpTx-1(1-34)	1230
DCLG[2-Abu]LRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Leu6;Pra13;Glu28]GpTx-1(1-34)	1231
DCLG[Nva]LRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Leu6;Pra13;Glu28]GpTx-1(1-34)	1232
DCLG[Nle]LRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Leu6;Pra13;Glu28]GpTx-1(1-34)	1233
DCLGVLRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Leu6;Pra13;Glu28]GpTx-1(1-34)	1234
DCLGLLRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5,6;Pra13;Glu28]GpTx-1(1-34)	1235
DCLGILRKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Leu6;Pra13;Glu28]GpTx-1(1-34)	1236
DCLGG[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Nle6;Pra13;Glu28]GpTx-1(1-34)	1237
DCLGA[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Nle6;Pra13;Glu28]GpTx-1(1-34)	1238
DCLG[2-Abu][Nle]RKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Nle6;Pra13;Glu28]GpTx-1(1-34)	1239
DCLG[Nva][Nle]RKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Nle6;Pra13;Glu28]GpTx-1(1-34)	1240
DCLG[Nle][Nle]RKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5,6;Pra13;Glu28]GpTx-1(1-34)	1241
DCLGV[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Nle6;Pra13;Glu28]GpTx-1(1-34)	1242
DCLGL[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Nle6;Pra13;Glu28]GpTx-1(1-34)	1243
DCLGI[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[ile5;Nle6;Pra13;Glu28]GpTx-1(1-34)	1244
DCLGFFRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Phe6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1245
DCLGFLRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu6,26;Glu11,28;2-Abu13]GpTx-1(1-34)	1246

DCLGF[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1247
DCLGGMRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1248
DCLGAMRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1249
DCLG[2-Abu]MRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Glu11,28;Leu26]GpTx-1(1-34)	1250
DCLG[Nva]MRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1251
DCLG[Nle]MRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1252
DCLGVMRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1253
DCLGLMRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Glu11,28;2-Abu13]GpTx-1(1-34)	1254
DCLGIMRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1255
DCLGFFRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Phe6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1256
DCLGFLRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu6,26;Glu10,28;2-Abu13]GpTx-1(1-34)	1257
DCLGF[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1258
DCLGGMRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1259
DCLGAMRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1260
DCLG[2-Abu]MRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Glu10,28;Leu26]GpTx-1(1-34)	1261
DCLG[Nva]MRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1262
DCLG[Nle]MRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1263
DCLGVMRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1264
DCLGLMRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Glu10,28;2-Abu13]GpTx-1(1-34)	1265
DCLGIMRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1266

DCLGFFRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Phe6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1267
DCLGFLRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu6,26;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1268
DCLGF[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1269
DCLGGMRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1270
DCLGAMRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1271
DCLG[2-Abu]MRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Asp10;Leu26;Glu28]GpTx-1(1-34)	1272
DCLG[Nva]MRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1273
DCLG[Nle]MRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1274
DCLGVMRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1275
DCLGLMRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1276
DCLGIMRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1277
DCLGGFRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Phe6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1278
DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Phe6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1279
DCLG[2-Abu]FRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Phe6;Leu26;Glu28]GpTx-1(1-34)	1280
DCLG[Nva]FRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Phe6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1281
DCLG[Nle]FRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Phe6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1282
DCLGVFRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Phe6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1283
DCLGLFRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Phe6;2-Abu13;Glu28]GpTx-1(1-34)	1284
DCLGIFRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Phe6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1285
DCLGGLRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Leu6,26;2-Abu13;Glu28]GpTx-1(1-34)	1286

DCLGALRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Leu6,26;2-Abu13;Glu28]GpTx-1(1-34)	1287
DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Glu28]GpTx-1(1-34)	1288
DCLG[Nva]LRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Leu6,26;2-Abu13;Glu28]GpTx-1(1-34)	1289
DCLG[Nle]LRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Leu6,26;2-Abu13;Glu28]GpTx-1(1-34)	1290
DCLGVLRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Leu6,26;2-Abu13;Glu28]GpTx-1(1-34)	1291
DCLGLLRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,6,26;2-Abu13;Glu28]GpTx-1(1-34)	1292
DCLGILRKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Leu6,26;2-Abu13;Glu28]GpTx-1(1-34)	1293
DCLGG[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Nle6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1294
DCLGA[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Nle6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1295
DCLG[2-Abu][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Nle6;Leu26;Glu28]GpTx-1(1-34)	1296
DCLG[Nva][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Nle6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1297
DCLG[Nle][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5,6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1298
DCLGV[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Nle6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1299
DCLGL[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Nle6;2-Abu13;Glu28]GpTx-1(1-34)	1300
DCLGI[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Nle6;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1301
DCLGFFRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Phe6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1302
DCLGFLRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu6,26;Glu11,28;Pra13]GpTx-1(1-34)	1303
DCLGF[Nle]RKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1304
DCLGGMRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1305
DCLGAMRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1306

DCLG[2-Abu]MRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1307
DCLG[Nva]MRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1308
DCLG[Nle]MRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1309
DCLGVMRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1310
DCLGLMRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Glu11,28;Pra13]GpTx-1(1-34)	1311
DCLGIMRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1312
DCLGFFRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Phe6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1313
DCLGFLRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu6,26;Glu10,28;Pra13]GpTx-1(1-34)	1314
DCLGF[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1315
DCLGGMRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1316
DCLGAMRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1317
DCLG[2-Abu]MRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1318
DCLG[Nva]MRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1319
DCLG[Nle]MRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1320
DCLGVMRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1321
DCLGLMRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Glu10,28;Pra13]GpTx-1(1-34)	1322
DCLGIMRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1323
DCLGFFRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Phe6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1324
DCLGFLRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu6,26;Asp10;Pra13;Glu28]GpTx-1(1-34)	1325
DCLGF[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1326

DCLGGMRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1327
DCLGAMRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1328
DCLG[2-Abu]MRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1329
DCLG[Nva]MRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1330
DCLG[Nle]MRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1331
DCLGVMRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1332
DCLGLMRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Asp10;Pra13;Glu28]GpTx-1(1-34)	1333
DCLGIMRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1334
DCLGGFRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Phe6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1335
DCLGAFRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Phe6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1336
DCLG[2-Abu]FRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Phe6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1337
DCLG[Nva]FRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Phe6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1338
DCLG[Nle]FRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Phe6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1339
DCLGVFRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Phe6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1340
DCLGLFRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Phe6;Pra13;Glu28]GpTx-1(1-34)	1341
DCLGIFRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Phe6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1342
DCLGGLRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Leu6,26;Pra13;Glu28]GpTx-1(1-34)	1343
DCLGALRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Leu6,26;Pra13;Glu28]GpTx-1(1-34)	1344
DCLG[2-Abu]LRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Leu6,26;Pra13;Glu28]GpTx-1(1-34)	1345
DCLG[Nva]LRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Leu6,26;Pra13;Glu28]GpTx-1(1-34)	1346

DCLG[Nle]LRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Leu6,26;Pra13;Glu28]GpTx-1(1-34)	1347
DCLGVLRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Leu6,26;Pra13;Glu28]GpTx-1(1-34)	1348
DCLGLLRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,6,26;Pra13;Glu28]GpTx-1(1-34)	1349
DCLGILRKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Leu6,26;Pra13;Glu28]GpTx-1(1-34)	1350
DCLGG[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Nle6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1351
DCLGA[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Nle6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1352
DCLG[2-Abu][Nle]RKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Nle6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1353
DCLG[Nva][Nle]RKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Nle6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1354
DCLG[Nle][Nle]RKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5,6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1355
DCLGV[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Nle6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1356
DCLGL[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Nle6;Pra13;Glu28]GpTx-1(1-34)	1357
DCLGI[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Nle6;Pra13;Leu26;Glu28]GpTx-1(1-34)	1358
DCLGGFRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Phe6;Glu11,28;2-Abu13]GpTx-1(1-34)	1359
DCLGAFRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Phe6;Glu11,28;2-Abu13]GpTx-1(1-34)	1360
DCLG[2-Abu]FRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu11,28]GpTx-1(1-34)	1361
DCLG[Nva]FRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Phe6;Glu11,28;2-Abu13]GpTx-1(1-34)	1362
DCLG[Nle]FRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Phe6;Glu11,28;2-Abu13]GpTx-1(1-34)	1363
DCLGVFRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Phe6;Glu11,28;2-Abu13]GpTx-1(1-34)	1364
DCLGLFRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Phe6;Glu11,28;2-Abu13]GpTx-1(1-34)	1365
DCLGIFRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Phe6;Glu11,28;2-Abu13]GpTx-1(1-34)	1366

DCLGGLRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Leu6;Glu11,28;2-Abu13]GpTx-1(1-34)	1367
DCLGALRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Leu6;Glu11,28;2-Abu13]GpTx-1(1-34)	1368
DCLG[2-Abu]LRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Leu6;Glu11,28]GpTx-1(1-34)	1369
DCLG[Nva]LRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Leu6;Glu11,28;2-Abu13]GpTx-1(1-34)	1370
DCLG[Nle]LRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Leu6;Glu11,28;2-Abu13]GpTx-1(1-34)	1371
DCLGVLRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Leu6;Glu11,28;2-Abu13]GpTx-1(1-34)	1372
DCLGLLRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5,6;Glu11,28;2-Abu13]GpTx-1(1-34)	1373
DCLGILRKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Leu6;Glu11,28;2-Abu13]GpTx-1(1-34)	1374
DCLGG[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Nle6;Glu11,28;2-Abu13]GpTx-1(1-34)	1375
DCLGA[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Nle6;Glu11,28;2-Abu13]GpTx-1(1-34)	1376
DCLG[2-Abu][Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu11,28]GpTx-1(1-34)	1377
DCLG[Nva][Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Nle6;Glu11,28;2-Abu13]GpTx-1(1-34)	1378
DCLG[Nle][Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5,6;Glu11,28;2-Abu13]GpTx-1(1-34)	1379
DCLGV[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Nle6;Glu11,28;2-Abu13]GpTx-1(1-34)	1380
DCLGL[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Nle6;Glu11,28;2-Abu13]GpTx-1(1-34)	1381
DCLGI[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Nle6;Glu11,28;2-Abu13]GpTx-1(1-34)	1382
DCLGGFRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Phe6;Glu10,28;2-Abu13]GpTx-1(1-34)	1383
DCLGAFRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Phe6;Glu10,28;2-Abu13]GpTx-1(1-34)	1384
DCLG[2-Abu]FRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu10,28]GpTx-1(1-34)	1385
DCLG[Nva]FRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Phe6;Glu10,28;2-Abu13]GpTx-1(1-34)	1386

DCLG[Nle]FRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Phe6;Glu10,28;2-Abu13]GpTx-1(1-34)	1387
DCLGVFRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Phe6;Glu10,28;2-Abu13]GpTx-1(1-34)	1388
DCLGLFRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Phe6;Glu10,28;2-Abu13]GpTx-1(1-34)	1389
DCLGIFRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Phe6;Glu10,28;2-Abu13]GpTx-1(1-34)	1390
DCLGGLRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Leu6;Glu10,28;2-Abu13]GpTx-1(1-34)	1391
DCLGALRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Leu6;Glu10,28;2-Abu13]GpTx-1(1-34)	1392
DCLG[2-Abu]LRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Leu6;Glu10,28]GpTx-1(1-34)	1393
DCLG[Nva]LRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Leu6;Glu10,28;2-Abu13]GpTx-1(1-34)	1394
DCLG[Nle]LRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Leu6;Glu10,28;2-Abu13]GpTx-1(1-34)	1395
DCLGVLRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Leu6;Glu10,28;2-Abu13]GpTx-1(1-34)	1396
DCLGLLRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5,6;Glu10,28;2-Abu13]GpTx-1(1-34)	1397
DCLGILRKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Leu6;Glu10,28;2-Abu13]GpTx-1(1-34)	1398
DCLGG[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Nle6;Glu10,28;2-Abu13]GpTx-1(1-34)	1399
DCLGA[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Nle6;Glu10,28;2-Abu13]GpTx-1(1-34)	1400
DCLG[2-Abu][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu10,28]GpTx-1(1-34)	1401
DCLG[Nva][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Nle6;Glu10,28;2-Abu13]GpTx-1(1-34)	1402
DCLG[Nle][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5,6;Glu10,28;2-Abu13]GpTx-1(1-34)	1403
DCLGV[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Nle6;Glu10,28;2-Abu13]GpTx-1(1-34)	1404
DCLGL[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Nle6;Glu10,28;2-Abu13]GpTx-1(1-34)	1405
DCLGI[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Nle6;Glu10,28;2-Abu13]GpTx-1(1-34)	1406

DCLGGFRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Phe6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1407
DCLGAFRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Phe6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1408
DCLG[2-Abu]FRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Phe6;Asp10;Glu28]GpTx-1(1-34)	1409
DCLG[Nva]FRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Phe6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1410
DCLG[Nle]FRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Phe6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1411
DCLGVFRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Phe6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1412
DCLGLFRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Phe6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1413
DCLGIFRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Phe6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1414
DCLGGLRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Leu6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1415
DCLGALRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Leu6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1416
DCLG[2-Abu]LRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Leu6;Asp10;Glu28]GpTx-1(1-34)	1417
DCLG[Nva]LRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Leu6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1418
DCLG[Nle]LRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Leu6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1419
DCLGVLRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Leu6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1420
DCLGLLRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5,6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1421
DCLGILRKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Leu6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1422
DCLGG[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Nle6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1423
DCLGA[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Nle6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1424
DCLG[2-Abu][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,13;Nle6;Asp10;Glu28]GpTx-1(1-34)	1425
DCLG[Nva][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Nle6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1426

DCLG[Nle][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5,6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1427
DCLGV[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Nle6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1428
DCLGL[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Nle6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1429
DCLGI[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Nle6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1430
DCLGGFRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Phe6;Glu11,28;Pra13]GpTx-1(1-34)	1431
DCLGAFRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Phe6;Glu11,28;Pra13]GpTx-1(1-34)	1432
DCLG[2-Abu]FRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Phe6;Glu11,28;Pra13]GpTx-1(1-34)	1433
DCLG[Nva]FRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Phe6;Glu11,28;Pra13]GpTx-1(1-34)	1434
DCLG[Nle]FRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Phe6;Glu11,28;Pra13]GpTx-1(1-34)	1435
DCLGVFRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Phe6;Glu11,28;Pra13]GpTx-1(1-34)	1436
DCLGLFRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Phe6;Glu11,28;Pra13]GpTx-1(1-34)	1437
DCLGIFRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Phe6;Glu11,28;Pra13]GpTx-1(1-34)	1438
DCLGGLRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Leu6;Glu11,28;Pra13]GpTx-1(1-34)	1439
DCLGALRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Leu6;Glu11,28;Pra13]GpTx-1(1-34)	1440
DCLG[2-Abu]LRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Leu6;Glu11,28;Pra13]GpTx-1(1-34)	1441
DCLG[Nva]LRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Leu6;Glu11,28;Pra13]GpTx-1(1-34)	1442
DCLG[Nle]LRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Leu6;Glu11,28;Pra13]GpTx-1(1-34)	1443
DCLGVLRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Leu6;Glu11,28;Pra13]GpTx-1(1-34)	1444
DCLGLLRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5,6;Glu11,28;Pra13]GpTx-1(1-34)	1445
DCLGILRKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Leu6;Glu11,28;Pra13]GpTx-1(1-34)	1446

DCLGG[Nle]RKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Nle6;Glu11,28;Pra13]GpTx-1(1-34)	1447
DCLGA[Nle]RKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Nle6;Glu11,28;Pra13]GpTx-1(1-34)	1448
DCLG[2-Abu][Nle]RKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Nle6;Glu11,28;Pra13]GpTx-1(1-34)	1449
DCLG[Nva][Nle]RKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Nle6;Glu11,28;Pra13]GpTx-1(1-34)	1450
DCLG[Nle][Nle]RKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5,6;Glu11,28;Pra13]GpTx-1(1-34)	1451
DCLGV[Nle]RKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Nle6;Glu11,28;Pra13]GpTx-1(1-34)	1452
DCLGL[Nle]RKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Nle6;Glu11,28;Pra13]GpTx-1(1-34)	1453
DCLGI[Nle]RKCIED[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Nle6;Glu11,28;Pra13]GpTx-1(1-34)	1454
DCLGGFRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Phe6;Glu10,28;Pra13]GpTx-1(1-34)	1455
DCLGAFRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Phe6;Glu10,28;Pra13]GpTx-1(1-34)	1456
DCLG[2-Abu]FRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Phe6;Glu10,28;Pra13]GpTx-1(1-34)	1457
DCLG[Nva]FRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Phe6;Glu10,28;Pra13]GpTx-1(1-34)	1458
DCLG[Nle]FRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Phe6;Glu10,28;Pra13]GpTx-1(1-34)	1459
DCLGVFRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Phe6;Glu10,28;Pra13]GpTx-1(1-34)	1460
DCLGLFRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Phe6;Glu10,28;Pra13]GpTx-1(1-34)	1461
DCLGIFRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Phe6;Glu10,28;Pra13]GpTx-1(1-34)	1462
DCLGGLRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Leu6;Glu10,28;Pra13]GpTx-1(1-34)	1463
DCLGALRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Leu6;Glu10,28;Pra13]GpTx-1(1-34)	1464
DCLG[2-Abu]LRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Leu6;Glu10,28;Pra13]GpTx-1(1-34)	1465
DCLG[Nva]LRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Leu6;Glu10,28;Pra13]GpTx-1(1-34)	1466

DCLG[Nle]LRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Leu6;Glu10,28;Pra13]GpTx-1(1-34)	1467
DCLGVLRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Leu6;Glu10,28;Pra13]GpTx-1(1-34)	1468
DCLGLLRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5,6;Glu10,28;Pra13]GpTx-1(1-34)	1469
DCLGILRKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Leu6;Glu10,28;Pra13]GpTx-1(1-34)	1470
DCLGG[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Nle6;Glu10,28;Pra13]GpTx-1(1-34)	1471
DCLGA[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Nle6;Glu10,28;Pra13]GpTx-1(1-34)	1472
DCLG[2-Abu]-[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,Nle6;Glu10,28;Pra13]GpTx-1(1-34)	1473
DCLG[Nva]-[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5,Nle6;Glu10,28;Pra13]GpTx-1(1-34)	1474
DCLG[Nle]-[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5,6;Glu10,28;Pra13]GpTx-1(1-34)	1475
DCLGV[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Nle6;Glu10,28;Pra13]GpTx-1(1-34)	1476
DCLGL[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Nle6;Glu10,28;Pra13]GpTx-1(1-34)	1477
DCLGI[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Nle6;Glu10,28;Pra13]GpTx-1(1-34)	1478
DCLGGFRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Phe6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1479
DCLGAFRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Phe6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1480
DCLG[2-Abu]FRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5,Phe6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1481
DCLG[Nva]FRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Phe6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1482
DCLG[Nle]FRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Phe6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1483
DCLGVFRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Phe6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1484
DCLGLFRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Phe6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1485
DCLGIFRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Phe6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1486

DCLGGLRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Leu6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1487
DCLGALRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Leu6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1488
DCLG[2-Abu]LRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Leu6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1489
DCLG[Nva]LRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Leu6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1490
DCLG[Nle]LRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5;Leu6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1491
DCLGVLRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Leu6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1492
DCLGLLRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5,6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1493
DCLGILRKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Leu6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1494
DCLGG[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Nle6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1495
DCLGA[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Nle6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1496
DCLG[2-Abu]{Nle]RKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Nle6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1497
DCLG[Nva]{Nle]RKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Nle6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1498
DCLG[Nle]{Nle]RKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nle5,6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1499
DCLGV[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Nle6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1500
DCLGL[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Leu5;Nle6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1501
DCLGI[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ile5;Nle6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1502
DCLGGFRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Phe6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1503
DCLGAFRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Phe6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1504
DCLG[2-Abu]FRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu11,28;Leu26]GpTx-1(1-34)	1505
DCLG[Nva]FRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Phe6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1506

DCLG[Nle]FRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Phe6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1507
DCLGVFRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Phe6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1508
DCLGLFRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Phe6;Glu11,28;2-Abu13]GpTx-1(1-34)	1509
DCLGIFRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Phe6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1510
DCLGGLRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Leu6,26;Glu11,28;2-Abu13]GpTx-1(1-34)	1511
DCLGALRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Leu6,26;Glu11,28;2-Abu13]GpTx-1(1-34)	1512
DCLG[2-Abu]LRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Glu11,28]GpTx-1(1-34)	1513
DCLG[Nva]LRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Leu6,26;Glu11,28;2-Abu13]GpTx-1(1-34)	1514
DCLG[Nle]LRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Leu6,26;Glu11,28;2-Abu13]GpTx-1(1-34)	1515
DCLGVLRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Leu6,26;Glu11,28;2-Abu13]GpTx-1(1-34)	1516
DCLGLLRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,6,26;Glu11,28;2-Abu13]GpTx-1(1-34)	1517
DCLGILRKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Leu6,26;Glu11,28;2-Abu13]GpTx-1(1-34)	1518
DCLGG[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Nle6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1519
DCLGA[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Nle6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1520
DCLG[2-Abu][Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu11,28;Leu26]GpTx-1(1-34)	1521
DCLG[Nva][Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Nle6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1522
DCLG[Nle][Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5,6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1523
DCLGV[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Nle6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1524
DCLGL[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Nle6;Glu11,28;2-Abu13]GpTx-1(1-34)	1525
DCLGI[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Nle6;Glu11,28;2-Abu13;Leu26]GpTx-1(1-34)	1526

DCLGGFRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Phe6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1527
DCLGAFRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Phe6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1528
DCLGI[2-Abu]FRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu10,28;Leu26]GpTx-1(1-34)	1529
DCLG[Nva]FRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Phe6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1530
DCLG[Nle]FRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Phe6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1531
DCLGVFRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Phe6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1532
DCLGLFRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Phe6;Glu10,28;2-Abu13]GpTx-1(1-34)	1533
DCLGIFRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Phe6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1534
DCLGGLRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Leu6,26;Glu10,28;2-Abu13]GpTx-1(1-34)	1535
DCLGALRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Leu6,26;Glu10,28;2-Abu13]GpTx-1(1-34)	1536
DCLGI[2-Abu]LRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Glu10,28]GpTx-1(1-34)	1537
DCLG[Nva]LRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Leu6,26;Glu10,28;2-Abu13]GpTx-1(1-34)	1538
DCLG[Nle]LRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Leu6,26;Glu10,28;2-Abu13]GpTx-1(1-34)	1539
DCLGVLRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Leu6,26;Glu10,28;2-Abu13]GpTx-1(1-34)	1540
DCLGLLRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,6,26;Glu10,28;2-Abu13]GpTx-1(1-34)	1541
DCLGILRKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Leu6,26;Glu10,28;2-Abu13]GpTx-1(1-34)	1542
DCLGG[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Nle6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1543
DCLGA[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Nle6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1544
DCLG[2-Abu][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu10,28;Leu26]GpTx-1(1-34)	1545
DCLG[Nva][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Nle6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1546

DCLG[Nle][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5,6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1547
DCLGV[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Nle6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1548
DCLGL[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Nle6;Glu10,28;2-Abu13]GpTx-1(1-34)	1549
DCLGI[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Nle6;Glu10,28;2-Abu13;Leu26]GpTx-1(1-34)	1550
DCLGGFRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Phe6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1551
DCLGAFRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Phe6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1552
DCLG[2-Abu]FRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Phe6;Asp10;Leu26;Glu28]GpTx-1(1-34)	1553
DCLG[Nva]FRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Phe6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1554
DCLG[Nle]FRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Phe6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1555
DCLGVFRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Phe6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1556
DCLGLFRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Phe6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1557
DCLGIFRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Phe6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1558
DCLGGLRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Leu6,26;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1559
DCLGALRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Leu6,26;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1560
DCLG[2-Abu]LRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Asp10;Glu28]GpTx-1(1-34)	1561
DCLG[Nva]LRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Leu6,26;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1562
DCLG[Nle]LRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Leu6,26;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1563
DCLGVLRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Leu6,26;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1564
DCLGLLRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,6,26;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1565
DCLGILRKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Leu6,26;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1566

DCLGG[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Nle6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1567
DCLGA[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Nle6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1568
DCLG[2-Abu][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5,13;Nle6;Asp10;Leu26;Glu28]GpTx-1(1-34)	1569
DCLG[Nva][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Nle6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1570
DCLG[Nle][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5,6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1571
DCLGV[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Nle6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1572
DCLGL[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Nle6;Asp10;2-Abu13;Glu28]GpTx-1(1-34)	1573
DCLGI[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Nle6;Asp10;2-Abu13;Leu26;Glu28]GpTx-1(1-34)	1574
DCLGGFRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Phe6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1575
DCLGAFRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Phe6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1576
DCLG[2-Abu]FRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Phe6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1577
DCLG[Nva]FRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Phe6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1578
DCLG[Nle]FRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Phe6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1579
DCLGVFRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Phe6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1580
DCLGLFRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Phe6;Glu11,28;Pra13]GpTx-1(1-34)	1581
DCLGIFRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Phe6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1582
DCLGGLRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Leu6,26;Glu11,28;Pra13]GpTx-1(1-34)	1583
DCLGALRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Leu6,26;Glu11,28;Pra13]GpTx-1(1-34)	1584
DCLG[2-Abu]LRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Leu6,26;Glu11,28;Pra13]GpTx-1(1-34)	1585
DCLG[Nva]LRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Leu6,26;Glu11,28;Pra13]GpTx-1(1-34)	1586

DCLG[Nle]LRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Leu6,26;Glu11,28;Pra13]GpTx-1(1-34)	1587
DCLGVLRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Leu6,26;Glu11,28;Pra13]GpTx-1(1-34)	1588
DCLGLLRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,6,26;Glu11,28;Pra13]GpTx-1(1-34)	1589
DCLGILRKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	*[Ile5;Leu6,26;Glu11,28;Pra13]GpTx-1(1-34)*	*1590*
DCLGG[Nle]RKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Nle6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1591
DCLGA[Nle]RKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Nle6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1592
DCLG[2-Abu][Nle]RKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Nle6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1593
DCLG[Nva][Nle]RKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Nle6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1594
DCLG[Nle][Nle]RKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5,6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1595
DCLGV[Nle]RKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Nle6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1596
DCLGL[Nle]RKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Nle6;Glu11,28;Pra13]GpTx-1(1-34)	1597
DCLGI[Nle]RKCIED[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Nle6;Glu11,28;Pra13;Leu26]GpTx-1(1-34)	1598
DCLGGFRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Phe6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1599
DCLGAFRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Phe6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1600
DCLG[2-Abu]FRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Phe6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1601
DCLG[Nva]FRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Phe6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1602
DCLG[Nle]FRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Phe6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1603
DCLGVFRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Phe6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1604
DCLGLFRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Phe6;Glu10,28;Pra13]GpTx-1(1-34)	1605
DCLGIFRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Phe6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1606

DCLGGLRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Leu6,26;Glu10,28;Pra13]GpTx-1(1-34)	1607
DCLGALRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Leu6,26;Glu10,28;Pra13]GpTx-1(1-34)	1608
DCLG[2-Abu]LRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Leu6,26;Glu10,28;Pra13]GpTx-1(1-34)	1609
DCLG[Nva]LRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Leu6,26;Glu10,28;Pra13]GpTx-1(1-34)	1610
DCLG[Nle]LRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Leu6,26;Glu10,28;Pra13]GpTx-1(1-34)	1611
DCLGVLRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Leu6,26;Glu10,28;Pra13]GpTx-1(1-34)	1612
DCLGLLRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,6,26;Glu10,28;Pra13]GpTx-1(1-34)	1613
DCLGILRKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Leu6,26;Glu10,28;Pra13]GpTx-1(1-34)	1614
DCLGG[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Nle6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1615
DCLGA[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Nle6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1616
DCLG[2-Abu][Nle]RKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Nle6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1617
DCLG[Nva][Nle]RKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Nle6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1618
DCLG[Nle][Nle]RKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5,6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1619
DCLGV[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Nle6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1620
DCLGL[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Nle6;Glu10,28;Pra13]GpTx-1(1-34)	1621
DCLGI[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Nle6;Glu10,28;Pra13;Leu26]GpTx-1(1-34)	1622
DCLGGFRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Phe6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1623
DCLGAFRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Phe6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1624
DCLG[2-Abu]FRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Phe6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1625
DCLG[Nva]FRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Phe6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1626

DCLG[Nle]FRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Phe6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1627
DCLGVFRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Phe6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1628
DCLGLFRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Phe6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1629
DCLGIFRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Phe6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1630
DCLGGLRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Leu6,26;Asp10;Pra13;Glu28]GpTx-1(1-34)	1631
DCLGALRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Leu6,26;Asp10;Pra13;Glu28]GpTx-1(1-34)	1632
DCLG[2-Abu]LRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Leu6,26;Asp10;Pra13;Glu28]GpTx-1(1-34)	1633
DCLG[Nva]LRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Leu6,26;Asp10;Pra13;Glu28]GpTx-1(1-34)	1634
DCLG[Nle]LRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5;Leu6,26;Asp10;Pra13;Glu28]GpTx-1(1-34)	1635
DCLGVLRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Leu6,26;Asp10;Pra13;Glu28]GpTx-1(1-34)	1636
DCLGLLRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,6,26;Asp10;Pra13;Glu28]GpTx-1(1-34)	1637
DCLGILRKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Leu6,26;Asp10;Pra13;Glu28]GpTx-1(1-34)	1638
DCLGG[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Gly5;Nle6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1639
DCLGA[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ala5;Nle6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1640
DCLG[2-Abu][Nle]RKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[2-Abu5;Nle6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1641
DCLG[Nva][Nle]RKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nva5;Nle6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1642
DCLG[Nle][Nle]RKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Nle5,6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1643
DCLGV[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Val5;Nle6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1644
DCLGL[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Leu5,26;Nle6;Asp10;Pra13;Glu28]GpTx-1(1-34)	1645
DCLGI[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHEWCKYVF-{Amide}	[Ile5;Nle6;Asp10;Pra13;Leu26;Glu28]GpTx-1(1-34)	1646

DCLGFMRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu13;Asp28]GpTx-1(1-34)	1647
DCLGFMRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Pra13;Asp28]GpTx-1(1-34)	1648
DCLGFMRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1649
DCLGFMRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Pra13;Leu26;Asp28]GpTx-1(1-34)	1650
DCLGFMRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1651
DCLGFMRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1652
DCLGFMRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Asp10,28;2-Abu13]GpTx-1(1-34)	1653
DCLGFFRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Phe6;2-Abu13;Asp28]GpTx-1(1-34)	1654
DCLGFLRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu6;2-Abu13;Asp28]GpTx-1(1-34)	1655
DCLGF[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle6;2-Abu13;Asp28]GpTx-1(1-34)	1656
DCLGGMRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;2-Abu13;Asp28]GpTx-1(1-34)	1657
DCLGAMRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;2-Abu13;Asp28]GpTx-1(1-34)	1658
DCLG[2-Abu]MRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Asp28]GpTx-1(1-34)	1659
DCLG[Nva]MRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;2-Abu13;Asp28]GpTx-1(1-34)	1660
DCLG[Nle]MRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;2-Abu13;Asp28]GpTx-1(1-34)	1661
DCLGVMRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;2-Abu13;Asp28]GpTx-1(1-34)	1662
DCLGLMRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;2-Abu13;Asp28]GpTx-1(1-34)	1663
DCLGIMRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;2-Abu13;Asp28]GpTx-1(1-34)	1664
DCLGFMRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Glu11;Pra13;Asp28]GpTx-1(1-34)	1665
DCLGFMRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Glu10;Pra13;Asp28]GpTx-1(1-34)	1666

DCLGFMRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Asp10,28;Pra13]GpTx-1(1-34)	1667
DCLGFFRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Phe6;Pra13;Asp28]GpTx-1(1-34)	1668
DCLGFLRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu6;Pra13;Asp28]GpTx-1(1-34)	1669
DCLGF[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle6;Pra13;Asp28]GpTx-1(1-34)	1670
DCLGGMRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Pra13;Asp28]GpTx-1(1-34)	1671
DCLGAMRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Pra13;Asp28]GpTx-1(1-34)	1672
DCLG[2-Abu]MRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Pra13;Asp28]GpTx-1(1-34)	1673
DCLG[Nva]MRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Pra13;Asp28]GpTx-1(1-34)	1674
DCLG[Nle]MRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Pra13;Asp28]GpTx-1(1-34)	1675
DCLGVMRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Pra13;Asp28]GpTx-1(1-34)	1676
DCLGLMRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Pra13;Asp28]GpTx-1(1-34)	1677
DCLGIMRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Pra13;Asp28]GpTx-1(1-34)	1678
DCLGFMRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1679
DCLGFMRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1680
DCLGFMRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	1681
DCLGFFRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Phe6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1682
DCLGFLRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu6,26;2-Abu13;Asp28]GpTx-1(1-34)	1683
DCLGF[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1684
DCLGGMRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1685
DCLGAMRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1686

DCLG[2-Abu]MRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Leu26;Asp28]GpTx-1(1-34)	1687
DCLG[Nva]MRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1688
DCLG[Nle]MRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1689
DCLGVMRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1690
DCLGLMRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;2-Abu13;Asp28]GpTx-1(1-34)	1691
DCLGIMRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1692
DCLGFMRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	1693
DCLGFMRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	1694
DCLGFMRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Asp10,28;Pra13;Leu26]GpTx-1(1-34)	1695
DCLGFFRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Phe6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1696
DCLGFLRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu6,26;Pra13;Asp28]GpTx-1(1-34)	1697
DCLGF[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1698
DCLGGMRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Pra13;Leu26;Asp28]GpTx-1(1-34)	1699
DCLGAMRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Pra13;Leu26;Asp28]GpTx-1(1-34)	1700
DCLG[2-Abu]MRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Pra13;Leu26;Asp28]GpTx-1(1-34)	1701
DCLG[Nva]MRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Pra13;Leu26;Asp28]GpTx-1(1-34)	1702
DCLG[Nle]MRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Pra13;Leu26;Asp28]GpTx-1(1-34)	1703
DCLGVMRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Pra13;Leu26;Asp28]GpTx-1(1-34)	1704
DCLGLMRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Pra13;Asp28]GpTx-1(1-34)	1705
DCLGIMRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Pra13;Leu26;Asp28]GpTx-1(1-34)	1706

DCLGFFRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Phe6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1707
DCLGFLRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1708
DCLGF[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1709
DCLGGMRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1710
DCLGAMRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1711
DCLG[2-Abu]MRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Glu11;Asp28]GpTx-1(1-34)	1712
DCLG[Nva]MRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1713
DCLG[Nle]MRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1714
DCLGVMRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1715
DCLGLMRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1716
DCLGIMRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1717
DCLGFFRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Phe6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1718
DCLGFLRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1719
DCLGF[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1720
DCLGGMRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1721
DCLGAMRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1722
DCLG[2-Abu]MRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Glu10;Asp28]GpTx-1(1-34)	1723
DCLG[Nva]MRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1724
DCLG[Nle]MRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1725
DCLGVMRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1726

DCLGLMRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1727
DCLGIMRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1728
DCLGFFRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Phe6;Asp10,28;2-Abu13]GpTx-1(1-34)	1729
DCLGFLRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu6;Asp10,28;2-Abu13]GpTx-1(1-34)	1730
DCLGF[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle6;Asp10,28;2-Abu13]GpTx-1(1-34)	1731
DCLGGMRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Asp10,28;2-Abu13]GpTx-1(1-34)	1732
DCLGAMRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Asp10,28;2-Abu13]GpTx-1(1-34)	1733
DCLG[2-Abu]MRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Asp10,28]GpTx-1(1-34)	1734
DCLG[Nva]MRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Asp10,28;2-Abu13]GpTx-1(1-34)	1735
DCLG[Nle]MRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Asp10,28;2-Abu13]GpTx-1(1-34)	1736
DCLGVMRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Asp10,28;2-Abu13]GpTx-1(1-34)	1737
DCLGLMRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Asp10,28;2-Abu13]GpTx-1(1-34)	1738
DCLGIMRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Asp10,28;2-Abu13]GpTx-1(1-34)	1739
DCLGGFRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Phe6;2-Abu13;Asp28]GpTx-1(1-34)	1740
DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Phe6;2-Abu13;Asp28]GpTx-1(1-34)	1741
DCLG[2-Abu]FRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Phe6;Asp28]GpTx-1(1-34)	1742
DCLG[Nva]FRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Phe6;2-Abu13;Asp28]GpTx-1(1-34)	1743
DCLG[Nle]FRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Phe6;2-Abu13;Asp28]GpTx-1(1-34)	1744
DCLGVFRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Phe6;2-Abu13;Asp28]GpTx-1(1-34)	1745
DCLGLFRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Phe6;2-Abu13;Asp28]GpTx-1(1-34)	1746

DCLGIFRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Phe6;2-Abu13;Asp28]GpTx-1(1-34)	1747
DCLGGLRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Leu6;2-Abu13;Asp28]GpTx-1(1-34)	1748
DCLGALRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Leu6;2-Abu13;Asp28]GpTx-1(1-34)	1749
DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Leu6;Asp28]GpTx-1(1-34)	1750
DCLG[Nva]LRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Leu6;2-Abu13;Asp28]GpTx-1(1-34)	1751
DCLG[Nle]LRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Leu6;2-Abu13;Asp28]GpTx-1(1-34)	1752
DCLGVLRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Leu6;2-Abu13;Asp28]GpTx-1(1-34)	1753
DCLGLLRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5,6;2-Abu13;Asp28]GpTx-1(1-34)	1754
DCLGILRKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Leu6;2-Abu13;Asp28]GpTx-1(1-34)	1755
DCLGG[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Nle6;2-Abu13;Asp28]GpTx-1(1-34)	1756
DCLGA[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Nle6;2-Abu13;Asp28]GpTx-1(1-34)	1757
DCLG[2-Abu][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Nle6;Asp28]GpTx-1(1-34)	1758
DCLG[Nva][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Nle6;2-Abu13;Asp28]GpTx-1(1-34)	1759
DCLG[Nle][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5,6;2-Abu13;Asp28]GpTx-1(1-34)	1760
DCLGV[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Nle6;2-Abu13;Asp28]GpTx-1(1-34)	1761
DCLGL[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Nle6;2-Abu13;Asp28]GpTx-1(1-34)	1762
DCLGI[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Nle6;2-Abu13;Asp28]GpTx-1(1-34)	1763
DCLGFFRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Phe6;Glu11;Pra13;Asp28]GpTx-1(1-34)	1764
DCLGFLRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu6;Glu11;Pra13;Asp28]GpTx-1(1-34)	1765
DCLGF[Nle]RKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle6;Glu11;Pra13;Asp28]GpTx-1(1-34)	1766

DCLGGMRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Glu11;Pra13;Asp28]GpTx-1(1-34)	1767
DCLGAMRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Glu11;Pra13;Asp28]GpTx-1(1-34)	1768
DCLG[2-Abu]MRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Glu11;Pra13;Asp28]GpTx-1(1-34)	1769
DCLG[Nva]MRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Glu11;Pra13;Asp28]GpTx-1(1-34)	1770
DCLG[Nle]MRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Glu11;Pra13;Asp28]GpTx-1(1-34)	1771
DCLGVMRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Glu11;Pra13;Asp28]GpTx-1(1-34)	1772
DCLGLMRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Glu11;Pra13;Asp28]GpTx-1(1-34)	1773
DCLGIMRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Glu11;Pra13;Asp28]GpTx-1(1-34)	1774
DCLGFFRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Phe6;Glu10;Pra13;Asp28]GpTx-1(1-34)	1775
DCLGFLRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu6;Glu10;Pra13;Asp28]GpTx-1(1-34)	1776
DCLGF[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle6;Glu10;Pra13;Asp28]GpTx-1(1-34)	1777
DCLGGMRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Glu10;Pra13;Asp28]GpTx-1(1-34)	1778
DCLGAMRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Glu10;Pra13;Asp28]GpTx-1(1-34)	1779
DCLG[2-Abu]MRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Glu10;Pra13;Asp28]GpTx-1(1-34)	1780
DCLG[Nva]MRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Glu10;Pra13;Asp28]GpTx-1(1-34)	1781
DCLG[Nle]MRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Glu10;Pra13;Asp28]GpTx-1(1-34)	1782
DCLGVMRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Glu10;Pra13;Asp28]GpTx-1(1-34)	1783
DCLGLMRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Glu10;Pra13;Asp28]GpTx-1(1-34)	1784
DCLGIMRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Glu10;Pra13;Asp28]GpTx-1(1-34)	1785
DCLGFFRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Phe6;Asp10,28;Pra13]GpTx-1(1-34)	1786

DCLGFLRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu6;Asp10,28;Pra13]GpTx-1(1-34)	1787
DCLGF[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle6;Asp10,28;Pra13]GpTx-1(1-34)	1788
DCLGGMRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Asp10,28;Pra13]GpTx-1(1-34)	1789
DCLGAMRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Asp10,28;Pra13]GpTx-1(1-34)	1790
DCLG[2-Abu]MRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Asp10,28;Pra13]GpTx-1(1-34)	1791
DCLG[Nva]MRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Asp10,28;Pra13]GpTx-1(1-34)	1792
DCLG[Nle]MRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Asp10,28;Pra13]GpTx-1(1-34)	1793
DCLGVMRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Asp10,28;Pra13]GpTx-1(1-34)	1794
DCLGLMRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Asp10,28;Pra13]GpTx-1(1-34)	1795
DCLGIMRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Asp10,28;Pra13]GpTx-1(1-34)	1796
DCLGGFRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Phe6;Pra13;Asp28]GpTx-1(1-34)	1797
DCLGAFRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Phe6;Pra13;Asp28]GpTx-1(1-34)	1798
DCLG[2-Abu]FRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Phe6;Pra13;Asp28]GpTx-1(1-34)	1799
DCLG[Nva]FRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Phe6;Pra13;Asp28]GpTx-1(1-34)	1800
DCLG[Nle]FRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Phe6;Pra13;Asp28]GpTx-1(1-34)	1801
DCLGVFRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Phe6;Pra13;Asp28]GpTx-1(1-34)	1802
DCLGLFRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Phe6;Pra13;Asp28]GpTx-1(1-34)	1803
DCLGIFRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Phe6;Pra13;Asp28]GpTx-1(1-34)	1804
DCLGGLRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Leu6;Pra13;Asp28]GpTx-1(1-34)	1805
DCLGALRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Leu6;Pra13;Asp28]GpTx-1(1-34)	1806

DCLG[2-Abu]LRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Leu6;Pra13;Asp28]GpTx-1(1-34)	1807
DCLG[Nva]LRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Leu6;Pra13;Asp28]GpTx-1(1-34)	1808
DCLG[Nle]LRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Leu6;Pra13;Asp28]GpTx-1(1-34)	1809
DCLGVLRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Leu6;Pra13;Asp28]GpTx-1(1-34)	1810
DCLGLLRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5,6;Pra13;Asp28]GpTx-1(1-34)	1811
DCLGILRKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Leu6;Pra13;Asp28]GpTx-1(1-34)	1812
DCLGG[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Nle6;Pra13;Asp28]GpTx-1(1-34)	1813
DCLGA[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Nle6;Pra13;Asp28]GpTx-1(1-34)	1814
DCLG[2-Abu][Nle]RKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Nle6;Pra13;Asp28]GpTx-1(1-34)	1815
DCLG[Nva][Nle]RKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Nle6;Pra13;Asp28]GpTx-1(1-34)	1816
DCLG[Nle][Nle]RKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5,6;Pra13;Asp28]GpTx-1(1-34)	1817
DCLGV[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Nle6;Pra13;Asp28]GpTx-1(1-34)	1818
DCLGL[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Nle6;Pra13;Asp28]GpTx-1(1-34)	1819
DCLGI[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Nle6;Pra13;Asp28]GpTx-1(1-34)	1820
DCLGFFRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Phe6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1821
DCLGFLRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu6,26;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1822
DCLGF[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1823
DCLGGMRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1824
DCLGAMRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1825
DCLG[2-Abu]MRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Glu11;Leu26;Asp28]GpTx-1(1-34)	1826

DCLG[Nva]MRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1827
DCLG[Nle]MRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1828
DCLGVMRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1829
DCLGLMRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1830
DCLGIMRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1831
DCLGFFRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Phe6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1832
DCLGFLRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu6,26;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1833
DCLGF[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1834
DCLGGMRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1835
DCLGAMRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1836
DCLG[2-Abu]MRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Glu10;Leu26;Asp28]GpTx-1(1-34)	1837
DCLG[Nva]MRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1838
DCLG[Nle]MRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1839
DCLGVMRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1840
DCLGLMRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1841
DCLGIMRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1842
DCLGFFRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Phe6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	1843
DCLGFLRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu6,26;Asp10,28;2-Abu13]GpTx-1(1-34)	1844
DCLGF[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	1845
DCLGGMRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	1846

DCLGAMRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	1847
DCLG[2-Abu]MRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Asp10,28;Leu26]GpTx-1(1-34)	1848
DCLG[Nva]MRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	1849
DCLG[Nle]MRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	1850
DCLGVMRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	1851
DCLGLMRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Asp10,28;2-Abu13]GpTx-1(1-34)	1852
DCLGIMRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	1853
DCLGGFRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Phe6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1854
DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Phe6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1855
DCLG[2-Abu]FRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Phe6;Leu26;Asp28]GpTx-1(1-34)	1856
DCLG[Nva]FRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Phe6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1857
DCLG[Nle]FRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Phe6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1858
DCLGVFRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Phe6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1859
DCLGLFRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Phe6;2-Abu13;Asp28]GpTx-1(1-34)	1860
DCLGIFRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Phe6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1861
DCLGGLRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Leu6,26;2-Abu13;Asp28]GpTx-1(1-34)	1862
DCLGALRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Leu6,26;2-Abu13;Asp28]GpTx-1(1-34)	1863
DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Asp28]GpTx-1(1-34)	1864
DCLG[Nva]LRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Leu6,26;2-Abu13;Asp28]GpTx-1(1-34)	1865
DCLG[Nle]LRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Leu6,26;2-Abu13;Asp28]GpTx-1(1-34)	1866

DCLGVLRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Leu6,26;2-Abu13;Asp28]GpTx-1(1-34)	1867
DCLGLLRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,6,26;2-Abu13;Asp28]GpTx-1(1-34)	1868
DCLGILRKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Leu6,26;2-Abu13;Asp28]GpTx-1(1-34)	1869
DCLGG[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Nle6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1870
DCLGA[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Nle6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1871
DCLG[2-Abu][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Nle6;Leu26;Asp28]GpTx-1(1-34)	1872
DCLG[Nva][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Nle6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1873
DCLG[Nle][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5,6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1874
DCLGV[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Nle6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1875
DCLGL[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Nle6;2-Abu13;Asp28]GpTx-1(1-34)	1876
DCLGI[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Nle6;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	1877
DCLGFFRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Phe6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	1878
DCLGFLRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu6,26;Glu11;Pra13;Asp28]GpTx-1(1-34)	1879
DCLGF[Nle]RKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	1880
DCLGGMRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	1881
DCLGAMRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	1882
DCLG[2-Abu]MRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	1883
DCLG[Nva]MRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	1884
DCLG[Nle]MRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	1885
DCLGVMRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	1886

DCLGLMRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Glu11;Pra13;Asp28]GpTx-1(1-34)	1887
DCLGIMRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	1888
DCLGFFRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Phe6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	1889
DCLGFLRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu6,26;Glu10;Pra13;Asp28]GpTx-1(1-34)	1890
DCLGF[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	1891
DCLGGMRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	1892
DCLGAMRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	1893
DCLG[2-Abu]MRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	1894
DCLG[Nva]MRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	1895
DCLG[Nle]MRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	1896
DCLGVMRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	1897
DCLGLMRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Glu10;Pra13;Asp28]GpTx-1(1-34)	1898
DCLGIMRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	1899
DCLGFFRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Phe6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	1900
DCLGFLRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu6,26;Asp10,28;Pra13]GpTx-1(1-34)	1901
DCLGF[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	1902
DCLGGMRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	1903
DCLGAMRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	1904
DCLG[2-Abu]MRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	1905
DCLG[Nva]MRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	1906

DCLG[Nle]MRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	1907
DCLGVMRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	1908
DCLGLMRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Asp10,28;Pra13]GpTx-1(1-34)	1909
DCLGIMRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	1910
DCLGGFRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Phe6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1911
DCLGAFRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Phe6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1912
DCLG[2-Abu]FRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Phe6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1913
DCLG[Nva]FRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Phe6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1914
DCLG[Nle]FRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Phe6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1915
DCLGVFRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Phe6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1916
DCLGLFRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Phe6;Pra13;Asp28]GpTx-1(1-34)	1917
DCLGIFRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Phe6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1918
DCLGGLRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Leu6,26;Pra13;Asp28]GpTx-1(1-34)	1919
DCLGALRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Leu6,26;Pra13;Asp28]GpTx-1(1-34)	1920
DCLG[2-Abu]LRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Leu6,26;Pra13;Asp28]GpTx-1(1-34)	1921
DCLG[Nva]LRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Leu6,26;Pra13;Asp28]GpTx-1(1-34)	1922
DCLG[Nle]LRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Leu6,26;Pra13;Asp28]GpTx-1(1-34)	1923
DCLGVLRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Leu6,26;Pra13;Asp28]GpTx-1(1-34)	1924
DCLGLLRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,6,26;Pra13;Asp28]GpTx-1(1-34)	1925
DCLGILRKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Leu6,26;Pra13;Asp28]GpTx-1(1-34)	1926

DCLGG[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Nle6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1927
DCLGA[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Nle6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1928
DCLG[2-Abu][Nle]RKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Nle6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1929
DCLG[Nva][Nle]RKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Nle6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1930
DCLG[Nle][Nle]RKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5,6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1931
DCLGV[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Nle6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1932
DCLGL[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Nle6;Pra13;Asp28]GpTx-1(1-34)	1933
DCLGI[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Nle6;Pra13;Leu26;Asp28]GpTx-1(1-34)	1934
DCLGGFRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Phe6;Glu11,2-Abu13;Asp28]GpTx-1(1-34)	1935
DCLGAFRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Phe6;Glu11,2-Abu13;Asp28]GpTx-1(1-34)	1936
DCLG[2-Abu]FRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu11;Asp28]GpTx-1(1-34)	1937
DCLG[Nva]FRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Phe6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1938
DCLG[Nle]FRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Phe6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1939
DCLGVFRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Phe6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1940
DCLGLFRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Phe6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1941
DCLGIFRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Phe6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1942
DCLGGLRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Leu6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1943
DCLGALRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Leu6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1944
DCLG[2-Abu]LRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Leu6;Glu11;Asp28]GpTx-1(1-34)	1945
DCLG[Nva]LRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Leu6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1946

DCLG[Nle]LRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Leu6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1947
DCLGVLRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Leu6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1948
DCLGLLRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5,6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1949
DCLGILRKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Leu6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1950
DCLGG[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Nle6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1951
DCLGA[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Nle6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1952
DCLG[2-Abu][Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu11;Asp28]GpTx-1(1-34)	1953
DCLG[Nva][Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Nle6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1954
DCLG[Nle][Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5,6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1955
DCLGV[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Nle6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1956
DCLGL[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Nle6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1957
DCLGI[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Nle6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	1958
DCLGGFRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Phe6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1959
DCLGAFRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Phe6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1960
DCLG[2-Abu]FRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu10;Asp28]GpTx-1(1-34)	1961
DCLG[Nva]FRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Phe6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1962
DCLG[Nle]FRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Phe6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1963
DCLGVFRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Phe6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1964
DCLGLFRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Phe6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1965
DCLGIFRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Phe6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1966

DCLGGLRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Leu6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1967
DCLGALRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Leu6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1968
DCLG[2-Abu]LRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Leu6;Glu10;Asp28]GpTx-1(1-34)	1969
DCLG[Nva]LRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Leu6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1970
DCLG[Nle]LRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Leu6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1971
DCLGVLRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Leu6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1972
DCLGLLRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5,6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1973
DCLGILRKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Leu6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1974
DCLGG[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Nle6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1975
DCLGA[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Nle6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1976
DCLG[2-Abu][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu10;Asp28]GpTx-1(1-34)	1977
DCLG[Nva][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Nle6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1978
DCLG[Nle][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5,6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1979
DCLGV[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Nle6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1980
DCLGL[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Nle6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1981
DCLGI[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Nle6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	1982
DCLGGFRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Phe6;Asp10,28;2-Abu13]GpTx-1(1-34)	1983
DCLGAFRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Phe6;Asp10,28;2-Abu13]GpTx-1(1-34)	1984
DCLG[2-Abu]FRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Phe6;Asp10,28]GpTx-1(1-34)	1985
DCLG[Nva]FRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Phe6;Asp10,28;2-Abu13]GpTx-1(1-34)	1986

DCLG[Nle]FRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Phe6;Asp10,28;2-Abu13]GpTx-1(1-34)	1987
DCLGVFRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Phe6;Asp10,28;2-Abu13]GpTx-1(1-34)	1988
DCLGLFRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Phe6;Asp10,28;2-Abu13]GpTx-1(1-34)	1989
DCLGIFRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Phe6;Asp10,28;2-Abu13]GpTx-1(1-34)	1990
DCLGGLRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Leu6;Asp10,28;2-Abu13]GpTx-1(1-34)	1991
DCLGALRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Leu6;Asp10,28;2-Abu13]GpTx-1(1-34)	1992
DCLG[2-Abu]LRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Leu6;Asp10,28]GpTx-1(1-34)	1993
DCLG[Nva]LRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Leu6;Asp10,28;2-Abu13]GpTx-1(1-34)	1994
DCLG[Nle]LRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Leu6;Asp10,28;2-Abu13]GpTx-1(1-34)	1995
DCLGVLRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Leu6;Asp10,28;2-Abu13]GpTx-1(1-34)	1996
DCLGLLRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5,6;Asp10,28;2-Abu13]GpTx-1(1-34)	1997
DCLGILRKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Leu6;Asp10,28;2-Abu13]GpTx-1(1-34)	1998
DCLGG[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Nle6;Asp10,28;2-Abu13]GpTx-1(1-34)	1999
DCLGA[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Nle6;Asp10,28;2-Abu13]GpTx-1(1-34)	2000
DCLG[2-Abu][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5,13;Nle6;Asp10,28]GpTx-1(1-34)	2001
DCLG[Nva][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Nle6;Asp10,28;2-Abu13]GpTx-1(1-34)	2002
DCLG[Nle][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5,6;Asp10,28;2-Abu13]GpTx-1(1-34)	2003
DCLGV[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Nle6;Asp10,28;2-Abu13]GpTx-1(1-34)	2004
DCLGL[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Nle6;Asp10,28;2-Abu13]GpTx-1(1-34)	2005
DCLGI[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Nle6;Asp10,28;2-Abu13]GpTx-1(1-34)	2006

DCLGGFRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Phe6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2007
DCLGAFRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Phe6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2008
DCLG[2-Abu]FRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Phe6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2009
DCLG[Nva]FRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Phe6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2010
DCLG[Nle]FRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Phe6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2011
DCLGVFRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Phe6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2012
DCLGLFRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Phe6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2013
DCLGIFRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Phe6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2014
DCLGGLRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Leu6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2015
DCLGALRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Leu6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2016
DCLG[2-Abu]LRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Leu6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2017
DCLG[Nva]LRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Leu6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2018
DCLG[Nle]LRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Leu6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2019
DCLGVLRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Leu6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2020
DCLGLLRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5,6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2021
DCLGILRKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Leu6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2022
DCLGG[Nle]RKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Nle6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2023
DCLGA[Nle]RKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Nle6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2024
DCLG[2-Abu][Nle]RKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Nle6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2025
DCLG[Nva][Nle]RKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Nle6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2026

DCLG[Nle][Nle]RKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5,6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2027
DCLGV[Nle]RKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Nle6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2028
DCLGL[Nle]RKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Nle6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2029
DCLGI[Nle]RKCIED[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Nle6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2030
DCLGGFRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Phe6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2031
DCLGAFRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Phe6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2032
DCLG[2-Abu]FRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Phe6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2033
DCLG[Nva]FRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Phe6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2034
DCLG[Nle]FRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Phe6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2035
DCLGVFRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Phe6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2036
DCLGLFRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Phe6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2037
DCLGIFRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Phe6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2038
DCLGGLRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Leu6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2039
DCLGALRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Leu6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2040
DCLG[2-Abu]LRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Leu6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2041
DCLG[Nva]LRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Leu6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2042
DCLG[Nle]LRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Leu6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2043
DCLGVLRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Leu6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2044
DCLGLLRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5,6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2045
DCLGILRKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Leu6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2046

DCLGG[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Nle6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2047
DCLGA[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Nle6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2048
DCLG[2-Abu][Nle]RKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Nle6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2049
DCLG[Nva][Nle]RKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Nle6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2050
DCLG[Nle][Nle]RKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5,6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2051
DCLGV[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Nle6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2052
DCLGL[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Nle6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2053
DCLGI[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Nle6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2054
DCLGGFRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Phe6;Asp10,28;Pra13]GpTx-1(1-34)	2055
DCLGAFRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Phe6;Asp10,28;Pra13]GpTx-1(1-34)	2056
DCLG[2-Abu]FRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Phe6;Asp10,28;Pra13]GpTx-1(1-34)	2057
DCLG[Nva]FRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Phe6;Asp10,28;Pra13]GpTx-1(1-34)	2058
DCLG[Nle]FRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Phe6;Asp10,28;Pra13]GpTx-1(1-34)	2059
DCLGVFRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Phe6;Asp10,28;Pra13]GpTx-1(1-34)	2060
DCLGLFRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Phe6;Asp10,28;Pra13]GpTx-1(1-34)	2061
DCLGIFRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Phe6;Asp10,28;Pra13]GpTx-1(1-34)	2062
DCLGGLRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Leu6;Asp10,28;Pra13]GpTx-1(1-34)	2063
DCLGALRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Leu6;Asp10,28;Pra13]GpTx-1(1-34)	2064
DCLG[2-Abu]LRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Leu6;Asp10,28;Pra13]GpTx-1(1-34)	2065
DCLG[Nva]LRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Leu6;Asp10,28;Pra13]GpTx-1(1-34)	2066

DCLG[Nle]LRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5;Leu6;Asp10,28;Pra13]GpTx-1(1-34)	2067
DCLGVLRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Leu6;Asp10,28;Pra13]GpTx-1(1-34)	2068
DCLGLLRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5,6;Asp10,28;Pra13]GpTx-1(1-34)	2069
DCLGILRKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Leu6;Asp10,28;Pra13]GpTx-1(1-34)	2070
DCLGG[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Gly5;Nle6;Asp10,28;Pra13]GpTx-1(1-34)	2071
DCLGA[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ala5;Nle6;Asp10,28;Pra13]GpTx-1(1-34)	2072
DCLG[2-Abu][Nle]RKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[2-Abu5;Nle6;Asp10,28;Pra13]GpTx-1(1-34)	2073
DCLG[Nva][Nle]RKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nva5;Nle6;Asp10,28;Pra13]GpTx-1(1-34)	2074
DCLG[Nle][Nle]RKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Nle5,6;Asp10,28;Pra13]GpTx-1(1-34)	2075
DCLGV[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Val5;Nle6;Asp10,28;Pra13]GpTx-1(1-34)	2076
DCLGL[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Leu5;Nle6;Asp10,28;Pra13]GpTx-1(1-34)	2077
DCLGI[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHDWCKYVF-{Amide}	[Ile5;Nle6;Asp10,28;Pra13]GpTx-1(1-34)	2078
DCLGGFRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Phe6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2079
DCLGAFRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Phe6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2080
DCLG[2-Abu]FRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu11;Leu26;Asp28]GpTx-1(1-34)	2081
DCLG[Nva]FRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Phe6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2082
DCLG[Nle]FRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Phe6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2083
DCLGVFRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Phe6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2084
DCLGLFRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Phe6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	2085
DCLGIFRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Phe6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2086

DCLGGLRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Leu6,26;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	2087
DCLGALRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Leu6,26;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	2088
DCLG[2-Abu]LRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Glu11;Asp28]GpTx-1(1-34)	2089
DCLG[Nva]LRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Leu6,26;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	2090
DCLG[Nle]LRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Leu6,26;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	2091
DCLGVLRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Leu6,26;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	2092
DCLGLLRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,6,26;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	2093
DCLGILRKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Leu6,26;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	2094
DCLGG[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Nle6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2095
DCLGA[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Nle6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2096
DCLG[2-Abu][Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu11;Leu26;Asp28]GpTx-1(1-34)	2097
DCLG[Nva][Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Nle6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2098
DCLG[Nle][Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5,6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2099
DCLGV[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Nle6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2100
DCLGL[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Nle6;Glu11;2-Abu13;Asp28]GpTx-1(1-34)	2101
DCLGI[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Nle6;Glu11;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2102
DCLGGFRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Phe6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2103
DCLGAFRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Phe6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2104
DCLG[2-Abu]FRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu10;Leu26;Asp28]GpTx-1(1-34)	2105
DCLG[Nva]FRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Phe6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2106

DCLG[Nle]FRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	*[Nle5;Phe6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)*	*2107*
DCLGVFRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Phe6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2108
DCLGLFRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Phe6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	2109
DCLGIFRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Phe6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2110
DCLGGLRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Leu6,26;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	2111
DCLGALRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Leu6,26;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	2112
DCLG[2-Abu]LRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Glu10;Asp28]GpTx-1(1-34)	2113
DCLG[Nva]LRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Leu6,26;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	2114
DCLG[Nle]LRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Leu6,26;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	2115
DCLGVLRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Leu6,26;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	2116
DCLGLLRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,6,26;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	2117
DCLGILRKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Leu6,26;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	2118
DCLGG[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Nle6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2119
DCLGA[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Nle6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2120
DCLG[2-Abu][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu10;Leu26;Asp28]GpTx-1(1-34)	2121
DCLG[Nva][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Nle6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2122
DCLG[Nle][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5,6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2123
DCLGV[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Nle6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2124
DCLGL[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Nle6;Glu10;2-Abu13;Asp28]GpTx-1(1-34)	2125
DCLGI[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Nle6;Glu10;2-Abu13;Leu26;Asp28]GpTx-1(1-34)	2126

DCLGGFRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Phe6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2127
DCLGAFRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Phe6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2128
DCLG[2-Abu]FRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Phe6;Asp10,28;Leu26]GpTx-1(1-34)	2129
DCLG[Nva]FRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Phe6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2130
DCLG[Nle]FRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Phe6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2131
DCLGVFRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Phe6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2132
DCLGLFRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Phe6;Asp10,28;2-Abu13]GpTx-1(1-34)	2133
DCLGIFRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Phe6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2134
DCLGGLRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Leu6,26;Asp10,28;2-Abu13]GpTx-1(1-34)	2135
DCLGALRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Leu6,26;Asp10,28;2-Abu13]GpTx-1(1-34)	2136
DCLG[2-Abu]LRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Asp10,28]GpTx-1(1-34)	2137
DCLG[Nva]LRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Leu6,26;Asp10,28;2-Abu13]GpTx-1(1-34)	2138
DCLG[Nle]LRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Leu6,26;Asp10,28;2-Abu13]GpTx-1(1-34)	2139
DCLGVLRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Leu6,26;Asp10,28;2-Abu13]GpTx-1(1-34)	2140
DCLGLLRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,6,26;Asp10,28;2-Abu13]GpTx-1(1-34)	2141
DCLGILRKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Leu6,26;Asp10,28;2-Abu13]GpTx-1(1-34)	2142
DCLGG[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Nle6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2143
DCLGA[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Nle6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2144
DCLG[2-Abu][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5,13;Nle6;Asp10,28;Leu26]GpTx-1(1-34)	2145
DCLG[Nva][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Nle6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2146

DCLG[Nle][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5,6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2147
DCLGV[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Nle6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2148
DCLGL[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Nle6;Asp10,28;2-Abu13]GpTx-1(1-34)	2149
DCLGI[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Nle6;Asp10,28;2-Abu13;Leu26]GpTx-1(1-34)	2150
DCLGGFRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Phe6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2151
DCLGAFRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Phe6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2152
DCLG[2-Abu]FRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Phe6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2153
DCLG[Nva]FRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Phe6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2154
DCLG[Nle]FRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Phe6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2155
DCLGVFRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Phe6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2156
DCLGLFRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Phe6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2157
DCLGIFRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Phe6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2158
DCLGGLRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Leu6,26;Glu11;Pra13;Asp28]GpTx-1(1-34)	2159
DCLGALRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Leu6,26;Glu11;Pra13;Asp28]GpTx-1(1-34)	2160
DCLG[2-Abu]LRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Leu6,26;Glu11;Pra13;Asp28]GpTx-1(1-34)	2161
DCLG[Nva]LRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Leu6,26;Glu11;Pra13;Asp28]GpTx-1(1-34)	2162
DCLG[Nle]LRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Leu6,26;Glu11;Pra13;Asp28]GpTx-1(1-34)	2163
DCLGVLRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Leu6,26;Glu11;Pra13;Asp28]GpTx-1(1-34)	2164
DCLGLLRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,6,26;Glu11;Pra13;Asp28]GpTx-1(1-34)	2165
DCLGILRKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Leu6,26;Glu11;Pra13;Asp28]GpTx-1(1-34)	2166

DCLGG[Nle]RKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Nle6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2167
DCLGA[Nle]RKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Nle6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2168
DCLG[2-Abu][Nle]RKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Nle6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2169
DCLG[Nva][Nle]RKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Nle6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2170
DCLG[Nle][Nle]RKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5,6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2171
DCLGV[Nle]RKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Nle6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2172
DCLGL[Nle]RKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Nle6;Glu11;Pra13;Asp28]GpTx-1(1-34)	2173
DCLGI[Nle]RKCIED[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Nle6;Glu11;Pra13;Leu26;Asp28]GpTx-1(1-34)	2174
DCLGGFRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Phe6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2175
DCLGAFRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Phe6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2176
DCLG[2-Abu]FRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Phe6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2177
DCLG[Nva]FRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Phe6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2178
DCLG[Nle]FRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Phe6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2179
DCLGVFRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Phe6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2180
DCLGLFRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Phe6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2181
DCLGIFRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Phe6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2182
DCLGGLRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Leu6,26;Glu10;Pra13;Asp28]GpTx-1(1-34)	2183
DCLGALRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Leu6,26;Glu10;Pra13;Asp28]GpTx-1(1-34)	2184
DCLG[2-Abu]LRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Leu6,26;Glu10;Pra13;Asp28]GpTx-1(1-34)	2185
DCLG[Nva]LRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Leu6,26;Glu10;Pra13;Asp28]GpTx-1(1-34)	2186

DCLG[Nle]LRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Leu6,26;Glu10;Pra13;Asp28]GpTx-1(1-34)	2187
DCLGVLRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Leu6,26;Glu10;Pra13;Asp28]GpTx-1(1-34)	2188
DCLGLLRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,6,26;Glu10;Pra13;Asp28]GpTx-1(1-34)	2189
DCLGILRKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Leu6,26;Glu10;Pra13;Asp28]GpTx-1(1-34)	2190
DCLGG[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Nle6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2191
DCLGA[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Nle6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2192
DCLG[2-Abu][Nle]RKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Nle6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2193
DCLG[Nva][Nle]RKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Nle6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2194
DCLG[Nle][Nle]RKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5,6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2195
DCLGV[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Nle6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2196
DCLGL[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Nle6;Glu10;Pra13;Asp28]GpTx-1(1-34)	2197
DCLGI[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Nle6;Glu10;Pra13;Leu26;Asp28]GpTx-1(1-34)	2198
DCLGGFRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Phe6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2199
DCLGAFRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Phe6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2200
DCLG[2-Abu]FRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Phe6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2201
DCLG[Nva]FRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Phe6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2202
DCLG[Nle]FRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Phe6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2203
DCLGVFRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Phe6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2204
DCLGLFRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Phe6;Asp10,28;Pra13]GpTx-1(1-34)	2205
DCLGIFRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Phe6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2206

DCLGGLRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Leu6,26;Asp10,28;Pra13]GpTx-1(1-34)	2207
DCLGALRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Leu6,26;Asp10,28;Pra13]GpTx-1(1-34)	2208
DCLG[2-Abu]LRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Leu6,26;Asp10,28;Pra13]GpTx-1(1-34)	2209
DCLG[Nva]LRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Leu6,26;Asp10,28;Pra13]GpTx-1(1-34)	2210
DCLG[Nle]LRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5;Leu6,26;Asp10,28;Pra13]GpTx-1(1-34)	2211
DCLGVLRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Leu6,26;Asp10,28;Pra13]GpTx-1(1-34)	2212
DCLGLLRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,6,26;Asp10,28;Pra13]GpTx-1(1-34)	2213
DCLGILRKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Leu6,26;Asp10,28;Pra13]GpTx-1(1-34)	2214
DCLGG[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Gly5;Nle6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2215
DCLGA[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ala5;Nle6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2216
DCLG[2-Abu][Nle]RKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[2-Abu5;Nle6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2217
DCLG[Nva][Nle]RKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nva5;Nle6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2218
DCLG[Nle][Nle]RKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Nle5,6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2219
DCLGV[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Val5;Nle6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2220
DCLGL[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Leu5,26;Nle6;Asp10,28;Pra13]GpTx-1(1-34)	2221
DCLGI[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHDWCKYVF-{Amide}	[Ile5;Nle6;Asp10,28;Pra13;Leu26]GpTx-1(1-34)	2222
DCLGFMRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu13;Gln28]GpTx-1(1-34)	2223
DCLGFMRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Pra13;Gln28]GpTx-1(1-34)	2224
DCLGFMRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2225
DCLGFMRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Pra13;Leu26;Gln28]GpTx-1(1-34)	2226

DCLGFMRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2227
DCLGFMRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2228
DCLGFMRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2229
DCLGFFRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Phe6;2-Abu13;Gln28]GpTx-1(1-34)	2230
DCLGFLRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu6;2-Abu13;Gln28]GpTx-1(1-34)	2231
DCLGF[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle6;2-Abu13;Gln28]GpTx-1(1-34)	2232
DCLGGMRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;2-Abu13;Gln28]GpTx-1(1-34)	2233
DCLGAMRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;2-Abu13;Gln28]GpTx-1(1-34)	2234
DCLG[2-Abu]MRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Gln28]GpTx-1(1-34)	2235
DCLG[Nva]MRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;2-Abu13;Gln28]GpTx-1(1-34)	2236
DCLG[Nle]MRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;2-Abu13;Gln28]GpTx-1(1-34)	2237
DCLGVMRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;2-Abu13;Gln28]GpTx-1(1-34)	2238
DCLGLMRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;2-Abu13;Gln28]GpTx-1(1-34)	2239
DCLGIMRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;2-Abu13;Gln28]GpTx-1(1-34)	2240
DCLGFMRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Glu11;Pra13;Gln28]GpTx-1(1-34)	2241
DCLGFMRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Glu10;Pra13;Gln28]GpTx-1(1-34)	2242
DCLGFMRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Asp10;Pra13;Gln28]GpTx-1(1-34)	2243
DCLGFFRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Phe6;Pra13;Gln28]GpTx-1(1-34)	2244
DCLGFLRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu6;Pra13;Gln28]GpTx-1(1-34)	2245
DCLGF[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle6;Pra13;Gln28]GpTx-1(1-34)	2246

DCLGGMRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Pra13;Gln28]GpTx-1(1-34)	2247
DCLGAMRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Pra13;Gln28]GpTx-1(1-34)	2248
DCLG[2-Abu]MRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Pra13;Gln28]GpTx-1(1-34)	2249
DCLG[Nva]MRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Pra13;Gln28]GpTx-1(1-34)	2250
DCLG[Nle]MRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Pra13;Gln28]GpTx-1(1-34)	2251
DCLGVMRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Pra13;Gln28]GpTx-1(1-34)	2252
DCLGLMRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Pra13;Gln28]GpTx-1(1-34)	2253
DCLGIMRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Pra13;Gln28]GpTx-1(1-34)	2254
DCLGFMRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2255
DCLGFMRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2256
DCLGFMRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2257
DCLGFFRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Phe6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2258
DCLGFLRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu6,26;2-Abu13;Gln28]GpTx-1(1-34)	2259
DCLGF[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2260
DCLGGMRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2261
DCLGAMRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2262
DCLG[2-Abu]MRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Leu26;Gln28]GpTx-1(1-34)	2263
DCLG[Nva]MRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2264
DCLG[Nle]MRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2265
DCLGVMRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2266

DCLGLMRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;2-Abu13;Gln28]GpTx-1(1-34)	2267
DCLGIMRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2268
DCLGFMRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Glu11,Pra13;Leu26;Gln28]GpTx-1(1-34)	2269
DCLGFMRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2270
DCLGFMRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2271
DCLGFFRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Phe6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2272
DCLGFLRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu6,26;Pra13;Gln28]GpTx-1(1-34)	2273
DCLGF[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2274
DCLGGMRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Pra13;Leu26;Gln28]GpTx-1(1-34)	2275
DCLGAMRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Pra13;Leu26;Gln28]GpTx-1(1-34)	2276
DCLG[2-Abu]MRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Pra13;Leu26;Gln28]GpTx-1(1-34)	2277
DCLG[Nva]MRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Pra13;Leu26;Gln28]GpTx-1(1-34)	2278
DCLG[Nle]MRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Pra13;Leu26;Gln28]GpTx-1(1-34)	2279
DCLGVMRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Pra13;Leu26;Gln28]GpTx-1(1-34)	2280
DCLGLMRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Pra13;Gln28]GpTx-1(1-34)	2281
DCLGIMRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Pra13;Leu26;Gln28]GpTx-1(1-34)	2282
DCLGFFRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Phe6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2283
DCLGFLRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2284
DCLGF[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2285
DCLGGMRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2286

DCLGAMRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2287
DCLG[2-Abu]MRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Glu11;Gln28]GpTx-1(1-34)	2288
DCLG[Nva]MRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2289
DCLG[Nle]MRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2290
DCLGVMRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2291
DCLGLMRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2292
DCLGIMRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2293
DCLGFFRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Phe6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2294
DCLGFLRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2295
DCLGF[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2296
DCLGGMRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2297
DCLGAMRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2298
DCLG[2-Abu]MRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Glu10;Gln28]GpTx-1(1-34)	2299
DCLG[Nva]MRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2300
DCLG[Nle]MRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2301
DCLGVMRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2302
DCLGLMRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2303
DCLGIMRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2304
DCLGFFRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Phe6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2305
DCLGFLRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2306

DCLGF[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2307
DCLGGMRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2308
DCLGAMRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2309
DCLG[2-Abu]MRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Asp10;Gln28]GpTx-1(1-34)	2310
DCLG[Nva]MRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2311
DCLG[Nle]MRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2312
DCLGVMRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2313
DCLGLMRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2314
DCLGIMRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2315
DCLGGFRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Phe6;2-Abu13;Gln28]GpTx-1(1-34)	2316
DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Phe6;2-Abu13;Gln28]GpTx-1(1-34)	2317
DCLG[2-Abu]FRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Phe6;Gln28]GpTx-1(1-34)	2318
DCLG[Nva]FRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Phe6;2-Abu13;Gln28]GpTx-1(1-34)	2319
DCLG[Nle]FRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Phe6;2-Abu13;Gln28]GpTx-1(1-34)	2320
DCLGVFRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Phe6;2-Abu13;Gln28]GpTx-1(1-34)	2321
DCLGLFRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Phe6;2-Abu13;Gln28]GpTx-1(1-34)	2322
DCLGIFRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Phe6;2-Abu13;Gln28]GpTx-1(1-34)	2323
DCLGGLRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Leu6;2-Abu13;Gln28]GpTx-1(1-34)	2324
DCLGALRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Leu6;2-Abu13;Gln28]GpTx-1(1-34)	2325
DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Leu6;Gln28]GpTx-1(1-34)	2326

DCLG[Nva]LRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Leu6;2-Abu13;Gln28]GpTx-1(1-34)	2327
DCLG[Nle]LRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Leu6;2-Abu13;Gln28]GpTx-1(1-34)	2328
DCLGVLRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Leu6;2-Abu13;Gln28]GpTx-1(1-34)	2329
DCLGLLRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5,6;2-Abu13;Gln28]GpTx-1(1-34)	2330
DCLGILRKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Leu6;2-Abu13;Gln28]GpTx-1(1-34)	2331
DCLGG[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Nle6;2-Abu13;Gln28]GpTx-1(1-34)	2332
DCLGA[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Nle6;2-Abu13;Gln28]GpTx-1(1-34)	2333
DCLG[2-Abu][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Nle6;Gln28]GpTx-1(1-34)	2334
DCLG[Nva][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Nle6;2-Abu13;Gln28]GpTx-1(1-34)	2335
DCLG[Nle][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5,6;2-Abu13;Gln28]GpTx-1(1-34)	2336
DCLGV[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Nle6;2-Abu13;Gln28]GpTx-1(1-34)	2337
DCLGL[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Nle6;2-Abu13;Gln28]GpTx-1(1-34)	2338
DCLGI[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Nle6;2-Abu13;Gln28]GpTx-1(1-34)	2339
DCLGFFRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Phe6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2340
DCLGFLRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2341
DCLGF[Nle]RKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2342
DCLGGMRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Glu11;Pra13;Gln28]GpTx-1(1-34)	2343
DCLGAMRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Glu11;Pra13;Gln28]GpTx-1(1-34)	2344
DCLG[2-Abu]MRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	*[2-Abu5;Glu11;Pra13;Gln28]GpTx-1(1-34)*	2345
DCLG[Nva]MRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Glu11;Pra13;Gln28]GpTx-1(1-34)	2346

DCLG[Nle]MRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Glu11;Pra13;Gln28]GpTx-1(1-34)	2347
DCLGVMRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Glu11;Pra13;Gln28]GpTx-1(1-34)	2348
DCLGLMRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Glu11;Pra13;Gln28]GpTx-1(1-34)	2349
DCLGIMRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Glu11;Pra13;Gln28]GpTx-1(1-34)	2350
DCLGFFRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Phe6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2351
DCLGFLRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2352
DCLGF[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2353
DCLGGMRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Glu10;Pra13;Gln28]GpTx-1(1-34)	2354
DCLGAMRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Glu10;Pra13;Gln28]GpTx-1(1-34)	2355
DCLG[2-Abu]MRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Glu10;Pra13;Gln28]GpTx-1(1-34)	2356
DCLG[Nva]MRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Glu10;Pra13;Gln28]GpTx-1(1-34)	2357
DCLG[Nle]MRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Glu10;Pra13;Gln28]GpTx-1(1-34)	2358
DCLGVMRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Glu10;Pra13;Gln28]GpTx-1(1-34)	2359
DCLGLMRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Glu10;Pra13;Gln28]GpTx-1(1-34)	2360
DCLGIMRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Glu10;Pra13;Gln28]GpTx-1(1-34)	2361
DCLGFFRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Phe6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2362
DCLGFLRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2363
DCLGF[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2364
DCLGGMRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Asp10;Pra13;Gln28]GpTx-1(1-34)	2365
DCLGAMRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Asp10;Pra13;Gln28]GpTx-1(1-34)	2366

DCLG[2-Abu]MRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Asp10;Pra13;Gln28]GpTx-1(1-34)	2367
DCLG[Nva]MRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Asp10;Pra13;Gln28]GpTx-1(1-34)	2368
DCLG[Nle]MRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Asp10;Pra13;Gln28]GpTx-1(1-34)	2369
DCLGVMRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Asp10;Pra13;Gln28]GpTx-1(1-34)	2370
DCLGLMRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Asp10;Pra13;Gln28]GpTx-1(1-34)	2371
DCLGIMRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Asp10;Pra13;Gln28]GpTx-1(1-34)	2372
DCLGGFRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Phe6;Pra13;Gln28]GpTx-1(1-34)	2373
DCLGAFRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Phe6;Pra13;Gln28]GpTx-1(1-34)	2374
DCLG[2-Abu]FRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Phe6;Pra13;Gln28]GpTx-1(1-34)	2375
DCLG[Nva]FRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Phe6;Pra13;Gln28]GpTx-1(1-34)	2376
DCLG[Nle]FRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Phe6;Pra13;Gln28]GpTx-1(1-34)	2377
DCLGVFRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Phe6;Pra13;Gln28]GpTx-1(1-34)	2378
DCLGLFRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Phe6;Pra13;Gln28]GpTx-1(1-34)	2379
DCLGIFRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Phe6;Pra13;Gln28]GpTx-1(1-34)	2380
DCLGGLRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Leu6;Pra13;Gln28]GpTx-1(1-34)	2381
DCLGALRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Leu6;Pra13;Gln28]GpTx-1(1-34)	2382
DCLG[2-Abu]LRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Leu6;Pra13;Gln28]GpTx-1(1-34)	2383
DCLG[Nva]LRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Leu6;Pra13;Gln28]GpTx-1(1-34)	2384
DCLG[Nle]LRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Leu6;Pra13;Gln28]GpTx-1(1-34)	2385
DCLGVLRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Leu6;Pra13;Gln28]GpTx-1(1-34)	2386

DCLGLLRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5,6;Pra13;Gln28]GpTx-1(1-34)	2387
DCLGILRKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Leu6;Pra13;Gln28]GpTx-1(1-34)	2388
DCLGG[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Nle6;Pra13;Gln28]GpTx-1(1-34)	2389
DCLGA[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Nle6;Pra13;Gln28]GpTx-1(1-34)	2390
DCLG[2-Abu][Nle]RKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Nle6;Pra13;Gln28]GpTx-1(1-34)	2391
DCLG[Nva][Nle]RKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Nle6;Pra13;Gln28]GpTx-1(1-34)	2392
DCLG[Nle][Nle]RKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5,6;Pra13;Gln28]GpTx-1(1-34)	2393
DCLGV[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Nle6;Pra13;Gln28]GpTx-1(1-34)	2394
DCLGL[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Nle6;Pra13;Gln28]GpTx-1(1-34)	2395
DCLGI[Nle]RKCIPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Nle6;Pra13;Gln28]GpTx-1(1-34)	2396
DCLGFFRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Phe6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2397
DCLGFLRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu6,26;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2398
DCLGF[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2399
DCLGGMRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2400
DCLGAMRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2401
DCLG[2-Abu]MRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Glu11;Leu26;Gln28]GpTx-1(1-34)	2402
DCLG[Nva]MRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2403
DCLG[Nle]MRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2404
DCLGVMRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2405
DCLGLMRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2406

DCLGIMRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2407
DCLGFFRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Phe6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2408
DCLGFLRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu6,26;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2409
DCLGF[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2410
DCLGGMRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2411
DCLGAMRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2412
DCLG[2-Abu]MRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Glu10;Leu26;Gln28]GpTx-1(1-34)	2413
DCLG[Nva]MRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2414
DCLG[Nle]MRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2415
DCLGVMRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2416
DCLGLMRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2417
DCLGIMRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2418
DCLGFFRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Phe6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2419
DCLGFLRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu6,26;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2420
DCLGF[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2421
DCLGGMRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2422
DCLGAMRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2423
DCLG[2-Abu]MRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Asp10;Leu26;Gln28]GpTx-1(1-34)	2424
DCLG[Nva]MRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2425
DCLG[Nle]MRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	*[Nle5;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)*	*2426*

DCLGVMRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2427
DCLGLMRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2428
DCLGIMRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2429
DCLGGFRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Phe6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2430
DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Phe6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2431
DCLG[2-Abu]FRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Phe6;Leu26;Gln28]GpTx-1(1-34)	2432
DCLG[Nva]FRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Phe6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2433
DCLG[Nle]FRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Phe6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2434
DCLGVFRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Phe6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2435
DCLGLFRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Phe6;2-Abu13;Gln28]GpTx-1(1-34)	2436
DCLGIFRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Phe6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2437
DCLGGLRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Leu6,26;2-Abu13;Gln28]GpTx-1(1-34)	2438
DCLGALRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Leu6,26;2-Abu13;Gln28]GpTx-1(1-34)	2439
DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Gln28]GpTx-1(1-34)	2440
DCLG[Nva]LRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Leu6,26;2-Abu13;Gln28]GpTx-1(1-34)	2441
DCLG[Nle]LRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Leu6,26;2-Abu13;Gln28]GpTx-1(1-34)	2442
DCLGVLRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Leu6,26;2-Abu13;Gln28]GpTx-1(1-34)	2443
DCLGLLRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,6,26;2-Abu13;Gln28]GpTx-1(1-34)	2444
DCLGILRKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Leu6,26;2-Abu13;Gln28]GpTx-1(1-34)	2445
DCLGG[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Nle6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2446

DCLGA[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Nle6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2447
DCLG[2-Abu][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Nle6;Leu26;Gln28]GpTx-1(1-34)	2448
DCLG[Nva][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Nle6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2449
DCLG[Nle][Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5,6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2450
DCLGV[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Nle6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2451
DCLGL[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Nle6;2-Abu13;Gln28]GpTx-1(1-34)	2452
DCLGI[Nle]RKCIPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Nle6;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2453
DCLGFFRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Phe6;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2454
DCLGFLRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu6,26;Glu11;Pra13;Gln28]GpTx-1(1-34)	2455
DCLGF[Nle]RKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle6;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2456
DCLGGMRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2457
DCLGAMRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2458
DCLG[2-Abu]MRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2459
DCLG[Nva]MRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2460
DCLG[Nle]MRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2461
DCLGVMRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2462
DCLGLMRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Glu11;Pra13;Gln28]GpTx-1(1-34)	2463
DCLGIMRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2464
DCLGFFRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Phe6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2465
DCLGFLRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu6,26;Glu10;Pra13;Gln28]GpTx-1(1-34)	2466

DCLGF[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2467
DCLGGMRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2468
DCLGAMRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2469
DCLG[2-Abu]MRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2470
DCLG[Nva]MRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2471
DCLG[Nle]MRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2472
DCLGVMRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2473
DCLGLMRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Glu10;Pra13;Gln28]GpTx-1(1-34)	2474
DCLGIMRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2475
DCLGFFRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Phe6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2476
DCLGFLRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu6,26;Asp10;Pra13;Gln28]GpTx-1(1-34)	2477
DCLGF[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2478
DCLGGMRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2479
DCLGAMRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2480
DCLG[2-Abu]MRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2481
DCLG[Nva]MRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2482
DCLG[Nle]MRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2483
DCLGVMRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2484
DCLGLMRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Asp10;Pra13;Gln28]GpTx-1(1-34)	2485
DCLGIMRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2486

DCLGGFRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Phe6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2487
DCLGAFRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Phe6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2488
DCLG[2-Abu]FRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Phe6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2489
DCLG[Nva]FRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Phe6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2490
DCLG[Nle]FRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Phe6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2491
DCLGVFRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Phe6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2492
DCLGLFRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Phe6;Pra13;Gln28]GpTx-1(1-34)	2493
DCLGIFRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Phe6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2494
DCLGGLRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Leu6,26;Pra13;Gln28]GpTx-1(1-34)	2495
DCLGALRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Leu6,26;Pra13;Gln28]GpTx-1(1-34)	2496
DCLG[2-Abu]LRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Leu6,26;Pra13;Gln28]GpTx-1(1-34)	2497
DCLG[Nva]LRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Leu6,26;Pra13;Gln28]GpTx-1(1-34)	2498
DCLG[Nle]LRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Leu6,26;Pra13;Gln28]GpTx-1(1-34)	2499
DCLGVLRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Leu6,26;Pra13;Gln28]GpTx-1(1-34)	2500
DCLGLLRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,6,26;Pra13;Gln28]GpTx-1(1-34)	2501
DCLGILRKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Leu6,26;Pra13;Gln28]GpTx-1(1-34)	2502
DCLGG[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Nle6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2503
DCLGA[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Nle6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2504
DCLG[2-Abu][Nle]RKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Nle6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2505
DCLG[Nva][Nle]RKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Nle6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2506

DCLG[Nle][Nle]RKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5,6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2507
DCLGV[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Nle6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2508
DCLGL[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Nle6;Pra13;Gln28]GpTx-1(1-34)	2509
DCLGI[Nle]RKCIPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Nle6;Pra13;Leu26;Gln28]GpTx-1(1-34)	2510
DCLGGFRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Phe6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2511
DCLGAFRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Phe6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2512
DCLG[2-Abu]FRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu11;Gln28]GpTx-1(1-34)	2513
DCLG[Nva]FRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Phe6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2514
DCLG[Nle]FRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Phe6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2515
DCLGVFRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Phe6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2516
DCLGLFRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Phe6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2517
DCLGIFRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Phe6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2518
DCLGGLRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Leu6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2519
DCLGALRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Leu6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2520
DCLG[2-Abu]LRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Leu6;Glu11;Gln28]GpTx-1(1-34)	2521
DCLG[Nva]LRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Leu6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2522
DCLG[Nle]LRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Leu6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2523
DCLGVLRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Leu6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2524
DCLGLLRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5,6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2525
DCLGILRKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Leu6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2526

DCLGG[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Nle6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2527
DCLGA[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Nle6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2528
DCLGI[2-Abu][Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu11;Gln28]GpTx-1(1-34)	2529
DCLG[Nva][Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Nle6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2530
DCLG[Nle][Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5,6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2531
DCLGV[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Nle6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2532
DCLGL[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Nle6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2533
DCLGI[Nle]RKCIED[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Nle6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2534
DCLGGFRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Phe6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2535
DCLGAFRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Phe6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2536
DCLG[2-Abu]FRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu10;Gln28]GpTx-1(1-34)	2537
DCLG[Nva]FRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Phe6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2538
DCLG[Nle]FRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Phe6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2539
DCLGVFRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Phe6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2540
DCLGLFRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Phe6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2541
DCLGIFRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Phe6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2542
DCLGGLRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Leu6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2543
DCLGALRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Leu6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2544
DCLG[2-Abu]LRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Leu6;Glu10;Gln28]GpTx-1(1-34)	2545
DCLG[Nva]LRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Leu6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2546

DCLG[Nle]LRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Leu6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2547
DCLGVLRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Leu6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2548
DCLGLLRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5,6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2549
DCLGILRKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Leu6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2550
DCLGG[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Nle6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2551
DCLGA[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Nle6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2552
DCLG[2-Abu][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu10;Gln28]GpTx-1(1-34)	2553
DCLG[Nva][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Nle6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2554
DCLG[Nle][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5,6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2555
DCLGV[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Nle6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2556
DCLGL[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Nle6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2557
DCLGI[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Nle6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2558
DCLGGFRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Phe6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2559
DCLGAFRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Phe6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2560
DCLG[2-Abu]FRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Phe6;Asp10;Gln28]GpTx-1(1-34)	2561
DCLG[Nva]FRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Phe6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2562
DCLG[Nle]FRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Phe6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2563
DCLGVFRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Phe6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2564
DCLGLFRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Phe6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2565
DCLGIFRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Phe6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2566

DCLGGLRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Leu6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2567
DCLGALRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Leu6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2568
DCLG[2-Abu]LRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Leu6;Asp10;Gln28]GpTx-1(1-34)	2569
DCLG[Nva]LRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Leu6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2570
DCLG[Nle]LRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Leu6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2571
DCLGVLRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Leu6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2572
DCLGLLRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5,6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2573
DCLGILRKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Leu6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2574
DCLGG[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Nle6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2575
DCLGA[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Nle6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2576
DCLG[2-Abu][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5,13;Nle6;Asp10;Gln28]GpTx-1(1-34)	2577
DCLG[Nva][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Nle6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2578
DCLG[Nle][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5,6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2579
DCLGV[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Nle6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2580
DCLGL[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Nle6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2581
DCLGI[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Nle6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2582
DCLGGFRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Phe6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2583
DCLGAFRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Phe6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2584
DCLG[2-Abu]FRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Phe6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2585
DCLG[Nva]FRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Phe6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2586

DCLG[Nle]FRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Phe6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2587
DCLGVFRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Phe6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2588
DCLGLFRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Phe6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2589
DCLGIFRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Phe6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2590
DCLGGLRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Leu6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2591
DCLGALRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Leu6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2592
DCLG[2-Abu]LRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Leu6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2593
DCLG[Nva]LRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Leu6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2594
DCLG[Nle]LRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Leu6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2595
DCLGVLRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Leu6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2596
DCLGLLRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5,6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2597
DCLGILRKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Leu6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2598
DCLGG[Nle]RKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Nle6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2599
DCLGA[Nle]RKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Nle6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2600
DCLG[2-Abu][Nle]RKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Nle6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2601
DCLG[Nva][Nle]RKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Nle6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2602
DCLG[Nle][Nle]RKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5,6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2603
DCLGV[Nle]RKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Nle6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2604
DCLGL[Nle]RKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Nle6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2605
DCLGI[Nle]RKCIED[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Nle6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2606

DCLGGFRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Phe6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2607
DCLGAFRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Phe6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2608
DCLG[2-Abu]FRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Phe6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2609
DCLG[Nva]FRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Phe6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2610
DCLG[Nle]FRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Phe6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2611
DCLGVFRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Phe6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2612
DCLGLFRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Phe6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2613
DCLGIFRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Phe6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2614
DCLGGLRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Leu6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2615
DCLGALRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Leu6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2616
DCLG[2-Abu]LRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Leu6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2617
DCLG[Nva]LRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Leu6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2618
DCLG[Nle]LRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Leu6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2619
DCLGVLRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Leu6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2620
DCLGLLRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5,6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2621
DCLGILRKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Leu6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2622
DCLGG[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Nle6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2623
DCLGA[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Nle6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2624
DCLG[2-Abu][Nle]RKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Nle6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2625
DCLG[Nva][Nle]RKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Nle6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2626

DCLG[Nle][Nle]RKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5,6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2627
DCLGV[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Nle6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2628
DCLGL[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Nle6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2629
DCLGI[Nle]RKCEPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Nle6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2630
DCLGGFRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Phe6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2631
DCLGAFRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Phe6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2632
DCLG[2-Abu]FRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Phe6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2633
DCLG[Nva]FRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Phe6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2634
DCLG[Nle]FRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Phe6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2635
DCLGVFRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Phe6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2636
DCLGLFRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Phe6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2637
DCLGIFRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Phe6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2638
DCLGGLRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Leu6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2639
DCLGALRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Leu6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2640
DCLG[2-Abu]LRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Leu6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2641
DCLG[Nva]LRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Leu6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2642
DCLG[Nle]LRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5;Leu6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2643
DCLGVLRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Leu6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2644
DCLGLLRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5,6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2645
DCLGILRKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Leu6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2646

DCLGG[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gly5;Nle6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2647
DCLGA[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ala5;Nle6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2648
DCLG[2-Abu][Nle]RKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[2-Abu5;Nle6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2649
DCLG[Nva][Nle]RKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nva5;Nle6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2650
DCLG[Nle][Nle]RKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Nle5,6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2651
DCLGV[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Val5;Nle6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2652
DCLGL[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Leu5;Nle6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2653
DCLGI[Nle]RKCDPD[Pra]DKCCRPNLVCSRTHQWCKYVF-{Amide}	[Ile5;Nle6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2654
DCLGGFRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Phe6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2655
DCLGAFRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Phe6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2656
DCLG[2-Abu]FRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu11;Leu26;Gln28]GpTx-1(1-34)	2657
DCLG[Nva]FRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Phe6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2658
DCLG[Nle]FRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Phe6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2659
DCLGVFRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Phe6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2660
DCLGLFRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Phe6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2661
DCLGIFRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Phe6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2662
DCLGGLRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Leu6,26;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2663
DCLGALRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Leu6,26;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2664
DCLG[2-Abu]LRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Glu11;Gln28]GpTx-1(1-34)	2665
DCLG[Nva]LRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Leu6,26;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2666

DCLG[Nle]LRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Leu6,26;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2667
DCLGVLRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Leu6,26;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2668
DCLGLLRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,6,26;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2669
DCLGILRKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Leu6,26;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2670
DCLGG[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Nle6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2671
DCLGA[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Nle6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2672
DCLG[2-Abu][Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu11;Leu26;Gln28]GpTx-1(1-34)	2673
DCLG[Nva][Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Nle6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2674
DCLG[Nle][Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5,6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2675
DCLGV[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Nle6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2676
DCLGL[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Nle6;Glu11;2-Abu13;Gln28]GpTx-1(1-34)	2677
DCLGI[Nle]RKCIED[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Nle6;Glu11;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2678
DCLGGFRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Phe6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2679
DCLGAFRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Phe6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2680
DCLG[2-Abu]FRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu10;Leu26;Gln28]GpTx-1(1-34)	2681
DCLG[Nva]FRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Phe6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2682
DCLG[Nle]FRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Phe6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2683
DCLGVFRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Phe6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2684
DCLGLFRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Phe6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2685
DCLGIFRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Phe6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2686

DCLGGLRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Leu6,26;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2687
DCLGALRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Leu6,26;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2688
DCLG[2-Abu]LRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Glu10;Gln28]GpTx-1(1-34)	2689
DCLG[Nva]LRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Leu6,26;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2690
DCLG[Nle]LRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Leu6,26;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2691
DCLGVLRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Leu6,26;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2692
DCLGLLRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,6,26;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2693
DCLGILRKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Leu6,26;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2694
DCLGG[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Nle6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2695
DCLGA[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Nle6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2696
DCLG[2-Abu][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu10;Leu26;Gln28]GpTx-1(1-34)	2697
DCLG[Nva][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Nle6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2698
DCLG[Nle][Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5,6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2699
DCLGV[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Nle6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2700
DCLGL[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Nle6;Glu10;2-Abu13;Gln28]GpTx-1(1-34)	2701
DCLGI[Nle]RKCEPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Nle6;Glu10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2702
DCLGGFRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Phe6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2703
DCLGAFRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Phe6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2704
DCLG[2-Abu]FRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Phe6;Asp10;Leu26;Gln28]GpTx-1(1-34)	2705
DCLG[Nva]FRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Phe6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2706

DCLG[Nle]FRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Phe6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2707
DCLGVFRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Phe6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2708
DCLGLFRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Phe6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2709
DCLGIFRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Phe6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2710
DCLGGLRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Leu6,26;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2711
DCLGALRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Leu6,26;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2712
DCLG[2-Abu]LRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Leu6,26;Asp10;Gln28]GpTx-1(1-34)	2713
DCLG[Nva]LRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Leu6,26;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2714
DCLG[Nle]LRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Leu6,26;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2715
DCLGVLRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Leu6,26;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2716
DCLGLLRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,6,26;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2717
DCLGILRKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Leu6,26;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2718
DCLGG[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Nle6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2719
DCLGA[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Nle6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2720
DCLG[2-Abu][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5,13;Nle6;Asp10;Leu26;Gln28]GpTx-1(1-34)	2721
DCLG[Nva][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Nle6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2722
DCLG[Nle][Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5,6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2723
DCLGV[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Nle6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2724
DCLGL[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Nle6;Asp10;2-Abu13;Gln28]GpTx-1(1-34)	2725
DCLGI[Nle]RKCDPD[2-Abu]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Nle6;Asp10;2-Abu13;Leu26;Gln28]GpTx-1(1-34)	2726

DCLGGFRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	{Gly5;Phe6;Glu11;Pra13;Leu26;Gln28}GpTx-1(1-34)	2727
DCLGAFRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Phe6;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2728
DCLG[2-Abu]FRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Phe6;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2729
DCLG[Nva]FRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	{Nva5;Phe6;Glu11;Pra13;Leu26;Gln28}GpTx-1(1-34)	2730
DCLG[Nle]FRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	{Nle5;Phe6;Glu11;Pra13;Leu26;Gln28}GpTx-1(1-34)	2731
DCLGVFRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	{Val5;Phe6;Glu11;Pra13;Leu26;Gln28}GpTx-1(1-34)	2732
DCLGLFRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	{Leu5,26;Phe6;Glu11;Pra13;Gln28}GpTx-1(1-34)	2733
DCLGIFRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	{Ile5;Phe6;Glu11;Pra13;Leu26;Gln28}GpTx-1(1-34)	2734
DCLGGLRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	{Gly5;Leu6,26;Glu11;Pra13;Gln28}GpTx-1(1-34)	2735
DCLGALRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	{Ala5;Leu6,26;Glu11;Pra13;Gln28}GpTx-1(1-34)	2736
DCLG[2-Abu]LRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Leu6,26;Glu11;Pra13;Gln28]GpTx-1(1-34)	2737
DCLG[Nva]LRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Leu6,26;Glu11;Pra13;Gln28]GpTx-1(1-34)	2738
DCLG[Nle]LRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Leu6,26;Glu11;Pra13;Gln28]GpTx-1(1-34)	2739
DCLGVLRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Leu6,26;Glu11;Pra13;Gln28]GpTx-1(1-34)	2740
DCLGLLRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,6,26;Glu11;Pra13;Gln28]GpTx-1(1-34)	2741
DCLGILRKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Leu6,26;Glu11;Pra13;Gln28]GpTx-1(1-34)	2742
DCLGG[Nle]RKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Nle6;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2743
DCLGA[Nle]RKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Nle6;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2744
DCLG[2-Abu][Nle]RKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Nle6;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2745
DCLG[Nva][Nle]RKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Nle6;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2746

DCLG[Nle][Nle]RKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5,6;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2747
DCLGV[Nle]RKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Nle6;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2748
DCLGL[Nle]RKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Nle6;Glu11;Pra13;Gln28]GpTx-1(1-34)	2749
DCLGI[Nle]RKCIED[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Nle6;Glu11;Pra13;Leu26;Gln28]GpTx-1(1-34)	2750
DCLGGFRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Phe6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2751
DCLGAFRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Phe6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2752
DCLG[2-Abu]FRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Phe6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2753
DCLG[Nva]FRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Phe6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2754
DCLG[Nle]FRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Phe6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2755
DCLGVFRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Phe6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2756
DCLGLFRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Phe6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2757
DCLGIFRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Phe6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2758
DCLGGLRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Leu6,26;Glu10;Pra13;Gln28]GpTx-1(1-34)	2759
DCLGALRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Leu6,26;Glu10;Pra13;Gln28]GpTx-1(1-34)	2760
DCLG[2-Abu]LRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Leu6,26;Glu10;Pra13;Gln28]GpTx-1(1-34)	2761
DCLG[Nva]LRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Leu6,26;Glu10;Pra13;Gln28]GpTx-1(1-34)	2762
DCLG[Nle]LRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Leu6,26;Glu10;Pra13;Gln28]GpTx-1(1-34)	2763
DCLGVLRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Leu6,26;Glu10;Pra13;Gln28]GpTx-1(1-34)	2764
DCLGLLRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,6,26;Glu10;Pra13;Gln28]GpTx-1(1-34)	2765
DCLGILRKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Leu6,26;Glu10;Pra13;Gln28]GpTx-1(1-34)	2766

DCLGG[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Nle6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2767
DCLGA[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Nle6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2768
DCLG[2-Abu][Nle]RKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Nle6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2769
DCLG[Nva][Nle]RKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Nle6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2770
DCLG[Nle][Nle]RKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5,6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2771
DCLGV[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Nle6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2772
DCLGL[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Nle6;Glu10;Pra13;Gln28]GpTx-1(1-34)	2773
DCLGI[Nle]RKCEPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Nle6;Glu10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2774
DCLGGFRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Phe6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2775
DCLGAFRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Phe6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2776
DCLG[2-Abu]FRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Phe6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2777
DCLG[Nva]FRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Phe6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2778
DCLG[Nle]FRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Phe6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2779
DCLGVFRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Phe6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2780
DCLGLFRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Phe6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2781
DCLGIFRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Phe6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2782
DCLGGLRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Leu6,26;Asp10;Pra13;Gln28]GpTx-1(1-34)	2783
DCLGALRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Leu6,26;Asp10;Pra13;Gln28]GpTx-1(1-34)	2784
DCLG[2-Abu]LRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Leu6,26;Asp10;Pra13;Gln28]GpTx-1(1-34)	2785
DCLG[Nva]LRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Leu6,26;Asp10;Pra13;Gln28]GpTx-1(1-34)	2786

DCLG[Nle]LRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5;Leu6,26;Asp10;Pra13;Gln28]GpTx-1(1-34)	2787
DCLGVLRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Leu6,26;Asp10;Pra13;Gln28]GpTx-1(1-34)	2788
DCLGLLRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,6,26;Asp10;Pra13;Gln28]GpTx-1(1-34)	2789
DCLGILRKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Leu6,26;Asp10;Pra13;Gln28]GpTx-1(1-34)	2790
DCLGG[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Gly5;Nle6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2791
DCLGA[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ala5;Nle6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2792
DCLG[2-Abu][Nle]RKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[2-Abu5;Nle6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2793
DCLG[Nva][Nle]RKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nva5;Nle6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2794
DCLG[Nle][Nle]RKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Nle5,6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2795
DCLGV[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Val5;Nle6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2796
DCLGL[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Leu5,26;Nle6;Asp10;Pra13;Gln28]GpTx-1(1-34)	2797
DCLGI[Nle]RKCDPD[Pra]DKCCRPNLVCSRLHQWCKYVF-{Amide}	[Ile5;Nle6;Asp10;Pra13;Leu26;Gln28]GpTx-1(1-34)	2798
DCLGFMRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu13;Glu26]GpTx-1(1-34)	2799
DCLGFMRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Pra13;Glu26]GpTx-1(1-34)	2800
DCLGFMRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Glu11,26;2-Abu13]GpTx-1(1-34)	2801
DCLGFMRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Glu10,26;2-Abu13]GpTx-1(1-34)	2802
DCLGFMRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2803
DCLGFFRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Phe6;2-Abu13;Glu26]GpTx-1(1-34)	2804
DCLGFLRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu6;2-Abu13;Glu26]GpTx-1(1-34)	2805
DCLGF[Nle]RKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle6;2-Abu13;Glu26]GpTx-1(1-34)	2806

DCLGGMRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;2-Abu13;Glu26]GpTx-1(1-34)	2807
DCLGAMRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;2-Abu13;Glu26]GpTx-1(1-34)	2808
DCLG[2-Abu]MRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Glu26]GpTx-1(1-34)	2809
DCLG[Nva]MRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;2-Abu13;Glu26]GpTx-1(1-34)	2810
DCLG[Nle]MRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;2-Abu13;Glu26]GpTx-1(1-34)	2811
DCLGVMRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;2-Abu13;Glu26]GpTx-1(1-34)	2812
DCLGLMRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;2-Abu13;Glu26]GpTx-1(1-34)	2813
DCLGIMRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;2-Abu13;Glu26]GpTx-1(1-34)	2814
DCLGFMRKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Glu11,26;Pra13]GpTx-1(1-34)	2815
DCLGFMRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Glu10,26;Pra13]GpTx-1(1-34)	2816
DCLGFMRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Asp10;Pra13;Glu26]GpTx-1(1-34)	2817
DCLGFFRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Phe6;Pra13;Glu26]GpTx-1(1-34)	2818
DCLGFLRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu6;Pra13;Glu26]GpTx-1(1-34)	2819
DCLGF[Nle]RKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle6;Pra13;Glu26]GpTx-1(1-34)	2820
DCLGGMRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Pra13;Glu26]GpTx-1(1-34)	2821
DCLGAMRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Pra13;Glu26]GpTx-1(1-34)	2822
DCLG[2-Abu]MRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Pra13;Glu26]GpTx-1(1-34)	2823
DCLG[Nva]MRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Pra13;Glu26]GpTx-1(1-34)	2824
DCLG[Nle]MRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Pra13;Glu26]GpTx-1(1-34)	2825
DCLGVMRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Pra13;Glu26]GpTx-1(1-34)	2826

DCLGLMRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Pra13;Glu26]GpTx-1(1-34)	2827
DCLGIMRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Pra13;Glu26]GpTx-1(1-34)	2828
DCLGFFRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Phe6;Glu11,26;2-Abu13]GpTx-1(1-34)	2829
DCLGFLRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu6;Glu11,26;2-Abu13]GpTx-1(1-34)	2830
DCLGF[Nle]RKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle6;Glu11,26;2-Abu13]GpTx-1(1-34)	2831
DCLGGMRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Glu11,26;2-Abu13]GpTx-1(1-34)	2832
DCLGAMRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Glu11,26;2-Abu13]GpTx-1(1-34)	2833
DCLG[2-Abu]MRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Glu11,26]GpTx-1(1-34)	2834
DCLG[Nva]MRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Glu11,26;2-Abu13]GpTx-1(1-34)	2835
DCLG[Nle]MRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Glu11,26;2-Abu13]GpTx-1(1-34)	2836
DCLGVMRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Glu11,26;2-Abu13]GpTx-1(1-34)	2837
DCLGLMRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Glu11,26;2-Abu13]GpTx-1(1-34)	2838
DCLGIMRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Glu11,26;2-Abu13]GpTx-1(1-34)	2839
DCLGFFRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Phe6;Glu10,26;2-Abu13]GpTx-1(1-34)	2840
DCLGFLRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu6;Glu10,26;2-Abu13]GpTx-1(1-34)	2841
DCLGF[Nle]RKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle6;Glu10,26;2-Abu13]GpTx-1(1-34)	2842
DCLGGMRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Glu10,26;2-Abu13]GpTx-1(1-34)	2843
DCLGAMRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Glu10,26;2-Abu13]GpTx-1(1-34)	2844
DCLG[2-Abu]MRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Glu10,26]GpTx-1(1-34)	2845
DCLG[Nva]MRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Glu10,26;2-Abu13]GpTx-1(1-34)	2846

DCLG[Nle]MRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Glu10,26;2-Abu13]GpTx-1(1-34)	2847
DCLGVMRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Glu10,26;2-Abu13]GpTx-1(1-34)	2848
DCLGLMRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Glu10,26;2-Abu13]GpTx-1(1-34)	2849
DCLGIMRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Glu10,26;2-Abu13]GpTx-1(1-34)	2850
DCLGFFRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Phe6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2851
DCLGFLRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2852
DCLGF[Nle]RKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2853
DCLGGMRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2854
DCLGAMRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2855
DCLG[2-Abu]MRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Asp10;Glu26]GpTx-1(1-34)	2856
DCLG[Nva]MRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2857
DCLG[Nle]MRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2858
DCLGVMRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2859
DCLGLMRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2860
DCLGIMRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2861
DCLGGFRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Phe6;2-Abu13;Glu26]GpTx-1(1-34)	2862
DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Phe6;2-Abu13;Glu26]GpTx-1(1-34)	2863
DCLG[2-Abu]FRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu26]GpTx-1(1-34)	2864
DCLG[Nva]FRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Phe6;2-Abu13;Glu26]GpTx-1(1-34)	2865
DCLG[Nle]FRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Phe6;2-Abu13;Glu26]GpTx-1(1-34)	2866

DCLGVFRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Phe6;2-Abu13;Glu26]GpTx-1(1-34)	2867
DCLGLFRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Phe6;2-Abu13;Glu26]GpTx-1(1-34)	2868
DCLGIFRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Phe6;2-Abu13;Glu26]GpTx-1(1-34)	2869
DCLGGLRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Leu6;2-Abu13;Glu26]GpTx-1(1-34)	2870
DCLGALRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Leu6;2-Abu13;Glu26]GpTx-1(1-34)	2871
DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Leu6;Glu26]GpTx-1(1-34)	2872
DCLG[Nva]LRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Leu6;2-Abu13;Glu26]GpTx-1(1-34)	2873
DCLG[Nle]LRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Leu6;2-Abu13;Glu26]GpTx-1(1-34)	2874
DCLGVLRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Leu6;2-Abu13;Glu26]GpTx-1(1-34)	2875
DCLGLLRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5,6;2-Abu13;Glu26]GpTx-1(1-34)	2876
DCLGILRKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Leu6;2-Abu13;Glu26]GpTx-1(1-34)	2877
DCLGG[Nle]RKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Nle6;2-Abu13;Glu26]GpTx-1(1-34)	2878
DCLGA[Nle]RKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Nle6;2-Abu13;Glu26]GpTx-1(1-34)	2879
DCLG[2-Abu][Nle]RKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu26]GpTx-1(1-34)	2880
DCLG[Nva][Nle]RKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Nle6;2-Abu13;Glu26]GpTx-1(1-34)	2881
DCLG[Nle][Nle]RKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	*[Nle5,6;2-Abu13;Glu26]GpTx-1(1-34)*	2882
DCLGV[Nle]RKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Nle6;2-Abu13;Glu26]GpTx-1(1-34)	2883
DCLGL[Nle]RKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Nle6;2-Abu13;Glu26]GpTx-1(1-34)	2884
DCLGI[Nle]RKCIPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Nle6;2-Abu13;Glu26]GpTx-1(1-34)	2885
DCLGFFRKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Phe6;Glu11,26;Pra13]GpTx-1(1-34)	2886

DCLGFLRKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu6;Glu11,26;Pra13]GpTx-1(1-34)	2887
DCLGF[Nle]RKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle6;Glu11,26;Pra13]GpTx-1(1-34)	2888
DCLGGMRKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Glu11,26;Pra13]GpTx-1(1-34)	2889
DCLGAMRKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Glu11,26;Pra13]GpTx-1(1-34)	2890
DCLG[2-Abu]MRKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Glu11,26;Pra13]GpTx-1(1-34)	2891
DCLG[Nva]MRKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Glu11,26;Pra13]GpTx-1(1-34)	2892
DCLG[Nle]MRKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Glu11,26;Pra13]GpTx-1(1-34)	2893
DCLGVMRKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Glu11,26;Pra13]GpTx-1(1-34)	2894
DCLGLMRKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Glu11,26;Pra13]GpTx-1(1-34)	2895
DCLGIMRKCIED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Glu11,26;Pra13]GpTx-1(1-34)	2896
DCLGFFRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Phe6;Glu10,26;Pra13]GpTx-1(1-34)	2897
DCLGFLRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu6;Glu10,26;Pra13]GpTx-1(1-34)	2898
DCLGF[Nle]RKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle6;Glu10,26;Pra13]GpTx-1(1-34)	2899
DCLGGMRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Glu10,26;Pra13]GpTx-1(1-34)	2900
DCLGAMRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Glu10,26;Pra13]GpTx-1(1-34)	2901
DCLG[2-Abu]MRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Glu10,26;Pra13]GpTx-1(1-34)	2902
DCLG[Nva]MRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Glu10,26;Pra13]GpTx-1(1-34)	2903
DCLG[Nle]MRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Glu10,26;Pra13]GpTx-1(1-34)	2904
DCLGVMRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Glu10,26;Pra13]GpTx-1(1-34)	2905
DCLGLMRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Glu10,26;Pra13]GpTx-1(1-34)	2906

DCLGIMRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Glu10,26;Pra13]GpTx-1(1-34)	2907
DCLGFFRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Phe6;Asp10;Pra13;Glu26]GpTx-1(1-34)	2908
DCLGFLRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu6;Asp10;Pra13;Glu26]GpTx-1(1-34)	2909
DCLGF[Nle]RKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle6;Asp10;Pra13;Glu26]GpTx-1(1-34)	2910
DCLGGMRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Asp10;Pra13;Glu26]GpTx-1(1-34)	2911
DCLGAMRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Asp10;Pra13;Glu26]GpTx-1(1-34)	2912
DCLG[2-Abu]MRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Asp10;Pra13;Glu26]GpTx-1(1-34)	2913
DCLG[Nva]MRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Asp10;Pra13;Glu26]GpTx-1(1-34)	2914
DCLG[Nle]MRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Asp10;Pra13;Glu26]GpTx-1(1-34)	2915
DCLGVMRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Asp10;Pra13;Glu26]GpTx-1(1-34)	2916
DCLGLMRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Asp10;Pra13;Glu26]GpTx-1(1-34)	2917
DCLGIMRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Asp10;Pra13;Glu26]GpTx-1(1-34)	2918
DCLGGFRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Phe6;Pra13;Glu26]GpTx-1(1-34)	2919
DCLGAFRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Phe6;Pra13;Glu26]GpTx-1(1-34)	2920
DCLG[2-Abu]FRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Phe6;Pra13;Glu26]GpTx-1(1-34)	2921
DCLG[Nva]FRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Phe6;Pra13;Glu26]GpTx-1(1-34)	2922
DCLG[Nle]FRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Phe6;Pra13;Glu26]GpTx-1(1-34)	2923
DCLGVFRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Phe6;Pra13;Glu26]GpTx-1(1-34)	2924
DCLGLFRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Phe6;Pra13;Glu26]GpTx-1(1-34)	2925
DCLGIFRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Phe6;Pra13;Glu26]GpTx-1(1-34)	2926

DCLGGLRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Leu6;Pra13;Glu26]GpTx-1(1-34)	2927
DCLGALRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Leu6;Pra13;Glu26]GpTx-1(1-34)	2928
DCLG[2-Abu]LRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Leu6;Pra13;Glu26]GpTx-1(1-34)	2929
DCLG[Nva]LRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Leu6;Pra13;Glu26]GpTx-1(1-34)	2930
DCLG[Nle]LRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Leu6;Pra13;Glu26]GpTx-1(1-34)	2931
DCLGVLRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Leu6;Pra13;Glu26]GpTx-1(1-34)	2932
DCLGLLRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5,6;Pra13;Glu26]GpTx-1(1-34)	2933
DCLGILRKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Leu6;Pra13;Glu26]GpTx-1(1-34)	2934
DCLGG[Nle]RKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Nle6;Pra13;Glu26]GpTx-1(1-34)	2935
DCLGA[Nle]RKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Nle6;Pra13;Glu26]GpTx-1(1-34)	2936
DCLG[2-Abu][Nle]RKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Nle6;Pra13;Glu26]GpTx-1(1-34)	2937
DCLG[Nva][Nle]RKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Nle6;Pra13;Glu26]GpTx-1(1-34)	2938
DCLG[Nle][Nle]RKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5,6;Pra13;Glu26]GpTx-1(1-34)	2939
DCLGV[Nle]RKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Nle6;Pra13;Glu26]GpTx-1(1-34)	2940
DCLGL[Nle]RKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Nle6;Pra13;Glu26]GpTx-1(1-34)	2941
DCLGI[Nle]RKCIPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Nle6;Pra13;Glu26]GpTx-1(1-34)	2942
DCLGGFRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Phe6;Glu11,26;2-Abu13]GpTx-1(1-34)	2943
DCLGAFRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Phe6;Glu11,26;2-Abu13]GpTx-1(1-34)	2944
DCLG[2-Abu]FRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu11,26]GpTx-1(1-34)	2945
DCLG[Nva]FRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Phe6;Glu11,26;2-Abu13]GpTx-1(1-34)	2946

DCLG[Nle]FRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Phe6;Glu11,26;2-Abu13]GpTx-1(1-34)	2947
DCLGVFRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Phe6;Glu11,26;2-Abu13]GpTx-1(1-34)	2948
DCLGLFRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Phe6;Glu11,26;2-Abu13]GpTx-1(1-34)	2949
DCLGIFRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Phe6;Glu11,26;2-Abu13]GpTx-1(1-34)	2950
DCLGGLRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Leu6;Glu11,26;2-Abu13]GpTx-1(1-34)	2951
DCLGALRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Leu6;Glu11,26;2-Abu13]GpTx-1(1-34)	2952
DCLG[2-Abu]LRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Leu6;Glu11,26]GpTx-1(1-34)	2953
DCLG[Nva]LRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Leu6;Glu11,26;2-Abu13]GpTx-1(1-34)	2954
DCLG[Nle]LRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Leu6;Glu11,26;2-Abu13]GpTx-1(1-34)	2955
DCLGVLRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Leu6;Glu11,26;2-Abu13]GpTx-1(1-34)	2956
DCLGLLRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5,6;Glu11,26;2-Abu13]GpTx-1(1-34)	2957
DCLGILRKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Leu6;Glu11,26;2-Abu13]GpTx-1(1-34)	2958
DCLGG[Nle]RKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Nle6;Glu11,26;2-Abu13]GpTx-1(1-34)	2959
DCLGA[Nle]RKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Nle6;Glu11,26;2-Abu13]GpTx-1(1-34)	2960
DCLG[2-Abu][Nle]RKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu11,26]GpTx-1(1-34)	2961
DCLG[Nva][Nle]RKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Nle6;Glu11,26;2-Abu13]GpTx-1(1-34)	2962
DCLG[Nle][Nle]RKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5,6;Glu11,26;2-Abu13]GpTx-1(1-34)	2963
DCLGV[Nle]RKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Nle6;Glu11,26;2-Abu13]GpTx-1(1-34)	2964
DCLGL[Nle]RKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Nle6;Glu11,26;2-Abu13]GpTx-1(1-34)	2965
DCLGI[Nle]RKCIED[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Nle6;Glu11,26;2-Abu13]GpTx-1(1-34)	2966

DCLGGFRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Phe6;Glu10,26;2-Abu13]GpTx-1(1-34)	2967
DCLGAFRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Phe6;Glu10,26;2-Abu13]GpTx-1(1-34)	2968
DCLG[2-Abu]FRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Phe6;Glu10,26]GpTx-1(1-34)	2969
DCLG[Nva]FRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Phe6;Glu10,26;2-Abu13]GpTx-1(1-34)	2970
DCLG[Nle]FRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Phe6;Glu10,26;2-Abu13]GpTx-1(1-34)	2971
DCLGVFRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Phe6;Glu10,26;2-Abu13]GpTx-1(1-34)	2972
DCLGLFRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Phe6;Glu10,26;2-Abu13]GpTx-1(1-34)	2973
DCLGIFRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Phe6;Glu10,26;2-Abu13]GpTx-1(1-34)	2974
DCLGGLRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Leu6;Glu10,26;2-Abu13]GpTx-1(1-34)	2975
DCLGALRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Leu6;Glu10,26;2-Abu13]GpTx-1(1-34)	2976
DCLG[2-Abu]LRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Leu6;Glu10,26]GpTx-1(1-34)	2977
DCLG[Nva]LRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Leu6;Glu10,26;2-Abu13]GpTx-1(1-34)	2978
DCLG[Nle]LRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Leu6;Glu10,26;2-Abu13]GpTx-1(1-34)	2979
DCLGVLRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Leu6;Glu10,26;2-Abu13]GpTx-1(1-34)	2980
DCLGLLRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5,6;Glu10,26;2-Abu13]GpTx-1(1-34)	2981
DCLGILRKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Leu6;Glu10,26;2-Abu13]GpTx-1(1-34)	2982
DCLGG[Nle]RKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Nle6;Glu10,26;2-Abu13]GpTx-1(1-34)	2983
DCLGA[Nle]RKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Nle6;Glu10,26;2-Abu13]GpTx-1(1-34)	2984
DCLG[2-Abu][Nle]RKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Nle6;Glu10,26]GpTx-1(1-34)	2985
DCLG[Nva][Nle]RKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Nle6;Glu10,26;2-Abu13]GpTx-1(1-34)	2986

DCLG[Nle][Nle]RKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5,6;Glu10,26;2-Abu13]GpTx-1(1-34)	2987
DCLGV[Nle]RKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Nle6;Glu10,26;2-Abu13]GpTx-1(1-34)	2988
DCLGL[Nle]RKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Nle6;Glu10,26;2-Abu13]GpTx-1(1-34)	2989
DCLGI[Nle]RKCEPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Nle6;Glu10,26;2-Abu13]GpTx-1(1-34)	2990
DCLGGFRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Phe6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2991
DCLGAFRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Phe6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2992
DCLG[2-Abu]FRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Phe6;Asp10;Glu26]GpTx-1(1-34)	2993
DCLG[Nva]FRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Phe6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2994
DCLG[Nle]FRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Phe6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2995
DCLGVFRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Phe6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2996
DCLGLFRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Phe6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2997
DCLGIFRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Phe6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2998
DCLGGLRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Leu6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	2999
DCLGALRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Leu6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3000
DCLG[2-Abu]LRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Leu6;Asp10;Glu26]GpTx-1(1-34)	3001
DCLG[Nva]LRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Leu6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3002
DCLG[Nle]LRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Leu6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3003
DCLGVLRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Leu6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3004
DCLGLLRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5,6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3005
DCLGILRKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Leu6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3006

DCLGG[Nle]RKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Nle6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3007
DCLGA[Nle]RKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Nle6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3008
DCLG[2-Abu][Nle]RKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5,13;Nle6;Asp10;Glu26]GpTx-1(1-34)	3009
DCLG[Nva][Nle]RKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Nle6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3010
DCLG[Nle][Nle]RKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5,6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3011
DCLGV[Nle]RKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Nle6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3012
DCLGL[Nle]RKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Nle6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3013
DCLGI[Nle]RKCDPD[2-Abu]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Nle6;Asp10;2-Abu13;Glu26]GpTx-1(1-34)	3014
DCLGGFRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Phe6;Glu11,26;Pra13]GpTx-1(1-34)	3015
DCLGAFRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Phe6;Glu11,26;Pra13]GpTx-1(1-34)	3016
DCLG[2-Abu]FRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Phe6;Glu11,26;Pra13]GpTx-1(1-34)	3017
DCLG[Nva]FRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Phe6;Glu11,26;Pra13]GpTx-1(1-34)	3018
DCLG[Nle]FRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Phe6;Glu11,26;Pra13]GpTx-1(1-34)	3019
DCLGVFRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Phe6;Glu11,26;Pra13]GpTx-1(1-34)	3020
DCLGLFRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Phe6;Glu11,26;Pra13]GpTx-1(1-34)	3021
DCLGIFRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Phe6;Glu11,26;Pra13]GpTx-1(1-34)	3022
DCLGGLRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Leu6;Glu11,26;Pra13]GpTx-1(1-34)	3023
DCLGALRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Leu6;Glu11,26;Pra13]GpTx-1(1-34)	3024
DCLG[2-Abu]LRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Leu6;Glu11,26;Pra13]GpTx-1(1-34)	3025
DCLG[Nva]LRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Leu6;Glu11,26;Pra13]GpTx-1(1-34)	3026

DCLG[Nle]LRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Leu6;Glu11,26;Pra13]GpTx-1(1-34)	3027
DCLGVLRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Leu6;Glu11,26;Pra13]GpTx-1(1-34)	3028
DCLGLLRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5,6;Glu11,26;Pra13]GpTx-1(1-34)	3029
DCLGILRKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Leu6;Glu11,26;Pra13]GpTx-1(1-34)	3030
DCLGG[Nle]RKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Nle6;Glu11,26;Pra13]GpTx-1(1-34)	3031
DCLGA[Nle]RKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Nle6;Glu11,26;Pra13]GpTx-1(1-34)	3032
DCLG[2-Abu][Nle]RKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Nle6;Glu11,26;Pra13]GpTx-1(1-34)	3033
DCLG[Nva][Nle]RKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Nle6;Glu11,26;Pra13]GpTx-1(1-34)	3034
DCLG[Nle][Nle]RKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5,6;Glu11,26;Pra13]GpTx-1(1-34)	3035
DCLGV[Nle]RKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Nle6;Glu11,26;Pra13]GpTx-1(1-34)	3036
DCLGL[Nle]RKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Nle6;Glu11,26;Pra13]GpTx-1(1-34)	3037
DCLGI[Nle]RKCiED[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Nle6;Glu11,26;Pra13]GpTx-1(1-34)	3038
DCLGGFRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Phe6;Glu10,26;Pra13]GpTx-1(1-34)	3039
DCLGAFRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Phe6;Glu10,26;Pra13]GpTx-1(1-34)	3040
DCLG[2-Abu]FRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Phe6;Glu10,26;Pra13]GpTx-1(1-34)	3041
DCLG[Nva]FRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Phe6;Glu10,26;Pra13]GpTx-1(1-34)	3042
DCLG[Nle]FRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Phe6;Glu10,26;Pra13]GpTx-1(1-34)	3043
DCLGVFRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Phe6;Glu10,26;Pra13]GpTx-1(1-34)	3044
DCLGLFRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Phe6;Glu10,26;Pra13]GpTx-1(1-34)	3045
DCLGIFRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Phe6;Glu10,26;Pra13]GpTx-1(1-34)	3046

DCLGGLRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Leu6;Glu10,26;Pra13]GpTx-1(1-34)	3047
DCLGALRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Leu6;Glu10,26;Pra13]GpTx-1(1-34)	3048
DCLG[2-Abu]LRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Leu6;Glu10,26;Pra13]GpTx-1(1-34)	3049
DCLG[Nva]LRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Leu6;Glu10,26;Pra13]GpTx-1(1-34)	3050
DCLG[Nle]LRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Leu6;Glu10,26;Pra13]GpTx-1(1-34)	3051
DCLGVLRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Leu6;Glu10,26;Pra13]GpTx-1(1-34)	3052
DCLGLLRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5,6;Glu10,26;Pra13]GpTx-1(1-34)	3053
DCLGILRKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Leu6;Glu10,26;Pra13]GpTx-1(1-34)	3054
DCLGG[Nle]RKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Nle6;Glu10,26;Pra13]GpTx-1(1-34)	3055
DCLGA[Nle]RKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Nle6;Glu10,26;Pra13]GpTx-1(1-34)	3056
DCLG[2-Abu][Nle]RKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Nle6;Glu10,26;Pra13]GpTx-1(1-34)	3057
DCLG[Nva][Nle]RKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Nle6;Glu10,26;Pra13]GpTx-1(1-34)	3058
DCLG[Nle][Nle]RKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5,6;Glu10,26;Pra13]GpTx-1(1-34)	3059
DCLGV[Nle]RKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Nle6;Glu10,26;Pra13]GpTx-1(1-34)	3060
DCLGL[Nle]RKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Nle6;Glu10,26;Pra13]GpTx-1(1-34)	3061
DCLGI[Nle]RKCEPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Nle6;Glu10,26;Pra13]GpTx-1(1-34)	3062
DCLGGFRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Phe6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3063
DCLGAFRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Phe6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3064
DCLG[2-Abu]FRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Phe6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3065
DCLG[Nva]FRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Phe6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3066

DCLG[Nle]FRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Phe6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3067
DCLGVFRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Phe6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3068
DCLGLFRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Phe6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3069
DCLGIFRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Phe6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3070
DCLGGLRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Leu6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3071
DCLGALRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Leu6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3072
DCLG[2-Abu]LRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Leu6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3073
DCLG[Nva]LRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Leu6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3074
DCLG[Nle]LRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5;Leu6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3075
DCLGVLRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Leu6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3076
DCLGLLRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5,6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3077
DCLGILRKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Leu6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3078
DCLGG[Nle]RKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Gly5;Nle6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3079
DCLGA[Nle]RKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Nle6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3080
DCLG[2-Abu][Nle]RKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[2-Abu5;Nle6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3081
DCLG[Nva][Nle]RKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nva5;Nle6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3082
DCLG[Nle][Nle]RKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Nle5,6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3083
DCLGV[Nle]RKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Val5;Nle6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3084
DCLGL[Nle]RKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Leu5;Nle6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3085
DCLGI[Nle]RKCDPD[Pra]DKCCRPNLVCSREHKWCKYVF-{Amide}	[Ile5;Nle6;Asp10;Pra13;Glu26]GpTx-1(1-34)	3086

[00229] As stated herein above, in accordance with the present invention, the peptide portions of the inventive composition of matter can also be chemically derivatized at one or more amino acid residues by known organic chemistry techniques. "Chemical derivative" or "chemically derivatized" refers to a subject peptide having one or more residues chemically derivatized by reaction of a functional side group. Such derivatized molecules include, for example, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups may be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may be derivatized to form N-im-benzylhistidine. Also included as chemical derivatives are those peptides which contain one or more naturally occurring amino acid derivatives of the twenty canonical amino acids, whether in L- or D- form. For example, 4-hydroxyproline may be substituted for proline; 5-hydroxylysine maybe substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may be substituted for lysine.

[00230] Useful derivatizations include, in some embodiments, those in which the amino terminal of the peptide is chemically blocked so that conjugation with the vehicle will be prevented from taking place at an N-terminal free amino group. There may also be other beneficial effects of such a modification, for example a reduction in the toxin peptide analog's susceptibility to enzymatic proteolysis. The N-terminus can be acylated or modified to a substituted amine, or derivatized with another functional group, such as an aromatic moiety (e.g., an indole acid, benzyl (Bzl or Bn), dibenzyl (DiBzl or Bn_2), or benzyloxycarbonyl (Cbz or Z)), *N,N*-dimethylglycine or creatine. For example, in some embodiments, an acyl moiety, such as, but not limited to, a formyl, acetyl (Ac), propanoyl, butanyl, heptanyl, hexanoyl, octanoyl, or nonanoyl, can be covalently linked to the N-terminal end of the peptide, which can prevent undesired side reactions during conjugation of the vehicle to the peptide. Other exemplary N-terminal derivative groups include $-NRR^1$ (other than $-NH_2$), $-NRC(O)R^1$, $-NRC(O)OR^1$, $-NRS(O)_2R^1$, $-NHC(O)NHR^1$, succinimide, or benzyloxycarbonyl-NH-

(Cbz-NH-), wherein R and R^1 are each independently hydrogen or lower alkyl and wherein the phenyl ring may be substituted with 1 to 3 substituents selected from C_1-C_4 alkyl, C_1-C_4 alkoxy, chloro, and bromo.

[00231] In some embodiments, one or more peptidyl [-C(O)NR-] linkages (bonds) between amino acid residues can be replaced by a non-peptidyl linkage. Exemplary non-peptidyl linkages are -CH_2-carbamate [-CH_2-OC(O)NR-], phosphonate , -CH_2-sulfonamide [-CH_2-$S(O)_2$NR-], urea [-NHC(O)NH-], -CH_2-secondary amine, and alkylated peptide [-$C(O)NR^6$- wherein R^6 is lower alkyl].

[00232] In some embodiments, one or more individual amino acid residues can be derivatized. Various derivatizing agents are known to react specifically with selected sidechains or terminal residues, as described in detail below by way of example.

[00233] Lysinyl residues and amino terminal residues may be reacted with succinic or other carboxylic acid anhydrides, which reverse the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4 pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[00234] Arginyl residues may be modified by reaction with any one or combination of several conventional reagents, including phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginyl residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

[00235] Specific modification of tyrosyl residues has been studied extensively, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively.

[00236] Carboxyl sidechain groups (aspartyl or glutamyl) may be selectively modified by reaction with carbodiimides (R'-N=C=N-R') such as 1-cyclohexyl-3-(2-morpholinyl-(4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl)

carbodiimide. Furthermore, aspartyl and glutamyl residues may be converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

[00237] Glutaminyl and asparaginyl residues may be deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[00238] Cysteinyl residues can be replaced by amino acid residues or other moieties either to eliminate disulfide bonding or, conversely, to stabilize cross-linking. (See, e.g., Bhatnagar et al., J. Med. Chem., 39:3814-3819 (1996)).

[00239] Derivatization with bifunctional agents is useful for cross-linking the peptides or their functional derivatives to a water-insoluble support matrix, if desired, or to other macromolecular vehicles. Commonly used cross-linking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates, e.g., as described in U.S. Pat. Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440, are employed for protein immobilization.

[00240] Other possible modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, oxidation of the sulfur atom in Cys, methylation of the alpha-amino groups of lysine, arginine, and histidine side chains. Creighton, Proteins: Structure and Molecule Properties (W. H. Freeman & Co., San Francisco), 79-86 (1983).

[00241] The above examples of derivatizations are not intended to be an exhaustive treatment, but merely illustrative.

[00242] The production of the composition of matter can also involve suitable protein purification techniques, when applicable. In some embodiments of the composition of matter of the invention, the molecule can be prepared to include a

suitable isotopic label (e.g., ^{125}I, ^{14}C, ^{13}C, ^{35}S, ^{3}H, ^{2}H, ^{13}N, ^{15}N, ^{18}O, ^{17}O, *etc.*), for ease of quantification or detection.

[00243] Half-life extending moieties. Optionally, for modulation of the pharmacokinetic profile of the molecule to fit the therapeutic need, the composition of the present invention can include one or more half-life extending moieties of various masses and configurations, which half-life extending moiety, or moieties, can be covalently fused, attached, linked or conjugated to the toxin peptide analog. A "half-life extending moiety" refers to a molecule that prevents or mitigates in vivo degradation by proteolysis or other activity-diminishing chemical modification, increases in vivo half-life or other pharmacokinetic properties such as but not limited to increasing the rate of absorption, reduces toxicity, reduces immunogenicity, improves solubility, increases biological activity and/or target selectivity of the toxin peptide analog with respect to a target of interest, and/or increases manufacturability, compared to an unconjugated form of the toxin peptide analog. In accordance with the invention, the half-life extending moiety is one that is pharmaceutically acceptable.

[00244] The half-life extending moiety can be selected such that the inventive composition achieves a sufficient hydrodynamic size to prevent clearance by renal filtration in vivo. For example, a half-life extending moiety can be selected that is a polymeric macromolecule, which is substantially straight chain, branched-chain (br), or dendritic in form. Alternatively, a half-life extending moiety can be selected such that, in vivo, the inventive composition of matter will bind to a serum protein to form a complex, such that the complex thus formed avoids substantial renal clearance. The half-life extending moiety can be, for example, a lipid; a cholesterol group (such as a steroid); a carbohydrate or oligosaccharide; or any natural or synthetic protein, polypeptide or peptide that binds to a salvage receptor.

[00245] Exemplary half-life extending moieties that can be used, in accordance with the present invention, include an immunoglobulin Fc domain, or a portion thereof, or a biologically suitable polymer or copolymer, for example, a polyalkylene glycol compound, such as a polyethylene glycol (PEG) or a polypropylene glycol. Other appropriate polyalkylene glycol compounds include, but are not limited to, charged or neutral polymers of the following types: dextran, polylysine, colominic acids or other carbohydrate based polymers, polymers of amino acids, and biotin derivatives. In some

monomeric fusion or conjugate protein embodiments an immunoglobulin (including light and heavy chains) or a portion thereof, can be used as a half-life-extending moiety, preferably an immunoglobulin of human origin, and including any of the immunoglobulins, such as, but not limited to, IgG1, IgG2, IgG3 or IgG4.

[00246] Other examples of the half-life extending moiety, in accordance with the invention, include a copolymer of ethylene glycol, a copolymer of propylene glycol, a carboxymethylcellulose, a polyvinyl pyrrolidone, a poly-1,3-dioxolane, a poly-1,3,6-trioxane, an ethylene maleic anhydride copolymer, a polyaminoacid (e.g., polylysine or polyornithine), a dextran n-vinyl pyrrolidone, a poly n-vinyl pyrrolidone, a propylene glycol homopolymer, a propylene oxide polymer, an ethylene oxide polymer, a polyoxyethylated polyol, a polyvinyl alcohol, a linear or branched glycosylated chain, a polyacetal, a long chain fatty acid, a long chain hydrophobic aliphatic group, or a polysialic acid (e.g., PolyXen™ technology; Gregoriadis et al., Improving the therapeutic efficacy of peptides and proteins: a role for polysialic acids, Intl. J. Pharmaceutics, 300:125-30 (2005), incorporated herein by reference in its entirety).

[00247] In other embodiments of the composition of matter, the half-life extending moiety is an anionically charged chemical entity, covalently linked to the N-terminus of the toxin peptide analog, which anionically charged chemical entities include, but are not limited to, phosphotyrosine, phosphoserine, p-phosphono(difluoro-methyl)-phenylalanine (Pfp), p-phosphono-methyl-phenylalanine (Pmp), p-phosphatidyl-phenylalanine (Ppa), or p-phosphono-methylketo-phenylalanine (Pkp), which can be covalently linked to the N-terminal of the toxin peptide analog, optionally indirectly, via an AEEA linker or other linker as described herein. (See, Chandy et al., Analogs of ShK toxin and their uses in selective inhibition of Kv1.3 potassium channels, WO 2006/042151 A2; Beeton et al., Targeting effector memory T cells with a selective peptide inhibitor of Kv1.3 channels for therapy of autoimmune diseases, Molec. Pharmacol. 67(4):1369-81 (2005); Pennington et al., Engineering a stable and selective peptide blocker of the Kv1.3 channel in T lymphocytes, Molecular Pharmacology Fast Forward, published January 2, 2009 as doi:10.1124/mol.108.052704 (2009), all of which references are incorporated herein by reference in their entireties). AEEA is 2-(2-(2-aminoethoxy)ethoxy)acetic acid (also known as 8-Amino-3,6-Dioxaoctanoic Acid). (See, e.g., Beeton et al., Targeting effector memory T cells with a

selective peptide inhibitor of Kv1.3 channels for therapy of autoimmune diseases, Molec. Pharmacol. 67(4):1369-81 (2005)).

[00248] Other embodiments of the half-life extending moiety, in accordance with the invention, include peptide ligands or small (organic) molecule ligands that have binding affinity for a long half-life serum protein under physiological conditions of temperature, pH, and ionic strength. Examples include an albumin-binding peptide or small molecule ligand, a transthyretin-binding peptide or small molecule ligand, a thyroxine-binding globulin-binding peptide or small molecule ligand, an antibody-binding peptide or small molecule ligand, or another peptide or small molecule that has an affinity for a long half-life serum protein. (See, e.g., Blancy et al., Method and compositions for increasing the serum half-life of pharmacologically active agents by binding to transthyretin-selective ligands, US Patent. No. 5,714,142; Sato et al., Serum albumin binding moieties, US 2003/0069395 A1; Jones et al., Pharmaceutical active conjugates, US Patent No. 6,342,225). A "long half-life serum protein" is one of the hundreds of different proteins dissolved in mammalian blood plasma, including so-called "carrier proteins" (such as albumin, transferrin and haptoglobin), fibrinogen and other blood coagulation factors, complement components, immunoglobulins, enzyme inhibitors, precursors of substances such as angiotensin and bradykinin and many other types of proteins. The invention encompasses the use of any single species of pharmaceutically acceptable half-life extending moiety, such as, but not limited to, those described herein, or the use of a combination of two or more different half-life extending moieties, such as PEG and immunoglobulin Fc domain or a portion thereof (see, e.g., Feige et al., Modified peptides as therapeutic agents, US Patent No. 6,660,843), such as a CH2 domain of Fc, albumin (e.g., human serum albumin (HSA); see, e.g., Rosen et al., Albumin fusion proteins, US Patent No. 6,926,898 and US 2005/0054051; Bridon et al., Protection of endogenous therapeutic peptides from peptidase activity through conjugation to blood components, US 6,887,470), a transthyretin (TTR; see, e.g., Walker et al., Use of transthyretin peptide/protein fusions to increase the serum half-life of pharmacologically active peptides/proteins, US 2003/0195154 A1; 2003/0191056 A1), or a thyroxine-binding globulin (TBG), or a combination such as immunoglobulin(light chain+heavy chain) and Fc domain (the heterotrimeric combination a so-called "hemibody"), for example as described in

Sullivan et al., Toxin Peptide Therapeutic Agents, PCT/US2007/022831, published as WO 2008/088422, which is incorporated herein by reference in its entirety.

[00249] Conjugation of the toxin peptide analogs(s) to the half-life extending moiety, or moieties, can be via the N-terminal and/or C-terminal of the toxin peptide, or can be intercalary as to its primary amino acid sequence, F1 being linked closer to the toxin peptide analog's N-terminus.

[00250] Particularly useful half-life extending moieties include immunoglobulins (e.g., human immunoglobulin, including IgG1, IgG2, IgG3 or IgG4). The term "immunoglobulin" encompasses full antibodies comprising two dimerized heavy chains (HC), each covalently linked to a light chain (LC); a single undimerized immunoglobulin heavy chain and covalently linked light chain (HC + LC); or a chimeric immunoglobulin (light chain + heavy chain)-Fc heterotrimer (a so-called "hemibody"). Figure 12A-N and Figures 88-91 illustrate several different embodiments of such immunoglobulin-toxin peptide conjugates.

[00251] Recombinant fusion or chemical conjugation of the inventive GpTx-1 peptide analogs to a recombinant immunoglobulin of any of the IgG1, IgG2, IgG3 or IgG4 isotypes can be useful to extend pharmacokinetic half life. (See, e.g., Doellgast et al., WO 2010/108153 A2). Any of the carrier immunoglobulins disclosed in Doellgast et al., WO 2010/108153 A2 or Walker et al., PCT/US2011/052841, or isotype conversions of any of them comprising different isotype constant domains, or other carrier immunoglobulins known in the art, can be used as half life extending moieties within the scope of the invention.

[00252] One example of a human IgG2 heavy chain (HC) constant domain has the amino acid sequence:

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPP
CPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVE
VHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTI
SKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK// SEQ. ID NO:3090.

[00253] Constant region sequences of other IgG isotypes are known in the art for an IgG1, IgG2, IgG3, or IgG4 immunoglobulin isotype, if desired. In general, human IgG2 can be used for targets where effector functions are not desired, and human IgG1 in situations where such effector functions (e.g., antibody-dependent cytotoxicity (ADCC)) are desired. Human IgG3 has a relatively short half life and human IgG4 forms antibody "half-molecules." There are four known allotypes of human IgG1. The preferred allotype is referred to as "hIgG1z", also known as the "KEEM" allotype. Human IgG1 allotypes "hIgG1za" (KDEL), "hIgG1f" (REEM), and "hIgG1fa" are also useful; all appear to have ADCC effector function.

[00254] Human hIgG1z heavy chain (HC) constant domain has the amino acid sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
QKSLSLSPGK// SEQ ID NO:3091.

[00232] Human hIgG1za heavy chain (HC) constant domain has the amino acid sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
KSLSLSPGK// SEQ ID NO:3092.

[00233] Human hIgG1f heavy chain (HC) constant domain has the amino acid sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
QKSLSLSPGK// SEQ ID NO:3093.

[00234] Human hIgG1fa heavy chain (HC) constant domain has the amino acid sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHT
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
KSLSLSPGK// SEQ ID NO:3094.

[00235] One example of a human immunoglobulin light chain (LC) constant region sequence is the following (designated "CL-1"):

GQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGV
ETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS//
SEQ ID NO:3095.

[00236] CL-1 is useful to increase the pI of antibodies and is convenient. There are three other human immunoglobulin light chain constant regions, designated "CL-2", "CL-3" and "CL-7", which can also be used within the scope of the present invention. CL-2 and CL-3 are more common in the human population.

[00237] CL-2 human light chain (LC) constant domain has the amino acid sequence:

GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS// SEQ ID NO:3096.

[00238] CL-3 human LC constant domain has the amino acid sequence:

GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPTECS// SEQ ID NO:3097.

[00239] CL-7 human LC constant domain has the amino acid sequence:

GQPKAAPSVTLFPPSSEELQANKATLVCLVSDFYPGAVTVAWKADGSPVKVGV ETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCRVTHEGSTVEKTVAPAECS// SEQ ID NO:3098.

[00240] Variable regions of immunoglobulin chains generally exhibit the same overall structure, comprising relatively conserved framework regions (FR) joined by three hypervariable regions, more often called "complementarity determining regions" or CDRs. The CDRs from the two chains of each heavy chain/light chain pair mentioned above typically are aligned by the framework regions to form a structure that binds specifically with a specific epitope or domain on the target protein, if any. From N-terminal to C-terminal, naturally-occurring light and heavy chain variable regions both typically conform with the following order of these elements: FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. A numbering system has been devised for assigning numbers to amino acids that occupy positions in each of these domains. This numbering system is defined in Kabat Sequences of Proteins of Immunological Interest (1987 and 1991, NIH, Bethesda, MD), or Chothia & Lesk, 1987, *J. Mol. Biol.* 196:901-917; Chothia *et al.*, 1989, *Nature* 342:878-883.

[00241] An "antibody", or interchangeably "Ab", is a tetrameric glycoprotein. In a naturally-occurring antibody, each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" chain of about 220 amino acids (about

25 kDa) and one "heavy" chain of about 440 amino acids (about 50-70 kDa). The amino-terminal portion of each chain includes a "variable" ("V") region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. The variable region differs among different antibodies. The constant region is the same among different antibodies. Within the variable region of each heavy or light chain, there are three hypervariable subregions that help determine the antibody's specificity for antigen. The variable domain residues between the hypervariable regions are called the framework residues and generally are somewhat homologous among different antibodies. Immunoglobulins can be assigned to different classes depending on the amino acid sequence of the constant domain of their heavy chains. Human light chains are classified as kappa (κ) and lambda (λ) light chains. Within light and heavy chains, the variable and constant regions are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. See generally, Fundamental Immunology, Ch. 7 (Paul, W., ed., 2nd ed. Raven Press, N.Y. (1989)). Within the scope of the invention, an "antibody" also encompasses a recombinantly made antibody, and antibodies that are lacking glycosylation.

[00242] The term "light chain" or "immunoglobulin light chain" includes a full-length light chain and fragments thereof having sufficient variable region sequence to confer binding specificity. A full-length light chain includes a variable region domain, VL, and a constant region domain, CL. The variable region domain of the light chain is at the amino-terminus of the polypeptide. Light chains include kappa chains and lambda chains. The term "heavy chain" or "immunoglobulin heavy chain" includes a full-length heavy chain and fragments thereof having sufficient variable region sequence to confer binding specificity. A full-length heavy chain includes a variable region domain, V_H, and three constant region domains, C_H1, C_H2, and C_H3. The V_H domain is at the amino-terminus of the polypeptide, and the C_H domains are at the carboxyl-terminus, with the C_H3 being closest to the carboxy-terminus of the polypeptide. Heavy chains are classified as mu (μ), delta (Δ), gamma (γ), alpha (α), and epsilon (ε), and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE,

respectively. In separate embodiments of the invention, heavy chains may be of any isotype, including IgG (including IgG1, IgG2, IgG3 and IgG4 subtypes), IgA (including IgA1 and IgA2 subtypes), IgM and IgE. Several of these may be further divided into subclasses or isotypes, e.g. IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2. The variable regions of each light/heavy chain pair typically form the antigen binding site of an antibody, but a useful carrier antibody need not have a known antigen binding site to be useful. (See, e.g., Doellgast et al., WO 2010/108153 A2; Walker et al., PCT/US2011/052841). Different IgG isotypes may have different effector functions (mediated by the Fc region), such as antibody-dependent cellular cytotoxicity (ADCC) and complement-dependent cytotoxicity (CDC). In ADCC, the Fc region of an antibody binds to Fc receptors (FcγRs) on the surface of immune effector cells such as natural killers and macrophages, leading to the phagocytosis or lysis of the targeted cells. In CDC, the antibodies kill the targeted cells by triggering the complement cascade at the cell surface.

[00243] An "Fc region", or used interchangeably herein, "Fc domain" or "immunoglobulin Fc domain", contains two heavy chain fragments, which in a full antibody comprise the C_H1 and C_H2 domains of the antibody. The two heavy chain fragments are held together by two or more disulfide bonds and by hydrophobic interactions of the C_H3 domains.

[00244] The term "salvage receptor binding epitope" refers to an epitope of the Fc region of an IgG molecule (*e.g.*, IgG_1, IgG_2, IgG_3, or IgG_4) that is responsible for increasing the in vivo serum half-life of the IgG molecule.

[00245] "Allotypes" are variations in antibody sequence, often in the constant region, that can be immunogenic and are encoded by specific alleles in humans. Allotypes have been identified for five of the human IGHC genes, the IGHG1, IGHG2, IGHG3, IGHA2 and IGHE genes, and are designated as G1m, G2m, G3m, A2m, and Em allotypes, respectively. At least 18 Gm allotypes are known: nG1m(1), nG1m(2), G1m (1, 2, 3, 17) or G1m (a, x, f, z), G2m (23) or G2m (n), G3m (5, 6, 10, 11, 13, 14, 15, 16, 21, 24, 26, 27, 28) or G3m (b1, c3, b5, b0, b3, b4, s, t, g1, c5, u, v, g5). There are two A2m allotypes A2m(1) and A2m(2).

[00246] For a detailed description of the structure and generation of antibodies, see Roth, D.B., and Craig, N.L., *Cell*, 94:411-414 (1998), herein incorporated by reference in its entirety. Briefly, the process for generating DNA encoding the heavy and light chain immunoglobulin sequences occurs primarily in developing B-cells. Prior to the rearranging and joining of various immunoglobulin gene segments, the V, D, J and constant (C) gene segments are found generally in relatively close proximity on a single chromosome. During B-cell-differentiation, one of each of the appropriate family members of the V, D, J (or only V and J in the case of light chain genes) gene segments are recombined to form functionally rearranged variable regions of the heavy and light immunoglobulin genes. This gene segment rearrangement process appears to be sequential. First, heavy chain D-to-J joints are made, followed by heavy chain V-to-DJ joints and light chain V-to-J joints. In addition to the rearrangement of V, D and J segments, further diversity is generated in the primary repertoire of immunoglobulin heavy and light chains by way of variable recombination at the locations where the V and J segments in the light chain are joined and where the D and J segments of the heavy chain are joined. Such variation in the light chain typically occurs within the last codon of the V gene segment and the first codon of the J segment. Similar imprecision in joining occurs on the heavy chain chromosome between the D and J_H segments and may extend over as many as 10 nucleotides. Furthermore, several nucleotides may be inserted between the D and J_H and between the V_H and D gene segments which are not encoded by genomic DNA. The addition of these nucleotides is known as N-region diversity. The net effect of such rearrangements in the variable region gene segments and the variable recombination which may occur during such joining is the production of a primary antibody repertoire.

[00247] The term "hypervariable" region refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region comprises amino acid residues from a complementarity determining region or CDR [i.e., residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the light chain variable domain and 31-35 (H1), 50-65 (H2) and 95-102 (H3) in the heavy chain variable domain as described by Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)]. Even a

single CDR may recognize and bind antigen, although with a lower affinity than the entire antigen binding site containing all of the CDRs.

[00248] An alternative definition of residues from a hypervariable "loop" is described by Chothia et al., *J. Mol.Biol. 196*: 901-917 (1987) as residues 26-32 (L1), 50-52 (L2) and 91-96 (L3) in the light chain variable domain and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the heavy chain variable domain.

[00249] "Framework" or "FR" residues are those variable region residues other than the hypervariable region residues.

[00250] "Antibody fragments" comprise a portion of an intact full length antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng.,8(10):1057-1062 (1995)); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

[00251] Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment which contains the constant region. The Fab fragment contains all of the variable domain, as well as the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. The Fc fragment displays carbohydrates and is responsible for many antibody effector functions (such as binding complement and cell receptors), that distinguish one class of antibody from another.

[00252] Pepsin treatment yields an $F(ab')_2$ fragment that has two "Single-chain Fv" or "scFv" antibody fragments comprising the VH and VL domains of antibody, wherein these domains are present in a single polypeptide chain. Fab fragments differ from Fab' fragments by the inclusion of a few additional residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Preferably, the Fv polypeptide further comprises a polypeptide linker between the VH and VL domains that enables the Fv to form the desired structure for antigen binding. For a review of scFv see Pluckthun in The Pharmacology of Monoclonal

Antibodies, vol. 1 13, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

[00253] A "Fab fragment" is comprised of one light chain and the C_H1 and variable regions of one heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule.

[00254] A "Fab' fragment" contains one light chain and a portion of one heavy chain that contains the V_H domain and the C_H1 domain and also the region between the C_H1 and C_H2 domains, such that an interchain disulfide bond can be formed between the two heavy chains of two Fab' fragments to form an $F(ab')_2$ molecule.

[00255] A "$F(ab')_2$ fragment" contains two light chains and two heavy chains containing a portion of the constant region between the C_H1 and C_H2 domains, such that an interchain disulfide bond is formed between the two heavy chains. A $F(ab')_2$ fragment thus is composed of two Fab' fragments that are held together by a disulfide bond between the two heavy chains.

[00256] "Fv" is the minimum antibody fragment that contains a complete antigen recognition and binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen binding site on the surface of the VH VL dimer. A single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[00257] "Single-chain antibodies" are Fv molecules in which the heavy and light chain variable regions have been connected by a flexible linker to form a single polypeptide chain, which forms an antigen-binding region. Single chain antibodies are discussed in detail in International Patent Application Publication No. WO 88/01649 and United States Patent No. 4,946,778 and No. 5,260,203, the disclosures of which are incorporated by reference in their entireties.

[00258] "Single-chain Fv" or "scFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain, and optionally comprising a polypeptide linker between the V_H and V_L domains that enables the Fv to form the desired structure for antigen binding (Bird et al., *Science* 242:423-426, 1988, and Huston et al., *Proc. Natl. Acad. Sci. USA* 85:5879-5883, 1988). An "Fd" fragment consists of the V_H and C_H1 domains.

[00259] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) in the same polypeptide chain (VH VL). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

[00260] A "domain antibody" is an immunologically functional immunoglobulin fragment containing only the variable region of a heavy chain or the variable region of a light chain. In some instances, two or more V_H regions are covalently joined with a peptide linker to create a bivalent domain antibody. The two V_H regions of a bivalent domain antibody may target the same or different antigens.

[00261] The term "epitope" is the portion of a molecule that is bound by an antigen binding protein (for example, an antibody). The term includes any determinant capable of specifically binding to an antigen binding protein, such as an antibody or to a T-cell receptor. An epitope can be contiguous or non-contiguous (e.g., in a single-chain polypeptide, amino acid residues that are not contiguous to one another in the polypeptide sequence but that within the context of the molecule are bound by the antigen binding protein). In certain embodiments, epitopes may be mimetic in that they comprise a three dimensional structure that is similar to an epitope used to generate the antigen binding protein, yet comprise none or only some of the amino acid residues found in that epitope used to generate the antigen binding protein. Most often, epitopes reside on proteins, but in some instances may reside on other kinds of molecules, such

as nucleic acids. Epitope determinants may include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl or sulfonyl groups, and may have specific three dimensional structural characteristics, and/or specific charge characteristics. Generally, antibodies specific for a particular target antigen will preferentially recognize an epitope on the target antigen in a complex mixture of proteins and/or macromolecules.

[00262] The term "identity" refers to a relationship between the sequences of two or more polypeptide molecules or two or more nucleic acid molecules, as determined by aligning and comparing the sequences. "Percent identity" means the percent of identical residues between the amino acids or nucleotides in the compared molecules and is calculated based on the size of the smallest of the molecules being compared. For these calculations, gaps in alignments (if any) must be addressed by a particular mathematical model or computer program (i.e., an "algorithm"). Methods that can be used to calculate the identity of the aligned nucleic acids or polypeptides include those described in Computational Molecular Biology, (Lesk, A. M., ed.), 1988, New York: Oxford University Press; Biocomputing Informatics and Genome Projects, (Smith, D. W., ed.), 1993, New York: Academic Press; Computer Analysis of Sequence Data, Part I, (Griffin, A. M., and Griffin, H. G., eds.), 1994, New Jersey: Humana Press; von Heinje, G., 1987, Sequence Analysis in Molecular Biology, New York: Academic Press; Sequence Analysis Primer, (Gribskov, M. and Devereux, J., eds.), 1991, New York: M. Stockton Press; and Carillo et al., 1988, SIAM J. Applied Math. 48:1073. For example, sequence identity can be determined by standard methods that are commonly used to compare the similarity in position of the amino acids of two polypeptides. Using a computer program such as BLAST or FASTA, two polypeptide or two polynucleotide sequences are aligned for optimal matching of their respective residues (either along the full length of one or both sequences, or along a pre-determined portion of one or both sequences). The programs provide a default opening penalty and a default gap penalty, and a scoring matrix such as PAM 250 [a standard scoring matrix; see Dayhoff et al., in *Atlas of Protein Sequence and Structure*, vol. 5, supp. 3 (1978)] can be used in conjunction with the computer program. For example, the percent identity can then be calculated as: the total number of identical matches multiplied by

100 and then divided by the sum of the length of the longer sequence within the matched span and the number of gaps introduced into the longer sequences in order to align the two sequences. In calculating percent identity, the sequences being compared are aligned in a way that gives the largest match between the sequences.

[00263] The GCG program package is a computer program that can be used to determine percent identity, which package includes GAP (Devereux et al., 1984, Nucl. Acid Res. 12:387; Genetics Computer Group, University of Wisconsin, Madison, WI). The computer algorithm GAP is used to align the two polypeptides or two polynucleotides for which the percent sequence identity is to be determined. The sequences are aligned for optimal matching of their respective amino acid or nucleotide (the "matched span", as determined by the algorithm). A gap opening penalty (which is calculated as 3x the average diagonal, wherein the "average diagonal" is the average of the diagonal of the comparison matrix being used; the "diagonal" is the score or number assigned to each perfect amino acid match by the particular comparison matrix) and a gap extension penalty (which is usually 1/10 times the gap opening penalty), as well as a comparison matrix such as PAM 250 or BLOSUM 62 are used in conjunction with the algorithm. In certain embodiments, a standard comparison matrix (see, Dayhoff et al., 1978, Atlas of Protein Sequence and Structure 5:345-352 for the PAM 250 comparison matrix; Henikoff et al., 1992, Proc. Natl. Acad. Sci. U.S.A. 89:10915-10919 for the BLOSUM 62 comparison matrix) is also used by the algorithm.

[00264] Recommended parameters for determining percent identity for polypeptides or nucleotide sequences using the GAP program include the following:

Algorithm: Needleman et al., 1970, J. Mol. Biol. 48:443-453;
Comparison matrix: BLOSUM 62 from Henikoff et al., 1992, supra;
Gap Penalty: 12 (but with no penalty for end gaps)
Gap Length Penalty: 4
Threshold of Similarity: 0

[00265] Certain alignment schemes for aligning two amino acid sequences may result in matching of only a short region of the two sequences, and this small aligned region

may have very high sequence identity even though there is no significant relationship between the two full-length sequences. Accordingly, the selected alignment method (GAP program) can be adjusted if so desired to result in an alignment that spans at least 50 contiguous amino acids of the target polypeptide.

[00266] The term "modification" when used in connection withimmmunoglobulins, including antibodies and antibody fragments, of the invention, include, but are not limited to, one or more amino acid changes (including substitutions, insertions or deletions); chemical modifications; covalent modification by conjugation to therapeutic or diagnostic agents; labeling (e.g., with radionuclides or various enzymes); covalent polymer attachment such as PEGylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of non-natural amino acids.

[00267] The term "derivative" when used in connection with an immunoglobulin (including antibodies and antibody fragments) within the scope of the invention refers to immunoglobulin proteins that are covalently modified by conjugation to therapeutic or diagnostic agents, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as PEGylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of non-natural amino acids. Derivatives of the invention will retain the binding properties of underivatized molecules of the invention.

[00268] In some embodiments of the invention, the half-life extending moiety is an immunoglobulin Fc domain (e.g., a human immunoglobulin Fc domain, including Fc of allotype IgG1, IgG2, IgG3 or IgG4) or a portion thereof (e.g., CH2 domain of the Fc domain), human serum albumin (HSA), or poly(ethylene glycol) (PEG), in particular PEG of molecular weight of about 1000 Da to about 100000 Da.

[00269] Monovalent dimeric or bivalent dimeric Fc-toxin peptide analog fusions or conjugates are useful embodiments of the inventive composition of matter. A "monovalent dimeric" Fc-toxin peptide analog fusion or conjugate, or interchangeably, "monovalent dimer", or interchangeably, "monovalent heterodimer", is a Fc-toxin peptide analog fusion or conjugate that includes a toxin peptide analog conjugated with only one of the dimerized Fc domains (e.g., as represented schematically in Figure 2B

of Sullivan et al., Toxin Peptide Therapeutic Agents, US2007/0071764 and Sullivan et al., Toxin Peptide Therapeutic Agents, PCT/US2007/022831, published as WO 2008/088422, which are both incorporated herein by reference in their entireties). A "bivalent dimeric" Fc-toxin peptide analog fusion, or interchangeably, "bivalent dimer" or "bivalent homodimer", is a Fc-toxin peptide analog fusion or conjugate having both of the dimerized Fc domains each conjugated separately with a toxin peptide analog (e.g., as represented schematically in Figure 2C of Sullivan et al., Toxin Peptide Therapeutic Agents, US2007/0071764 and Sullivan et al., Toxin Peptide Therapeutic Agents, PCT/US2007/022831, published as WO 2008/088422).

[00270] Immunoglobulin Fc domains include Fc variants, which are suitable half-life extending moieties within the scope of this invention. A native Fc can be extensively modified to form an Fc variant in accordance with this invention, provided binding to the salvage receptor is maintained; see, for example WO 97/34631, WO 96/32478, and WO 04/110 472. In such Fc variants, one can remove one or more sites of a native Fc that provide structural features or functional activity not required by the fusion or conjugate molecules of this invention. One can remove these sites by, for example, substituting or deleting residues, inserting residues into the site, or truncating portions containing the site. The inserted or substituted residues can also be altered amino acids, such as peptidomimetics or D-amino acids. Fc variants can be desirable for a number of reasons, several of which are described below. Exemplary Fc variants include molecules and sequences in which:

[00271] 1. Sites involved in disulfide bond formation are removed. Such removal can avoid reaction with other cysteine-containing proteins present in the host cell used to produce the molecules of the invention. For this purpose, the cysteine-containing segment at the N-terminus can be truncated or cysteine residues can be deleted or substituted with other amino acids (e.g., alanyl, seryl). In particular, one can truncate the N-terminal 20-amino acid segment of SEQ ID NO: 478:

Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly
Val His Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys// SEQ ID NO:478.

or delete or substitute the cysteine residues at positions 7 and 10 of SEQ ID NO: 478. Even when cysteine residues are removed, the single chain Fc domains can still form a dimeric Fc domain that is held together non-covalently.

[00272] 2. A native Fc is modified to make it more compatible with a selected host cell. For example, one can remove the PA dipeptide sequence near the N-terminus of a typical native Fc, which can be recognized by a digestive enzyme in *E. coli* such as proline iminopeptidase. One can also add an N-terminal methionine residue, especially when the molecule is expressed recombinantly in a bacterial cell such as *E. coli*. The Fc domain of SEQ ID NO: 478 is one such Fc variant.

[00273] 3. A portion of the N-terminus of a native Fc is removed to prevent N-terminal heterogeneity when expressed in a selected host cell. For this purpose, one can delete any of the first 20 amino acid residues at the N-terminus, particularly those at positions 1, 2, 3, 4 and 5.

[00274] 4. One or more glycosylation sites are removed. Residues that are typically glycosylated (e.g., asparagine) can confer cytolytic response. Such residues can be deleted or substituted with unglycosylated residues (e.g., alanine).

[00275] 5. Sites involved in interaction with complement, such as the C1q binding site, are removed. For example, one can delete or substitute the EKK tripeptide sequence of human IgG1. Complement recruitment may not be advantageous for the molecules of this invention and so can be avoided with such an Fc variant.

[00276] 5. Sites are removed that affect binding to Fc receptors other than a salvage receptor. A native Fc can have sites for interaction with certain white blood cells that are not required for the fusion or conjugate molecules of the present invention and so can be removed.

[00277] 7. The ADCC site is removed to decrease or eliminate ADCC effector function, or alternatively, modified for enhanced ADCC effector function by non-fucosylation or de-fucosylation. ADCC sites are known in the art; see, for example, Molec. Immunol. 29 (5): 633-9 (1992) with regard to ADCC sites in IgG1. These sites, as well, are not required for the fusion or conjugate molecules of the present invention and so can be removed, or enhanced for ADCC effector function, as may be desired. (See, Iida et al., Two mechanisms of the enhanced antibody-dependent cellular cytotoxicity (ADCC) efficacy of non-fucosylated therapeutic antibodies in human blood, BMC Cancer 9:58 doi:10.1186/1471-2407-9-58 (2009)).

[00278] 8. When the native Fc is derived from a non-human antibody, the native Fc can be humanized. Typically, to humanize a native Fc, one will substitute selected residues in the non-human native Fc with residues that are normally found in human native Fc. Techniques for antibody humanization are well known in the art.

[00279] 9. One or more toxin peptide analog sequences can be inserted into an internal conjugation site, or sites, within a loop region of an immunoglobulin Fc domain, as disclosed in U.S. Patent Nos.7,442,778; 7,645,861; 7,655,764; 7,655,765; 7,662,931; 7,750,127, and 7,750,128. The term "loop" region or "Fc-loop" region refers to a primary sequence of amino acid residues which connects two regions comprising secondary structure, such as an α-helix or a β-sheet, in the immediate N-terminal and C-terminal directions of primary structure from the loop region. Examples include, but are not limited to, CH2 or CH3 loop regions. One of skill in the art understands that a loop region, while not itself comprising secondary structure, may

influence or contribute to secondary or higher order protein structure. The term "internal" conjugation site means that the toxin peptide analog moiety, or moieties, is non-terminal, i.e., not through the α-amino site or the α-carboxy site of the Fc domain, although there optionally can also be additional moieties conjugated terminally at the N-terminal and/or C-terminal of the Fc domain.

[00280] 10. A linker of suitable length and neutral charge, such as "L25" (GGGGSGGGGSGGGGSGGGGSGGGGS; SEQ ID NO:493) or "L20" (GGGGSGGGGSGGGGSGGGGS; SEQ ID NO:477), can be covalently fused between the C-terminal of one monomer of an Fc domain and the N-terminal of a second Fc domain monomer, with a toxin peptide analog fused to the N-terminal of the first Fc domain monomer or the C-terminal of the second Fc domain monomer, or within a loop region of the first and/or second Fc domain monomer. Such a molecule can be recombinantly expressed in bacterial or mammalian cells to produce a variant "monovalent dimeric" Fc-toxin peptide analog fusion or conjugate with the typical disulfide bond formation between the Fc monomers. (See, e.g., Example 13 herein). Other examples of Fc variants include the following: In SEQ ID NO: 478, the leucine at position 15 can be substituted with glutamate; the glutamate at position 99, with alanine; and the lysines at positions 101 and 103, with alanines. In addition, phenyalanine residues can replace one or more tyrosine residues. For purposes of the invention, a variant Fc domain can also be part of a monomeric immunoglobulin heavy chain, an antibody, or a heterotrimeric hemibody (LC+HC+Fc).

[00281] An alternative half-life extending moiety would be a protein, polypeptide, peptide, antibody, antibody fragment, or small molecule (e.g., a peptidomimetic compound) capable of binding to a salvage receptor. For example, one could use as a half-life extending moiety a polypeptide as described in U.S. Pat. No. 5,739,277, issued April 14, 1998 to Presta et al. Peptides could also be selected by phage display for binding to the FcRn salvage receptor. Such salvage receptor-binding compounds are also included within the meaning of "half-life extending moiety" and are within the scope of this invention. Such half-life extending moieties should be selected for increased half-life (e.g., by avoiding sequences recognized by proteases) and decreased

immunogenicity (e.g., by favoring non-immunogenic sequences, as discovered in antibody humanization).

[00282] As noted above, polymer half-life extending moieties can also be used. Various means for attaching chemical moieties useful as half-life extending moieties are currently available, see, e.g., Patent Cooperation Treaty ("PCT") International Publication No. WO 96/11953, entitled "N-Terminally Chemically Modified Protein Compositions and Methods," herein incorporated by reference in its entirety. This PCT publication discloses, among other things, the selective attachment of water-soluble polymers to the N-terminus of proteins.

[00283] In some embodiments of the inventive compositions, the polymer half-life extending moiety is polyethylene glycol (PEG), covalently linked at the N-terminal, C-terminal or at one or more intercalary side chains of toxin peptide analog. Some embodiments of the inventive composition of matter further include one or more PEG moieties conjugated to a non-PEG half-life extending moiety or to the toxin peptide analog, or to any combination of any of these. For example, an Fc domain or portion thereof in the inventive composition can be made mono-PEGylated, di-PEGylated, or otherwise multi-PEGylated, by the process of reductive alkylation.

[00284] Covalent conjugation of proteins and peptides with poly(ethylene glycol) (PEG) has been widely recognized as an approach to significantly extend the in vivo circulating half-lives of therapeutic proteins. PEGylation achieves this effect predominately by retarding renal clearance, since the PEG moiety adds considerable hydrodynamic radius to the protein. (Zalipsky, S., et al., Use of functionalized poly(ethylene glycol)s for modification of polypeptides., in poly(ethylene glycol) chemistry: Biotechnical and biomedical applications., J.M. Harris, Ed., Plenum Press: New York., 347-370 (1992)). Additional benefits often conferred by PEGylation of proteins and peptides include increased solubility, resistance to proteolytic degradation, and reduced immunogenicity of the therapeutic polypeptide. The merits of protein PEGylation are evidenced by the commercialization of several PEGylated proteins including PEG-Adenosine deaminase (Adagen™/Enzon Corp.), PEG-L-asparaginase (Oncaspar™/Enzon Corp.), PEG-Interferon α-2b (PEG-Intron™/Schering/Enzon),

PEG-Interferon α-2a (PEGASYS™/Roche) and PEG-G-CSF (Neulasta™/Amgen) as well as many others in clinical trials.

[00285] By "PEGylated peptide" or "PEGylated protein" is meant a peptide having a polyethylene glycol (PEG) moiety covalently bound to an amino acid residue of the peptide itself or to a peptidyl or non-peptidyl linker that is covalently bound to a residue of the peptide, either directly or indirectly through another linker moiety. A non-limiting example is N-terminal conjugation of the peptide with 3-(1-(1-bromo-2-oxo-6,9,12,15,18,21,24,27,30,33,36-undecaoxa-3-azaoctatriacontan-38-yl)-1H-1,2,3-triazol-4-yl)propanoyl (designated herein by the abbreviation "{bromoacetamide-PEG11-triazole}-").

[00286] By "polyethylene glycol" or "PEG" is meant a polyalkylene glycol compound or a derivative thereof, with or without coupling agents or derivatization with coupling or activating moieties (e.g., with aldehyde, hydroxysuccinimidyl, hydrazide, thiol, triflate, tresylate, azirdine, oxirane, orthopyridyl disulphide, vinylsulfone, iodoacetamide or a maleimide moiety). In accordance with the present invention, useful PEG includes substantially linear, straight chain PEG, branched PEG (brPEG), or dendritic PEG. (See, e.g., Merrill, US Patent No. 5,171,264; Harris et al., Multiarmed, monofunctional, polymer for coupling to molecules and surfaces, US Patent No. 5,932,462; Shen, N-maleimidyl polymer derivatives, US Patent No. 6,602,498).

[00287] Briefly, the PEG groups are generally attached to the peptide portion of the composition of the invention via acylation or reductive alkylation (or reductive amination) through a reactive group on the PEG moiety (e.g., an aldehyde, amino, thiol, or ester group) to a reactive group on the inventive compound (e.g., an aldehyde, amino, or ester group). A useful strategy for the PEGylation of synthetic peptides consists of combining, through forming a conjugate linkage in solution, a peptide and a PEG moiety, each bearing a special functionality that is mutually reactive toward the other. The peptides can be easily prepared with conventional solid phase synthesis (see, for example, Figures 5 and 6 and the accompanying text herein). The peptides are "preactivated" with an appropriate functional group at a specific site. The precursors are

purified and fully characterized prior to reacting with the PEG moiety. Ligation of the peptide with PEG usually takes place in aqueous phase and can be easily monitored by reverse phase analytical HPLC. The PEGylated peptides can be easily purified by preparative HPLC and characterized by analytical HPLC, amino acid analysis and laser desorption mass spectrometry.

[00288] PEG is a well-known, water soluble polymer that is commercially available or can be prepared by ring-opening polymerization of ethylene glycol according to methods well known in the art (Sandler and Karo, Polymer Synthesis, Academic Press, New York, Vol. 3, pages 138-161). In the present application, the term "PEG" is used broadly to encompass any polyethylene glycol molecule, in mono-, bi-, or poly-functional form, without regard to size or to modification at an end of the PEG, and can be represented by the formula:

$$X\text{-}O(CH_2CH_2O)_{n-1}CH_2CH_2OH, \qquad (I)$$

where n is 20 to 2300 and X is H or a terminal modification, e.g., a C_{1-4} alkyl.

[00289] In some useful embodiments, a PEG used in the invention terminates on one end with hydroxy or methoxy, i.e., X is H or CH_3 ("methoxy PEG"). It is noted that the other end of the PEG, which is shown in formula (I) terminating in OH, covalently attaches to an activating moiety via an ether oxygen bond, an amine linkage, or amide linkage. When used in a chemical structure, the term "PEG" includes the formula (I) above without the hydrogen of the hydroxyl group shown, leaving the oxygen available to react with a free carbon atom of a linker to form an ether bond. More specifically, in order to conjugate PEG to a peptide, the peptide must be reacted with PEG in an "activated" form. Activated PEG can be represented by the formula:

$$(PEG)\text{-}(A) \qquad (II)$$

where PEG (defined supra) covalently attaches to a carbon atom of the activation moiety (A) to form an ether bond, an amine linkage, or amide linkage, and (A) contains a reactive group which can react with an amino, azido, alkyne, imino, maleimido, N-succinimidyl, carboxyl, aminooxy, seleno, or thiol group on an amino acid residue of a peptide or a linker moiety covalently attached to the peptide, e.g., the toxin peptide analog.

[00290] Techniques for the preparation of activated PEG and its conjugation to biologically active peptides are well known in the art. (E.g., see U.S. Pat. Nos. 5,643,575, 5,919,455, 5,932,462, and 5,990,237; Kinstler et al., N-terminally chemically modified protein compositions and methods, US Patent Nos. 5,985,265, and 5,824,784; Thompson et al., PEGylation of polypeptides, EP 0575545 B1; Petit, Site specific protein modification, US Patent Nos. 6,451,986, and 6,548,644; S. Herman et al., Poly(ethylene glycol) with reactive endgroups: I. Modification of proteins, J. Bioactive Compatible Polymers, 10:145-187 (1995); Y. Lu et al., PEGylated peptides III: Solid-phase synthesis with PEGylating reagents of varying molecular weight: synthesis of multiply PEGylated peptides, Reactive Polymers, 22:221-229 (1994); A.M. Felix et al., PEGylated Peptides IV: Enhanced biological activity of site-directed PEGylated GRF analogs, Int. J. Peptide Protein Res., 46:253-264 (1995); A.M. Felix, Site-specific poly(ethylene glycol)ylation of peptides, ACS Symposium Series 680(poly(ethylene glycol)): 218-238 (1997); Y. Ikeda et al., Polyethylene glycol derivatives, their modified peptides, methods for producing them and use of the modified peptides, EP 0473084 B1; G.E. Means et al., Selected techniques for the modification of protein side chains, in: Chemical modification of proteins, Holden Day, Inc., 219 (1971)).

[00291] Activated PEG, such as PEG-aldehydes or PEG-aldehyde hydrates, can be chemically synthesized by known means or obtained from commercial sources, e.g., Shearwater Polymers, (Huntsville, Al) or Enzon, Inc. (Piscataway, N.J.).

[00292] An example of a useful activated PEG for purposes of the present invention is a PEG-aldehyde compound (e.g., a methoxy PEG-aldehyde), such as PEG-propionaldehyde, which is commercially available from Shearwater Polymers

(Huntsville, Al). PEG-propionaldehyde is represented by the formula PEG-CH_2CH_2CHO. (See, e.g., U.S. Pat. No. 5,252,714). Also included within the meaning of "PEG aldehyde compound" are PEG aldehyde hydrates, e.g., PEG acetaldehyde hydrate and PEG bis aldehyde hydrate, which latter yields a bifunctionally activated structure. (See., e.g., Bentley et al., Poly(ethylene glycol) aldehyde hydrates and related polymers and applications in modifying amines, US Patent No. 5,990,237) (See., e.g., Bentley et al., Poly(ethylene glycol) aldehyde hydrates and related polymers and applications in modifying amines, US Patent No. 5,990,237). An activated multi-branched PEG-aldehyde compound can be used (PEG derivatives comprising multiple arms to give divalent, trivalent, tetravalent, octavalent constructs). Using a 4-arm PEG derivative four (4) toxin peptide analogs are attached to each PEG molecule. For example, in accordance with the present invention, the toxin peptide analog can be conjugated to a polyethylene glycol (PEG) at 1, 2, 3 or 4 amino functionalized sites of the PEG.

[00293] In being conjugated in accordance with the inventive method, the polyethylene glycol (PEG), as described herein, is covalently bound by reductive amination directly to at least one solvent-exposed free amine moiety of an amino acid residue of the toxin peptide analog itself. In some embodiments of the inventive method, the toxin peptide analog is conjugated to a PEG at one or more primary or secondary amines on the toxin peptide analog, or to two PEG groups at a single primary amine site on the toxin peptide analog (e.g., this can occur when the reductive amination reaction involves the presence of excess PEG-aldehyde compound). We have observed that when PEGylation by reductive amination is at a primary amine on the peptide, it is not uncommon to have amounts (1 to 100% range) of reaction product that have two or more PEGs present per molecule, and if the desired PEGylation product is one with only one PEG per molecule, then this "over-PEGylation" may be undesirable. When PEGylated product with a single PEG per PEGylation product molecule is desired, an embodiment of the inventive method can be employed that involves PEGylation using secondary amines of the pharmacologically active peptide, because only one PEG group per molecule will be transferred in the reductive amination reaction.

[00294] Amino acid residues that can provide a primary amine moiety include residues of lysine, homolysine, ornithine, α, β-diaminopropionic acid (Dap), α, β-diaminopropionoic acid (Dpr), and α, γ-diaminobutyric acid (Dab), aminobutyric acid (Abu), and α-amino-isobutyric acid (Aib). The polypeptide N-terminus also provides a useful α-amino group for PEGylation. Amino acid residues that can provide a secondary amine moiety include ε-N-alkyl lysine, α-N-alkyl lysine, δ-N-alkyl ornithine, α-N-alkyl ornithine, or an N-terminal proline, where the alkyl is C_1 to C_6.

[00295] Another useful activated PEG for generating the PEGylated toxin peptide analogs of the present invention is a PEG-maleimide compound, such as, but not limited to, a methoxy PEG-maleimide, such as maleimido monomethoxy PEG, are particularly useful for generating the PEG-conjugated peptides of the invention. (E.g., Shen, *N*-maleimidyl polymer derivatives, US Patent No. 6,602,498; C. Delgado et al., The uses and properties of PEG-linked proteins., Crit. Rev. Therap. Drug Carrier Systems, 9:249-304 (1992); S. Zalipsky et al., Use of functionalized poly(ethylene glycol)s for modification of polypeptides, in: Poly(ethylene glycol) chemistry: Biotechnical and biomedical applications (J.M. Harris, Editor, Plenum Press: New York, 347-370 (1992); S. Herman et al., Poly(ethylene glycol) with reactive endgroups: I. Modification of proteins, J. Bioactive Compatible Polymers, 10:145-187 (1995); P.J. Shadle et al., Conjugation of polymer to colony stimulating factor-1, U.S. Patent No. 4,847,325; G. Shaw et al., Cysteine added variants IL-3 and chemical modifications thereof, U.S. Patent No. 5,166,322 and EP 0469074 B1; G. Shaw et al., Cysteine added variants of EPO and chemical modifications thereof, EP 0668353 A1; G. Shaw et al., Cysteine added variants G-CSF and chemical modifications thereof, EP 0668354 A1; N.V. Katre et al., Interleukin-2 muteins and polymer conjugation thereof, U.S. Patent No. 5,206,344; R.J. Goodson and N.V. Katre, Site-directed pegylation of recombinant interleukin-2 at its glycosylation site, Biotechnology, 8:343-346 (1990)).

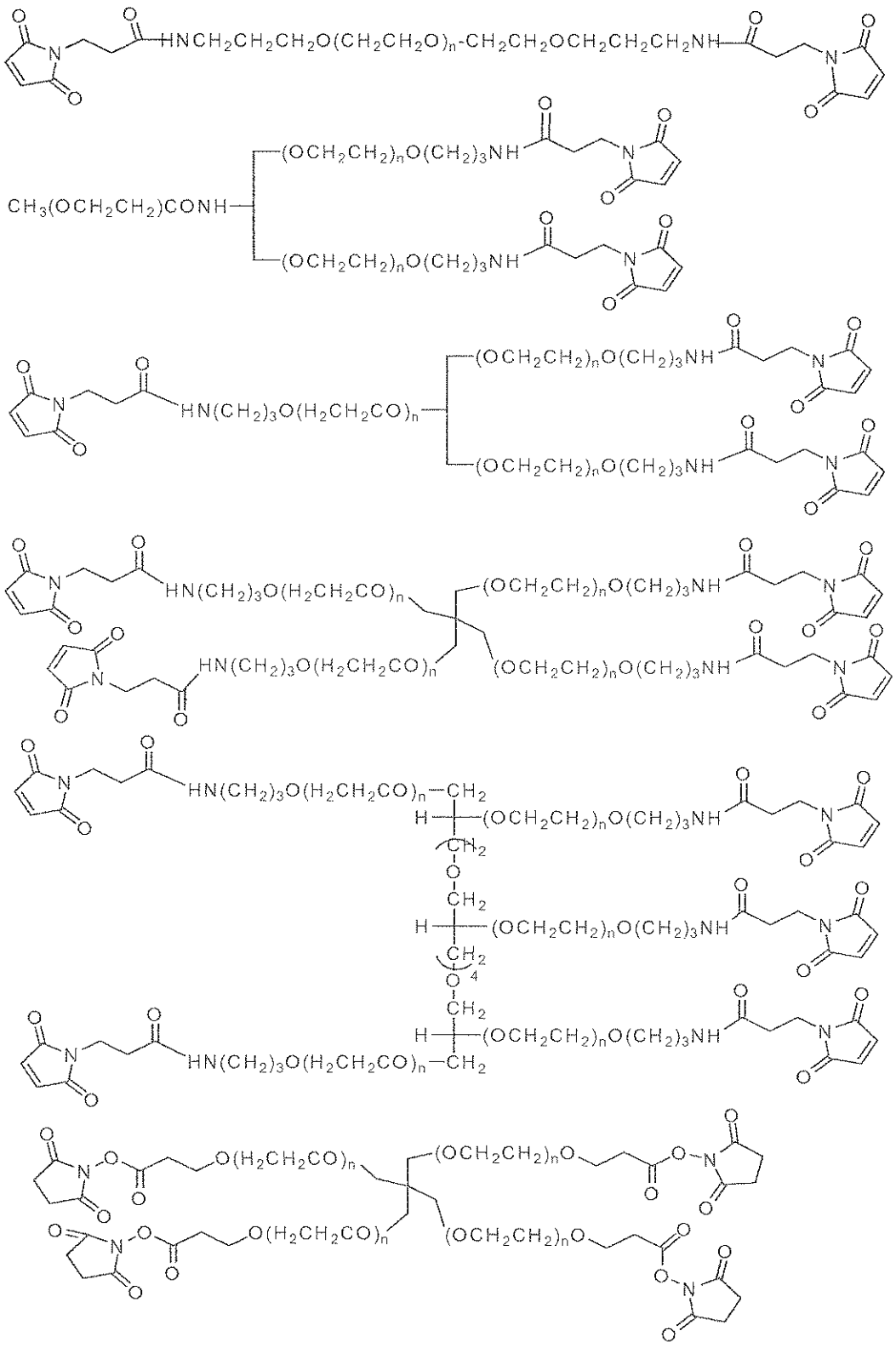
[00296] A poly(ethylene glycol) vinyl sulfone is another useful activated PEG for generating the PEG-conjugated toxin peptide analogs of the present invention by conjugation at thiolated amino acid residues, e.g., at C residues. (E.g., M. Morpurgo et al., Preparation and characterization of poly(ethylene glycol) vinyl sulfone, Bioconj. Chem., 7:363-368 (1996); see also Harris, Functionalization of polyethylene glycol for

formation of active sulfone-terminated PEG derivatives for binding to proteins and biologically compatible materials, U.S. Patent Nos. 5,446,090; 5,739,208; 5,900,461; 6,610,281 and 6,894,025; and Harris, Water soluble active sulfones of poly(ethylene glycol), WO 95/13312 A1). Another activated form of PEG that is useful in accordance with the present invention, is a PEG-N-hydroxysuccinimide ester compound, for example, methoxy PEG-N-hydroxysuccinimidyl (NHS) ester.

[00297] Heterobifunctionally activated forms of PEG are also useful. (See, e.g., Thompson et al., PEGylation reagents and biologically active compounds formed therewith, U.S. Patent No. 6,552,170).

[00298] In still other embodiments of the inventive method of producing a composition of matter, the toxin peptide analog is reacted by known chemical techniques with an activated PEG compound, such as but not limited to, a thiol-activated PEG compound, a diol-activated PEG compound, a PEG-hydrazide compound, a PEG-oxyamine compound, or a PEG-bromoacetyl compound. (See, e.g., S. Herman, Poly(ethylene glycol) with Reactive Endgroups: I. Modification of Proteins, J. Bioactive and Compatible Polymers, 10:145-187 (1995); S. Zalipsky, Chemistry of Polyethylene Glycol Conjugates with Biologically Active Molecules, Advanced Drug Delivery Reviews, 16:157-182 (1995); R. Greenwald et al., Poly(ethylene glycol) conjugated drugs and prodrugs: a comprehensive review, Critical Reviews in Therapeutic Drug Carrier Systems, 17:101-161 (2000)).

[00299] An even more preferred activated PEG for generating the PEG-conjugated toxin peptide analogs of the present invention is a multivalent PEG having more than one activated residues. Preferred multivalent PEG moieties include, but are not limited to, those shown below:



[00300] In still other embodiments of making the composition of matter, the inventive toxin peptide analog is reacted by known chemical techniques with an activated multi-

branched PEG compound (PEG derivatives comprising multiple arms to give divalent, trivalent, tetravalent, octavalent constructs), such as but not limited to, pentaerythritol tetra-polyethyleneglycol ether. Functionalization and activated derivatives , such as, but not limited to, N-succinimidyloxycarbonyl)propyl, p-nitrophenyloxycarbonyl, (—CO_2-p-$C_6H_4NO_2$), 3-(N-maleimido)propanamido, 2-sulfanylethyl, and 3-aminopropyl. Using a 4-arm PEG derivative, four toxin peptide analogs are attached to each PEG molecule. For example, in accordance with the present invention, the toxin peptide analog can be conjugated to a polyethylene glycol (PEG) at:

(a) 1, 2, 3 or 4 amino functionalized sites of the PEG;
(b) 1, 2, 3 or 4 thiol functionalized sites of the PEG;
(c) 1, 2, 3 or 4 maleimido functionalized sites of the PEG;
(d) 1, 2, 3 or 4 N-succinimidyl functionalized sites of the PEG;
(e) 1, 2, 3 or 4 carboxyl functionalized sites of the PEG; or
(f) 1, 2, 3 or 4 *p*-nitrophenyloxycarbonyl functionalized sites of the PEG.

[00301] The smallest practical size of PEG is about 500 Daltons (Da), below which PEG becomes toxic. Above about 500 Da, any molecular mass for a PEG can be used as practically desired, e.g., from about 1,000 Daltons (Da) to 100,000 Da (n is 20 to 2300). The number of PEG monomers (n) is approximated from the average molecular mass using a MW = 44 Da for each monomer. It is preferred that the combined molecular mass of PEG on an activated linker is suitable for pharmaceutical use. Thus, the combined molecular mass of the PEG molecule should not exceed about 100,000 Da. In some embodiments, the combined or total average molecular mass of PEG used in a PEG-conjugated toxin peptide analog of the present invention is from about 3,000 Da to 60,000 Da (total n is from 70 to 1,400), more preferably from about 10,000 Da to 40,000 Da (total n is about 230 to about 910). The most preferred combined mass for PEG is from about 20,000 Da to 30,000 Da (total n is about 450 to about 680).

[00302] It will be appreciated that "multimers" of the composition of matter can be made, since the half-life extending moiety employed for conjugation to the toxin peptide analog (with or without an intervening linker moiety) can be multivalent (e.g., bivalent, trivalent, tetravalent or a higher order valency) as to the number of amino acid

residues at which the half-life extending moiety can be conjugated. In some embodiments the peptide portion of the inventive composition of matter can be multivalent (e.g., bivalent, trivalent, tetravalent or a higher order valency), and, thus, some "multimers" of the inventive composition of matter may have more that one half life extending moiety. Consequently, it is possible by the inventive method of producing a composition of matter to produce a variety of conjugated half-life extending moiety peptide structures. By way of example, a univalent half-life extending moiety and a univalent peptide will produce a 1:1 conjugate; a bivalent peptide and a univalent half-life extending moiety may form conjugates wherein the peptide conjugates bear two half-life extending moiety moieties, whereas a bivalent half-life extending moiety and a univalent peptide may produce species where two peptide entities are linked to a single half-life extending moiety; use of higher-valence half-life extending moiety can lead to the formation of clusters of peptide entities bound to a single half-life extending moiety, whereas higher-valence peptides may become encrusted with a plurality of half-life extending moiety moieties. By way of further example, if the site of conjugation of a multivalent half-life extending moiety to the toxin peptide analog is a cysteine or other aminothiol the methods disclosed by D'Amico et al. may be employed (D'Amico et al., Method of conjugating aminothiol containing molecules to vehicles, published as US 2006/0199812, which application is incorporated herein by reference in its entirety).

[00303] The peptide moieties may have more than one reactive group which will react with the activated half-life extending moiety and the possibility of forming complex structures must always be considered; when it is desired to form simple structures such as 1:1 adducts of half-life extending moiety and peptide, or to use bivalent half-life extending moiety to form peptide:half-life extending moiety:peptide adducts, it will be beneficial to use predetermined ratios of activated half-life extending moiety and peptide material, predetermined concentrations thereof and to conduct the reaction under predetermined conditions (such as duration, temperature, pH, etc.) so as to form a proportion of the described product and then to separate the described product from the other reaction products. The reaction conditions, proportions and concentrations of the reagents can be obtained by relatively simple trial-and-error experiments which are

within the ability of an ordinarily skilled artisan with appropriate scaling-up as necessary. Purification and separation of the products is similarly achieved by conventional techniques well known to those skilled in the art.

[00304] Additionally, physiologically acceptable salts of the half-life extending moiety-fused or conjugated to the toxin peptide analogs of this invention are also encompassed within the composition of matter of the present invention.

[00305] The above-described half-life extending moieties and other half-life extending moieties described herein are useful, either individually or in combination, and as further described in the art, for example, in Sullivan et al., Toxin Peptide Therapeutic Agents, US2007/0071764 and Sullivan et al., Toxin Peptide Therapeutic Agents, PCT/US2007/022831, published as WO 2008/088422, which are both incorporated herein by reference in their entireties. The invention encompasses the use of any single species of pharmaceutically acceptable half-life extending moiety, such as, but not limited to, those described herein, in conjugation with the toxin peptide analog, or the use of a combination of two or more like or different half-life extending moieties.

[00306] Linkers. A "linker moiety" as used herein refers to a biologically acceptable peptidyl or non-peptidyl organic group that is covalently bound to an amino acid residue of a toxin peptide analog or other polypeptide chain (e.g., an immunoglobulin HC or LC or immunoglobulin Fc domain) contained in the inventive composition, which linker moiety covalently joins or conjugates the toxin peptide analog or other polypeptide chain to another peptide or polypeptide chain in the composition, or to a half-life extending moiety. In some embodiments of the composition, a half-life extending moiety, as described herein, is conjugated, i.e., covalently bound directly to an amino acid residue of the toxin peptide analog itself, or optionally, to a peptidyl or non-peptidyl linker moiety (including but not limited to aromatic or aryl linkers) that is covalently bound to an amino acid residue of the toxin peptide analog. The presence of any linker moiety is optional. When present, its chemical structure is not critical, since it serves primarily as a spacer to position, join, connect, or optimize presentation or position of one functional moiety in relation to one or more other functional moieties of a molecule of the inventive composition. The presence of a linker moiety can be useful

in optimizing pharamcologial activity of some embodiments of the inventive composition. The linker is preferably made up of amino acids linked together by peptide bonds. The linker moiety, if present, can be independently the same or different from any other linker, or linkers, that may be present in the inventive composition. As stated above, the linker moiety, if present (whether within the primary amino acid sequence of the toxin peptide analog, or as a linker for attaching a half-life extending moiety to the toxin peptide analog), can be "peptidyl" in nature (i.e., made up of amino acids linked together by peptide bonds) and made up in length, preferably, of from 1 up to about 40 amino acid residues, more preferably, of from 1 up to about 20 amino acid residues, and most preferably of from 1 to about 10 amino acid residues. Preferably, but not necessarily, the amino acid residues in the linker are from among the twenty canonical amino acids, more preferably, cysteine, glycine, alanine, proline, asparagine, glutamine, and /or serine. Even more preferably, a peptidyl linker is made up of a majority of amino acids that are sterically unhindered, such as glycine, serine, and alanine linked by a peptide bond. It is also desirable that, if present, a peptidyl linker be selected that avoids rapid proteolytic turnover in circulation *in vivo*. Some of these amino acids may be glycosylated, as is well understood by those in the art. For example, a useful linker sequence constituting a sialylation site is $X_1X_2NX_4X_5G$ (SEQ ID NO:479), wherein X_1, X_2,X_4 and X_5 are each independently any amino acid residue.

[00307] In other embodiments, the 1 to 40 amino acids of the peptidyl linker moiety are selected from glycine, alanine, proline, asparagine, glutamine, and lysine. Preferably, a linker is made up of a majority of amino acids that are sterically unhindered, such as glycine and alanine. Thus, preferred linkers include polyglycines, polyserines, and polyalanines, or combinations of any of these. Some exemplary peptidyl linkers are poly$(Gly)_{1-8}$, particularly $(Gly)_3$, $(Gly)_4$ (SEQ ID NO:480), $(Gly)_5$ (SEQ ID NO:481) and $(Gly)_7$ (SEQ ID NO:482), as well as, GlySer and poly$(Gly)_4$Ser, such as "L15" (GGGGSGGGGSGGGGS; SEQ ID NO:483), poly$(Gly\text{-}Ala)_{2-4}$ and poly$(Ala)_{1-8}$. Other specific examples of peptidyl linkers include $(Gly)_5$Lys (SEQ ID NO:484), and $(Gly)_5$LysArg (SEQ ID NO:485). Other examples of useful peptidyl linkers are: Other examples of useful peptidyl linkers are:

$(Gly)_3Lys(Gly)_4$ (SEQ ID NO:486);

$(Gly)_3AsnGlySer(Gly)_2$ (SEQ ID NO:487);
$(Gly)_3Cys(Gly)_4$ (SEQ ID NO:488); and
GlyProAsnGlyGly (SEQ ID NO:489).

To explain the above nomenclature, for example, $(Gly)_3Lys(Gly)_4$ means Gly-Gly-Gly-Lys-Gly-Gly-Gly-Gly (SEQ ID NO:490). Other combinations of Gly and Ala are also useful.

[00308] Other preferred linkers are those identified herein as "L5" (GGGGS; or "G_4S"; SEQ ID NO:491), "L10" (GGGGSGGGGS; SEQ ID NO:492); "L20" (GGGGSGGGGSGGGGSGGGGS; SEQ ID NO:477) ; "L25" (GGGGSGGGGSGGGGSGGGGSGGGGS; SEQ ID NO:493) and any linkers used in the working examples hereinafter.

[00309] In some embodiments of the compositions of this invention, which comprise a peptide linker moiety, acidic residues, for example, glutamate or aspartate residues, are placed in the amino acid sequence of the linker moiety. Examples include the following peptide linker sequences:

GGEGGG (SEQ ID NO:494);
GGEEEGGG (SEQ ID NO:495);
GEEEG (SEQ ID NO:496);
GEEE (SEQ ID NO:497);
GGDGGG (SEQ ID NO:498);
GGDDDGG (SEQ ID NO:499);
GDDDG (SEQ ID NO:500);
GDDD (SEQ ID NO:501);
GGGGSDDSDEGSDGEDGGGGS (SEQ ID NO:502);
WEWEW (SEQ ID NO:503);
FEFEF (SEQ ID NO:504);
EEEWWW (SEQ ID NO:505);
EEEFFF (SEQ ID NO:506);
WWEEEWW (SEQ ID NO:507); or

FFEEEFF (SEQ ID NO:508).

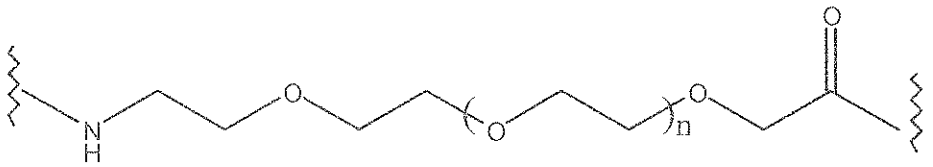
[00310] In other embodiments, the linker constitutes a phosphorylation site, e.g., $X_1X_2YX_4X_5G$ (SEQ ID NO:509), wherein X_1, X_2, X_4, and X_5 are each independently any amino acid residue; $X_1X_2SX_4X_5G$ (SEQ ID NO:510), wherein X_1, X_2,X_4 and X_5 are each independently any amino acid residue; or $X_1X_2TX_4X_5G$ (SEQ ID NO:511), wherein X_1, X_2, X_4 and X_5 are each independently any amino acid residue.

[00311] The linkers shown here are exemplary; peptidyl linkers within the scope of this invention may be much longer and may include other residues. A peptidyl linker can contain, e.g., a cysteine, another thiol, or nucleophile for conjugation with a half-life extending moiety. In another embodiment, the linker contains a cysteine or homocysteine residue, or other 2-amino-ethanethiol or 3-amino-propanethiol moiety for conjugation to maleimide, iodoacetaamide or thioester, functionalized half-life extending moiety.

[00312] Another useful peptidyl linker is a large, flexible linker comprising a random Gly/Ser/Thr sequence, for example: GSGSATGGSGSTASSGSGSATH (SEQ ID NO:512) or HGSGSATGGSGSTASSGSGSAT (SEQ ID NO:513), that is estimated to be about the size of a 1 kDa PEG molecule. Alternatively, a useful peptidyl linker may be comprised of amino acid sequences known in the art to form rigid helical structures (e.g., Rigid linker: -AEAAAKEAAAKEAAAKAGG-// SEQ ID NO:514). Additionally, a peptidyl linker can also comprise a non-peptidyl segment such as a 6 carbon aliphatic molecule of the formula $-CH_2-CH_2-CH_2-CH_2-CH_2-CH_2-$. The peptidyl linkers can be altered to form derivatives as described herein.

[00313] Optionally, a non-peptidyl linker moiety is also useful for conjugating the half-life extending moiety to the peptide portion of the half-life extending moiety-conjugated toxin peptide analog. For example, alkyl linkers such as $-NH-(CH_2)_s-C(O)-$, wherein s = 2-20 can be used. These alkyl linkers may further be substituted by any non-sterically hindering group such as lower alkyl (e.g., C_1-C_6) lower acyl, halogen (e.g., Cl, Br), CN, NH_2, phenyl, *etc*. Exemplary non-peptidyl linkers are PEG linkers (e.g., shown below):

(III)



wherein n is such that the linker has a molecular weight of about 100 to about 5000 Daltons (Da), preferably about 100 to about 500 Da.

[00314] In one embodiment, the non-peptidyl linker is aryl. The linkers may be altered to form derivatives in the same manner as described herein. In addition, PEG moieties may be attached to the N-terminal amine or selected side chain amines by either reductive alkylation using PEG aldehydes or acylation using hydroxysuccinimido or carbonate esters of PEG, or by thiol conjugation.

[00315] "Aryl" is phenyl or phenyl vicinally-fused with a saturated, partially-saturated, or unsaturated 3-, 4-, or 5 membered carbon bridge, the phenyl or bridge being substituted by 0, 1, 2 or 3 substituents selected from C_{1-8} alkyl, C_{1-4} haloalkyl or halo. "Heteroaryl" is an unsaturated 5 , 6 or 7 membered monocyclic or partially-saturated or unsaturated 6-, 7-, 8-, 9-, 10- or 11 membered bicyclic ring, wherein at least one ring is unsaturated, the monocyclic and the bicyclic rings containing 1, 2, 3 or 4 atoms selected from N, O and S, wherein the ring is substituted by 0, 1, 2 or 3 substituents selected from C_{1-8} alkyl, C_{1-4} haloalkyl and halo.

[00316] Non-peptide portions of the inventive composition of matter, such as non-peptidyl linkers or non-peptide half-life extending moieties can be synthesized by conventional organic chemistry reactions.

[00317] The above is merely illustrative and not an exhaustive treatment of the kinds of linkers that can optionally be employed in accordance with the present invention.

[00318] Compositions of this invention incorporating the isolated polypeptide antagonists of the voltage-gated sodium channel $Na_V1.3$ and/or $Na_V1.7$, in particular GpTx-1 and GpTx-1 toxin peptide analogs of the present invention, whether or not conjugated to a half-life extending moiety, are useful as therapeutic agents in the treatment of pain, for example in humans. Clinical genetic information, replicated independently by several groups, shows unambiguously that the product of the Nav1.7 (*SCN9A*) gene is a key control point for the perception of pain. In humans, loss-of-function truncation mutations of the gene lead to complete insensitivity to all forms of pain measured, whereas the human chronic pain syndromes primary erythromelalgia and paroxysmal extreme pain disorder are caused by gain-of-function mutations in $Na_V1.7$ that lead to easier or more prolonged Nav1.7 channel opening. Remarkably, no other major neurological abnormalities are present in patients carrying either truncation or gain-of-function mutations in $Na_V1.7$ (Goldberg et al., Clin Genet 71:311-319 (2007); Cox et al., Nature 444:894-898 (2006); Ahmad et al., Hum Mol Genet 16:2114-2121 (2007); Fertleman et al., Neurology 69:586-595 (2007)). Accordingly, a therapeutic that blocks $Na_V1.7$ can be expected to be of great utility for the treatment of pain in humans.

[00319] Specific clinical chronic pain syndromes include, but are not limited to, pain associated with, or due to, cancer, chemotherapy, osteoarthritis, fibromyalgia, primary erythromelalgia, post-herpetic neuralgia, painful diabetic neuropathy, idiopathic painful neuropathy, neuromas, paroxysmal extreme pain disorder, migraine, trigeminal neuralgia, orofacial pain, cluster or other headaches, complex regional pain syndrome (CRPS), failed back surgery syndrome, sciatica (including lower back pain), interstitial cystitis and pelvic pain, inflammation-induced pain including cellulitis, and rheumatic or joint pain. A $Na_V1.7$ inhibitor can also have great utility for treatment of acute or persistent pain, including but not limited to pain following trauma, burns, or surgery. Notably, inhibition of $Na_V1.7$ is not expected to result in the adverse effects on cognition and on the gastrointestinal system that limit the use of opioid drugs. Again unlike opioids, $Na_V1.7$ inhibitors should not produce respiratory depression, patient tolerance, or addiction. Moreover, $Na_V1.7$ expression in humans and in non-human primates is overwhelmingly in the peripheral nervous system, with little or no message

or protein in the brain or spinal cord (Ahmad et al., Hum Mol Genet 16:2114-2121, 2007). Consistent with these studies, our data show that among CNS areas from post-mortem humans examined with in situ hybridization, message RNA for $Na_V1.7$ was found only in light amounts in hypothalamic nuclei and in ventral motor areas of the spinal cord and spinal ependyma, areas with no known involvement in the pain response. By contrast, no $Na_V1.7$ was found in cerebral cortex, cerebellum, adrenal medulla, pituitary, or dorsal or deep regions of lumbar spinal cord. Strong $Na_V1.7$ expression was found in peripheral nerves including dorsal root ganglia, trigeminal ganglia, and myenteric plexes of the stomach and intestine. (See, Figure 13A-E). This suggests that an inhibitor of $Na_V1.7$ would exert analgesic efficacy via the peripheral nervous system without a need for CNS penetrance. As peptides generally do not cross the blood-brain barrier, a peptide inhibitor thus has an advantage over small molecules with some CNS-penetrance in that a peptide should not produce common off-target side effects mediated by the brain such as dizziness, confusion, or sedation.

[00320] The clinical genetic data for $Na_V1.7$ do not address whether $Na_V1.7$ maintains its key role in pain perception in patients with damage to and subsequent remodeling of the nervous system. Such remodeling is likely a feature of many chronic pain syndromes (Woolf and Ma, Neuron 55:353-364 (2007)). For such cases, antagonism of the $Na_V1.3$ sodium channel may prove of great therapeutic benefit. Published results show up-regulation of mRNA encoding $Na_V1.3$ in sensory neurons of rats subjected to spinal nerve ligation surgery, a standard model for neuropathic pain in humans (Hains et al., J Neurosci 24:4832-4839, 2004). This implies that for some chronic pain syndromes, especially neuropathic pain, inhibition of $Na_V1.3$ in addition to $Na_V1.7$ may produce the best analgesic efficacy. Electrophysiological studies of the cell bodies of rat sensory neurons show that spinal nerve ligation causes a dramatic shift in sodium channel expression to the fast, tetrodotoxin-sensitive subtype most likely encoded by *SCN9A* ($Na_V1.7$) and *SCN3A* ($Na_V1.3$) (see, Figure 14A-E). Again this implies that for some pain syndromes, simultaneous dual inhibition of Nav1.7 and Nav1.3 can produce the most effective suppression of pain.

[00321] Accordingly, the present invention also relates to the use of one or more of the inventive compositions of matter in the manufacture of a medicament for the

treatment or prevention of a disease, disorder, or other medical condition described herein, for example, but not limited to, chronic pain, acute pain, or persistent pain, or any of the pain syndromes described herein.

[00322] Such pharmaceutical compositions can be configured for administration to a patient by a wide variety of delivery routes, e.g., an intravascular delivery route such as by injection or infusion, subcutaneous ("s.c."), intravenous ("i.v."), intramuscular, intraperitoneal ("i.p."), epidural, or intrathecal delivery routes, or for oral, enteral, pulmonary (e.g., inhalant), intranasal, transmucosal (e.g., sublingual administration), transdermal or other delivery routes and/or forms of administration known in the art. Delivery of a drug or pharmaceutical composition containing GpTx-1, or other compositions of matter of the invention, may take place via standard injectable modalities, whether self-administered or in hospital setting, or also via an implantable delivery pump to achieve the most accurate dosing and the most stable plasma exposure levels. The inventive pharmaceutical compositions may be prepared in liquid form, or may be in dried powder form, such as lyophilized form, or crystalline form. For oral or enteral use, the pharmaceutical compositions can be configured, for example, as tablets, troches, lozenges, aqueous or oily suspensions, dispersible powders or granules, emulsions, hard or soft capsules, syrups, elixirs or enteral formulas.

[00323] Pharmaceutical Compositions

[00324] In General. The present invention also provides pharmaceutical compositions comprising the inventive composition of matter and a pharmaceutically acceptable carrier. Such pharmaceutical compositions can be configured for administration to a patient by a wide variety of delivery routes, e.g., an intravascular delivery route such as by injection or infusion, subcutaneous, intramuscular, intraperitoneal, epidural, or intrathecal delivery routes, or for oral, enteral, pulmonary (e.g., inhalant), intranasal, transmucosal (e.g., sublingual administration), transdermal or other delivery routes and/or forms of administration known in the art. The inventive pharmaceutical compositions may be prepared in liquid form, or may be in dried powder form, such as lyophilized form. For oral or enteral use, the pharmaceutical compositions can be configured, for example, as tablets, troches, lozenges, aqueous or oily suspensions,

dispersible powders or granules, emulsions, hard or soft capsules, syrups, elixirs or enteral formulas.

[00325] In the practice of this invention the "pharmaceutically acceptable carrier" is any physiologically tolerated substance known to those of ordinary skill in the art useful in formulating pharmaceutical compositions, including, any pharmaceutically acceptable diluents, excipients, dispersants, binders, fillers, glidants, anti-frictional agents, compression aids, tablet-disintegrating agents (disintegrants), suspending agents, lubricants, flavorants, odorants, sweeteners, permeation or penetration enhancers, preservatives, surfactants, solubilizers, emulsifiers, thickeners, adjuvants, dyes, coatings, encapsulating material(s), and/or other additives singly or in combination. Such pharmaceutical compositions can include diluents of various buffer content (*e.g.*, Tris-HCl, acetate, phosphate), pH and ionic strength; additives such as detergents and solubilizing agents (*e.g.*, Tween® 80, Polysorbate 80), anti-oxidants (*e.g.*, ascorbic acid, sodium metabisulfite), preservatives (*e.g.*, Thimersol®, benzyl alcohol) and bulking substances (*e.g.*, lactose, mannitol); incorporation of the material into particulate preparations of polymeric compounds such as polylactic acid, polyglycolic acid, etc. or into liposomes. Hyaluronic acid can also be used, and this can have the effect of promoting sustained duration in the circulation. Such compositions can influence the physical state, stability, rate of in vivo release, and rate of in vivo clearance of the present proteins and derivatives. See, e.g., Remington's Pharmaceutical Sciences, 18th Ed. (1990, Mack Publishing Co., Easton, PA 18042) pages 1435-1712, which are herein incorporated by reference in their entirety. The compositions can be prepared in liquid form, or can be in dried powder, such as lyophilized form. Implantable sustained release formulations are also useful, as are transdermal or transmucosal formulations. Additionally (or alternatively), the present invention provides compositions for use in any of the various slow or sustained release formulations or microparticle formulations known to the skilled artisan, for example, sustained release microparticle formulations, which can be administered via pulmonary, intranasal, or subcutaneous delivery routes. (See, e.g., Murthy et al., Injectable compositions for the controlled delivery of pharmacologically active compound, U.S. Patent No.6,887,487; Manning et al., Solubilization of pharmaceutical substances in an

organic solvent and preparation of pharmaceutical powders using the same, U.S. Patent Nos. 5,770,559 and 5,981,474; Lieberman et al., Lipophilic complexes of pharmacologically active inorganic mineral acid esters of organic compounds, U.S. Patent No. 5,002,936; Gen, Formative agent of protein complex, US 2002/0119946 A1; Goldenberg et al., Sustained release formulations, WO 2005/105057 A1).

[00326] One can dilute the inventive compositions or increase the volume of the pharmaceutical compositions of the invention with an inert material. Such diluents can include carbohydrates, especially, mannitol, α-lactose, anhydrous lactose, cellulose, sucrose, modified dextrans and starch. Certain inorganic salts may also be used as fillers, including calcium triphosphate, magnesium carbonate and sodium chloride. Some commercially available diluents are Fast-Flo, Emdex, STA-Rx 1500, Emcompress and Avicell.

[00327] A variety of conventional thickeners are useful in creams, ointments, suppository and gel configurations of the pharmaceutical composition, such as, but not limited to, alginate, xanthan gum, or petrolatum, may also be employed in such configurations of the pharmaceutical composition of the present invention. A permeation or penetration enhancer, such as polyethylene glycol monolaurate, dimethyl sulfoxide, N-vinyl-2-pyrrolidone, N-(2-hydroxyethyl)-pyrrolidone, or 3-hydroxy-N-methyl-2-pyrrolidone can also be employed. Useful techniques for producing hydrogel matrices are known. (E.g., Feijen, Biodegradable hydrogel matrices for the controlled release of pharmacologically active agents, U.S. Patent No. 4,925,677; Shah et al., Biodegradable pH/thermosensitive hydrogels for sustained delivery of biologically active agents, WO 00/38651 A1). Such biodegradable gel matrices can be formed, for example, by crosslinking a proteinaceous component and a polysaccharide or mucopolysaccharide component, then loading with the inventive composition of matter to be delivered.

[00328] Liquid pharmaceutical compositions of the present invention that are sterile solutions or suspensions can be administered to a patient by injection, for example, intramuscularly, intrathecally, epidurally, intravascularly (e.g., intravenously or intraarterially), intraperitoneally or subcutaneously. (See, e.g., Goldenberg et al.,

Suspensions for the sustained release of proteins, U.S. Patent No. 6,245,740 and WO 00/38652 A1). Sterile solutions can also be administered by intravenous infusion. The inventive composition can be included in a sterile solid pharmaceutical composition, such as a lyophilized powder, which can be dissolved or suspended at a convenient time before administration to a patient using sterile water, saline, buffered saline or other appropriate sterile injectable medium.

[00329] Implantable sustained release formulations are also useful embodiments of the inventive pharmaceutical compositions. For example, the pharmaceutically acceptable carrier, being a biodegradable matrix implanted within the body or under the skin of a human or non-human vertebrate, can be a hydrogel similar to those described above. Alternatively, it may be formed from a poly-alpha-amino acid component. (Sidman, Biodegradable, implantable drug delivery device, and process for preparing and using same, U.S. Patent No. 4,351,337). Other techniques for making implants for delivery of drugs are also known and useful in accordance with the present invention.

[00330] In powder forms, the pharmaceutically acceptable carrier is a finely divided solid, which is in admixture with finely divided active ingredient(s), including the inventive composition. For example, in some embodiments, a powder form is useful when the pharmaceutical composition is configured as an inhalant. (See, e.g., Zeng et al., Method of preparing dry powder inhalation compositions, WO 2004/017918; Trunk et al., Salts of the CGRP antagonist BIBN4096 and inhalable powdered medicaments containing them, U.S. Patent No. 6,900,317).

[00331] One can dilute or increase the volume of the compound of the invention with an inert material. These diluents could include carbohydrates, especially mannitol, α-lactose, anhydrous lactose, cellulose, sucrose, modified dextrans and starch. Certain inorganic salts can also be used as fillers including calcium triphosphate, magnesium carbonate and sodium chloride. Some commercially available diluents are Fast-Flo™, Emdex™, STA-Rx™ 1500, Emcompress™ and Avicell™.

[00332] Disintegrants can be included in the formulation of the pharmaceutical composition into a solid dosage form. Materials used as disintegrants include but are not limited to starch including the commercial disintegrant based on starch, Explotab™.

Sodium starch glycolate, Amberlite™, sodium carboxymethylcellulose, ultramylopectin, sodium alginate, gelatin, orange peel, acid carboxymethyl cellulose, natural sponge and bentonite can all be used. Insoluble cationic exchange resin is another form of disintegrant. Powdered gums can be used as disintegrants and as binders and these can include powdered gums such as agar, Karaya or tragacanth. Alginic acid and its sodium salt are also useful as disintegrants.

[00333] Binders can be used to hold the therapeutic agent together to form a hard tablet and include materials from natural products such as acacia, tragacanth, starch and gelatin. Others include methyl cellulose (MC), ethyl cellulose (EC) and carboxymethyl cellulose (CMC). Polyvinyl pyrrolidone (PVP) and hydroxypropylmethyl cellulose (HPMC) could both be used in alcoholic solutions to granulate the therapeutic. An antifrictional agent can be included in the formulation of the therapeutic to prevent sticking during the formulation process. Lubricants can be used as a layer between the therapeutic and the die wall, and these can include but are not limited to; stearic acid including its magnesium and calcium salts, polytetrafluoroethylene (PTFE), liquid paraffin, vegetable oils and waxes. Soluble lubricants can also be used such as sodium lauryl sulfate, magnesium lauryl sulfate, polyethylene glycol of various molecular weights, Carbowax 4000 and 6000.

[00334] Glidants that might improve the flow properties of the drug during formulation and to aid rearrangement during compression might be added. The glidants can include starch, talc, pyrogenic silica and hydrated silicoaluminate.

[00335] To aid dissolution of the compound of this invention into the aqueous environment a surfactant might be added as a wetting agent. Surfactants can include anionic detergents such as sodium lauryl sulfate, dioctyl sodium sulfosuccinate and dioctyl sodium sulfonate. Cationic detergents might be used and could include benzalkonium chloride or benzethonium chloride. The list of potential nonionic detergents that could be included in the formulation as surfactants are lauromacrogol 400, polyoxyl 40 stearate, polyoxyethylene hydrogenated castor oil 10, 50 and 60, glycerol monostearate, polysorbate 40, 60, 65 and 80, sucrose fatty acid ester, methyl

cellulose and carboxymethyl cellulose. These surfactants could be present in the formulation of the protein or derivative either alone or as a mixture in different ratios.

[00336] Oral dosage forms. Also useful are oral dosage forms of the inventive compositionss. If necessary, the composition can be chemically modified so that oral delivery is efficacious. Generally, the chemical modification contemplated is the attachment of at least one moiety to the molecule itself, where said moiety permits (a) inhibition of proteolysis; and (b) uptake into the blood stream from the stomach or intestine. Also desired is the increase in overall stability of the compound and increase in circulation time in the body. Moieties useful as covalently attached half-life extending moieties in this invention can also be used for this purpose. Examples of such moieties include: PEG, copolymers of ethylene glycol and propylene glycol, carboxymethyl cellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone and polyproline. See, for example, Abuchowski and Davis (1981), Soluble Polymer-Enzyme Adducts, Enzymes as Drugs (Hocenberg and Roberts, eds.), Wiley-Interscience, New York, NY, pp 367-83; Newmark, et al. (1982), J. Appl. Biochem. 4:185-9. Other polymers that could be used are poly-1,3-dioxolane and poly-1,3,6-tioxocane. Preferred for pharmaceutical usage, as indicated above, are PEG moieties.

[00337] For oral delivery dosage forms, it is also possible to use a salt of a modified aliphatic amino acid, such as sodium N-(8-[2-hydroxybenzoyl] amino) caprylate (SNAC), as a carrier to enhance absorption of the therapeutic compounds of this invention. The clinical efficacy of a heparin formulation using SNAC has been demonstrated in a Phase II trial conducted by Emisphere Technologies. See US Patent No. 5,792,451, "Oral drug delivery composition and methods."

[00338] In one embodiment, the pharmaceutically acceptable carrier can be a liquid and the pharmaceutical composition is prepared in the form of a solution, suspension, emulsion, syrup, elixir or pressurized composition. The active ingredient(s) (e.g., the inventive composition of matter) can be dissolved, diluted or suspended in a pharmaceutically acceptable liquid carrier such as water, an organic solvent, a mixture of both, or pharmaceutically acceptable oils or fats. The liquid carrier can contain other suitable pharmaceutical additives such as detergents and/or solubilizers (e.g., Tween 80,

Polysorbate 80), emulsifiers, buffers at appropriate pH (e.g., Tris-HCl, acetate, phosphate), adjuvants, anti-oxidants (e.g., ascorbic acid, sodium metabisulfite), preservatives (e.g., Thimersol, benzyl alcohol), sweeteners, flavoring agents, suspending agents, thickening agents, bulking substances (e.g., lactose, mannitol), colors, viscosity regulators, stabilizers, electrolytes, osmolutes or osmo-regulators. Additives can also be included in the formulation to enhance uptake of the inventive composition. Additives potentially having this property are for instance the fatty acids oleic acid, linoleic acid and linolenic acid.

[00339] Useful are oral solid dosage forms, which are described generally in Remington's Pharmaceutical Sciences (1990), supra, in Chapter 89, which is hereby incorporated by reference in its entirety. Solid dosage forms include tablets, capsules, pills, troches or lozenges, cachets or pellets. Also, liposomal or proteinoid encapsulation can be used to formulate the present compositions (as, for example, proteinoid microspheres reported in U.S. Patent No. 4,925,673). Liposomal encapsulation can be used and the liposomes can be derivatized with various polymers (e.g., U.S. Patent No. 5,013,556). A description of possible solid dosage forms for the therapeutic is given in Marshall, K., Modern Pharmaceutics (1979), edited by G. S. Banker and C. T. Rhodes, in Chapter 10, which is hereby incorporated by reference in its entirety. In general, the formulation will include the inventive compound, and inert ingredients that allow for protection against the stomach environment, and release of the biologically active material in the intestine.

[00340] The composition of this invention can be included in the formulation as fine multiparticulates in the form of granules or pellets of particle size about 1 mm. The formulation of the material for capsule administration could also be as a powder, lightly compressed plugs or even as tablets. The therapeutic could be prepared by compression.

[00341] Colorants and flavoring agents can all be included. For example, the protein (or derivative) can be formulated (such as by liposome or microsphere encapsulation) and then further contained within an edible product, such as a refrigerated beverage containing colorants and flavoring agents.

[00342] In tablet form, the active ingredient(s) are mixed with a pharmaceutically acceptable carrier having the necessary compression properties in suitable proportions and compacted in the shape and size desired.

[00343] The powders and tablets preferably contain up to 99% of the active ingredient(s). Suitable solid carriers include, for example, calcium phosphate, magnesium stearate, talc, sugars, lactose, dextrin, starch, gelatin, cellulose, polyvinylpyrrolidine, low melting waxes and ion exchange resins.

[00344] Controlled release formulation can be desirable. The composition of this invention can be incorporated into an inert matrix that permits release by either diffusion or leaching mechanisms e.g., gums. Slowly degenerating matrices can also be incorporated into the formulation, e.g., alginates, polysaccharides. Another form of a controlled release of the compositions of this invention is by a method based on the Oros™ therapeutic system (Alza Corp.), i.e., the drug is enclosed in a semipermeable membrane which allows water to enter and push drug out through a single small opening due to osmotic effects. Some enteric coatings also have a delayed release effect.

[00345] Other coatings can be used for the formulation. These include a variety of sugars that could be applied in a coating pan. The therapeutic agent could also be given in a film-coated tablet and the materials used in this instance are divided into 2 groups. The first are the nonenteric materials and include methylcellulose, ethyl cellulose, hydroxyethyl cellulose, methylhydroxy-ethyl cellulose, hydroxypropyl cellulose, hydroxypropyl-methyl cellulose, sodium carboxymethyl cellulose, providone and the polyethylene glycols. The second group consists of the enteric materials that are commonly esters of phthalic acid.

[00346] A mix of materials might be used to provide the optimum film coating. Film coating can be carried out in a pan coater or in a fluidized bed or by compression coating.

[00347] Pulmonary delivery forms. Pulmonary delivery of the inventive compositions is also useful. The protein (or derivative) is delivered to the lungs of a

mammal while inhaling and traverses across the lung epithelial lining to the blood stream. (Other reports of this include Adjei et al., Pharma. Res. (1990) 7: 565-9; Adjei et al. (1990), Internatl. J. Pharmaceutics 63: 135-44 (leuprolide acetate); Braquet et al. (1989), J. Cardiovasc. Pharmacol. 13 (suppl.5): s.143-146 (endothelin-1); Hubbard et al. (1989), Annals Int. Med. 3: 206-12 (α1-antitrypsin); Smith et al. (1989), J. Clin. Invest. 84: 1145-6 (α1-proteinase); Oswein et al. (March 1990), "Aerosolization of Proteins," Proc. Symp. Resp. Drug Delivery II, Keystone, Colorado (recombinant human growth hormone); Debs et al. (1988), J. Immunol. 140: 3482-8 (interferon-γ and tumor necrosis factor α) and Platz et al., U.S. Patent No. 5,284,656 (granulocyte colony stimulating factor).

[00348] Useful in the practice of this invention are a wide range of mechanical devices designed for pulmonary delivery of therapeutic products, including but not limited to nebulizers, metered dose inhalers, and powder inhalers, all of which are familiar to those skilled in the art. Some specific examples of commercially available devices suitable for the practice of this invention are the Ultravent nebulizer, manufactured by Mallinckrodt, Inc., St. Louis, Missouri; the Acorn II nebulizer, manufactured by Marquest Medical Products, Englewood, Colorado; the Ventolin metered dose inhaler, manufactured by Glaxo Inc., Research Triangle Park, North Carolina; and the Spinhaler powder inhaler, manufactured by Fisons Corp., Bedford, Massachusetts. (See, e.g., Helgesson et al., Inhalation device, U.S. Patent No. 6,892,728; McDerment et al., Dry powder inhaler, WO 02/11801 A1; Ohki et al., Inhalant medicator, U.S. Patent No. 6,273,086). All such devices require the use of formulations suitable for the dispensing of the inventive compound. Typically, each formulation is specific to the type of device employed and can involve the use of an appropriate propellant material, in addition to diluents, adjuvants and/or carriers useful in therapy.

[00349] The inventive compound should most advantageously be prepared in particulate form with an average particle size of less than 10 μm (or microns), most preferably 0.5 to 5 μm, for most effective delivery to the distal lung.

[00350] Pharmaceutically acceptable excipients include carbohydrates such as trehalose, mannitol, xylitol, sucrose, lactose, and sorbitol. Other ingredients for use in formulations can include DPPC, DOPE, DSPC and DOPC. Natural or synthetic surfactants can be used. PEG can be used (even apart from its use in derivatizing the protein or analog). Dextrans, such as cyclodextran, can be used. Bile salts and other related enhancers can be used. Cellulose and cellulose derivatives can be used. Amino acids can be used, such as use in a buffer formulation.

[00351] Also, the use of liposomes, microcapsules or microspheres, inclusion complexes, or other types of carriers is contemplated.

[00352] Formulations suitable for use with a nebulizer, either jet or ultrasonic, will typically comprise the inventive compound dissolved in water at a concentration of about 0.1 to 25 mg of biologically active protein per mL of solution. The formulation can also include a buffer and a simple sugar (e.g., for protein stabilization and regulation of osmotic pressure). The nebulizer formulation can also contain a surfactant, to reduce or prevent surface induced aggregation of the protein caused by atomization of the solution in forming the aerosol.

[00353] Formulations for use with a metered-dose inhaler device will generally comprise a finely divided powder containing the inventive compound suspended in a propellant with the aid of a surfactant. The propellant can be any conventional material employed for this purpose, such as a chlorofluorocarbon, a hydrochlorofluorocarbon, a hydrofluorocarbon, or a hydrocarbon, including trichlorofluoromethane, dichlorodifluoromethane, dichlorotetrafluoroethanol, and 1,1,1,2-tetrafluoroethane, or combinations thereof. Suitable surfactants include sorbitan trioleate and soya lecithin. Oleic acid can also be useful as a surfactant. (See, e.g., Bäckström et al., Aerosol drug formulations containing hydrofluoroalkanes and alkyl saccharides, U.S. Patent No. 6,932,962).

[00354] Formulations for dispensing from a powder inhaler device will comprise a finely divided dry powder containing the inventive compound and can also include a bulking agent, such as lactose, sorbitol, sucrose, mannitol, trehalose, or xylitol in

amounts which facilitate dispersal of the powder from the device, e.g., 50 to 90% by weight of the formulation.

[00355] Nasal delivery forms. In accordance with the present invention, intranasal delivery of the inventive composition of matter and/or pharmaceutical compositions is also useful, which allows passage thereof to the blood stream directly after administration to the inside of the nose, without the necessity for deposition of the product in the lung. Formulations suitable for intransal administration include those with dextran or cyclodextran, and intranasal delivery devices are known. (See, e.g, Freezer, Inhaler, U.S. Patent No. 4,083,368).

[00356] Transdermal and transmucosal (e.g., buccal) delivery forms). In some embodiments, the inventive composition is configured as a part of a pharmaceutically acceptable transdermal or transmucosal patch or a troche. Transdermal patch drug delivery systems, for example, matrix type transdermal patches, are known and useful for practicing some embodiments of the present pharmaceutical compositions. (E.g., Chien et al., Transdermal estrogen/progestin dosage unit, system and process, U.S. Patent Nos. 4,906,169 and 5,023,084; Cleary et al., Diffusion matrix for transdermal drug administration and transdermal drug delivery devices including same, U.S. Patent No. 4,911,916; Teillaud et al., EVA-based transdermal matrix system for the administration of an estrogen and/or a progestogen, U.S. Patent No. 5.605,702; Venkateshwaran et al., Transdermal drug delivery matrix for coadministering estradiol and another steroid, U.S. Patent No. 5,783,208; Ebert et al., Methods for providing testosterone and optionally estrogen replacement therapy to women, U.S. Patent No. 5,460,820). A variety of pharmaceutically acceptable systems for transmucosal delivery of therapeutic agents are also known in the art and are compatible with the practice of the present invention. (E.g., Heiber et al., Transmucosal delivery of macromolecular drugs, U.S. Patent Nos. 5,346,701 and 5,516,523; Longenecker et al., Transmembrane formulations for drug administration, U.S. Patent No. 4,994,439).

[00357] Buccal delivery of the inventive compositions is also useful. Buccal delivery formulations are known in the art for use with peptides. For example, known tablet or patch systems configured for drug delivery through the oral mucosa (e.g., sublingual

mucosa), include some embodiments that comprise an inner layer containing the drug, a permeation enhancer, such as a bile salt or fusidate, and a hydrophilic polymer, such as hydroxypropyl cellulose, hydroxypropyl methylcellulose, hydroxyethyl cellulose, dextran, pectin, polyvinyl pyrrolidone, starch, gelatin, or any number of other polymers known to be useful for this purpose. This inner layer can have one surface adapted to contact and adhere to the moist mucosal tissue of the oral cavity and can have an opposing surface adhering to an overlying non-adhesive inert layer. Optionally, such a transmucosal delivery system can be in the form of a bilayer tablet, in which the inner layer also contains additional binding agents, flavoring agents, or fillers. Some useful systems employ a non-ionic detergent along with a permeation enhancer. Transmucosal delivery devices may be in free form, such as a cream, gel, or ointment, or may comprise a determinate form such as a tablet, patch or troche. For example, delivery of the inventive composition can be via a transmucosal delivery system comprising a laminated composite of, for example, an adhesive layer, a backing layer, a permeable membrane defining a reservoir containing the inventive composition, a peel seal disc underlying the membrane, one or more heat seals, and a removable release liner. (E.g., Ebert et al., Transdermal delivery system with adhesive overlay and peel seal disc, U.S. Patent No. 5,662,925; Chang et al., Device for administering an active agent to the skin or mucosa, U.S. Patent Nos. 4,849,224 and 4,983,395). These examples are merely illustrative of available transmucosal drug delivery technology and are not limiting of the present invention.

[00358] Dosages. The dosage regimen involved in a method for treating the above-described conditions will be determined by the attending physician, considering various factors which modify the action of drugs, e.g. the age, condition, body weight, sex and diet of the patient, the severity of any infection, time of administration and other clinical factors. Generally, the daily regimen should be in the range of 0.1-1000 micrograms of the inventive compound per kilogram of body weight, preferably 0.1-150 micrograms per kilogram.

[00359] By way of further illustration, the following numbered embodiments are encompassed by the present invention:

[00360] 1. A composition of matter comprising an isolated polypeptide comprising the amino acid sequence of the formula:

$X_{aa}^{1}X_{aa}^{2}X_{aa}^{3}X_{aa}^{4}X_{aa}^{5}X_{aa}^{6}X_{aa}^{7}X_{aa}^{8}X_{aa}^{9}X_{aa}^{10}X_{aa}^{11}X_{aa}^{12}X_{aa}^{13}X_{aa}^{14}Asp^{15}$
$X_{aa}^{16}X_{aa}^{17}$
$X_{aa}^{18}X_{aa}^{19}X_{aa}^{20}X_{aa}^{21}X_{aa}^{22}X_{aa}^{23}X_{aa}^{24}X_{aa}^{25}X_{aa}^{26}X_{aa}^{27}X_{aa}^{28}X_{aa}^{29}X_{aa}^{30}$
$X_{aa}^{31}Lys^{32}X_{aa}^{33}X_{aa}^{34}X_{aa}^{35}X_{aa}^{36}X_{aa}^{37}X_{aa}^{38}$//SEQ ID NO:475

or a pharmaceutically acceptable salt thereof,

wherein:

$X_{aa}^{1}X_{aa}^{2}$ is absent; or X_{aa}^{1} is any amino acid residue and X_{aa}^{2} is any amino acid residue; or X_{aa}^{1} is absent and X_{aa}^{2} is any amino acid residue;

X_{aa}^{3} is Cys, if X_{aa}^{18} is Cys; or X_{aa}^{3} is SeCys, if X_{aa}^{18} is SeCys; or X_{aa}^{3} is an alkyl amino acid residue, if X_{aa}^{18} is an alkyl amino acid residue;

X_{aa}^{4} is an acidic, hydrophobic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{5} is a Gly, Ala, hydrophobic, or basic amino acid residue;

X_{aa}^{6} is a Gly, Ala, 2-Abu, Nle, Nva, or hydrophobic amino acid residue;

X_{aa}^{7} is a Gly, Ala, aromatic, or hydrophobic amino acid residue;

X_{aa}^{8} is a basic, acidic, or neutral hydrophilic amino acid residue, or an Ala residue;

X_{aa}^{9} is a basic or neutral hydrophilic amino acid residue;

X_{aa}^{10} is Cys if X_{aa}^{24} is Cys; or X_{aa}^{10} is SeCys if X_{aa}^{24} is SeCys;

X_{aa}^{11} is any amino acid residue;

X_{aa}^{12} is a Pro, acidic, neutral, or hydrophobic amino acid residue;

X_{aa}^{13} is any amino acid residue;

X_{aa}^{14} is any amino acid residue;

X_{aa}^{16} is a basic, neutral hydrophilic, or acidic amino acid residue, or an Ala residue;

X_{aa}^{17} is a Cys if X_{aa}^{31} is Cys; or X_{aa}^{17} is a SeCys if X_{aa}^{31} is SeCys;

X_{aa}^{18} is a Cys, SeCys, or an alkyl amino acid residue;

X_{aa}^{19} is any amino acid residue;

X_{aa}^{20} is a Pro, Gly, basic, or neutral hydrophilic residue;

X_{aa}^{21} is a basic, hydrophobic, or neutral hydrophilic amino acid residue;

X_{aa}^{22} is a hydrophobic or basic amino acid residue;

X_{aa}^{23} is a hydrophobic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{24} is a Cys or SeCys residue;

X_{aa}^{25} is a Ser, Ala, or a neutral hydrophilic amino acid residue;

X_{aa}^{26} is an Ala, acidic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{27} is an acidic, basic, neutral hydrophilic or hydrophobic residue;

X_{aa}^{28} is an aromatic or basic amino acid residue;

X_{aa}^{29} is an acidic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{30} is a Trp, 5-bromoTrp, 6-bromoTrp, 5-chloroTrp, 6-chloroTrp, 1-Nal, 2-Nal, or thioTrp residue;

X_{aa}^{31} is a Cys or SeCys;

X_{aa}^{33} is a hydrophobic or aromatic amino acid residue;

X_{aa}^{34} is any amino acid residue;

X_{aa}^{35} is a hydrophobic amino acid residue;

each of X_{aa}^{36}, X_{aa}^{37}, and X_{aa}^{38} is independently absent or is independently a neutral, basic, or hydrophobic amino acid residue;

and wherein:

if X_{aa}^{3} and X_{aa}^{18} are both Cys residues, there is a disulfide bond between residue X_{aa}^{3} and residue X_{aa}^{18}; or if X_{aa}^{3} and X_{aa}^{18} are both SeCys residues, there is a diselenide bond between residue X_{aa}^{3} and residue X_{aa}^{18};

if X_{aa}^{10} and X_{aa}^{24} are both Cys residues, there is a disulfide bond between residue X_{aa}^{10} and residue X_{aa}^{24}; or if X_{aa}^{10} and X_{aa}^{24} are both SeCys residues, there is a diselenide bond between residue X_{aa}^{10} and residue X_{aa}^{24};

if X_{aa}^{17} and X_{aa}^{31} are both Cys residues, there is a disulfide bond between residue X_{aa}^{17} and residue X_{aa}^{31}; or if X_{aa}^{17} and X_{aa}^{31} are both SeCys residues, there is a diselenide bond between residue X_{aa}^{17} and residue X_{aa}^{31};

the amino-terminal residue is optionally acetylated, biotinylated, or 4-pentynoylated, or PEGylated; and

the carboxy-terminal residue is optionally amidated.

[00361] 2. The composition of matter of Embodiment 1 wherein X_{aa}^{4} is selected from Ala, Glu, Asp, Phe, Pro, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His,

homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, cyclohexylglycine (Chg), cyclohexylalanine (Cha), glycine, norleucine, norvaline, 1-Nal, 2-Nal, 4-phenyl-phenylalanine (Bip), Gln, Asn, Ser, Thr, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, and Cit residues.

[00362] 3. The composition of matter of Embodiments 1-2, wherein X_{aa}^5 is selected from Ala, Phe, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, glycine, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

[00363] 4. The composition of matter of Embodiments 1-3, wherein X_{aa}^6 is selected from Ala, Gly, 2-Abu, Phe, Ile, Leu, Met, Val, Trp, Tyr, proline, thiaproline, methionine, glycine, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclopentylglycine (Cpg), phenylglycine, N-methylleucine, N-methylphenylalanine, N-methylvaline, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, and 4-phenyl-phenylalanine (Bip) residues.

[00364] 5. The composition of matter of Embodiments 1-4, wherein X_{aa}^7 is selected from Gly, Ala, Phe, Ile, Leu, Met, Val, Trp, Tyr, norleucine, norvaline, Pro, 2-pyridinylalanine, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, and 4-phenyl-phenylalanine (Bip) residues.

[00365] 6. The composition of matter of Embodiments 1-5, wherein X_{aa}^8 is selected from Ala, Arg, Lys, His, homolysine, ornithine, N-methyl-arginine, ω-

aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Ser, Thr, Asn, Gln, Cit, Asp, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, and Glu residues.

[00366] 7. The composition of matter of Embodiments 1-6, wherein X_{aa}^{9} is selected from Ala, Pro, Met, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Gln, Asn, Ser, Thr, and Cit residues.

[00367] 8. The composition of matter of Embodiments 1-7, wherein X_{aa}^{11} is selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

[00368] 9. The composition of matter of Embodiments 1-8, wherein X_{aa}^{12} is selected from alanine, valine, leucine, isoleucine, proline, serine, threonine, aspartic acid, glutamatic acid, glycine, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, Cha, and 4-phenyl-phenylalanine (Bip), cyclohexylglycine (Chg), cyclohexylalanine (Cha), asparagine, glutamine, methionine, hydroxyproline, phenylalanine, tryptophan, and tyrosine.

[00369] 10. The composition of matter of Embodiments 1-9, wherein X_{aa}^{13} is selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine,

homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

[00370] 11. The composition of matter of Embodiments 1-10, wherein X_{aa}^{14} is selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

[00371] 12. The composition of matter of Embodiments 1-11, wherein X_{aa}^{16} is selected from Ala, Pro, Met, Arg, Lys, His, Pra, Atz, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Gln, Asn, Ser, Thr, Cit, Asp, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, and Glu residues.

[00372] 13. The composition of matter of Embodiments 1-12, wherein X_{aa}^{19} is selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

[00373] 14. The composition of matter of Embodiments 1-13, wherein X_{aa}^{20} is selected from Ala, Gly, Pro, Met, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-

histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Gln, Asn, Ser, Thr, and Cit residues.

[00374] 15. The composition of matter of Embodiments 1-14, wherein X_{aa}^{21} is selected from Ala, Phe, Pro, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, cyclohexylglycine (Chg), cyclohexylalanine (Cha), glycine, norleucine, norvaline, 1-Nal, 2-Nal, 4-phenyl-phenylalanine (Bip), Gln, Asn, Ser, Thr, and Cit residues.

[00375] 16. The composition of matter of Embodiments 1-15, wherein X_{aa}^{22} is selected from Ala, Phe, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, glycine, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

[00376] 17. The composition of matter of Embodiments 1-16, wherein X_{aa}^{23} is selected from Ala, Phe, Pro, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, cyclohexylglycine (Chg), cyclohexylalanine (Cha), glycine, norleucine, norvaline, 1-Nal, 2-Nal, 4-phenyl-phenylalanine (Bip), Gln, Asn, Ser, Thr, and Cit residues.

[00377] 18. The composition of matter of Embodiments 1-17, wherein X_{aa}^{25} is selected from Ala, Gly Pro, Met, Gln, Asn, Ser, Thr, and Cit residues.

[00378] 19. The composition of matter of Embodiments 1-18, wherein X_{aa}^{26} is selected from Ala, Pro, Met, Arg, Lys, His, homolysine, ornithine, N-methyl-

arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, glycine, Glu, Asp, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, Gln, Asn, Ser, Thr, and Cit residues.

[00379] 20. The composition of matter of Embodiments 1-19, wherein X_{aa}^{27} is selected from Thr, Leu, Ile, Val, Ser, Met, Gln, Asn, Phe, Tyr, Trp, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 4-phenyl-phenylalanine (Bip), Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Asp, Glu, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, and Gly residues.

[00380] 21. The composition of matter of Embodiments 1-20, wherein X_{aa}^{28} is selected from Phe, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, 1-Nal, 2-Nal, 2-pyridyl-alanine, 3-pyridyl-alanine, 4-pyridyl-alanine, 4-piperidinyl-alanine, and 4-phenyl-phenylalanine (Bip) residues.

[00381] 22. The composition of matter of Embodiments 1-21, wherein X_{aa}^{29} is selected from Ala, Asp, Glu, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, Phe, Gly, His, Lys, Asn, Pro, Gln, Arg, Ser, Thr, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, and Dab residues.

[00382] 23. The composition of matter of Embodiments 1-22, wherein X_{aa}^{33} is selected from Phe, Ile, Leu, Met, Val, Trp, Tyr, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-

phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, 2-pyridyl-alanine, 3-pyridyl-alanine, 4-pyridyl-alanine, 4-piperidinyl-alanine, and 4-phenyl-phenylalanine (Bip) residues.

[00383] 24. The composition of matter of Embodiments 1-23, wherein X_{aa}^{34} is selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, 2-pyridyl-alanine, 3-pyridyl-alanine, 4-carboxy-phenylalanine, and 4-phenyl-phenylalanine (Bip) residues.

[00384] 25. The composition of matter of Embodiments 1-24, wherein X_{aa}^{35} is selected from Phe, Ile, Leu, Met, Val, Trp, Tyr, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, and 4-phenyl-phenylalanine (Bip) residues.

[00385] 26. The composition of matter of Embodiments 1-25, wherein each of X_{aa}^{36}, X_{aa}^{37}, and X_{aa}^{38} is independently absent or is independently selected from Ala, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

[00386] 27. The composition of matter of Embodiments 1-26, wherein $X_{aa}^{3}$and X_{aa}^{18} are alkyl residues.

[00387] 28. The composition of matter of Embodiment 27, wherein $X_{aa}^{3}$and X_{aa}^{18} are, independently, Ala or 2-Abu residues.

[00388] 29. The composition of matter of Embodiments 1-28, wherein the carboxy-terminal residue is amidated.

[00389] 30. The composition of matter of Embodiments 1-29, wherein the isolated polypeptide comprises the amino acid sequence of the formula:

$X_{aa}^{1}X_{aa}^{2}$ $Cys^{3}X_{aa}^{4}$ $X_{aa}^{5}Ala^{6}$ $X_{aa}^{7}X_{aa}^{8}X_{aa}^{9}Cys^{10}X_{aa}^{11}X_{aa}^{12}X_{aa}^{13}X_{aa}^{14}Asp^{15}$
X_{aa}^{16} $Cys^{17}Cys^{18}X_{aa}^{19}$ X_{aa}^{20} $X_{aa}^{21}X_{aa}^{22}X_{aa}^{23}$ $Cys^{24}X_{aa}^{25}$
$X_{aa}^{26}X_{aa}^{27}X_{aa}^{28}X_{aa}^{29}X_{aa}^{30}$
$Cys^{31}Lys^{32}X_{aa}^{33}X_{aa}^{34}X_{aa}^{35}$ $X_{aa}^{36}X_{aa}^{37}X_{aa}^{38}$// SEQ ID NO:476.

[00390] 31. The composition of matter of Embodiments 1-29, wherein X_{aa}^{6} is Ala.

[00391] 32. The composition of matter of Embodiment 31, wherein X_{aa}^{27} is Glu.

[00392] 33. The composition of matter of Embodiments 31-32, wherein X_{aa}^{29} is Asp, Glu, or Gln.

[00393] 34. The composition of matter of Embodiment 31, comprising an amino acid sequence selected from SEQ ID NOS: 22, 252-263, 419-439, 518-521, 524, 525, 562-580, 602, 691, 692, 696-703, 715, 721-735, 737-749, 756, 757, 761, 762, 764-

771, 787-796, 798, 800, 802, 803, 809-812, 1028, 1030-1040, 1043-1047, 1062-1065, and 1068-1070.

[00394] 35. The composition of matter of Embodiment 31, comprising an amino acid sequence selected from SEQ ID NOS: 1082, 1096, 1110, 1124, 1135, 1146, 1157, 1165, 1173, 1181, 1192, 1203, 1214, 1222, 1230, 1238, 1249, 1260, 1271, 1279, 1287, 1295, 1306, 1317, 1328, 1336, 1344, 1352, 1360, 1368, 1376, 1384, 1392, 1400, 1408, 1416, 1424, 1432, 1440, 1448, 1456, 1464, 1472, 1480, 1488, 1496, 1504, 1512, 1520, 1528, 1536, 1544, 1552, 1560, 1568, 1576, 1584, 1592, 1600, 1608, 1616, 1624, 1632, 1640, 1658, 1672, 1686, 1700, 1711, 1722, 1733, 1741, 1749, 1757, 1768, 1779, 1790, 1798, 1806, 1814, 1825, 1836, 1847, 1855, 1863, 1871, 1882, 1893, 1904, 1912, 1920, 1928, 1936, 1944, 1952, 1960, 1968, 1976, 1984, 1992, 2000, 2008, 2016, 2024, 2032, 2040, 2048, 2056, 2064, 2072, 2080, 2088, 2096, 2104, 2112, 2120, 2128, 2136, 2144, 2152, 2160, 2168, 2176, 2184, 2192, 2200, 2208, 2216, 2234, 2248, 2262, 2276, 2287, 2298, 2309, 2317, 2325, 2333, 2344, 2355, 2366, 2374, 2382, 2390, 2401, 2412, 2423, 2431, 2439, 2447, 2458, 2469, 2480, 2488, 2496, 2504, 2512, 2520, 2528, 2536, 2544, 2552, 2560, 2568, 2576, 2584, 2592, 2600, 2608, 2616, 2624, 2632, 2640, 2648, 2656, 2664, 2672, 2680, 2688, 2696, 2704, 2712, 2720, 2728, 2736, 2744, 2752, 2760, 2768, 2776, 2784, 2792, 2808, 2822, 2833, 2844, 2855, 2863, 2871, 2879, 2890, 2901, 2912, 2920, 2928, 2936, 2944, 2952, 2960, 2968, 2976, 2984, 2992, 3000, 3008, 3016, 3024, 3032, 3040, 3048, 3056, 3064, 3072, and 3080.

[00395] 36. The composition of matter of Embodiment 31, comprising an amino acid sequence selected from SEQ ID NOS: 597-601 and 813-1027.

[00396] 37. The composition of matter of Embodiments 1-29, wherein X_{aa}^{6} is Gly.

[00397] 38. The composition of matter of Embodiment 37, wherein X_{aa}^{27} is Glu.

[00398] 39. The composition of matter of Embodiments 37-38, wherein X_{aa}^{29} is Asp, Glu, or Gln.

[00399] 40. The composition of matter of Embodiment 37, comprising an amino acid sequence selected from SEQ ID NOS: 265, 751, 752, 754, 755, 1081, 1095, 1109, 1123, 1134, 1145, 1156, 1164, 1172, 1180, 1191, 1202, 1213, 1221, 1229, 1237, 1248, 1259, 1270, 1278, 1286, 1294, 1305, 1316, 1327, 1335, 1343, 1351, 1359, 1367, 1375, 1383, 1391, 1399, 1407, 1415, 1423, 1431, 1439, 1447, 1455, 1463, 1471, 1479, 1487, 1495, 1503, 1511, 1519, 1527, 1535, 1543, 1551, 1559, 1567, 1575, 1583, 1591, 1599, 1607, 1615, 1623, 1631, 1639, 1657, 1671, 1685, 1699, 1710, 1721, 1732, 1740, 1748, 1756, 1767, 1778, 1789, 1797, 1805, 1813, 1824, 1835, 1846, 1854, 1862, 1870, 1881, 1892, 1903, 1911, 1919, 1927, 1935, 1943, 1951, 1959, 1967, 1975, 1983, 1991, 1999, 2007, 2015, 2023, 2031, 2039, 2047, 2055, 2063, 2071, 2079, 2087, 2095, 2103, 2111, 2119, 2127, 2135, 2143, 2151, 2159, 2167, 2175, 2183, 2191, 2199, 2207, 2215, 2233, 2247, 2261, 2275, 2286, 2297, 2308, 2316, 2324, 2332, 2343, 2354, 2365, 2373, 2381, 2389, 2400, 2411, 2422, 2430, 2438, 2446, 2457, 2468, 2479, 2487, 2495, 2503, 2511, 2519, 2527, 2535, 2543, 2551, 2559, 2567, 2575, 2583, 2591, 2599, 2607, 2615, 2623, 2631, 2639, 2647, 2655, 2663, 2671, 2679, 2687, 2695, 2703, 2711, 2719, 2727, 2735, 2743, 2751, 2759, 2767, 2775, 2783, 2791, 2807, 2821, 2832, 2843, 2854, 2862, 2870, 2878, 2889, 2900, 2911, 2919, 2927, 2935, 2943, 2951, 2959, 2967, 2975, 2983, 2991, 2999, 3007, 3015, 3023, 3031, 3039, 3047, 3055, 3063, 3071, and 3079.

[00400] 41. The composition of matter of Embodiments 1-29, wherein X_{aa}^{6} is 2-Abu.

[00401] 42. The composition of matter of Embodiment 41, wherein X_{aa}^{27} is Glu.

[00402] 43. The composition of matter of Embodiments 41-42, wherein X_{aa}^{29} is Asp, Glu, or Gln.

[00403] 44. The composition of matter of Embodiment 41, comprising an amino acid sequence selected from SEQ ID NOS: 605, 636, 649, 706, 707, 718, 753, 758, 797, 799, 801, 804, 807, 808, 1029, 1041, 1042, 1048, 1066, 1067, 1083, 1097, 1111, 1125, 1136, 1147, 1158, 1166, 1174, 1182, 1193, 1204, 1215, 1223, 1231, 1239, 1250, 1261, 1272, 1280, 1288, 1296, 1307, 1318, 1329, 1337, 1345, 1353, 1361, 1369, 1377, 1385, 1393, 1401, 1409, 1417, 1425, 1433, 1441, 1449, 1457, 1465, 1473, 1481, 1489, 1497, 1505, 1513, 1521, 1529, 1537, 1545, 1553, 1561, 1569, 1577, 1585, 1593, 1601, 1609, 1617, 1625, 1633, 1641, 1659, 1673, 1687, 1701, 1712, 1723, 1734, 1742, 1750, 1758, 1769, 1780, 1791, 1799, 1807, 1815, 1826, 1837, 1848, 1856, 1864, 1872, 1883, 1894, 1905, 1913, 1921, 1929, 1937, 1945, 1953, 1961, 1969, 1977, 1985, 1993, 2001, 2009, 2017, 2025, 2033, 2041, 2049, 2057, 2065, 2073, 2081, 2089, 2097, 2105, 2113, 2121, 2129, 2137, 2145, 2153, 2161, 2169, 2177, 2185, 2193, 2201, 2209, 2217, 2235, 2249, 2263, 2277, 2288, 2299, 2310, 2318, 2326, 2334, 2345, 2356, 2367, 2375, 2383, 2391, 2402, 2413, 2424, 2432, 2440, 2448, 2459, 2470, 2481, 2489, 2497, 2505, 2513, 2521, 2529, 2537, 2545, 2553, 2561, 2569, 2577, 2585, 2593, 2601, 2609, 2617, 2625, 2633, 2641, 2649, 2657, 2665, 2673, 2681, 2689, 2697, 2705, 2713, 2721, 2729, 2737, 2745, 2753, 2761, 2769, 2777, 2785, 2793, 2809, 2823, 2834, 2845, 2856, 2864, 2872, 2880, 2891, 2902, 2913, 2921, 2929, 2937, 2945, 2953, 2961, 2969, 2977, 2985, 2993, 3001, 3009, 3017, 3025, 3033, 3041, 3049, 3057, 3065, 3073, and 3081.

[00404] 45. The composition of matter of Embodiments 1-29, wherein X_{aa}^{6} is Nle.

[00405] 46. The composition of matter of Embodiment 45, wherein X_{aa}^{27} is Glu.

[00406] 47. The composition of matter of Embodiments 45-46, wherein X_{aa}^{29} is Asp, Glu, or Gln.

[00407] 48. The composition of matter of Embodiment 45, comprising an amino acid sequence selected from SEQ ID NOS: 607, 638, 651, 1085, 1099, 1113, 1127, 1138, 1149, 1160, 1168, 1176, 1184, 1195, 1206, 1217, 1225, 1233, 1241, 1252, 1263, 1274, 1282, 1290, 1298, 1309, 1320, 1331, 1339, 1347, 1355, 1363, 1371, 1379, 1387, 1395, 1403, 1411, 1419, 1427, 1435, 1443, 1451, 1459, 1467, 1475, 1483, 1491, 1499, 1507, 1515, 1523, 1531, 1539, 1547, 1555, 1563, 1571, 1579, 1587, 1595, 1603, 1611, 1619, 1627, 1635, 1643, 1661, 1675, 1689, 1703, 1714, 1725, 1736, 1744, 1752, 1760, 1771, 1782, 1793, 1801, 1809, 1817, 1828, 1839, 1850, 1858, 1866, 1874, 1885, 1896, 1907, 1915, 1923, 1931, 1939, 1947, 1955, 1963, 1971, 1979, 1987, 1995, 2003, 2011, 2019, 2027, 2035, 2043, 2051, 2059, 2067, 2075, 2083, 2091, 2099, 2107, 2115, 2123, 2131, 2139, 2147, 2155, 2163, 2171, 2179, 2187, 2195, 2203, 2211, 2219, 2237, 2251, 2265, 2279, 2290, 2301, 2312, 2320, 2328, 2336, 2347, 2358, 2369, 2377, 2385, 2393, 2404, 2415, 2426, 2434, 2442, 2450, 2461, 2472, 2483, 2491, 2499, 2507, 2515, 2523, 2531, 2539, 2547, 2555, 2563, 2571, 2579, 2587, 2595, 2603, 2611, 2619, 2627, 2635, 2643, 2651, 2659, 2667, 2675, 2683, 2691, 2699, 2707, 2715, 2723, 2731, 2739, 2747, 2755, 2763, 2771, 2779, 2787, 2795, 2811, 2825, 2836, 2847, 2858, 2866, 2874, 2882, 2893, 2904, 2915, 2923, 2931, 2939, 2947, 2955, 2963, 2971, 2979, 2987, 2995, 3003, 3011, 3019, 3027, 3035, 3043, 3051, 3059, 3067, 3075, and 3083.

[00408] 49. The composition of matter of Embodiments 1-29, wherein X_{aa}^{6} is Nva.

[00409] 50. The composition of matter of Embodiment 49, wherein X_{aa}^{27} is Glu.

[00410] 51. The composition of matter of Embodiments 49-50, wherein X_{aa}^{29} is Asp, Glu, or Gln.

[00411] 52. The composition of matter of Embodiment 49, comprising an amino acid sequence selected from SEQ ID NOS: 606, 637, 650, 705, 708, 717, 759, 760, 805, 806, 1084, 1098, 1112, 1126, 1137, 1148, 1159, 1167, 1175, 1183, 1194, 1205, 1216, 1224, 1232, 1240, 1251, 1262, 1273, 1281, 1289, 1297, 1308, 1319, 1330, 1338, 1346, 1354, 1362, 1370, 1378, 1386, 1394, 1402, 1410, 1418, 1426, 1434, 1442, 1450, 1458, 1466, 1474, 1482, 1490, 1498, 1506, 1514, 1522, 1530, 1538, 1546, 1554, 1562, 1570, 1578, 1586, 1594, 1602, 1610, 1618, 1626, 1634, 1642, 1660, 1674, 1688, 1702, 1713, 1724, 1735, 1743, 1751, 1759, 1770, 1781, 1792, 1800, 1808, 1816, 1827, 1838, 1849, 1857, 1865, 1873, 1884, 1895, 1906, 1914, 1922, 1930, 1938, 1946, 1954, 1962, 1970, 1978, 1986, 1994, 2002, 2010, 2018, 2026, 2034, 2042, 2050, 2058, 2066, 2074, 2082, 2090, 2098, 2106, 2114, 2122, 2130, 2138, 2146, 2154, 2162, 2170, 2178, 2186, 2194, 2202, 2210, 2218, 2236, 2250, 2264, 2278, 2289, 2300, 2311, 2319, 2327, 2335, 2346, 2357, 2368, 2376, 2384, 2392, 2403, 2414, 2425, 2433, 2441, 2449, 2460, 2471, 2482, 2490, 2498, 2506, 2514, 2522, 2530, 2538, 2546, 2554, 2562, 2570, 2578, 2586, 2594, 2602, 2610, 2618, 2626, 2634, 2642, 2650, 2658, 2666, 2674, 2682, 2690, 2698, 2706, 2714, 2722, 2730, 2738, 2746, 2754, 2762, 2770, 2778, 2786, 2794, 2810, 2824, 2835, 2846, 2857, 2865, 2873, 2881, 2892, 2903, 2914, 2922, 2930, 2938, 2946, 2954, 2962, 2970, 2978, 2986, 2994, 3002, 3010, 3018, 3026, 3034, 3042, 3050, 3058, 3066, 3074, and 3082.

[00412] 53. The composition of matter of Embodiment 1, comprising an amino acid sequence selected from SEQ ID NOS: 3-30, 32-72, 74-134, 136-178, 180-211, 218-239, 241-305, 307-363, 366-386, 388-432, 434-474, 515-527, 532-588, 590, 591, 593-775, 777, 778, 780-788, 790-1049, and 1062-3086.

[00413] 54. A composition of matter, comprising an amino acid sequence selected from SEQ ID NOS: 3-134, 136-305, 307-386, 388-474, 515-527, 532-588, 590, 591, 593-1049, and 1062-3086.

[00414] 55. An isolated nucleic acid encoding any of SEQ ID NOS: 3-134, 136-305, 307-386, 388-474, 515-527, 532-588, 590, 591, 593-1049, or 1062-3086 that does not include a non-canonical amino acid.

[00415] 56. An expression vector comprising the nucleic acid of Embodiment 55.

[00416] 57. A recombinant host cell comprising the expression vector of Embodiment 56.

[00417] 58. The composition of matter of any of Embodiments 1-54, further comprising an optional linker moiety and a pharmaceutically acceptable, covalently linked half-life extending moiety.

[00418] 59. The composition of matter of Embodiment 58, wherein the half-life extending moiety is polyethylene glycol of molecular weight of about 1000 Da to about 100000 Da, an IgG Fc domain, a transthyretin, or a human serum albumin.

[00419] 60. The composition of matter of Embodiment 58, wherein the half-life extending moiety comprises a human immunoglobulin or a human immunoglobulin Fc domain, or both.

[00420] 61. The composition of matter of Embodiment 60 having a configuration as set forth in any of Figures 12A-N, or Figures 88-91.

[00421] 62. The composition of matter of Embodiment 60, wherein the composition comprises a monovalent immunoglobulin-peptide or Fc-peptide conjugate.

[00422] 63. The composition of matter of Embodiment 60, wherein the composition comprises a bivalent immunoglobulin-peptide or Fc-peptide conjugate.

[00423] 64. A pharmaceutical composition, comprising the composition of matter of any of Embodiments 1-54 or 58-63, and a pharmaceutically acceptable carrier.

[00424] 65. A method of preventing pain, comprising administering a prophylactically effective amount of the composition of matter of any of Embodiments 1-54 or 58-63.

[00425] 66. A method of treating pain, comprising administering a therapeutically effective amount of the composition of matter of any of Embodiments 1-54, or 58-63.

[00426] 67. The method of Embodiment 66, wherein the pain is chronic pain, acute pain, or persistent pain.

[00427] 68. The method of Embodiment 67, wherein the chronic pain is associated with cancer, chemotherapy, osteoarthritis, fibromyalgia, primary erythromelalgia, post-herpetic neuralgia, painful diabetic neuropathy, idiopathic painful neuropathy, neuromas, paroxysmal extreme pain disorder, migraine, trigeminal neuralgia, orofacial pain, cluster headaches, complex regional pain syndrome (CRPS), failed back surgery syndrome, sciatica, interstitial cystitis, pelvic pain, lower back pain, inflammation-induced pain, or joint pain.

[00428] 69. The method of Embodiment 67, wherein the acute or persistent pain is associated with trauma, burn, or surgery.

[00429] 70. The composition of matter of Embodiments 1-30, wherein X_{aa}^{29} is an acidic or neutral hydrophilic residue.

[00430] 71. The composition of matter of Embodiment 70, wherein X_{aa}^{29} is selected from Ala, Asp, Glu, Gly, Asn, Gln, Ser, Thr, phosphoserine, phosphotyrosine, and gamma-carboxyglutamic acid residues.

[00431] 72. The composition of matter of Embodiment 70, comprising an amino acid sequence selected from SEQ ID NOS: 1071-2798.

[00432] The following working examples are illustrative and not to be construed in any way as limiting the scope of the present invention.

[00433] EXAMPLES

[00434] Example 1: Isolation and purification of GpTx-1 from venom

[00435] Venom Sample Preparation. Venom from the tarantula *Gammostola porteri* was extracted via electrical stimulation of an anesthetized spider. Venom samples were collected, lyophilized, and dissolved in 0.1% trifluoroacetic acid (TFA) in water to approximately 1 mg venom/mL. The crude venom solutions were desalted by solid-phase extraction (SPE) with Sep-Pak C18 cartridges (Waters, Milford, MA, USA) equilibrated in 0.1% TFA, and eluted with 60% aqueous acetonitrile and then evaporated. The dried material was dissolved in 0.1% TFA to 1 mg venom/mL concentration and higher molecular components removed with a 10kDa molecular weight cut-off Ultrafree-CL (Millipore). The <10 kDa venom extract was then dried under in vacuo and stored at -80°C.

[00436] Fractionation. The crude venom was fractionated by reversed phase (RP) HPLC, collecting 84 samples in time slices. Less than 10 kDa venom extracts were dissolved in 0.1% TFA to approximately 1mg venom/mL, and then separated by C18 RP HPLC chromatography and collected into approximately 1 minute wide fractions. HPLC method: Buffer A (0.1% TFA in water) and buffer B (90% acetonitrile/10% water containing 0.1% TFA) at 1 mL/min with a 1% /min gradient 0-100% buffer B. The fractions were then transferred into a plate format, dried under in vacuo, and then stored at -80°C.

[00437] The venom fractions were screened for activity in the $Na_V1.7$ and $Na_V1.3$ IonWorks® Quattro (IWQ) assays. (See, Example 3 and Figure 1). Several fractions with significant (>80% of control) Nav1.7 inhibitory activity were identified, the first of which was fraction 31. A second aliquot of fraction 31 was tested in the $Na_V1.7$, $Na_V1.3$, and $Na_V1.5$ IWQ assays to confirm the activity of the "hit" and evaluate selectivity. The sample was then analyzed by high-resolution electro-spray ionization (ESI) and matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry (MS), which indicated that the fraction was a mixture of at least four distinct peptide species. (See, Figure 2 and Figure 3). Fraction 31 was then separated by RP-HPLC, and the corresponding sub-fractions were screened for activity in the $Na_V1.7$ and $Na_V1.5$ assays. Sub-fraction 11 was the major peak in the RP-HPLC chromatogram and showed > 90% inhibition of $Na_V1.7$ activity. (See Figure 4). Deconvolution of sub-fraction 11 revealed the primary peptide sequence of GpTx-1. As with all proteins, GpTx-1 is expected to have essentially zero access to the central nervous system.

[00438] GpTx-2 through GpTx-7 (SEQ ID NOS:467-474; see, Table 5A) were identified through transcriptomic analysis of the venom gland of *Grammostola porteri* using expressed sequence tag methodologies. (See, Siang AS, Doley R, Vonk FJ, Kini RM., "Transcriptomic analysis of the venom gland of the red-headed krait (Bungarus flaviceps) using expressed sequence tags", *BMC Molecular Biology* 2010, 11:24; Jiang Y, Li Y, Lee W, Xu X, Zhang Y, Zhao R, Zhang Y, Wang W., "Venom gland transcriptomes of two elapid snakes (Bungarus multicinctus and Naja atra) and evolution of toxin genes", *BMC Genomics* 2011, 12:1; Wagstaff SC, Sanz L, Juárez P,

Harrison RA, Calvete JJ., "Combined snake venomics and venom gland transcriptomic analysis of the ocellated carpet viper, Echis ocellatus.", *J Proteomics*. 2009 71(6):609-23; Magalhães GS, Junqueira-de-Azevedo IL, Lopes-Ferreira M, Lorenzini DM, Ho PL, Moura-da-Silva AM. "Transcriptome analysis of expressed sequence tags from the venom glands of the fish Thalassophryne nattereri", *Biochimie* 2006 88(6):693-9; Wagstaff SC, Harrison RA., "Venom gland EST analysis of the saw-scaled viper, Echis ocellatus, reveals novel alpha9beta1 integrin-binding motifs in venom metalloproteinases and a new group of putative toxins, renin-like aspartic proteases." *Gene* 2006 377:21-32).

[00439] Peptide Sequencing: Edman degradation and de novo MS/MS. N-terminal sequencing of peptides were performed by Edman degradation (Reference: (1) Edman, P. (1950), "Method for determination of the amino acid sequence in peptides", Acta Chem. Scand. 4: 283–293; (2) Niall, H.D. (1973). "Automated Edman degradation: the protein sequenator". Meth. Enzymol. 27: 942–1010). Phenylthiohydantoin (PTH)- amino acid derivatives were analyzed with an Applied Biosystems automatic 473A sequencer.

[00440] De novo peptide sequencing was accomplished by tandem mass spectrometry (References: Vlado Dančík, Theresa A. Addona, Karl R. Clauser, James E. Vath, Pavel A. Pevzner., J. Comp. Biol., Volume 6, 3/4, (1999); (2) Favreau, P., Menin, L., Michalet, S., Perret, F., Cheneval, Stöcklin, M., Bulet, A. and Stöcklin, R., Toxicon, 47(6),676-687, (2006), (3) Favreau, P., Cheneval, O., Menin, L., Michalet, S., Gaertner, H., Principaud, F., Thai, R., Ménez, A., Bulet, P. and Stöcklin, R. (2007), The venom of the snake genus Atheris contains a new class of peptides with clusters of histidine and glycine residues. Rapid Communications in Mass Spectrometry, 21: 406–412).

[00441] Example 2: Synthesis of GpTx-1 peptide analogs

[00442] Small-scale peptide synthesis. Peptides were assembled using N^{α}-Fmoc solid-phase peptide synthesis methodologies with appropriate orthogonal protection and resin linker strategies. The peptides were synthesized on a 0.012 mmol scale using Rink

Amide MBHA resin (100-200 mesh, 1% DVB, RFR-1063-PI, 0.52 meq/g initial loading, 408291, Peptides International, Louisville, KY). Dry resin (17 mg per well) was added to a Phenomenex deep well protein precipitation plate (CEO-7565, 38710-1) using a resin loader (Radley). Amino acids were added to the growing peptide chain by stepwise addition using standard solid phase methods on an automated peptide synthesizer (Intavis Multipep). Amino acids (5 molar equivalents, 120 µL, 0.5 M in DMF) were pre-activated (1 min) with (1-Cyano-2-ethoxy-2-oxoethylidenaminooxy)dimethylamino-morpholino-carbenium hexafluorophosphate (COMU®; 5 molar equivalents, 170 µL, 0.35 M in dimethylformamide (DMF)) and N,N-Diisopropylethylamine (DIEA; 7.5 molar equivalents, 70 µL, 1.25 M in dichloromethane (DCM)). Pre-activated amino acids were transferred to the appropriate well. Resins were incubated for 30 min, drained, and the cycle repeated. Following the 2nd amino acid incubation the plates were drained and washed with DMF 8 times (3 mL per column of 8 wells). The Fmoc groups were then removed by 2 sequential incubations in 500 µL of a 20% piperidine in DMF solution. The 1st incubation was 5 min, the resin drained, and the 2nd incubation was for 20 min. The resin was drained and washed with DMF 10 times (3 mL per column of 8 wells). After removal of the final Fmoc protecting group, the resin was washed with DCM 5 times (3 mL per column of 8 wells) and allowed to air dry.

[00443] Cleavage. To the bottom of the filter plate was affixed a drain port sealing mat (ArcticWhite, AWSM-1003DP). To the resin in each well was added triisopropylsilane (100 µL), DODT (100 µL), and water (100 µL) using a multichannel pipette. To the resin in each well was added TFA (1 mL) using a Dispensette Organic dispenser. To the resin was added a triangular micro stir bar, and the mixture was stirred for 3 h. The sealing mat was removed, and the cleavage solution was eluted into a solid bottom 96-well deep well plate. The resin in each well was washed with and additional 1 mL of TFA. The solutions were concentrated using rotary evaporation (Genevac). To each well in a new 96-well filter plate with a bottom sealing mat attached was added 1 mL of cold diethyl ether using a Dispensette Organic dispenser. To the ether was added the concentrated peptide solutions using a multichannel pipette with wide bore tips. The solution was agitated with the pipette to ensure complete

mixing and precipitation. The white solid was filtered, washed with a second 1 mL of cold ether, filtered, and dried under vacuum.

[00444] Folding. To the crude peptide in each well was added 0.9 mL of 50:50 water/acetonitrile with a multichannel pipette and a micro stir bar. The mixture was stirred for 1 h. The solution was filtered into a solid bottom 96-well deep well plate. To the crude peptide in each well was added another 0.9 mL of 50:50 water/acetonitrile with a multichannel pipette. The solution was filtered into the same solid bottom 96-well deep well plate. In a 4 L bottle was prepared 4.0 L of folding buffer (3.3 L water, 300 mL acetonitrile, 2.0 g oxidized glutathione, 1.0 g reduced glutathione, 400 mL 1 M Tris-HCl pH 7.5). To 96 50-mL centrifuge tubes was added 40 mL of peptide folding buffer using a Dispensette dispenser. To the folding buffer was added the 1.8 mL of dissolved peptide using the Tecan automated liquid handler. The pH of the folding solutions was measured to about 7.7. The folding reactions were allowed to stand overnight. To each tube was added 1 mL of glacial acetic acid. To a 96-well filter plate was added SP Sepharose High Performance as a slurry (1 mL per well) with a multichannel pipette. Using the Tecan automated liquid handler, the gel was conditioned with folding buffer (3 x 0.9 mL), loaded with the folded peptide solution (50 x 0.9 mL, pH = 4.0, on the Tecan automated liquid handler), washed (4 x 0.9 mL, 20 mM NaOAc, pH = 4.0), and eluted manually on a vacuum manifold with 2 x 1 mL (1 M NaCl, 20 mM NaOAc, pH = 4.0) into a solid bottom 96-well deep well plate.

[00445] Conjugation of peptides to PEG. Some GpTx-1 peptide analogs were conjugated to azido-NPEG10 (e.g., see, Table 30, Table 31, and Table 32, below). To 1 mL of the folded peptide in the IEX elution buffer was added in order 32-azido-3,6,9,12,15,18,21,24,27,30-decaoxadotriacontan-1-amine (70 µL, 50 mM aq.), tris(2-phenyl-1-(1H-1,2,3-triazol-4-yl)ethyl)amine (TBTA; 88 µL, 10 mM in DMSO), L-ascorbic acid sodium salt (438 µL, 75 mM aq.), and copper(ii) sulfate, anhydrous, powder (188 µL, 35 mM aq.). The reaction mixture turned slightly cloudy after the addition of the TBTA. After overnight incubation, the plate was centrifuged for 1 h at 1600 rpm to pellet any precipitate. The supernatant was transferred to a 96-well filter plate with a multichannel pipette and filtered into a solid bottom 96-well plate.

[00446] Purification and characterization of molecules. The folded (conjugated) peptide (2 mL) was purified by mass-triggered semi-prep HPLC (Agilent/LEAP 'Ariel',

Jupiter 5u C18 300 A, 100 x 10 mm 5 micron) with a gradient of 15-35% B over 45 min, with a 5 min flush, and 5 min equilibration at 8 mL/min. The collected fractions were pooled and reformatted into vials on the Tecan. Final QC (Phenomenex Jupiter 20 × 2 mm, 100 Å, 5 micron column eluted with a 10 to 60% B over 10 min gradient at a 0.750 mL/min flow rate monitoring absorbance at 220 nm) and CLND quantification were performed. Peptides with > 95% purity and correct (m/z) ratio were screened. (See Figures 5 and 6 for LC-MS characterization of synthetic GpTx-1).

[00447] Large-scale peptide synthesis. Rink Amide Chem Matrix resin (0.2 mmol, 0.45 mmol/g loading, 0.444g, Matrix Innovation) was weighed into a CS BIO reaction vessel. The reaction vessel was connected to a channel of the CS BIO 336X automated peptide synthesizer, and the resin was washed 2 x DMF and allowed to swell in DMF for 15 min. Fmoc-amino acid (1.0 mmol, Midwest Biotech or Novabiochem) was dissolved in 2.5 mL of 0.4 M 6-chloro-1-hydroxybenzotriazole (6-Cl-HOBt, Matrix Innovation) in DMF. To the solution was added 1.0 mL of 1.0 M 1,3-diisopropylcarbodiimide (DIC, Sigma-Aldrich) in DMF. The solution was agitated with nitrogen bubbling for 15 min to accomplish pre-activation and then added to the resin. The mixture was shaken for 2 h. The resin was filtered and washed 3 x DMF, 2 x DCM, and 3 x DMF. Fmoc-removal was accomplished by treatment with 20% piperdine in DMF (5 mL, 2 x 15 min, Fluka). The resin was filtered and washed 3 x DMF. All residues were single coupled through repetition of the Fmoc-amino acid coupling and Fmoc removal steps described above.

[00448] Cleavage and linear peptide purification. After final Fmoc-removal from the N-terminal residue, resin-bound linear peptide (0.2 mmol scale) was transferred to a 25 mL solid phase extraction (SPE) filter tube, washed 3 x DMF and 3 x DCM, and dried under vacuum. To the resin was added triisopropylsilane (1.0 mL), 3,6-dioxa-1,8-octane-dithiol (DODT, 1.0 mL), water (1.0 mL), trifluoroacetic acid (TFA, 15 mL), and a stir bar, and the mixture was stirred for 3 h. The mixture was filtered into a 50 mL centrifuge tube. The resin was washed with TFA (~ 5 mL), and the combined filtrate was concentrated by rotary evaoporation in a Genevac HT-12 (30°C chamber temperature, pressure ramp from 500 to 50 mbar over 40 min and a final pressure of 8 mbar for 2 h). To the residue (~5 mL) was added 40 mL cold diethyl ether. A white precipitate formed. The solid was stirred in the ether. The mixture was centrifuged (4

min, 4,400 rpm), and the ether was decanted. To the tube was added another 40 mL of cold ether, and the precipitate was stirred. The mixture was centrifuged, and the ether was decanted. The solid was dried overnight under vacuum. The crude linear peptide was purified by preparative LC-MS. The filtered sample (500 mg in 10 mL DMSO) was injected onto a preparative HPLC column (Jupiter 10u C18 300A, 250 x 50 mm 10 micron). The peptide was eluted with a 10-40%B over 60 min gradient at 50 mL/min, followed by a 10 min flush and a 10 min equilibration. The fractions were analyzed by LC-MS, pooled, and lyophilized to afford pure the linear peptide precursor.

[00449] Folding. In a 2L FEP bottle was prepared a folding buffer with water (944 mL), acetonitrile (55.5 mL), Tris-HCl pH 7.5 (111 mL), (-)-glutathione, oxidized (680 mg, 1.110 mmol), and l-glutathione reduced (340 mg, 1.110 mmol). To the pure linear peptide (111 mg, 0.028 mmol) was added 2.5 mL acetonitrile and 2.5 mL water. The mixture was vortexed to complete dissolution of the peptide. The peptide solution was added to the folding buffer (0.1 mg/mL peptide concentration, 1 mM oxidized glutathione, 1 mM reduced glutathione, 10% v/v acetonitrile, 0.1 M Tris pH 7.5). The pH value was measured to be 7.7. The folding mixture was stirred at 80 rpm at room temperature overnight. A small aliquot was removed and the sample was analyzed by LC-MS to ensure that the folding was complete. The solution was quenched by the addition of 4 mL AcOH and 4 mL TFA (pH = 2.5). The aqueous solution was filtered (0.45 uM cellulose membrane).

[00450] Purification. The filtered solution (1110 mL, 111 mg peptide) was loaded onto a preparative HPLC column (Phenomenex Synergi 4u MAX-RP 80A AXIA, 250 x 30 mm) at 30 mL/min using an Agilent preparative loading pump. The column was was flushed for 10 min with 10% B at 30 mL/min to elute the AcOH/TFA. The column was attached to a prep HPLC, Agilent/LEAP prep LC-MS, and the peptide was eluted with a 10-40% B gradient over 60 min, followed by a 10 min flush and a 10 min equilibration. The fractions were analyzed by LC-MS, pooled, and lyophilized to afford pure folded peptide.

[00451] Counterion exchange for peptide in vivo studies. A 4 mL SPE tube containing VariPure IPE (Varian, PL-HCO3 MP-Resin, polymer-supported hydrogencarbonate, 1.8 mmol/g, 100A, 150-300μm) was pre-conditioned with 2mL of MeOH, followed by 2mL of water, draining by gravity. 2.0 mL of a ≤5.0 mM solution

of purified folded peptide in water was applied to the bed. The device was washed with 4 x 2.0 mL of water to elute all of the peptide. To the eluent was added 50 μL of acetic acid. The solution was concentrated by rotary evaporation (Genevac) to afford the acetate salt of the purified folded peptide. A 100 mM stock solution of trifluoroethanol (TFE) in deuterium oxide (D2O) was prepared fresh by weighing 50 mg of TFE into a 5 mL volumetric flask, followed by addition of D2O to a final volume of 5 mL. A 5 mM solution of TFE in D2O was then prepared by dilution for dissolving all samples for 19F-NMR. The solution was used to dissolve peptide to a concentration of 1 mM, and the sample was analyzed by 19F-NMR using a fluorine long delay (d1 = 5 sec) method. The TFE integral (triplet at -76.75 ppm) was normalized to 5 and the integral of TFA (singlet at -75.6) recorded. NMR tube was cut, and sample was recovered by rotary evaporation (Genevac).

[00452] Example 3: Electrophysiology

[00453] Cell lines expressing Nav channels. Stable cell lines constitutively expressing human (h) voltage-gated sodium (Nav) channels (HEK293-hNav1.2, CHO-hNav1.3, HEK293-hNav1.4, HEK293-hNav1.5, and HEK293-hNav1.7) or CHO cells expressing hNav1.8 under an inducible promoter were used for experiments.

[00454] Ion-Works® Quatro population patch clamp electrophysiology. Adherent cells were isolated from tissue culture flasks using 0.25% trypsin-EDTA treatment for 10 minutes and were resuspended in external solution consisting of 140 mM NaCl, 5.0 mM KCl, 10 mM HEPES, 2 mM $CaCl_2$, 1 mM $MgCl_2$, 10 mM Glucose, pH 7.4. Internal solution consisted of 70 mM KCl, 70mM KF, 10 HEPES, 5mM EDTA, pH 7.3. Cells were voltage clamped, using the perforated patch clamp configuration at room temperature (~22°C), to -110mV and depolarized to -10mV before and 5 min after test compound addition. Compound dilutions contained 0.1% bovine serum albumin to minimize non-specific binding. Peak inward currents were measured from different cells for each compound concentration and IC_{50} values were calculated with Excel software. All compounds were tested in duplicate (n = 2).

[00455] PatchXpress® 7000A electrophysiology. Adherent cells were isolated from tissue culture flasks using 1:10 diluted 0.25% trypsin-EDTA treatment for 2-3 minutes and then were incubated in complete culture medium containing 10% fetal bovine serum for at least 15 minutes prior to resuspension in external solution consisting of 70 mM NaCl, 140 mM D-Mannitol, 10 mM HEPES, 2 mM $CaCl_2$, 1 mM $MgCl_2$, pH 7.4 with NaOH. Internal solution consisted of 62.5 mM CsCl, 75mM CsF, 10 HEPES, 5 mM EGTA, 2.5 mM $MgCl_2$, pH 7.25 with CsOH. Cells were voltage clamped using the whole cell patch clamp configuration at room temperature (~22°C) at a holding potential of -125mV with test potentials to -10mV (hNav1.2, hNav1.3, hNav1.4, and hNav1.7) or -20mV (hNav1.5). To record from partially inactivated channels, cells were switched to a voltage that yielded ~20% channel inactivation. Test compounds were added and Nav currents were monitored at 0.1 Hz at the appropriate test potential. All compound dilutions contained 0.1% bovine serum albumin to minimize non-specific binding. Cells were used for additional compound testing if currents recovered to >80% of starting values following compound washout. IC_{50} values were calculated by pooling single point determinations at different compound concentrations and fitting the resulting dataset with a Hill (4-parameter logistic) fit in DataXpress 2.0 software.

[00456] Whole cell patch clamp electrophysiology. Cells were voltage clamped using the whole cell patch clamp configuration at room temperature (~22°C). Pipette resistances were between 1.5 and 2.0 MΩ. Whole cell capacitance and series resistance were uncompensated. Currents were digitized at 50 kHz and filtered (4-pole Bessel) at 10 kHz using pClamp10.2. Cells were lifted off the culture dish and positioned directly in front of a micropipette connected to a solution exchange manifold for compound perfusion. To record from non-inactivated channels, cells were held at -140 mV and depolarized to -10 mV (0 mV for hNav1.8). To record from partially inactivated channels, cells were held at -140 mV initially and then switched to a voltage that yielded ~20% channel inactivation. 10 ms pulses were delivered every 10 seconds and peak inward currents were recorded before and after compound addition. Compound dilutions contained 0.1% bovine serum albumin to minimize non-specific binding. For hNav1.8 channel recordings, tetrodotoxin (TTX, 0.5 uM) was added to inhibit endogenous TTX-sensitive voltage-gated sodium channels and record only Nav1.8-

mediated TTX-resistant currents. External solution consisted of: 140 mM NaCl, 5.0 mM KCl, 2.0 mM $CaCl_2$, 1.0 mM $MgCl_2$, 10 mM HEPES, and 11 mM Glucose, pH 7.4 by NaOH. Internal solution consisted of: 62.5 mM CsCl, 75 mM CsF, 2.5 mM $MgCl_2$, 5 mM EGTA, and 10 mM HEPES, pH 7.25 by CsOH. Escalating compound concentrations were analyzed on the same cell and IC_{50} values were calculated with Clampfit 10.2 software and by fitting the resulting dataset with a Hill (4-parameter logistic) fit in Origin Pro 8 software.

[00457] DRG neuron isolation. Adult male and female C57BL/6 mice (Harlan Laboratories, Indianapolis, IN) were euthanized with sodium pentobarbital (Nembutal, 80 mg/kg, i.p., Western Med Supply, Arcadia, CA) followed by decapitation. DRG from cervical, thoracic and lumbar regions were removed, placed in Ca^{2+} and Mg^{2+}-free Hanks' Balanced Salt Solution (Invitrogen, Carlsbad, CA), and trimmed of attached fibers under a dissecting microscope. DRG were sequentially digested at 37°C with papain (20 U/ml, Worthington Biochemical Corporation, Lakewood, NJ) and L-cysteine (25 μM) in Ca^{2+} and Mg^{2+}-free Hanks' (pH 7.4) for 20-30 min and then with collagenase type 2 (0.9% w/v, Worthington Biochemical Corporation) for 20-30 min. Digestions were quenched with a 1:1 mixture of DMEM and Ham's F-12 Nutrient Mixture (Invitrogen) supplemented with 10% calf serum (Invitrogen), and cells were triturated with a fire-polished Pasteur pipette prior to plating on Poly-D-Lysine-coated glass coverslips (Cole-Parmer, Vernon Hills, IL). Cells were maintained in a humidified incubator at 28°C with 5% CO_2 for 3-7 days in the presence of 1% NSF-1 (Lonza, Basel, Switzerland) to increase the expression of tetrodotoxin-sensitive sodium channel currents.

[00458] Manual patch-clamp electrophysiology for DRG neurons. DRG neurons were voltage clamped using the whole-cell patch clamp configuration at room temperature (21-24°C) using an Axopatch 200 B or MultiClamp 700 B amplifier and DIGIDATA 1322A with pCLAMP software (Molecular Devices, Sunnyvale, CA). Pipettes, pulled from borosilicate glass capillaries (World Precision Instruments, Sarasota, FL), had resistances between 1.0 and 3.0 MΩ. Voltage errors were minimized using >80% series resistance compensation. A P/4 protocol was used for leak subtraction. Currents were digitized at 50 kHz and filtered (4-pole Bessel) at 10 kHz. Cells were lifted off the culture dish and positioned directly in front of a micropipette

connected to a solution exchange manifold for compound perfusion. Cells were held at -140 mV or a voltage yielding approximately 20% inactivation and depolarized to -10 mV for 40 msec every 10 seconds. Tetrodotoxin (TTX, Sigma) was used following peptide addition to block any residual TTX-sensitive sodium currents. Pipette solution contained (in mM): 62.5 CsCl, 75 CsF, 2.5 $MgCl_2$, 5 EGTA, and 10 HEPES, pH 7.25 by CsOH. Bath solution contained (in mM): 70 NaCl, 5.0 KCl, 2.0 $CaCl_2$, 1.0 $MgCl_2$, 10 HEPES, and 11 glucose, 140 mannitol, pH 7.4 by NaOH. Data were analyzed with Clampfit and Origin Pro8 (OriginLab Corp, Northampton, MA).

[00459] Results of electrophysiology studies and structure-activity relationship. Results of electrophysiology studies are shown in Table 6 through Table 32, below. Extensive systematic analoging has given considerable insight into how individual positions within GpTx-1 (SEQ ID NO:1) contribute to its overall VGSC activity profile. Concerning the overall molecular framework, the disulfide bonds (or diselenide bonds) between Cys9 (or SeCys9) and Cys23 (or SeCys23) (C2—C5) and between Cys16 (or SeCys16) and Cys30 (or SeCys30) (C3—C6) are essential for function. However, simultaneous substitution of Cys2 and Cys17, as in [2-Abu2,17]GpTx-1 (SEQ ID NO: 125), which removes the (C1—C4) disulfide bond, retains significant activity against $Na_V1.7$ and $Na_V1.3$ with potentially improved selectivity against Nav1.4. (See, Table 29).

[00460] The N-terminal portion of GpTx-1, including the N-terminus, Asp1, Leu3, and Gly4, is amenable to modification without affecting either VGSC potency or selectivity in comparison with GpTx-1. (See, Table 7, Table 8, Table 9, and Table 10). Extension of the polypeptide chain by coupling additional amino acid(s) to to the N-terminus is well-tolerated. (See Table 7). Acetylation of the N-terminal aspartic acid residue to give Ac-GpTx-1 (SEQ ID NO:132) maintains potency at $Na_V1.7$ and increases selectivity against $Na_V1.3$ and $Na_V1.4$ in the PatchXpress® (PX) format. (See, Table 30). Asp1 of GpTx-1 can be truncated or substituted with a variety of amino acids with no impact on potency at $Na_V1.7$ and $Na_V1.3$ or selectivity against $Na_V1.4$ and $Na_V1.5$. (See Table 8). Leu3 and Gly4 in GpTx-1 may be individually replaced with a hydrophobic or a basic amino acid and still retain potency against $Na_V1.7$ and $Na_V1.3$, but these positions are less tolerant of substitution with acidic

residues. (See Table 9 and Table 10). However, substitution of glutamic acid for Leu3 increases selectivity against Nav1.4 in the PX assay format. (See Table 30).

[00461] Hydrophobic residues at positions 5 and 6 (Phe5 and Met6 in GpTx-1), in relation to SEQ ID NO:1, are essential to $Na_V1.7$ and $Na_V1.3$ inhibitory potency. (See Table 11 and Table 12). The identity of the amino acid at position 5 in GpTx-1 (SEQ ID NO:1) also has great impact on the selectivity of the peptide between $Na_V1.7$, $Na_V1.3$, and $Na_V1.4$. Substitution of aliphatic or aromatic hydrophobic residues for the native phenylalanine maintains or increases potency against $Na_V1.7$ while increasing selectivity against $Na_V1.4$ and not reducing the selectivity against $Na_V1.5$. (See Table 11). Incorporation of alanine in [Ala5]GpTx-1 (SEQ ID NO:22) retains potency against $Na_V1.7$ while greatly increasing selectivity against $Na_V1.3$ and Nav1.4 in the PX format. Besides alanine, many other aliphatic residues may be incorporated at position 5 to improve selectivity against Nav1.4, including but not limited to glycine, 2-aminobutyric acid (Abu), 2-aminoisobutyric acid (Aib), norvaline, valine, leucine, and isoleucine. (See Table 30). Two para-substituted phenylalanine derivatives, [pI-Phe5]GpTx-1 (SEQ ID NO:247) and [Bip5]GpTx-1 (SEQ ID NO:242) have increased potency against $Na_V1.3$ and are selective against $Na_V1.7$. (See Table 30). Incorporation of hydrophobic residues at position 6 increases potency against all four Na_V sub-types tested in proportion to their size. (See Table 12). A variety of hydrophobic residues including leucine and phenylalanine can be incorporated at position 6 in combination with alanine at position 5 to maintain good potency against Nav1.7 and selectivity against Nav1.4 in the PX assay format. (See Table 30).

[00462] While each position has recognizable preferences, the sequence of amino acids from Arg8 to Thr26 is quite tolerant of individual substitutions, with the exception of Asp14 relative to SEQ ID NO:1. Peptides synthesized without an aspartic acid residue at position 14 of GpTx-1 have not been isolated in sufficiently pure form for screening, indicating this residue may be critical for proper folding of the peptide. Basic or neutral hydrophilic amino acids are acceptable as substitutions for Arg7 and Lys8, relative to SEQ ID NO:1, to maintain $Na_V1.7$ and $Na_V1.3$ inhibitory potency. (See Table 13). However, substitution of glutamic acid for Arg7 increases selectivity against Nav1.4 in the PX assay format. (See Table 30). Ile10, Pro11, Asp12, Asn13, Lys15, Arg18, and Pro19, relative to SEQ ID NO:1, can be substituted with a variety of amino

acids with little effect on potency against $Na_V1.7$ and $Na_V1.3$. (See Table 14, Table 15, Table 16, Table 17, and Table 18). The ability to substitute alternative residues for Pro11, i.e., [Glu11]GpTx-1 (SEQ ID NO:147) and [Trp11]GpTx-1 (SEQ ID NO:171), without affecting Nav1.7 activity is notable, since this residue is conserved in the peptide sequences of HWTX-IV SEQ ID NO:528) and HWTX-I (SEQ ID NO:529). (See Table 15; Figure 15A-B). Substitutions of acidic residues at positions 10 or 11 can improve selectivity against Nav1.4, i.e., [Asp10]GpTx-1 (SEQ ID NO:119) , [Glu10]GpTx-1 (SEQ ID NO:146) , and [Glu11]GpTx-1 (SEQ ID NO:147) (See Table 30). Substitution of Asn13 improves the Fmoc solid-phase synthesis of the peptide analogs, likely through reduction of aspartimide formation during subsequent Fmoc-removal steps. Substitutions at position 18 can improve selectivity against Nav1.4. (See Table 18 and Table 30). Asn20, Leu21, Val22, Ser24, Arg25, and Thr26, relative to SEQ ID NO:1, may be individually substituted with non-acidic amino acids and retain full Nav1.7 and Nav1.3 inhibitory potencies. (See Table 19, Table 20, Table 21, and Table 22). The threonine at position 26 of GpTx-1 (SEQ ID NO:1) differs from the conserved lysine in HWTX-IV (SEQ ID NO:528) and HWTX-I (SEQ ID NO:529; see Figure 15A-B). Substitutions at this position increase selectivity against $Na_V1.4$ as in [Leu26]GpTx-1 (SEQ ID NO:121) and [Glu26]GpTx-1 (SEQ ID NO:152). (See Table 30). The loop in GpTx-1 (SEQ ID NO:1) between Cys17 and Cys23 may be increased or decreased in length by insertion or deletion of one amino acid residue without substantial impact on the activity of the peptide against the VGSCs tested, as shown by [Ser-Ser19]GpTx-1 (SEQ ID NO:93) and [Glu18;desAsn20]GpTx-1 (SEQ ID NO:134). (See Table 18 and Table 29).

[00463] The C-terminal portion of the GpTx-1 sequence is most critical for the activity of the peptide against $Na_V1.7$ and $Na_V1.3$. Substitution of His27 in GpTx-1 (SEQ ID NO:1) with retention of potency and selectivity is best accomplished with aromatic and basic residues. See Table 23). Residues Lys28 and Val33, relative to SEQ ID NO:1, are most tolerant to substitution with a variety of different amino acids without affecting $Na_V1.7$ and $Na_V1.3$ inhibitory potency. (See Table 23 and Table 26). [Arg28]GpTx-1 (SEQ ID NO:72), [Glu28]GpTx-1 (SEQ ID NO:153), [Asp28]GpTx-1 (SEQ ID NO:750), [Gln28]GpTx-1 (SEQ ID NO:763), and [Glu33]GpTx-1 (SEQ ID NO:33), show increased selectivity against $Na_V1.4$. (See Table 30). A trytophan (or

thiotryptophan) at position 29 of GpTx-1 (SEQ ID NO:1) appears to be important to obtain high levels of potency against $Na_V1.7$ and $Na_V1.3$. (See Table 24). Analogs with large hydrophobic substitutions, [1-Nal29]GpTx-1 (SEQ ID NO:79) and [2-Nal29]GpTx-1 (SEQ ID NO:129), retain the most activity but are still 5-fold less potent than GpTx-1, though they may have increased selectivity against Nav1.4. (See Table 30). Lys31, relative to SEQ ID NO:1, is also apparently important for potent inhibition of Nav1.7 and $Na_V1.3$ by GpTx-1. (See Table 25). The tyrosine at position 32 of GpTx-1 (SEQ ID NO:1) can be substituted with aliphatic or aromatic hydrophobic amino acids with retention of potency against $Na_V1.7$ and $Na_V1.3$, but these substitutions often increase activity against $Na_V1.5$ and $Na_V1.4$, leading to reduced selectivity. (See Table 25). The phenylalanine at position 34 of GpTx-1 (SEQ ID NO:1) can only be substituted with other hydrophobic amino acids without losing potency against $Na_V1.7$ and $Na_V1.3$, though large hydrophobic amino acids tend to increase potency and hence reduce selectivity against $Na_V1.4$ and $Na_V1.5$. (See Table 27). The C-terminus of GpTx-1 (SEQ ID NO:1) is amenable to extension by at least one amino acid with retention of Na_V inhibitory activity, but truncation of the C-terminus of GpTx-1 or substitution of the native C-terminal amide with a free acid reduces potency against $Na_V1.7$ and $Na_V1.3$. (See Table 28). Additional analogs of GpTx-1 (SEQ ID NO:1) that combine individual substitutions have demonstrated further improvements in selectivity against $Na_V1.4$ and $Na_V1.5$ and potency toward Nav1.7 and Nav1.3, i.e., [Ala5,Phe6,Leu26,Arg28]GpTx-1 (SEQ ID NO:262) and [Ala5,Phe6,Glu10,2-Abu13,Leu26,Arg28]GpTx-1 (SEQ ID NO:1035). (See Table 29 and Table 30). The IC_{50} of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) against partially inactivated hNav1.2 channels was 0.265 μM.

[00464] Manual whole cell patch clamp electrophysiology was performed on GpTx-1 (SEQ ID NO:1) and [Ala5]GpTx-1 (SEQ ID NO:22) on human clones of Nav1.7, Nav1.3, Nav1.4, and Nav1.5. Testing with 100 nM GpTx-1 showed complete inhibition of the Nav1.7 current. (See Figure 20). The IC_{50} value of Nav1.7 inhibition for GpTx-1 was 7.40 nM. (See Figure 21). The effects of GpTx-1 addition in increasing concentrations and wash out on Nav1.7 current were recorded. (See Figure 22). Testing with 300 nM GpTx-1 showed complete inhibition of the Nav1.3 current. (See Figure 23). The IC_{50} value of Nav1.3 inhibition for GpTx-1 was 16.8 nM. (See Figure 24).

The effects of GpTx-1 addition in increasing concentrations and wash out on Nav1.3 current were recorded. (See Figure 25). Testing with 3.0 μM GpTx-1 showed partial inhibition of the Nav1.4 current. (See Figure 26). The IC_{50} value of Nav1.4 inhibition for GpTx-1 was 2.9 μM and 0.26 μM for the closed and partially inactivated states, respectively. (See Figures 27 and 28). The effects of GpTx-1 addition in increasing concentrations and wash out on Nav1.4 current were recorded on the closed and partially inactivated states, respectively. (See Figures 29 and 30). GpTx-1 is more potent against hNav1.4 when channels are partially inactivated. Testing with 3.0 μM GpTx-1 showed weak inhibition of the Nav1.5 current. (See Figure 31). The IC_{50} value of Nav1.5 inhibition for GpTx-1 was 8.9 μM. (See Figure 32). The effects of GpTx-1 addition in increasing concentrations and wash out on Nav1.5 current were recorded. (See Figure 33). These results demonstrate that GpTx-1 (SEQ ID NO:1) is a potent dual peptide inhibitor of Nav1.7 and Nav1.3 with selectivity against Nav1.4 and Nav1.5. Testing with 300 nM [Ala5]GpTx-1 (SEQ ID NO:22) showed complete inhibition of the Nav1.7 current. (See Figure 34). The IC_{50} value of Nav1.7 inhibition for [Ala5]GpTx-1 was 13.2 nM. (See Figure 35). The effects of [Ala5]GpTx-1 addition in increasing concentrations and wash out on Nav1.7 current were recorded. (See Figure 36). These results demonstrate that [Ala5]GpTx-1 (SEQ ID NO:22) is also a potent inhibitor of Nav1.7.

[00465] Manual patch clamp electrophysiology was performed on GpTx-1 (SEQ ID NO:1) and [Ala5]GpTx-1 (SEQ ID NO:22) on isolated mouse DRG neurons. The effects of GpTx-1 addition in increasing concentrations and wash out on sodium channel current in mouse DRG neurons were recorded. (See Figure 37). The IC_{50} value of TTX-sensitive sodium channel current inhibition for GpTx-1 was 7.1 nM. (See Figure 38). Testing with 200 nM GpTx-1 showed almost complete inhibition of the TTX-sensitive sodium current in mouse DRG neurons. (See, Figure 39). The effects of GpTx-1 addition in increasing concentrations and wash out on sodium channel current in mouse DRG neurons at a holding voltage that produced 20% inactivation were recorded. (See Figure 40). The IC_{50} value of TTX-sensitive sodium channel current inhibition with a holding voltage yielding 20% inactivation for GpTx-1 was 4.7 nM. (See Figure 41). Testing with 200 nM GpTx-1 showed complete inhibition of the TTX-sensitive sodium current in mouse DRG neurons with a holding voltage that yielded

20% inactivation (See, Figure 42). The effects of [Ala5]GpTx-1 (SEQ ID NO:22) addition in increasing concentrations and wash out on sodium channel current in mouse DRG neurons were recorded. (See, Figure 43). The IC_{50} value of TTX-sensitive sodium channel current inhibition for [Ala5]GpTx-1 (SEQ ID NO:22) was 17.0 nM. (See Figure 44). Testing with 300 nM GpTx-1 showed almost complete inhibition of the TTX-sensitive sodium current in mouse DRG neurons. (See, Figure 45).

[00466] Manual whole cell patch clamp electrophysiology was performed on Homodimeric Conjugate 1 on human clones of Nav1.7 and Nav1.5 (see, Example 5). The effects of adding Homodimeric Conjugate 1 in increasing concentrations and wash out on Nav1.7 current were recorded. (See Figure 46). The IC_{50} value of Nav1.7 inhibition for Homodimeric Conjugate 1 was 1.2 nM. (See, Figure 47). Testing with 3 nM Homodimeric Conjugate 1 showed that the compound was very slow to wash out during an extended wash (10min), and testing with 300 nM Homodimeric Conjugate 1 showed that the compound did not wash out during an extended wash (10 min). (See Figure 48). Testing with 300 nM Homodimeric Conjugate 1 gave complete inhibition of the Nav1.7 current. (See Figure 49). The effects of Homodimeric Conjugate 1 addition in increasing concentrations and wash out on Nav1.7 current with a holding votage that yielded ~20% inactivation were recorded. (See Figure 50). The IC_{50} value of Nav1.7 inhibition with a holding votage that yielded ~20% inactivation for Homodimeric Conjugate 1 was 0.66 nM. (See Figure 51). Testing with 3 nM Homodimeric Conjugate 1 gave complete inhibition of the Nav1.7 current with a holding votage that yielded ~20% inactivation. (See Figure 52). The effects of Homodimeric Conjugate 1 addition in increasing concentrations and wash out on Nav1.5 current were recorded. (See Figure 53). The IC_{50} value of Nav1.5 inhibition for Homodimeric Conjugate 1 was 75.5 nM. (See Figure 54). Testing with 2 μM Homodimeric Conjugate 1 gave complete inhibition of the Nav1.5 current. (See Figure 55). The effects of Homodimeric Conjugate 1 addition in increasing concentrations and wash out on Nav1.5 current with a holding votage that yielded ~20% inactivation were recorded. (See Figure 56). The IC_{50} value of Nav1.5 inhibition with a holding votage that yielded ~20% inactivation for Homodimeric Conjugate 1 was 57 nM. (See Figure 57). Testing with 2 μM Homodimeric Conjugate 1 gave complete inhibition of

the Nav1.5 current with a holding votage that yielded ~20% inactivation. (See Figure 58).

[00467] Potassium channel study. Dorsal root ganglia were harvested from adult Sprague-Dawley rats (aged 14 to 15 weeks), trimmed of connective tissue, and enzymatically dissociated with papain (3 mL calcium and magnesium-free Hank's buffer + 1 mg L-cysteine + 4 uL saturated sodium bicarbonate + 60 microliters papain, Worthington biochemical) for 30 minutes at 37°C. The preparation was spun at 1000 rpm for 2 minutes and the pellet was resuspended for a second enzymatic incubation in collagenase and dispase (4 mL calcium and magnesium-free Hank's buffer + 120 microliters of collagenase / dispase mix 100 mg/mL from Roche) for 60 minutes with gentle trituration every 10 minutes. Cells were spun again at 2000 rpm for 2 minutes, resuspended in F-12 medium, plated on poly-D-laminin coated coverslips, placed in a humidified 37°C incubator with 5% CO_2, and used for electrophysiological recording on the same day.

[00468] Electrophysiological recordings were made with the whole-cell configuration of the patch-clamp technique (Hamill OP et al., "Improved patch-clamp techniques for high-resolution current recording from cells and cell-free membrane patches, Pfluger's Archiv 391:85-100, 1981), with internal (pipette) solution containing, in millimolar, 70 KF, 70 KCl, 10 HEPES, 5 HEDTA, pH 7.25 with KOH. External solution contained, in millimolar, 140 NaCl, 5 KCl, 2 $CaCl_2$, 1 $MgCl_2$, 10 HEPES, 10 glucose, pH 7.4 with NaOH. After formation of the whole-cell configuration of the patch clamp, the cell was lifted off the dish bottom by moving the patch pipette and manually positioned in front of a gravity-driven microperfusion array under electronic control (BioLogique). Combined sodium and potassium currents were evoked every 5 seconds by a 20 ms test depolarization to 0 mV delivered from a holding potential of -90 mV. [Ala5]GpTx-1 (SEQ ID NO:22; 500 nM) peptide was added by switching perfusion tubes, and while fast sodium currents (presumably tetrodotoxin-sensitive, encoded at least partially by Nav1.7) steadily decreased, reflecting block by peptide, there was no change in the outward potassium currents. Currents shown in Figure 94 are not leak-subtracted, but as the test pulse was to 0 mV, contamination by leak currents should be minimal. The results shown in Figure 94 demonstrate that 500 nM [Ala5]GpTx-1 (SEQ ID NO:22) did not block voltage-gated potassium currents.

Table 6. Electrophysiology by IonWorks® Quattro: comparison of GpTx-1 (SEQ ID NO:1) and other toxins from *Grammostola porteri*.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1. 3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
467	{H}-DCLGFMRKCSPDNDKCCRPNLVCSRKHKWCKYEI-{Amide}	GpTx-2(1-34)	4.34	7.21	11.73	1.15	2.7	10.2	3.8
468	{H}-DCLGWFKGCDPDNDKCCEGYKCNRRDKWCKYKL-{Amide}	GpTx-3(1-33)	8.93	7.80	20.00	9.37	2.2	2.1	1.0
469	{H}-DCLGWFKGCDPDNDKCCENYKCNRREQWCKYKL-{Amide}	GpTx-4(1-33)	9.25	10.38	11.00	4.92	1.2	2.2	1.9
473	{H}-DCLGWFKGCDPDNDKCCENYKCNRRDKWCKYKLWK-{FreeAcid}	GpTx-7(1-35)	10.4	7.6	10.0	3.5	1.0	2.8	2.9
474	{H}-DCLGWFKGCDPDNDKCCENYKCNRRDKWCKYKLW-{FreeAcid}	GpTx-7(1-34)	4.0	7.9	10.5	1.4	2.6	7.7	2.9
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 7. Electrophysiology by IonWorks® Quattro: Position 0 additions relative to GpTx-1 (SEQ ID NO:1) and Ac-GpTx-1 (SEQ ID NO:132).

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1. 3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
100	{H}-ADCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	Ala-GpTx-1(1-34)	0.37	19.58	7.07	0.32	19.2	21.9	1.1
17	{H}-EDCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	Glu-GpTx-1(1-34)	0.26	12.77	3.63	0.19	13.9	18.7	1.3
36	{H}-KDCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	Lys-GpTx-1(1-34)	0.11	8.35	2.38	0.10	20.8	23.6	1.1
61	{H}-RDCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	Arg-GpTx-1(1-34)	0.17	15.08	2.58	0.08	15.6	31.8	2.0
106	{H}-WDCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	Trp-GpTx-1(1-34)	0.22	21.96	3.83	0.25	17.5	15.1	0.9
201	{H}-[1-Nal]DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	1-Nal-GpTx-1(1-34)							
132	{Acetyl}DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	Ac-GpTx-1(1-34)	0.31	12.69	2.86	0.22	9.3	12.9	1.4
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 8. Electrophysiology by IonWorks® Quattro Position 1 substitutions or deletions relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
20	{H}-ACLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala1]GpTx-1(1-34)	0.10	9.86	1.68	0.08	16.8	21.1	1.3
18	{H}-ECLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu1]GpTx-1(1-34)	0.22	14.16	3.46	0.15	15.7	23.2	1.5
37	{H}-KCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Lys1]GpTx-1(1-34)	0.15	7.29	1.49	0.07	10.2	21.0	2.1
62	{H}-RCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Arg1]GpTx-1(1-34)	0.11	8.78	1.45	0.10	12.9	15.2	1.2
81	{H}-WCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Trp1]GpTx-1(1-34)	0.05	8.79	3.06	0.10	56.1	30.9	0.6
77	{H}-[1-Nal]CLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal1]GpTx-1(1-34)	0.11	13.38	6.77	0.14	62.9	48.0	0.8
97	{H}-YCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Tyr1]GpTx-1(1-34)	0.16	10.61	3.89	0.13	24.5	29.0	1.2
108	{H}-CLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(2-34)	0.07	8.22	1.10	0.05	14.8	20.3	1.4
188	{H}-[PE]CLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[PE1]GpTx-1(1-34)	0.17	10.69	2.64	0.11	15.7	24.2	1.5
189	{H}-ICLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ile1]GpTx-1(1-34)	0.10	8.15	1.34	0.07	13.1	20.3	1.5
190	{H}-PCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Pro1]GpTx-1(1-34)	0.09	9.73	1.19	0.04	13.7	29.4	2.2
191	{H}-SCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ser1]GpTx-1(1-34)	0.07	9.40	1.14	0.05	15.7	21.2	1.4
192	{H}-TCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Thr1]GpTx-1(1-34)	0.11	9.21	1.41	0.07	12.5	20.5	1.6
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 9. Electrophysiology by IonWorks® Quattro: Position 3 substitutions relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav 1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
21	{H}-DCAGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala3]GpTx-1(1-34)	0.51	19.01	14.46	0.10	28.2	138.2	4.9
19	{H}-DCEGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu3]GpTx-1(1-34)	0.67	10.47	8.34	0.83	12.5	10.0	0.8
38	{H}-DCKGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Lys3]GpTx-1(1-34)	0.08	6.95	1.87	0.06	23.0	33.1	1.4
155	{H}-DCRGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Arg3]GpTx-1(1-34)	0.03	8.45	0.85	0.05	26.7	16.0	0.6
98	{H}-DCQGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Gln3]GpTx-1(1-34)	0.25	16.40	5.25	0.24	20.7	21.5	1.0
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 10. Electrophysiology by IonWorks® Quattro: Position 4 substitutions relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
141	{H}-DCLAFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala4]GpTx-1(1-34)	0.27	11.30	3.24	0.21	12.0	15.4	1.3
24	{H}-DCLEFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu4]GpTx-1(1-34)	1.74	17.61	8.50	1.33	4.9	6.4	1.3
39	{H}-DCLKFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Lys4]GpTx-1(1-34)	0.20	9.82	6.49	0.18	32.7	36.2	1.1
53	{H}-DCLRFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Arg4]GpTx-1(1-34)	0.21	20.09	5.82	0.23	27.1	24.8	0.9
169	{H}-DCLWFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Trp4]GpTx-1(1-34)	0.05	10.33	0.52	0.03	10.0	19.3	1.9
160	{H}-DCL[1-Nal]FMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal4]GpTx-1(1-34)	0.04	5.09	0.50	0.03	13.7	18.9	1.4
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 11. Electrophysiology by IonWorks® Quattro: Position 5 substitutions relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4 / Nav1.3	Nav1.7 / Nav1.3
22	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5]GpTx-1(1-34)	0.64	10.34	11.07	1.75	17.4	6.3	0.4
143	{H}-DCLGEMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu5]GpTx-1(1-34)	17.67	10.01	22.26	22.29	1.3	1.0	0.8
156	{H}-DCLGRMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Arg5]GpTx-1(1-34)	3.63	12.64	25.69	4.09	7.1	6.3	0.9
82	{H}-DCLGWMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Trp5]GpTx-1(1-34)	0.15	9.32	2.30	0.11	15.6	21.4	1.4
105	{H}-DCLG[1-Nal]MRKCIPDND KCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal5]GpTx-1(1-34)	0.08	13.41	2.13	0.10	26.4	21.7	0.8
88	{H}-DCLGIMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ile5]GpTx-1(1-34)	0.36	6.65	10.78	0.62	30.0	17.3	0.6
128	{H}-DCLG[2-Nal]MRKCIPDND KCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Nal5]GpTx-1(1-34)	0.11	6.11	0.94	0.06	8.2	17.3	2.1
242	{H}-DCLG[Bip]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Bip5]GpTx-1(1-34)	0.06	3.38	0.14	-	2.3	-	-
243	{H}-DCLG[Cha]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Cha5]GpTx-1(1-34)	0.01	6.99	0.64	0.02	47.6	34.8	0.7
247	{H}-DCLG[pI-Phe]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[pI-Phe5]GpTx-1(1-34)	0.16	6.16	19.68	0.02	121.9	1152.0	9.4
264	{H}-DCLG[1'NMeW]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1'NMeW5]GpTx-1(1-34)	0.09	8.17	2.81	0.09	32.9	30.5	0.9
265	{H}-DCLGGMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Gly5]GpTx-1(1-34)	0.75	7.47	10.73	1.24	14.3	8.6	0.6
266	{H}-DCLGHMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[His5]GpTx-1(1-34)	4.74	6.62	14.86	8.37	3.1	1.8	0.6
267	{H}-DCLGLMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Leu5]GpTx-1(1-34)	0.17	7.40	12.14	0.30	70.9	40.0	0.6

268	{H}-DCLGMMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Met5]GpTx-1(1-34)	0.10	12.81	11.20	0.24	113.6	45.9	0.4
269	{H}-DCLGPMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Pro5]GpTx-1(1-34)	1.17	6.61	11.40	1.73	9.7	6.6	0.7
270	{H}-DCLGTMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Thr5]GpTx-1(1-34)	1.22	15.25	15.54	2.19	12.7	7.1	0.6
271	{H}-DCLGYMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Tyr5]GpTx-1(1-34)	1.43	15.58	6.48	1.64	4.5	3.9	0.9
272	{H}-DCLGVMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Val5]GpTx-1(1-34)	0.71	13.22	13.88	1.03	19.7	13.5	0.7
273	{H}-DCLGfMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[D-Phe5]GpTx-1(1-34)	1.23	>5	>5	3.00	-	-	0.4
274	{H}-DCLG[NMeTrp]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMeTrp5]GpTx-1(1-34)	0.19	>5	2.40	0.15	12.8	16.3	1.3
275	{H}-DCLG[Phg]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Phg5]GpTx-1(1-34)	0.09	>5	2.55	0.17	28.4	15.4	0.5
276	{H}-DCLG[4CO2-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4CO2-F5]GpTx-1(1-34)	15.96	8.12	21.45	5.42	1.3	4.0	2.9
277	{H}-DCLG[2PAL]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[2PAL5]GpTx-1(1-34)	2.07	9.25	11.86	4.58	5.7	2.6	0.5
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 12. Electrophysiology by IonWorks® Quattro: Position 6 substitutions relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
23	{H}-DCLGFARKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala6]GpTx-1(1-34)	0.51	17.38	3.71	0.21	7.3	17.5	2.4
144	{H}-DCLGFERKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu6]GpTx-1(1-34)	3.51	9.39	22.42	20.36	6.4	1.1	0.2
154	{H}-DCLGFKRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Lys6]GpTx-1(1-34)	14.52	13.95	24.95	8.49	1.7	2.9	1.7
64	{H}-DCLGFRRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Arg6]GpTx-1(1-34)	6.98	17.59	14.74	5.90	2.1	2.5	1.2
170	{H}-DCLGFWRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Trp6]GpTx-1(1-34)	0.015	3.58	0.25	0.002	19.1	123.5	6.5
161	{H}-DCLGF[1-Nal]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal6]GpTx-1(1-34)	0.007	2.34	0.27	0.006	39.3	43.8	1.1
89	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Phe6]GpTx-1(1-34)	0.05	9.21	1.39	0.03	28.2	40.7	1.4
3	{H}-DCLGF[SeMet]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[SeMet6]GpTx-1(1-34)	0.10	13.89	2.25	0.10	23.5	22.6	1.0
123	{H}-DCLGF[Nle]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Nle6]GpTx-1(1-34)	0.05	4.50	0.43	0.02	8.1	23.3	2.9
124	{H}-DCLGF[2-Abu]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Abu6]GpTx-1(1-34)	0.11	10.59	2.09	0.10	18.6	21.3	1.1
244	{H}-DCLGFLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Leu6]GpTx-1(1-34)	0.06	6.42	15.94	0.04	270.6	364.7	1.3
245	{H}-DCLGF[Cha]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Cha6]GpTx-1(1-34)	0.02	2.37	0.10	-	6.3	-	-
278	{H}-DCLGFNRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Asn6]GpTx-1(1-34)	6.89	10.27	21.16	6.28	3.1	3.4	1.1
279	{H}-DCLGFQRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Gln6]GpTx-1(1-34)	8.62	7.57	14.08	5.96	1.6	2.4	1.4

280	{H}-DCLGFGRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Gly6]GpTx-1(1-34)	0.18	8.20	2.89	0.14	15.7	20.5	1.3
281	{H}-DCLGFHRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[His6]GpTx-1(1-34)	4.72	10.06	17.82	7.77	3.8	2.3	0.6
282	{H}-DCLGFIRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ile6]GpTx-1(1-34)	0.07	8.63	1.19	0.06	16.6	18.9	1.1
283	{H}-DCLGFPRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Pro6]GpTx-1(1-34)	0.79	10.00	11.00	0.76	13.8	14.4	1.0
284	{H}-DCLGFSRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ser6]GpTx-1(1-34)	1.02	16.94	21.30	0.71	20.8	30.1	1.4
285	{H}-DCLGFTRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Thr6]GpTx-1(1-34)	0.59	18.71	4.25	0.28	7.2	15.4	2.1
286	{H}-DCLGFYRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Tyr6]GpTx-1(1-34)	0.97	6.38	11.59	0.52	11.9	22.2	1.9
287	{H}-DCLGFVRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Val6]GpTx-1(1-34)	0.09	9.23	1.77	0.08	18.8	23.4	1.2
288	{H}-DCLGF[Phg]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Phg6]GpTx-1(1-34)	0.15	>5	2.88	0.09	19.5	32.2	1.7
289	{H}-DCLGF[NMeTrp]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMeTrp6]GpTx-1(1-34)	0.14	21.45	3.69	0.24	26.5	15.4	0.6
290	{H}-DCLGF[NMePhe]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMePhe6]GpTx-1(1-34)	0.24	10.56	2.59	0.14	10.7	18.8	1.8
291	{H}-DCLGF[pI-Phe]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[pI-Phe6]GpTx-1(1-34)	0.02	0.95	0.04	-	2.6	-	-
292	{H}-DCLGF[1'NMeW]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1'NMeW6]GpTx-1(1-34)	0.04	5.66	0.42	0.03	10.2	16.6	1.6
293	{H}-DCLGF[4CO2-F]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4CO2-F6]GpTx-1(1-34)	15.79	11.11	21.50	13.78	1.4	1.6	1.1
294	{H}-DCLGF[2PAL]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[2PAL6]GpTx-1(1-34)	0.37	9.11	7.04	0.09	18.8	75.3	4.0
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 13. Electrophysiology by IonWorks® Quattro: Substitutions at position 7 or 8 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
43	{H}-DCLGFMAKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala7]GpTx-1(1-34)	0.94	21.55	4.72	0.83	5.0	5.7	1.1
145	{H}-DCLGFMEKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu7]GpTx-1(1-34)	0.88	19.11	20.15	1.68	22.9	12.0	0.5
40	{H}-DCLGFMKKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Lys7]GpTx-1(1-34)	0.53	23.28	6.48	0.47	12.1	13.8	1.1
115	{H}-DCLGFM[Cit]KCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Cit7]GpTx-1(1-34)	0.63	14.37	6.52	0.56	10.3	11.7	1.1
295	{H}-DCLGFM[K(Me2)]KCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[K(Me2)7]GpTx-1(1-34)	0.82	13.27	10.69	0.27	13.0	39.0	3.0
296	{H}-DCLGFM[SDMA]KCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[SDMA7]GpTx-1(1-34)	0.24	10.34	4.89	0.12	20.2	39.2	1.9
44	{H}-DCLGFMRACIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala8]GpTx-1(1-34)	0.49	16.77	4.73	0.41	9.6	11.4	1.2
25	{H}-DCLGFMRECIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu8]GpTx-1(1-34)	1.70	24.85	13.46	1.36	7.9	9.9	1.2
65	{H}-DCLGFMRRCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Arg8]GpTx-1(1-34)	0.14	13.76	1.78	0.12	13.1	14.4	1.1
118	{H}-DCLGFMRTCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Thr8]GpTx-1(1-34)	0.35	9.86	6.13	0.15	17.4	41.3	2.4
297	{H}-DCLGFMR[SDMA]CIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[SDMA8]GpTx-1(1-34)	0.20	9.05	5.47	0.20	28.0	27.1	1.0
298	{H}-DCLGFMR[K(Me2)]CIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[K(Me2)8]GpTx-1(1-34)	0.19	9.46	4.43	0.18	23.1	25.2	1.1
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 14. Electrophysiology by IonWorks® Quattro: Substitutions at position 10 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
45	{H}-DCLGFMRKCAPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala10]GpTx-1(1-34)	0.21	16.48	2.95	0.19	14.1	15.5	1.1
146	{H}-DCLGFMRKCEPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu10]GpTx-1(1-34)	6.09	9.55	4.47	0.15	60.9	29.8	0.6
41	{H}-DCLGFMRKCKPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Lys10]GpTx-1(1-34)	0.24	9.00	2.57	0.15	10.9	17.3	1.6
66	{H}-DCLGFMRKCRPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Arg10]GpTx-1(1-34)	0.16	15.24	0.89	0.11	5.4	8.0	1.5
83	{H}-DCLGFMRKCWPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Trp10]GpTx-1(1-34)	0.10	8.02	4.35	0.19	44.1	23.1	0.5
78	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal10]GpTx-1(1-34)	0.15	10.03	9.02	0.21	58.3	42.9	0.7
90	{H}-DCLGFMRKCNPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Asn10]GpTx-1(1-34)	0.49	14.14	9.33	0.19	19.2	49.4	2.6
119	{H}-DCLGFMRKCDPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Asp10]GpTx-1(1-34)	0.22	11.34	8.36	0.16	37.4	52.9	1.4
299	{H}-DCLGFMRKCYPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Tyr10]GpTx-1(1-34)	0.14	5.41	0.96	0.07	6.7	14.5	2.2
300	{H}-DCLGFMRKC[NMeTrp]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMeTrp10]GpTx-1(1-34)	0.08	9.89	1.93	0.07	24.4	28.9	1.2
301	{H}-DCLGFMRKCVPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Val10]GpTx-1(1-34)	0.10	7.88	1.41	0.09	13.6	15.3	1.1
302	{H}-DCLGFMRKCFPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Phe10]GpTx-1(1-34)	0.11	5.33	1.08	0.08	9.7	12.8	1.3
303	{H}-DCLGFMRKCLPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Leu10]GpTx-1(1-34)	0.13	8.13	2.54	0.08	19.1	30.9	1.6
304	{H}-DCLGFMRKCHPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[His10]GpTx-1(1-34)	0.05	6.36	0.69	0.03	15.0	20.8	1.4
305	{H}-DCLGFMRKCSPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ser10]GpTx-1(1-34)	0.05	4.64	1.95	0.09	36.6	22.2	0.6
307	{H}-DCLGFMRKCMPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Met10]GpTx-1(1-	0.09	3.38	3.09	0.10	32.9	32.4	1.0

		34)							
308	{H}-DCLGFMRKCPPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Pro10]GpTx-1(1-34)	0.40	>5	1.19	0.24	3.0	5.0	1.7
309	{H}-DCLGFMRKCTPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Thr10]GpTx-1(1-34)	0.10	>5	1.08	0.06	10.7	17.7	1.7
310	{H}-DCLGFMRKC[4CO2-F]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4CO2-F10]GpTx-1(1-34)	0.28	6.87	3.94	0.23	14.2	17.3	1.2
311	{H}-DCLGFMRKC[2PAL]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[2PAL10]GpTx-1(1-34)	0.19	8.83	2.91	0.04	15.4	66.3	4.3
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.06	13.09	1.93	0.08	24.9	22.8	0.9

Table 15. Electrophysiology by IonWorks® Quattro: Substitutions at position 11 or 12 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
46	{H}-DCLGFMRKCIADNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala11]GpTx-1(1-34)	0.21	16.05	2.97	0.18	14.4	16.6	1.2
147	{H}-DCLGFMRKCIEDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu11]GpTx-1(1-34)	0.22	15.61	6.64	0.21	30.7	32.0	1.0
171	{H}-DCLGFMRKCIWDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Trp11]GpTx-1(1-34)	0.07	9.50	1.66	0.04	22.4	36.9	1.6
4	{H}-DCLGFMRKCIPANDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala12]GpTx-1(1-34)	0.12	8.05	0.70	0.13	6.0	5.4	0.9
26	{H}-DCLGFMRKCIPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu12]GpTx-1(1-34)	0.26	6.45	2.24	0.19	8.5	11.9	1.4
42	{H}-DCLGFMRKCIPKNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Lys12]GpTx-1(1-34)	0.12	6.51	0.53	0.09	4.5	5.8	1.3
67	{H}-DCLGFMRKCIPRNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Arg12]GpTx-1(1-34)	0.11	5.00	0.52	0.14	4.6	3.8	0.8
172	{H}-DCLGFMRKCIPWNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Trp12]GpTx-1(1-34)	0.05	8.04	0.49	0.04	10.4	12.7	1.2
162	{H}-DCLGFMRKCIP[1-Nal]NDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal12]GpTx-1(1-34)	0.06	9.88	0.55	0.04	9.4	12.3	1.3
91	{H}-DCLGFMRKCIPSNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ser12]GpTx-1(1-34)	0.08	9.58	1.68	0.19	20.5	8.9	0.4
194	{H}-DCLGFMRKCIPGNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Gly12]GpTx-1(1-34)	0.075	8.764	0.510	0.047	6.8	10.9	1.6
195	{H}-DCLGFMRKCIPINDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ile12]GpTx-1(1-34)	0.662	18.322	5.834	0.607	8.8	9.6	1.1
193	{H}-DCLGFMRKCIPLNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Leu12]GpTx-1(1-34)	0.080	6.832	0.586	0.071	7.4	8.2	1.1
196	{H}-DCLGFMRKCIPTNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Thr12]GpTx-1(1-34)	0.097	7.079	0.649	0.074	6.7	8.8	1.3

197	{H}-DCLGFMRKCIPYNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Tyr12]GpTx-1(1-34)	0.088	6.920	0.475	0.042	4.8	11.2	2.3
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 16. Electrophysiology by IonWorks® Quattro: Substitutions at position 13 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
5	{H}-DCLGFMRKCIPDADKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala13]GpTx-1(1-34)	0.17	8.15	2.64	0.16	15.9	16.9	1.1
27	{H}-DCLGFMRKCIPDEDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu13]GpTx-1(1-34)	0.26	9.38	4.41	0.22	17.2	19.8	1.2
48	{H}-DCLGFMRKCIPDKDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Lys13]GpTx-1(1-34)	0.21	9.72	2.44	0.13	11.5	19.1	1.7
103	{H}-DCLGFMRKCIPDRDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Arg13]GpTx-1(1-34)	0.16	15.96	4.64	0.22	29.4	21.4	0.7
173	{H}-DCLGFMRKCIPDWDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Trp13]GpTx-1(1-34)	0.09	17.29	2.28	0.05	26.2	49.3	1.9
163	{H}-DCLGFMRKCIPD[1-Nal]DKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal13]GpTx-1(1-34)	0.11	8.27	2.84	0.09	24.9	32.4	1.3
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.68	13.09	1.93	0.08	24.9	22.8	0.9

Table 17. Electrophysiology by IonWorks® Quattro: Substitutions at position 15 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
6	{H}-DCLGFMRKCIPDNDACCRPNLVCSRTHKWCKYVF-{Amide}	[Ala15]GpTx-1(1-34)	0.22	9.64	4.68	0.19	21.5	24.2	1.1
28	{H}-DCLGFMRKCIPDNDECCRPNLVCSRTHKWCKYVF-{Amide}	[Glu15]GpTx-1(1-34)	0.59	12.09	8.75	0.49	14.8	17.8	1.2
68	{H}-DCLGFMRKCIPDNDRCCRPNLVCSRTHKWCKYVF-{Amide}	[Arg15]GpTx-1(1-34)	0.20	18.14	2.27	0.14	11.2	16.0	1.4
92	{H}-DCLGFMRKCIPDNDQCCRPNLVCSRTHKWCKYVF-{Amide}	[Gln15]GpTx-1(1-34)	0.13	7.60	2.42	0.12	19.3	20.9	1.1
312	{H}-DCLGFMRKCIPDND[SDMA]CCRPNLVCSRTHKWCKYVF-{Amide}	[SDMA15]GpTx-1(1-34)	0.14	9.67	1.96	0.15	14.0	13.0	0.9
313	{H}-DCLGFMRKCIPDND[K(Me2)]CCRPNLVCSRTHKWCKYVF-{Amide}	[K(Me2)15]GpTx-1(1-34)	0.19	10.13	4.75	0.13	24.4	36.6	1.5
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 18. Electrophysiology by IonWorks® Quattro: Substitutions at position 18 or 19 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.7	Nav1.7/ Nav1.3
148	{H}-DCLGFMRKCIPDNDKCCEPNLVCSRTHKWCKYVF-{Amide}	[Glu18]GpTx-1(1-34)	0.22	14.60	4.95	0.21	22.8	23.7	1.0
49	{H}-DCLGFMRKCIPDNDKCCKPNLVCSRTHKWCKYVF-{Amide}	[Lys18]GpTx-1(1-34)	0.30	17.56	3.78	0.21	12.5	18.1	1.4
174	{H}-DCLGFMRKCIPDNDKCCWPNLVCSRTHKWCKYVF-{Amide}	[Trp18]GpTx-1(1-34)	0.19	14.73	8.66	0.08	46.6	108.0	2.3
116	{H}-DCLGFMRKCIPDNDKCC[Cit]PNLVCSRTHKWCKYVF-{Amide}	[Cit18]GpTx-1(1-34)	0.17	11.00	5.24	0.23	30.2	23.1	0.8
314	{H}-DCLGFMRKCIPDNDKCC[K(Me2)]PNLVCSRTHKWCKYVF-{Amide}	[K(Me2)18]GpTx-1(1-34)	0.21	6.55	6.70	0.08	31.8	82.8	2.6
315	{H}-DCLGFMRKCIPDNDKCC[SDMA]PNLVCSRTHKWCKYVF-{Amide}	[SDMA18]GpTx-1(1-34)	0.14	10.48	3.41	0.10	25.1	32.8	1.3
316	{H}-DCLGFMRKCIPDNDKCC[2PAL]PNLVCSRTHKWCKYVF-{Amide}	[2PAL18]GpTx-1(1-34)	0.19	9.17	9.85	0.06	51.9	167.0	3.2
50	{H}-DCLGFMRKCIPDNDKCCRKNLVCSRTHKWCKYVF-{Amide}	[Lys19]GpTx-1(1-34)	0.12	10.63	4.29	0.18	36.2	24.2	0.7
157	{H}-DCLGFMRKCIPDNDKCCRRNLVCSRTHKWCKYVF-{Amide}	[Arg19]GpTx-1(1-34)	0.07	6.16	1.42	0.06	21.0	23.4	1.1
181	{H}-DCLGFMRKCIPDNDKCCRSNLVCSRTHKWCKYVF-{Amide}	[Ser19]GpTx-1(1-34)	0.088	11.392	3.107	0.031	35.5	101.2	2.9
93	{H}-DCLGFMRKCIPDNDKCCRSSNLVCSRTHKWCKYVF-{Amide}	[Ser-Ser19]GpTx-1(1-34)	0.27	13.92	6.67	0.32	24.3	20.6	0.8
126	{H}-DCLGFMRKCIPDNDKCCRGNLVCSRTHKWCKYVF-{Amide}	[Gly19]GpTx-1(1-34)	0.10	11.92	1.82	0.11	18.6	17.2	0.9
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 19. Electrophysiology by IonWorks® Quattro: Substitutions at position 20 or 21 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
7	{H}-DCLGFMRKCIPDNDKCCRPALVCSRTHKWCKYVF-{Amide}	[Ala20]GpTx-1(1-34)	0.69	19.53	7.13	0.41	10.4	17.5	1.7
149	{H}-DCLGFMRKCIPDNDKCCRPELVCSRTHKWCKYVF-{Amide}	[Glu20]GpTx-1(1-34)	1.42	7.49	20.92	1.02	14.7	20.6	1.4
51	{H}-DCLGFMRKCIPDNDKCCRPKLVCSRTHKWCKYVF-{Amide}	[Lys20]GpTx-1(1-34)	0.61	18.96	3.72	0.33	6.1	11.4	1.9
69	{H}-DCLGFMRKCIPDNDKCCRPRLVCSRTHKWCKYVF-{Amide}	[Arg20]GpTx-1(1-34)	0.17	14.91	1.42	0.08	8.5	17.8	2.1
175	{H}-DCLGFMRKCIPDNDKCCRPWLVCSRTHKWCKYVF-{Amide}	[Trp20]GpTx-1(1-34)	0.05	7.39	0.85	0.02	16.7	37.6	2.3
164	{H}-DCLGFMRKCIPDNDKCCRP[1-Nal]LVCSRTHKWCKYVF-{Amide}	[1-Nal20]GpTx-1(1-34)	0.07	7.36	0.42	0.06	5.7	6.4	1.1
200	{H}-DCLGFMRKCIPDNDKCCRPYLVCSRTHKWCKYVF-{Amide}	[Tyr20]GpTx-1(1-34)	0.116	9.054	1.145	0.055	9.8	20.8	2.1
198	{H}-DCLGFMRKCIPDNDKCCRPGLVCSRTHKWCKYVF-{Amide}	[Gly20]GpTx-1(1-34)	0.229	9.754	2.629	0.126	11.5	20.9	1.8
199	{H}-DCLGFMRKCIPDNDKCCRPFLVCSRTHKWCKYVF-{Amide}	[Phe20]GpTx-1(1-34)	0.154	10.787	1.837	0.067	12.0	27.4	2.3
176	{H}-DCLGFMRKCIPDNDKCCRPNWVCSRTHKWCKYVF-{Amide}	[Trp21]GpTx-1(1-34)	0.10	13.75	2.65	0.05	26.8	48.6	1.8
165	{H}-DCLGFMRKCIPDNDKCCRPN[1-Nal]VCSRTHKWCKYVF-{Amide}	[1-Nal21]GpTx-1(1-34)	0.08	10.63	3.17	0.09	38.9	35.5	0.9
120	{H}-DCLGFMRKCIPDNDKCCRPNMVCSRTHKWCKYVF-{Amide}	[Met21]GpTx-1(1-34)	0.14	9.54	1.79	0.09	12.9	19.3	1.5
317	{H}-DCLGFMRKCIPDNDKCCRPN[4CO2-F]VCSRTHKWCKYVF-{Amide}	[4CO2-F21]GpTx-1(1-34)	3.98	8.90	19.74	3.67	5.0	5.4	1.1

318	{H}-DCLGFMRKCIPDNDKCCRPN[2PAL]VCSRTHKWCKYVF-{Amide}	[2PAL21]GpTx-1(1-34)	0.18	7.52	3.48	0.08	19.8	41.6	2.1
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 20. Electrophysiology by IonWorks® Quattro: Substitutions at position 22 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
8	{H}-DCLGFMRKCIPDNDKCCRPNLACSRTHKWCKYVF-{Amide}	[Ala22]GpTx-1(1-34)	0.38	20.43	13.76	0.32	36.1	43.2	1.2
102	{H}-DCLGFMRKCIPDNDKCCRPNLECSRTHKWCKYVF-{Amide}	[Glu22]GpTx-1(1-34)	1.40	20.78	8.31	2.14	6.0	3.9	0.7
52	{H}-DCLGFMRKCIPDNDKCCRPNLKCSRTHKWCKYVF-{Amide}	[Lys22]GpTx-1(1-34)	0.19	15.03	1.96	0.08	10.4	25.7	2.5
158	{H}-DCLGFMRKCIPDNDKCCRPNLRCSRTHKWCKYVF-{Amide}	[Arg22]GpTx-1(1-34)	0.09	8.20	0.70	0.03	11.7	24.3	2.1
177	{H}-DCLGFMRKCIPDNDKCCRPNLWCSRTHKWCKYVF-{Amide}	[Trp22]GpTx-1(1-34)	0.03	8.02	4.23	0.06	137.2	75.1	0.5
319	{H}-DCLGFMRKCIPDNDKCCRPNLFCSRTHKWCKYVF-{Amide}	[Phe22]GpTx-1(1-34)	0.70	>5	>5	1.02	-	-	0.7
320	{H}-DCLGFMRKCIPDNDKCCRPNLPCSRTHKWCKYVF-{Amide}	[Pro22]GpTx-1(1-34)	>5	>5	>5	>5	-	-	-
321	{H}-DCLGFMRKCIPDNDKCCRPNLICSRTHKWCKYVF-{Amide}	[Ile22]GpTx-1(1-34)	0.08	11.51	1.54	0.07	19.3	20.6	1.1
322	{H}-DCLGFMRKCIPDNDKCCRPNLLCSRTHKWCKYVF-{Amide}	[Leu22]GpTx-1(1-34)	0.09	9.58	0.83	0.07	9.3	11.4	1.2
323	{H}-DCLGFMRKCIPDNDKCCRPNLSCSRTHKWCKYVF-{Amide}	[Ser22]GpTx-1(1-34)	0.10	4.42	1.44	0.09	14.7	16.1	1.1
324	{H}-DCLGFMRKCIPDNDKCCRPNLGCSRTHKWCKYVF-{Amide}	[Gly22]GpTx-1(1-34)	0.14	10.86	4.66	0.10	33.5	45.2	1.4
325	{H}-DCLGFMRKCIPDNDKCCRPNLNCSRTHKWCKYVF-{Amide}	[Asn22]GpTx-1(1-34)	0.24	8.07	1.78	0.09	7.5	19.3	2.6
326	{H}-DCLGFMRKCIPDNDKCCRPNLHCSRTHKWCKYVF-{Amide}	[His22]GpTx-1(1-34)	0.41	15.64	2.51	0.10	6.0	24.1	4.0
327	{H}-DCLGFMRKCIPDNDKCCRPNLDCSRTHKWCKYVF-{Amide}	[Asp22]GpTx-1(1-34)	1.50	13.26	7.31	0.63	4.9	11.7	2.4
328	{H}-DCLGFMRKCIPDNDKCCRPNL[NMePhe]CSRTHKWCKYVF-{Amide}	[NMePhe22]GpTx-1(1-34)	20.60	20.39	18.40	7.37	0.9	2.5	2.8

329	{H}-DCLGFMRKCIPDNDKCCRPNLTCSRTHKWCKYVF-{Amide}	[Thr22]GpTx-1(1-34)	0.12	4.59	1.38	0.08	11.3	18.2	1.6
330	{H}-DCLGFMRKCIPDNDKCCRPNL[Phg]CSRTHKWCKYVF-{Amide}	[Phg22]GpTx-1(1-34)	0.18	4.69	1.82	0.07	10.0	25.0	2.5
331	{H}-DCLGFMRKCIPDNDKCCRPNLYCSRTHKWCKYVF-{Amide}	[Tyr22]GpTx-1(1-34)	0.56	4.26	7.91	0.50	14.1	15.9	1.1
332	{H}-DCLGFMRKCIPDNDKCCRPNLMCSRTHKWCKYVF-{Amide}	[Met22]GpTx-1(1-34)	0.09	4.61	0.43	0.08	4.9	5.5	1.1
333	{H}-DCLGFMRKCIPDNDKCCRPNL[4CO2-F]CSRTHKWCKYVF-{Amide}	[4CO2-F22]GpTx-1(1-34)	5.77	7.50	22.51	4.47	3.9	5.0	1.3
334	{H}-DCLGFMRKCIPDNDKCCRPNL[2PAL]CSRTHKWCKYVF-{Amide}	[2PAL22]GpTx-1(1-34)	0.33	10.96	6.80	0.14	20.5	49.4	2.4
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 21. Electrophysiology by IonWorks® Quattro: Substitutions at position 24 or 25 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
142	{H}-DCLGFMRKCIPDNDKCCRPNLVCARTHKWCKYVF-{Amide}	[Ala24]GpTx-1(1-34)	0.47	8.20	1.93	0.25	4.1	7.8	1.9
150	{H}-DCLGFMRKCIPDNDKCCRPNLVCERTHKWCKYVF-{Amide}	[Glu24]GpTx-1(1-34)	6.12	11.48	23.12	6.78	3.8	3.4	0.9
9	{H}-DCLGFMRKCIPDNDKCCRPNLVCSATHKWCKYVF-{Amide}	[Ala25]GpTx-1(1-34)	0.30	18.78	6.19	0.84	20.8	7.3	0.4
151	{H}-DCLGFMRKCIPDNDKCCRPNLVCSETHKWCKYVF-{Amide}	[Glu25]GpTx-1(1-34)	0.71	13.99	16.27	1.17	22.8	13.9	0.6
53	{H}-DCLGFMRKCIPDNDKCCRPNLVCSKTHKWCKYVF-{Amide}	[Lys25]GpTx-1(1-34)	0.38	15.21	3.89	0.24	10.4	16.2	1.6
117	{H}-DCLGFMRKCIPDNDKCCRPNLVCS[Cit]THKWCKYVF-{Amide}	[Cit25]GpTx-1(1-34)	0.32	8.87	10.49	0.51	32.3	20.6	0.6
335	{H}-DCLGFMRKCIPDNDKCCRPNLVCS[K(Me2)]THKWCKYVF-{Amide}	[K(Me2)25]GpTx-1(1-34)	0.31	7.93	13.57	0.11	43.2	126.4	2.9
336	{H}-DCLGFMRKCIPDNDKCCRPNLVCS[SDMA]THKWCKYVF-{Amide}	[SDMA25]GpTx-1(1-34)	0.14	9.22	2.68	0.11	19.8	23.5	1.2
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 22. Electrophysiology by IonWorks® Quattro: Substitutions at position 26 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
10	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRAHKWCKYVF-{Amide}	[Ala26]GpTx-1(1-34)	0.25	10.45	3.16	0.17	12.5	18.2	1.5
152	{H}-DCLGFMRKCIPDNDKCCRPNLVCSREHKWCKYVF-{Amide}	[Glu26]GpTx-1(1-34)	0.68	17.15	23.59	0.71	34.5	33.5	1.0
54	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRKHKWCKYVF-{Amide}	[Lys26]GpTx-1(1-34)	0.05	7.96	0.75	0.02	14.5	43.0	3.0
70	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRRHKWCKYVF-{Amide}	[Arg26]GpTx-1(1-34)	0.03	3.06	0.53	0.008	15.5	68.3	4.4
178	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRWHKWCKYVF-{Amide}	[Trp26]GpTx-1(1-34)	0.03	5.84	0.63	0.02	19.7	27.4	1.4
94	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRKTKWCKYVF-{Amide}	[Lys26;Thr27]GpTx-1(1-34)	0.10	9.29	3.52	0.05	36.2	65.7	1.8
121	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	[Leu26]GpTx-1(1-34)	0.07	10.20	3.45	0.07	51.9	46.8	0.9
337	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRHHKWCKYVF-{Amide}	[His26]GpTx-1(1-34)	0.10	4.52	10.31	0.08	100.6	124.4	1.2
338	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRSHKWCKYVF-{Amide}	[Ser26]GpTx-1(1-34)	0.10	12.32	1.12	0.09	11.2	12.9	1.2
339	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRQHKWCKYVF-{Amide}	[Gln26]GpTx-1(1-34)	0.14	17.95	1.90	0.09	13.2	21.5	1.6
340	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRYHKWCKYVF-{Amide}	[Tyr26]GpTx-1(1-34)	0.08	5.51	1.24	0.06	16.2	19.7	1.2
341	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRFHKWCKYVF-{Amide}	[Phe26]GpTx-1(1-34)	0.08	5.88	1.47	0.10	18.8	15.2	0.8
342	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRNHKWCKYVF-{Amide}	[Asn26]GpTx-1(1-34)	0.09	6.29	1.08	0.10	11.6	10.9	0.9
343	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRGHKWCKYVF-{Amide}	[Gly26]GpTx-1(1-34)	0.10	4.07	0.99	0.09	10.1	11.1	1.1

344	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRVHKWCKYVF-{Amide}	[Val26]GpTx-1(1-34)	0.06	8.93	1.57	0.04	24.9	37.9	1.5
345	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRPHKWCKYVF-{Amide}	[Pro26]GpTx-1(1-34)	0.18	6.65	1.78	0.16	9.7	11.5	1.2
346	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRMHKWCKYVF-{Amide}	[Met26]GpTx-1(1-34)	0.04	4.24	1.28	0.02	31.8	73.1	2.3
347	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRDHKWCKYVF-{Amide}	[Asp26]GpTx-1(1-34)	0.96	14.12	5.38	0.64	5.6	8.4	1.5
348	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRIHKWCKYVF-{Amide}	[Ile26]GpTx-1(1-34)	0.05	8.15	2.05	0.03	42.2	58.8	1.4
349	{H}-DCLGFMRKCIPDNDKCCRPNLVCSR[2PAL]HKWCKYVF-{Amide}	[2PAL26]GpTx-1(1-34)	0.26	10.60	5.14	0.06	19.6	86.3	4.4
350	{H}-DCLGFMRKCIPDNDKCCRPNLVCSR[4CO2-F]HKWCKYVF-{Amide}	[4CO2-F26]GpTx-1(1-34)	0.40	6.46	18.59	2.62	46.3	7.1	0.2
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

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Table 23. Electrophysiology by IonWorks® Quattro: Substitutions at position 27 or 28 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1 7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
11	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTAKWCKYVF-{Amide}	[Ala27]GpTx-1(1-34)	0.95	14.71	3.94	1.15	4.1	3.4	0.8
29	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTEKWCKYVF-{Amide}	[Glu27]GpTx-1(1-34)	8.54	15.16	21.40	12.26	2.5	1.7	0.7
55	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTKKWCKYVF-{Amide}	[Lys27]GpTx-1(1-34)	1.51	11.53	6.16	2.48	4.1	2.5	0.6
71	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTRKWCKYVF-{Amide}	[Arg27]GpTx-1(1-34)	0.51	5.22	2.61	0.51	5.2	5.1	1.0
84	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTWKWCKYVF-{Amide}	[Trp27]GpTx-1(1-34)	0.32	5.59	2.57	0.59	8.0	4.4	0.5
166	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRT[1-Nal]KWCKYVF-{Amide}	[1-Nal27]GpTx-1(1-34)	0.30	0.88	0.62	0.43	2.0	1.5	0.7
109	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTFKWCKYVF-{Amide}	[Phe27]GpTx-1(1-34)	0.22	2.06	2.92	0.53	13.2	5.5	0.4
110	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTYKWCKYVF-{Amide}	[Tyr27]GpTx-1(1-34)	0.19	6.39	5.78	0.31	29.9	18.4	0.6
111	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTLKWCKYVF-{Amide}	[Leu27]GpTx-1(1-34)	1.15	6.19	9.04	1.01	7.9	8.9	1.1
351	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRT[4CO2-F]KWCKYVF-{Amide}	[4CO2-F27]GpTx-1(1-34)	15.44	6.65	19.35	8.41	1.3	2.3	1.8

352	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRT[2PAL]KWCKYVF-{Amide}	[2PAL27]GpTx-1(1-34)	0.09	7.82	2.93	0.05	33.5	61.4	1.8
353	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRT[SDMA]KWCKYVF-{Amide}	[SDMA27]GpTx-1(1-34)	2.00	8.32	9.84	2.42	4.9	4.1	0.8
354	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRT[K(Me2)]KWCKYVF-{Amide}	[K(Me2)27]GpTx-1(1-34)	7.00	12.39	11.94	3.82	1.7	3.1	1.8
12	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHAWCKYVF-{Amide}	[Ala28]GpTx-1(1-34)	0.36	17.34	6.86	0.66	19.2	10.4	0.5
153	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[Glu28]GpTx-1(1-34)	0.34	14.07	13.93	0.80	41.4	17.5	0.4
72	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	[Arg28]GpTx-1(1-34)	0.08	8.95	7.55	0.13	93.8	58.1	0.6
355	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTH[K(Me2)]WCKYVF-{Amide}	[K(Me2)28]GpTx-1(1-34)	0.27	8.73	14.42	0.19	54.4	76.5	1.4
356	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTH[SDMA]WCKYVF-{Amide}	[SDMA28]GpTx-1(1-34)	0.18	9.52	5.01	0.23	28.1	22.1	0.8
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.09	24.9	22.8	0.9

Table 24. Electrophysiology by IonWorks® Quattro: Substitutions at position 29 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
47	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKACKYVF-{Amide}	[Ala29]GpTx-1(1-34)	11.74	16.17	4.49	27.50	0.4	0.2	0.4
30	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKECKYVF-{Amide}	[Glu29]GpTx-1(1-34)	18.06	18.91	23.53	16.05	1.3	1.5	1.1
56	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKKCKYVF-{Amide}	[Lys29]GpTx-1(1-34)	20.10	14.74	27.34	24.53	1.4	1.1	0.8
104	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKRCKYVF-{Amide}	[Arg29]GpTx-1(1-34)	9.73	18.76	7.35	11.39	0.8	0.6	0.9
79	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[1-Nal]CKYVF-{Amide}	[1-Nal29]GpTx-1(1-34)	0.46	9.25	16.23	1.55	35.1	10.5	0.3
113	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKYCKYVF-{Amide}	[Tyr29]GpTx-1(1-34)	1.46	9.49	9.52	4.03	6.5	2.4	0.4
114	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKLCKYVF-{Amide}	[Leu29]GpTx-1(1-34)	6.99	7.27	23.17	9.80	3.3	2.4	0.7
112	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKFCKYVF-{Amide}	[Phe29]GpTx-1(1-34)	2.18	6.21	15.19	4.82	7.0	3.1	0.5
129	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[2-Nal]CKYVF-{Amide}	[2-Nal29]GpTx-1(1-34)	0.58	11.67	9.46	0.73	16.2	12.9	0.8
357	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[NMeTrp]CKYVF-{Amide}	[NMeTrp29]GpTx-1(1-34)	>5	>5	>5	>5	-	-	-
358	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[pI-Phe]CKYVF-{Amide}	[pI-Phe29]GpTx-1(1-34)	1.01	14.90	12.98	1.27	12.9	10.2	0.8
359	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[NMePhe]CKYVF-{Amide}	[NMePhe29]GpTx-1(1-34)	19.15	18.84	15.35	7.39	0.8	2.1	2.6
360	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[Bip]CKYVF-{Amide}	[Bip29]GpTx-1(1-34)	4.79	9.77	19.69	6.95	4.1	2.8	0.7

361	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[1'NMeW]CKYVF-{Amide}	[1'NMeW29]GpTx-1(1-34)	3.89	12.24	7.04	4.58	1.8	1.5	0.9
362	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[Phg]CKYVF-{Amide}	[Phg29]GpTx-1(1-34)	5.52	7.85	16.33	3.18	3.0	5.1	1.7
363	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHK[4CO2-F]CKYVF-{Amide}	[4CO2-F29]GpTx-1(1-34)	15.03	18.77	19.34	14.94	1.3	1.3	1.0
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.05	13.09	1.93	0.08	24.9	22.8	0.9

Table 25. Electrophysiology by IonWorks® Quattro: Substitutions at position 31 or 32 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
13	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCAYVF-{Amide}	[Ala31]GpTx-1(1-34)	7.94	14.54	5.96	7.39	0.7	0.8	1.1
31	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCEYVF-{Amide}	[Glu31]GpTx-1(1-34)	22.96	21.69	20.41	13.06	0.9	1.6	1.8
73	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCRYVF-{Amide}	[Arg31]GpTx-1(1-34)	1.36	9.17	7.14	4.95	5.2	1.4	0.3
179	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCWYVF-{Amide}	[Trp31]GpTx-1(1-34)	23.61	10.84	21.31	10.17	0.9	2.1	2.3
364	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWC[2PAL]YVF-{Amide}	[2PAL31]GpTx-1(1-34)	10.95	9.49	21.73	16.93	2.0	1.3	0.6
365	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWC[SDMA]YVF-{Amide}	[SDMA31]GpTx-1(1-34)	4.15	14.21	10.75	4.55	2.6	2.4	0.9
14	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKAVF-{Amide}	[Ala32]GpTx-1(1-34)	0.80	20.61	5.96	0.77	7.5	7.8	1.0
32	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKEVF-{Amide}	[Glu32]GpTx-1(1-34)	13.95	22.80	22.80	9.14	1.6	2.5	1.5
57	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKKVF-{Amide}	[Lys32]GpTx-1(1-34)	4.96	10.89	15.71	4.19	3.2	3.8	1.2
159	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKRVF-{Amide}	[Arg32]GpTx-1(1-34)	1.02	8.65	18.71	0.87	18.4	21.5	1.2
85	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKWVF-{Amide}	[Trp32]GpTx-1(1-34)	0.09	6.74	4.99	0.16	53.5	31.3	0.6
167	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[1-Nal]VF-{Amide}	[1-Nal32]GpTx-1(1-34)	0.004	3.96	0.15	0.001	35.0	135.0	3.8
246	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[1'NMeW]VF-{Amide}	[1'NMeW32]GpTx-1(1-34)	0.06	14.44	21.36	0.03	372.6	806.3	2.2
366	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKQVF-{Amide}	[Gln32]GpTx-1(1-34)	4.87	21.01	12.08	2.39	2.5	5.1	2.0

367	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKIVF-{Amide}	[Ile32]GpTx-1(1-34)	0.07	8.71	1.33	0.06	19.9	23.0	1.2
368	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKMVF-{Amide}	[Met32]GpTx-1(1-34)	0.35	6.21	5.99	0.14	17.1	42.9	2.5
369	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKTVF-{Amide}	[Thr32]GpTx-1(1-34)	3.54	11.05	11.19	3.29	3.2	3.4	1.1
370	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[NMePhe]VF-{Amide}	[NMePhe32]GpTx-1(1-34)	>5	>5	>5	>5	-	-	-
371	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[NMeTrp]VF-{Amide}	[NMeTrp32]GpTx-1(1-34)	4.88	>5	>5	>5	-	-	-
372	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKVVF-{Amide}	[Val32]GpTx-1(1-34)	0.15	14.81	1.59	0.08	10.7	19.5	1.8
373	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKLVF-{Amide}	[Leu32]GpTx-1(1-34)	0.12	8.83	1.19	0.08	10.0	14.1	1.4
374	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[Phg]VF-{Amide}	[Phg32]GpTx-1(1-34)	0.14	7.06	1.80	0.10	13.2	18.9	1.4
375	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[Cha]VF-{Amide}	[Cha32]GpTx-1(1-34)	0.05	8.88	0.39	0.02	8.0	16.7	2.1
376	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[Bip]VF-{Amide}	[Bip32]GpTx-1(1-34)	0.03	2.90	0.19	0.00	7.0	68.6	9.8
377	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKFVF-{Amide}	[Phe32]GpTx-1(1-34)	0.05	6.84	0.67	0.05	12.3	13.7	1.1
378	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKGVF-{Amide}	[Gly32]GpTx-1(1-34)	0.71	11.18	7.97	0.62	11.3	12.8	1.1
379	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKNVF-{Amide}	[Asn32]GpTx-1(1-34)	4.86	10.56	8.40	6.85	1.7	1.2	0.7
380	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKHVF-{Amide}	[His32]GpTx-1(1-34)	0.60	10.16	7.18	0.75	11.9	9.6	0.8
381	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[pI-Phe]VF-{Amide}	[pI-Phe32]GpTx-1(1-34)	0.03	4.44	0.30	0.01	11.7	49.6	4.3
382	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKSVF-{Amide}	[Ser32]GpTx-1(1-34)	3.95	>5	>5	1.47	-	-	2.7
383	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKPVF-{Amide}	[Pro32]GpTx-1(1-34)	>5	>5	>5	>5	-	-	-

384	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[2PAL]VF-{Amide}	[2PAL32]GpTx-1(1-34)	0.81	7.65	19.08	0.66	23.4	28.8	1.2
385	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[4CO2-F]VF-{Amide}	[4CO2-F32]GpTx-1(1-34)	11.42	7.70	19.26	4.05	1.7	4.8	2.8
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 26. Electrophysiology by IonWorks® Quattro: Substitutions at position 33 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
15	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYAF-{Amide}	[Ala33]GpTx-1(1-34)	0.33	18.60	4.40	0.35	13.5	12.5	0.9
33	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYEF-{Amide}	[Glu33]GpTx-1(1-34)	0.56	11.48	10.26	0.39	18.4	26.3	1.4
58	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYKF-{Amide}	[Lys33]GpTx-1(1-34)	0.07	9.56	1.28	0.07	18.6	19.3	1.0
74	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYRF-{Amide}	[Arg33]GpTx-1(1-34)	0.08	9.55	2.11	0.05	26.7	40.0	1.5
180	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYWF-{Amide}	[Trp33]GpTx-1(1-34)	0.05	9.06	0.63	0.009	12.0	70.3	5.9
168	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[1-Nal]F-{Amide}	[1-Nal33]GpTx-1(1-34)	0.06	15.74	0.57	0.02	9.2	26.7	2.9
95	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYQF-{Amide}	[Gln33]GpTx-1(1-34)	0.12	10.59	9.56	0.11	81.2	85.7	1.1
248	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYIF-{Amide}	[Ile33]GpTx-1(1-34)	0.15	6.89	21.63	0.09	142.1	238.9	1.7
249	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[pI-Phe]F-{Amide}	[pI-Phe33]GpTx-1(1-34)	0.09	7.78	11.54	0.06	127.3	192.9	1.5
250	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[1'NMeW]F-{Amide}	[1'NMeW33]GpTx-1(1-34)	0.09	5.35	7.87	0.07	88.9	120.1	1.4
386	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[Cha]F-{Amide}	[Cha33]GpTx-1(1-34)	0.07	12.18	1.12	0.07	15.4	15.5	1.0
388	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[NMePhe]F-{Amide}	[NMePhe33]GpTx-1(1-34)	1.28	>5	4.91	1.09	3.8	4.5	1.2

389	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[NMeTrp]F-{Amide}	[NMeTrp33]GpTx-1(1-34)	0.35	>5	1.55	0.29	4.5	5.4	1.2
390	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYFF-{Amide}	[Phe33]GpTx-1(1-34)	0.06	8.66	0.74	0.04	12.7	18.5	1.5
391	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYMF-{Amide}	[Met33]GpTx-1(1-34)	0.07	15.06	1.54	0.08	20.8	20.3	1.0
392	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYHF-{Amide}	[His33]GpTx-1(1-34)	0.02	8.16	0.32	0.01	19.6	33.2	1.7
393	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[Phg]F-{Amide}	[Phg33]GpTx-1(1-34)	0.02	7.63	0.50	0.04	22.9	13.1	0.6
394	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYNF-{Amide}	[Asn33]GpTx-1(1-34)	0.36	7.94	1.22	0.07	3.4	16.3	4.8
395	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYDF-{Amide}	[Asp33]GpTx-1(1-34)	0.77	8.79	3.87	0.17	5.0	22.4	4.4
396	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYTF-{Amide}	[Thr33]GpTx-1(1-34)	0.02	3.78	1.29	0.04	70.8	28.9	0.4
397	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYSF-{Amide}	[Ser33]GpTx-1(1-34)	0.04	6.28	1.14	0.06	26.0	19.0	0.7
398	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYPF-{Amide}	[Pro33]GpTx-1(1-34)	5.19	6.93	6.87	3.34	1.3	2.1	1.6
399	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYYF-{Amide}	[Tyr33]GpTx-1(1-34)	0.07	>5	2.03	0.03	30.3	69.4	2.3
400	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYLF-{Amide}	[Leu33]GpTx-1(1-34)	0.13	>5	0.82	0.07	6.3	11.3	1.8
401	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYGF-{Amide}	[Gly33]GpTx-1(1-34)	0.29	>5	1.62	0.04	5.6	40.0	7.1
402	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[2PAL]F-{Amide}	[2PAL33]GpTx-1(1-34)	0.12	8.36	11.61	0.16	98.2	72.3	0.7
403	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY[4CO2-F]F-{Amide}	[4CO2-F33]GpTx-1(1-34)	0.16	9.06	9.23	0.31	59.1	29.8	0.5
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.08	24.9	22.8	0.9

Table 27. Electrophysiology by IonWorks® Quattro: Substitutions at position 34 relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
101	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVA-{Amide}	[Ala34]GpTx-1(1-34)	7.19	9.33	16.41	4.76	2.3	3.5	1.5
34	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVE-{Amide}	[Glu34]GpTx-1(1-34)	16.98	16.76	16.97	11.17	1.0	1.5	1.5
59	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVK-{Amide}	[Lys34]GpTx-1(1-34)	5.68	18.06	20.19	7.74	3.6	2.6	0.7
75	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVR-{Amide}	[Arg34]GpTx-1(1-34)	3.58	8.99	22.67	4.69	6.3	4.8	0.8
86	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVW-{Amide}	[Trp34]GpTx-1(1-34)	0.26	10.02	6.70	0.18	25.7	36.3	1.4
80	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[1-Nal]-{Amide}	[1-Nal34]GpTx-1(1-34)	0.02	10.24	0.94	0.03	40.9	31.5	0.8
96	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVI-{Amide}	[Ile34]GpTx-1(1-34)	0.28	10.79	5.33	0.28	18.8	19.0	1.0
122	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVL-{Amide}	[Leu34]GpTx-1(1-34)	0.24	8.46	3.31	0.13	13.5	25.4	1.9
130	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[2-Nal]-{Amide}	[2-Nal34]GpTx-1(1-34)	0.04	3.59	0.34	0.02	8.7	14.3	1.6
404	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVf-{Amide}	[D-Phe34]GpTx-1(1-34)	0.98	20.72	6.15	0.52	6.3	11.8	1.9
405	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[Cha]-{Amide}	[Cha34]GpTx-1(1-34)	0.02	5.53	0.63	0.01	26.3	57.7	2.2
406	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[Phg]-{Amide}	[Phg34]GpTx-1(1-34)	0.04	5.95	0.27	0.02	6.2	11.9	1.9

407	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[NMeTrp]-{Amide}	[NMeTrp34]GpTx-1(1-34)	6.85	10.16	10.29	4.64	1.5	2.2	1.5
408	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[NMePhe]-{Amide}	[NMePhe34]GpTx-1(1-34)	10.05	18.85	9.29	4.56	0.9	2.0	2.2
409	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[1'NMeW]-{Amide}	[1'NMeW34]GpTx-1(1-34)	0.09	5.61	1.22	0.07	14.1	18.3	1.3
410	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[4CO2-F]-{Amide}	[4CO2-F34]GpTx-1(1-34)	9.19	7.11	21.92	6.31	2.4	3.5	1.5
411	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[2PAL]-{Amide}	[2PAL34]GpTx-1(1-34)	5.82	8.16	21.31	4.83	3.7	4.4	1.2
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.08	13.09	1.93	0.03	24.9	22.8	0.9

Table 28. Electrophysiology by IonWorks® Quattro: Substitutions at position 35 and C-terminal deletions relative to SEQ ID NO:1 and free acids

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
16	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFA-{Amide}	GpTx-1(1-34)-Ala	0.41	14.15	7.13	0.26	17.6	27.2	1.5
35	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFE-{Amide}	GpTx-1(1-34)-Glu	4.47	19.59	21.73	2.47	4.9	8.8	1.8
60	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFK-{Amide}	GpTx-1(1-34)-Lys	0.59	12.53	7.00	0.21	11.8	32.7	2.8
76	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFR-{Amide}	GpTx-1(1-34)-Arg	0.30	9.73	5.53	0.10	18.5	56.3	3.0
131	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF[2-Nal]-{Amide}	GpTx-1(1-34)-2-Nal	0.05	2.55	0.44	0.02	9.2	18.2	2.0
87	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFW-{Amide}	GpTx-1(1-34)-Trp	0.03	7.87	2.69	0.07	55.0	36.0	0.7
133	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVFW-{FreeAcid}	GpTx-1(1-34)-Trp-FreeAcid	0.48	8.28	2.15	0.11	4.5	19.9	4.4
412	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF[2-Nal]-{Amide}	GpTx-1(1-34)-2-Nal	0.05	2.55	0.44	0.02	9.2	18.2	2.0
413	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF[4CO2-F]-{Amide}	GpTx-1(1-34)-4CO2-F	1.15	8.65	12.34	5.35	10.7	2.3	0.2
414	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF[2PAL]-{Amide}	GpTx-1(1-34)-2PAL	0.26	9.29	9.78	0.63	38.1	15.5	0.4

415	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV-{Amide}	GpTx-1(1-33)	2.35	10.84	10.61	1.30	4.5	8.1	1.8
416	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKY-{Amide}	GpTx-1(1-32)	1.50	8.64	11.48	0.88	7.6	13.1	1.7
417	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK-{Amide}	GpTx-1(1-31)	18.32	11.88	6.94	9.09	0.4	0.8	2.0
107	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-*{FreeAcid}*	GpTx-1(1-34)-*FreeAcid*	1.98	9.44	6.75	0.54	3.4	12.5	3.7
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34)	0.03	13.09	1.93	0.08	24.9	22.8	0.9

Table 29. Electrophysiology by IonWorks® Quattro: Substitutions, additions or deletions at multiple positions relative to SEQ ID NO:1.

SEQ ID NO.	Amino Acid Sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/ Nav1.7	Nav1.4/ Nav1.3	Nav1.7/ Nav1.3
2	{H}-dclgfmrkcipdndkccrpnlvcsrthkwckyvf-{Amide}	[All D-isomer]GpTx-1(1-34)	7.51	11.27	18.01	21.05	2.4	0.9	0.4
140	{H}-DALGFMRKCIPDNDKCARPNLVCSRTHKWCKYVF-{Amide}	[Ala2,17]GpTx-1(1-34)	2.45	18.95	15.39	0.79	6.3	19.4	3.1
125	{H}-D[2-Abu]LGFMRKCIPDNDKC[2-Abu]RPNLVCSRTHKWCKYVF-{Amide}	[2-Abu2,17]GpTx-1(1-34)	0.30	9.51	11.58	0.24	38.9	48.6	1.2
135	{H}-DCLGFMRK[2-Abu]IPDNDKCCRPNLV[2-Abu]SRTHKWCKYVF-{Amide}	[2-Abu9,23]GpTx-1(1-34)	8.14	9.21	20.81	12.27	2.6	1.7	0.7
139	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[2-Nal]W-{Amide}	[2-Nal34]GpTx-1(1-34)-Trp	0.11	2.12	0.30	0.05	2.7	6.5	2.4
99	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKKV[1-Nal]W-{Amide}	[Lys32;1-Nal34]GpTx-1(1-34)-Trp	0.11	9.14	3.19	0.16	28.0	20.3	0.7
136	{H}-DCLG[2-Nal]MRKCIPDNDKCCRPNLVCSRTHKWCKYV[2-Nal]-{Amide}	[2-Nal5,34]GpTx-1(1-34)	0.14	5.14	0.29	0.03	2.1	10.7	5.1
137	{H}-DCLG[2-Nal]MRKCIPDNDKCCRPNLVCSRTHKWCKYV[1-Nal]-{Amide}	[2-Nal5;1-Nal34]GpTx-1(1-34)	0.11	3.15	0.24	0.02	2.2	10.4	4.7
134	{H}-DCLGFMRKCIPDNDKCCEGLVCSRTHKWCKYVF-{Amide}	[Glu18;desAsn20]GpTx-1(1-34)	0.89	11.54	8.95	0.51	10.0	17.7	1.8
138	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYV[1-Nal]W-{Amide}	[1-Nal34]GpTx-1(1-34)-Trp	0.13	2.57	0.55	0.07	4.3	7.8	1.8
127	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKKVFW-{Amide}	[Lys32]GpTx-1(1-34)-Trp	0.73	18.91	8.41	0.70	11.5	12.0	1.0

252	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYWF-{Amide}	[Ala5;Trp33]GpTx-1(1-34)	0.23	5.00	3.86	0.40	16.7	9.7	0.6
253	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKWVF-{Amide}	[Ala5;Trp32]GpTx-1(1-34)	0.27	5.00	5.00	0.53	18.6	9.5	0.5
254	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCK[1-Nal]VF-{Amide}	[Ala5;1-Nal32]GpTx-1(1-34)	0.06	5.00	4.43	0.20	77.9	21.6	0.3
255	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	[Ala5;Leu26]GpTx-1(1-34)	0.28	5.00	5.00	0.68	17.7	7.4	0.4
256	{H}-DCLGA[1-Nal]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;1-Nal6]GpTx-1(1-34)	0.10	5.00	1.15	0.06	11.4	19.5	1.7
257	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6]GpTx-1(1-34)	0.07	5.00	2.24	0.05	32.0	48.8	1.5
258	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKY[1-Nal]F-{Amide}	[Ala5;1-Nal33]GpTx-1(1-34)	0.38	5.00	4.83	0.80	12.6	6.0	0.5
259	{H}-DCLGAMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;1-Nal10]GpTx-1(1-34)	1.50	5.00	5.00	3.12	3.3	1.6	0.5
260	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	[Ala5;Arg28]GpTx-1(1-34)	0.33	5.00	5.00	0.24	15.2	20.6	1.4
261	{H}-DCLGAWRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Trp6]GpTx-1(1-34)	1.01	5.00	5.00	0.67	5.0	7.5	1.5
262	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRLHRWCKYVF-{Amide}	[Ala5;Phe6;Leu26;Arg28]GpTx-1(1-34)	0.05	5.00	5.00	0.04	110.5	131.1	1.2
263	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	[Ala5;Phe6;Leu26]GpTx-1(1-34)	0.08	5.00	5.00	0.05	63.1	105.1	1.7

419	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYEF-{Amide}	[Ala5;Glu33]GpTx-1(1-34)	4.00	9.04	11.46	3.58	2.9	3.2	1.1
420	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHRWCKY[1-Nal]F-{Amide}	[Ala5;Arg28;1-Nal33]GpTx-1(1-34)	0.20	7.50	12.77	0.32	62.9	39.9	0.6
421	{H}-DCLGAMRKCIPDNDKCCRP[1-Nal]LVCSRTHKWCKYVF-{Amide}	[Ala5;1-Nal20]GpTx-1(1-34)	0.16	4.42	0.25	0.25	1.6	1.0	0.6
422	{H}-DCLGAMRKCIPDNDKCCRPWLVCSRTHKWCKYVF-{Amide}	[Ala5;Trp20]GpTx-1(1-34)	0.28	>5	>5	0.39	-	-	0.7
423	{H}-DCLGAMRKCIPWNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Trp12]GpTx-1(1-34)	0.43	>5	>5	1.09	-	-	0.4
424	{H}-DCLWAMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Trp4;Ala5]GpTx-1(1-34)	0.49	>5	>5	1.17	-	-	0.4
425	{H}-[1-Nal]CLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal1;Ala5]GpTx-1(1-34)	0.50	>5	>5	0.77	-	-	0.6
426	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYAF-{Amide}	[Ala5,33]GpTx-1(1-34)	0.58	>5	>5	1.58	-	-	0.4
427	{H}-DCLGAMRKCIPD[1-Nal]DKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;1-Nal13]GpTx-1(1-34)	0.65	>5	>5	1.18	-	-	0.6
428	{H}-DCLGAMRKCIPDWDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Trp13]GpTx-1(1-34)	0.67	>5	>5	1.10	-	-	0.6
429	{H}-DCLEAMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu4;Ala5]GpTx-1(1-34)	4.64	>5	>5	3.99	-	-	1.2
430	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYVE-{Amide}	[Ala5;Glu34]GpTx-1(1-34)	>5	>5	>5	>5	-	-	-
431	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCKYVA-{Amide}	[Ala5,34]GpTx-1(1-34)	>5	>5	>5	>5	-	-	-

432	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCK AVF-{Amide}	[Ala5,32]GpTx-1(1-34)	>5	>5	>5	>5	-	-	-	-
433	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCA YVF-{Amide}	[Ala5,31]GpTx-1(1-34)	>5	>5	>5	>5	-	-	-	-
434	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKACK YVF-{Amide}	[Ala5,29]GpTx-1(1-34)	>5	>5	>5	>5	-	-	-	-
435	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHEWCK YVF-{Amide}	[Ala5;Glu28]GpTx-1(1-34)	>5	3.66	0.23	>5	-	-	-	-
436	{H}-DCLGAMEKCIPDNDKCCRPNLVCSRTHKWCK YVF-{Amide}	[Ala5;Glu7]GpTx-1(1-34)	>5	>5	>5	>5	-	-	-	-
437	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKECK YVF-{Amide}	[Ala5;Glu29]GpTx-1(1-34)	11.93	9.26	22.27	6.09	1.9	3.7	2.0	
438	{H}-DCLGAMRKCIPDNDKCCRPNLVCSETHKWCK YVF-{Amide}	[Ala5;Glu25]GpTx-1(1-34)	5.50	18.21	21.08	5.95	3.8	3.5	0.9	
439	{H}-DCLGAMRKCIPDNDECCRPNLVCSRTHKWCK YVF-{Amide}	[Ala5;Glu15]GpTx-1(1-34)	2.41	10.81	20.47	4.80	8.5	4.3	0.5	
251	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHRWCK[1-Nal]VF-{Amide}	[Arg28;1-Nal32]GpTx-1(1-34)	0.005	2.56	0.19	0.002	35.9	112.3	3.1	
440	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKWVF-{Amide}	[1-Nal10;Trp32]GpTx-1(1-34)	0.37	>5	4.58	0.26	12.5	17.9	1.4	
441	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	[1-Nal10;Arg28]GpTx-1(1-34)	0.02	>5	1.29	0.04	52.7	36.4	0.7	
442	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHRWCK Y[1-Nal]F-{Amide}	[Arg28;1-Nal33]GpTx-1(1-34)	0.03	>5	0.60	0.04	20.2	13.6	0.7	

443	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHRWCK WVF-{Amide}	[Arg28,Trp32]GpTx-1(1-34)	0.07	4.92	2.49	0.07	38.2	35.0	0.9
444	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHRWCK YWF-{Amide}	[Arg28,Trp33]GpTx-1(1-34)	0.03	>5	0.68	0.04	19.6	18.2	0.9
445	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHRWCK YVF-{Amide}	[Leu26;Arg28]GpTx-1(1-34)	0.03	>5	>5	0.06	-	-	0.6
446	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHKWCK WVF-{Amide}	[Leu26;Trp32]GpTx-1(1-34)	0.04	>5	2.92	0.06	75.9	51.8	0.7
447	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHKWCK YWF-{Amide}	[Leu26;Trp33]GpTx-1(1-34)	0.03	>5	0.95	0.02	36.7	43.5	1.2
448	{H}-DCLGFWRKCIPDNDKCCRPNLVCSRTHRWCK YVF-{Amide}	[Trp6;Arg28]GpTx-1(1-34)	0.01	2.91	0.33	0.01	28.7	37.9	1.3
449	{H}-DCLGFWRKCIPDNDKCCRPNLVCSRTHKWCK WVF-{Amide}	[Trp6,32]GpTx-1(1-34)	0.03	2.93	0.25	0.01	8.6	29.2	3.4
450	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK WWF-{Amide}	[Trp32,33]GpTx-1(1-34)	0.05	11.50	0.38	0.03	7.1	11.0	1.6
451	{H}-DCLGF[1-Nal]RKCIPDNDKCCRPNLVCSRTHKWCKWVF-{Amide}	[1-Nal6;Trp32]GpTx-1(1-34)	0.004	>5	2.53	0.02	572.7	161.3	0.3
452	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCK[1-Nal]VF-{Amide}	[1-Nal10,32]GpTx-1(1-34)	0.005	>5	4.51	0.003	956.6	1322.1	1.4
453	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHKWCK[1-Nal]VF-{Amide}	[Leu26;1-Nal32]GpTx-1(1-34)	0.01	>5	1.69	0.01	289.5	161.2	0.6
454	{H}-DCLGF[1-Nal]RKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	[1-Nal6;Arg28]GpTx-1(1-34)	0.01	>5	4.42	0.01	732.2	661.7	0.9

455	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK W[1-Nal]IF-{Amide}	[Trp32;1-Nal33]GpTx-1(1-34)	0.02	>5	>5	0.04	-	-	0.6
456	{H}-DCLGFWRKCIPDNDKCCRPNLVCSRLHKWCK YVF-{Amide}	[Trp6;Leu26]GpTx-1(1-34)	0.03	>5	2.91	0.01	91.6	228.8	2.5
457	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	[1-Nal10;Leu26]GpTx-1(1-34)	0.06	>5	2.53	0.03	44.2	76.0	1.7
458	{H}-DCLGFWRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Trp6;1-Nal10]GpTx-1(1-34)	0.06	>5	>5	0.05	-	-	1.2
459	{H}-DCLGFMRKC[1-Nal]PWNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal10;Trp12]GpTx-1(1-34)	0.08	>5	0.70	0.09	8.5	7.8	0.9
460	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCK[1-Nal]WF-{Amide}	[1-Nal32;Trp33]GpTx-1(1-34)	0.08	>5	1.43	0.03	17.1	47.8	2.8
461	{H}-DCLGFWRKCIPDNDKCCRPNLVCSRTHKWCK Y[1-Nal]F-{Amide}	[Trp6;1-Nal33]GpTx-1(1-34)	0.10	>5	1.38	0.05	13.4	28.5	2.1
462	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKY[1-Nal]F-{Amide}	[1-Nal10,33]GpTx-1(1-34)	0.11	>5	0.88	0.07	8.2	13.0	1.6
463	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRLHKWCK Y[1-Nal]F-{Amide}	[Leu26;1-Nal33]GpTx-1(1-34)	0.13	>5	>5	0.18	-	-	0.7
464	{H}-WDCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	Trp-[1-Nal10]GpTx-1(1-34)	0.20	>5	2.61	0.22	13.1	12.0	0.9
465	{H}-WCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Trp1;1-Nal10]GpTx-1(1-34)	0.23	>5	1.98	0.15	8.7	13.0	1.5
466	{H}-[1-Nal]CLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal1,10]GpTx-1(1-34)	0.61	>5	>5	0.43	-	-	1.4

467	{H}-DCLGFMRKCSPDNDKCCRPNLVCSRKHKWCKYEI-{Amide}	GpTx-2	4.34	7.21	11.73	1.15	2.7	10.2	3.8
468	{H}-DCLGWFKGCDPDNDKCCEGYKCNRRDKWCKYKL-{Amide}	GpTx-3	8.93	7.80	20.00	9.37	2.2	2.1	1.0
469	{H}-DCLGWFKGCDPDNDKCCENYKCNRREQWCKYKL-{Amide}	GpTx-4	9.25	10.38	11.00	4.92	1.2	2.2	1.9
1	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	GpTx-1(1-34) GpTx-6(1-35)	0.08	13.09	1.93	0.08	24.9	22.8	0.9
471	{H}-DCLGWFKGCDPDNDKCCEGYKCNRRDKWCKYKLWK-{FreeAcid}		9.6	14.6	17.4	1.7	1.8	10.0	5.5
472	{H}-DCLGWFKGCDPDNDKCCEGYKCNRRDKWCKYKLW-{FreeAcid}	GpTx-6(1-34)	1.3	7.3	4.1	0.54	3.2	7.6	2.4
593	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTH[Atz(20kDa PEG)]WCKYVF-{Amide}	[Phe6,Atz(20kDa Peg)28]GpTx-1(1-34)	3.5	15.6	13.4	4.5	3.8	3.0	0.8
594	{H}-DCLGFFRKCIPDNDKCCRPNL[Atz(20kDa PEG)]CSRTHKWCKYVF-{Amide}	[Phe6,Atz(20kDa Peg)22]GpTx-1(1-34)	3.2	11.0	12.9	5.7	4.0	2.3	0.6
595	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKECKYVF-{Amide}	[1-Nal10;Glu29]GpTx-1(1-34)	9.8	18.9	11.2	10.8	1.1	1.0	0.9
596	{H}-DCLG[3Pal]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[3Pal5]GpTx-1(1-34)	2.6	>5	>5	>5	1.9	1.0	0.5
597	{H}-DCLGAFRKCIPDYDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Tyr13;Arg28]GpTx-1(1-34)-FreeAcid	>5	7.35	>5	1.1	-	-	-
598	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHGWCKYVF-{FreeAcid}	[Ala5;Leu6;Gly28]GpTx-1(1-34)-FreeAcid	>5	12.57	>5	4.0	-	-	-
599	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHHWCKYVF-{FreeAcid}	[Ala5;Leu6;His28]GpTx-1(1-34)-FreeAcid	>5	12.65	>5	2.2	-	-	-

600	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{FreeAcid}	[Ala5;Leu6]GpTx-1(1-34)-FreeAcid	>5	12.63	>5	3.1	-	-	-
601	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHNWCKYVF-{FreeAcid}	[Ala5;Leu6;Asn28]GpTx-1(1-34)-FreeAcid	>5	10.02	>5	2.6	-	-	-
602	{H}-DCLGaFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[D-Ala5;Phe6]GpTx-1(1-34)	2.1	13.1	8.1	2.7	3.8	3.0	0.8
603	{H}-DCLG[bAla]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[bAla5;Phe6]GpTx-1(1-34)	15.3	9.5	9.1	11.8	0.6	0.8	1.3
604	{H}-DCLG[Aib]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Aib5;Phe6]GpTx-1(1-34)	0.44	6.4	7.9	0.61	17.9	12.8	0.7
605	{H}-DCLG[2-Abu]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Abu5;Phe6]GpTx-1(1-34)	0.17	9.5	5.6	0.36	33.2	15.5	0.5
606	{H}-DCLG[Nva]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Nva5;Phe6]GpTx-1(1-34)	0.084	7.8	2.7	0.17	32.3	16.1	0.5
607	{H}-DCLG[Nle]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Nle5;Phe6]GpTx-1(1-34)	0.016	11.3	1.0	0.067	64.4	15.1	0.2
608	{H}-DCLG[OctylG]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[OctylG5;Phe6]GpTx-1(1-34)	11.3	20.2	15.8	21.8	1.4	0.7	0.5
609	{H}-DCLG[Tle]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Tle5;Phe6]GpTx-1(1-34)	0.081	6.7	4.6	0.26	56.4	17.6	0.3
610	{H}-DCLG[hLeu]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[hLeu5;Phe6]GpTx-1(1-34)	0.011	8.2	0.76	0.041	70.1	18.7	0.3
611	{H}-DCLGMFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Met5;Phe6]GpTx-1(1-34)	0.043	13.3	2.4	0.11	55.7	20.9	0.4
612	{H}-DCLGLFRKCIPDNDKCCRPNLVCSRTHKWCKY	[Leu5;Phe6]GpTx-1(1-34)	0.057	20.1	3.4	0.22	59.8	15.6	0.3

	VF-{Amide}											
613	{H}-DCLG[3Pal]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[3Pal5;Phe6]GpTx-1{1-34}	0.095	18.7	21.6	3.6	22.7	5.9	0.3			
614	{H}-DCLG[Thi]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Thi5;Phe6]GpTx-1{1-34}	0.012	4.1	1.1	0.077	88.3	14.3	0.2			
615	{H}-DCLG[Cpg]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Cpg5;Phe6]GpTx-1{1-34}	0.035	5.6	2.0	0.12	55.9	16.7	0.3			
616	{H}-DCLG[Chg]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Chg5;Phe6]GpTx-1{1-34}	0.023	6.9	1.2	0.075	54.0	16.6	0.3			
617	{H}-DCLGSFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ser5;Phe6]GpTx-1{1-34}	0.76	11.9	13.9	1.7	18.2	8.0	0.4			
618	{H}-DCLGVFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Val5;Phe6]GpTx-1{1-34}	0.12	9.4	2.3	0.099	19.1	23.3	1.2			
619	{H}-DCLG[4-Bz-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4-Bz-F5;Phe6]GpTx-1{1-34}	0.14	7.7	0.57	0.042	4.0	13.8	3.4			
620	{H}-DCLG[DiMeO-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[DiMeO-F5;Phe6]GpTx-1{1-34}	0.64	10.4	10.1	0.99	15.7	10.2	0.6			
621	{H}-DCLG[DiCl-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[DiCl-F5;Phe6]GpTx-1{1-34}	0.048	4.1	0.16	0.005	3.4	29.7	8.8			
622	{H}-DCLG[pI-Phe]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[pI-Phe5;Phe6]GpTx-1{1-34}	12.3	12.9	22.9	21.0	1.9	1.1	0.6			
623	{H}-DCLG[4CF3-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4CF3-F5;Phe6]GpTx-1{1-34}	0.096	7.1	0.23	0.013	2.3	17.1	7.3			
624	{H}-DCLG[4-F-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4-F-F5;Phe6]GpTx-1{1-34}	0.060	11.7	0.27	0.020	4.5	13.7	3.1			
625	{H}-DCLG[4-Me-	[4-Me-F5;Phe6]GpTx-	0.063	6.5	0.70	0.051	11.1	13.8	1.2			

	F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	1(1-34)							
626	{H}-DCLG[4tBu-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4tBu-F5;Phe6]GpTx-1(1-34)	0.052	4.7	0.26	0.021	5.0	12.6	2.5
627	{H}-DCLG[NMeVal]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMeVal5;Phe6]GpTx-1(1-34)	0.19	6.0	4.2	0.25	22.6	16.9	0.7
628	{H}-DCLG[NMeLeu]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMeLeu5;Phe6]GpTx-1(1-34)	0.076	8.4	1.4	0.091	17.9	15.0	0.8
629	{H}-DCLG[NMePhe]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMePhe5;Phe6]GpTx-1(1-34)	0.077	13.6	1.3	0.095	17.3	14.0	0.8
630	{H}-DCLG[2-Cl-F]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Cl-F5;Phe6]GpTx-1(1-34)	0.060	5.8	0.35	0.009	5.9	38.9	6.6
631	{H}-DCLG[hPhe]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[hPhe5;Phe6]GpTx-1(1-34)	0.019	4.9	0.18	0.005	9.4	38.4	4.1
632	{H}-DCLG[Sar]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Sar5;Phe6]GpTx-1(1-34)	0.68	10.5	7.6	0.45	11.2	17.0	1.5
633	{H}-DCLGaLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[D-Ala5;Leu6]GpTx-1(1-34)	10.7	7.1	10.6	11.5	1.0	0.9	0.9
634	{H}-DCLG[bAla]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[bAla5;Leu6]GpTx-1(1-34)	0.3	14.1	22.0	19.1	2.4	1.2	0.5
635	{H}-DCLG[Aib]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Aib5;Leu6]GpTx-1(1-34)	0.23	14.8	14.8	0.38	64.6	39.1	0.6
636	{H}-DCLG[2-Abu]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Abu5;Leu6]GpTx-1(1-34)	0.29	16.7	6.8	1.0	23.8	6.7	0.3
637	{H}-DCLG[Nva]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Nva5;Leu6]GpTx-1(1-34)	0.095	8.0	5.1	0.71	53.7	7.2	0.1

638	{H}-DCLG[Nle]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Nle5;Leu6]GpTx-1(1-34)	0.025	10.6	1.9	0.099	76.6	19.2	0.3
639	{H}-DCLG[OctylG]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[OctylG5;Leu6]GpTx-1(1-34)	0.015	1.7	0.11	0.033	7.8	3.5	0.4
640	{H}-DCLGAFRKCIPD[Pra]DKCCRPNLVCSRLHRWCKYVF-{Amide}	[Ala5,Phe6,Pra13,Leu26,Arg28]GpTx-1(1-34)	0.103	>5	4.9	0.090	47.3	54.6	1.2
641	{H}-DCLGMLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Met5;Leu6]GpTx-1(1-34)	0.069	>5	4.4	0.24	64.7	18.5	0.3
642	{H}-DCLG[3Pal]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[3Pal5;Leu6]GpTx-1(1-34)	1.7	>5	>5	3.9	-	-	0.4
643	{H}-DCLGSLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ser5;Leu6]GpTx-1(1-34)	1.3	>5	>5	3.2	-	-	0.4
644	{H}-DCLGVLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Val5;Leu6]GpTx-1(1-34)	0.15	>5	>5	0.48	-	-	0.3
645	{H}-DCLG[DiMeO-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[DiMeO-F5;Leu6]GpTx-1(1-34)	2.4	>5	>5	2.6	-	-	0.9
646	{H}-DCLG[Sar]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Sar5;Leu6]GpTx-1(1-34)	0.92	>5	>5	1.7	-	-	0.6
647	{H}-DCLGaMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[D-Ala5]GpTx-1(1-34)	4.5	>5	>5	>5	-	-	-
648	{H}-DCLG[bAla]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[bAla5]GpTx-1(1-34)	4.7	>5	>5	>5	-	-	-
649	{H}-DCLG[2-Abu]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Abu5]GpTx-1(1-34)	0.69	>5	>5	1.3	-	-	0.5
650	{H}-DCLG[Nva]MRKCIPDNDKCCRPNLVCSRTHKW	[Nva5]GpTx-1(1-34)	0.20	>5	>5	0.67	-	-	0.3

	CKYVF-{Amide}								
651	{H}-DCLG[Nle]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Nle5]GpTx-1(1-34)	0.077	>5	3.0	0.17	39.6	17.6	0.4
652	{H}-DCLG[DiMeO-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[DiMeO-F5]GpTx-1(1-34)	2.9	>5	>5	3.6	-	-	0.8
653	{H}-DCLG[DiCl-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[DiCl-F5]GpTx-1(1-34)	0.14	>5	1.2	0.069	8.8	17.7	2.0
654	{H}-DCLG[4CF3-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4CF3-F5]GpTx-1(1-34)	0.32	>5	1.3	0.072	4.1	18.4	4.4
655	{H}-DCLG[4-F-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4-F-F5]GpTx-1(1-34)	0.26	>5	1.9	0.070	7.1	26.6	3.8
656	{H}-DCLG[NMeVal]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMeVal5]GpTx-1(1-34)	1.2	>5	>5	2.5	-	-	0.5
657	{H}-DCLG[NMePhe]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMePhe5]GpTx-1(1-34)	0.36	>5	>5	0.28	-	-	1.3
658	{H}-DCLG[Sar]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Sar5]GpTx-1(1-34)	1.5	>5	>5	2.0	-	-	0.7
659	{H}-DCLG[Tle]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Tle5;Leu6]GpTx-1(1-34)	0.26	>5	>5	0.55	-	-	0.4
660	{H}-DCLG[hLeu]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[hLeu5;Leu6]GpTx-1(1-34)	0.031	>5	0.80	0.059	25.6	13.6	0.5
661	{H}-DCLGLLRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Leu5,6]GpTx-1(1-34)	0.005	>5	3.4	0.32	36.0	10.6	0.3
662	{H}-DCLG[Thi]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Thi5;Leu6]GpTx-1(1-34)	0.022	>5	0.93	0.068	42.7	13.6	0.3
663	{H}-	[Cpg5;Leu6]GpTx-1(1-	0.050	>5	2.2	0.24	36.6	9.1	0.2

	DCLG[Cpg]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	34)							
664	{H}-DCLG{Chg]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Chg5;Leu6]GpTx-1(1-34)	0.019	>5	1.3	0.11	65.3	11.4	0.2
665	{H}-DCLG[4-Bz-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4-Bz-F5;Leu6]GpTx-1(1-34)	0.23	>5	0.57	0.030	2.5	19.1	7.7
666	{H}-DCLG[DiCl-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[DiCl-F5;Leu6]GpTx-1(1-34)	0.029	4.5	0.32	0.016	10.9	20.2	1.9
667	{H}-DCLG[pI-Phe]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[pI-Phe5;Leu6]GpTx-1(1-34)	0.12	>5	0.39	0.017	3.2	23.3	7.3
668	{H}-DCLG[4CF3-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4CF3-F5;Leu6]GpTx-1(1-34)	0.18	4.4	0.47	0.011	2.6	42.8	16.3
669	{H}-DCLG[4-F-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4-F-F5;Leu6]GpTx-1(1-34)	0.091	>5	0.78	0.037	8.6	20.9	2.4
670	{H}-DCLG[4-Me-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4-Me-F5;Leu6]GpTx-1(1-34)	0.19	>5	0.99	0.055	5.2	17.9	3.4
671	{H}-DCLG[4tBu-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4tBu-F5;Leu6]GpTx-1(1-34)	0.14	>5	0.43	0.050	3.1	8.5	2.8
672	{H}-DCLG[NMeVal]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMeVal5;Leu6]GpTx-1(1-34)	0.47	>5	>5	0.75	-	-	0.6
673	{H}-DCLG[NMeLeu]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMeLeu5;Leu6]GpTx-1(1-34)	0.17	>5	>5	0.69	-	-	0.2
674	{H}-DCLG[NMePhe]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[NMePhe5;Leu6]GpTx-1(1-34)	0.24	>5	3.5	0.31	14.3	11.3	0.8
675	{H}-DCLG[2-Cl-F]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Cl-F5;Leu6]GpTx-1(1-34)	0.066	>5	0.92	0.072	14.0	12.9	0.9

676	{H}-DCLG[hPhe]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[hPhe5;Leu6]GpTx-1(1-34)	0.016	>5	0.90	0.061	56.2	14.6	0.3
677	{H}-DCLG[OctylG]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[OctylG5]GpTx-1(1-34)	0.17	>5	0.89	0.17	5.2	5.1	1.0
678	{H}-DCLG[Tle]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Tle5]GpTx-1(1-34)	0.70	>5	>5	1.36	-	-	0.5
679	{H}-DCLG[hLeu]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[hLeu5]GpTx-1(1-34)	0.086	>5	2.2	0.24	26.0	9.4	0.4
680	{H}-DCLG[Cha]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Cha5;Phe6]GpTx-1(1-34)	0.019	3.5	0.38	0.062	20.1	11.9	0.6
681	{H}-DCLG[Cha]LRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Cha5;Leu6]GpTx-1(1-34)	0.023	>5	0.86	0.079	37.9	10.9	0.3
682	{H}-DCLG[Thi]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Thi5]GpTx-1(1-34)	0.11	>5	2.8	0.28	26.6	10.3	0.4
683	{H}-DCLG[Cpg]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Cpg5]GpTx-1(1-34)	0.23	>5	>5	0.63	-	-	0.4
684	{H}-DCLG[Chg]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Chg5]GpTx-1(1-34)	0.13	>5	4.6	0.36	34.1	12.6	0.4
685	{H}-DCLG[4-Bz-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4-Bz-F5]GpTx-1(1-34)	0.68	>5	3.3	0.15	4.8	21.2	4.4
686	{H}-DCLG[4-Me-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4-Me-F5]GpTx-1(1-34)	0.19	>5	2.2	0.18	4.5	12.5	2.8
687	{H}-DCLG[4tBu-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[4tBu-F5]GpTx-1(1-34)	0.27	>5	1.2	0.13	4.5	9.4	2.1
688	{H}-DCLG[NMeLeu]MRKCIPDNDKCCRPNLVCSRT	[NMeLeu5]GpTx-1(1-34)	0.29	>5	>5	0.73	-	-	0.4

	HKWCKYVF-{Amide}								
689	{H}-DCLG[2-Cl-F]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Cl-F5]GpTx-1(1-34)	0.13	>5	1.9	0.11	14.2	18.2	1.3
690	{H}-DCLG[hPhe]MRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[hPhe5]GpTx-1(1-34)	0.090	>5	2.3	0.18	25.8	13.0	0.5
691	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Glu28]GpTx-1(1-34)	>5	>5	>5	>5	-	-	-
692	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCK[1'NMeW]VF-{Amide}	[Ala5;1'NMeW32]GpTx-1(1-34)	0.18	>5	>5	0.63	-	-	0.3
693	{H}-DCLGMMRKCIPDNDKCCRPNLVCSRTHKWCK[1'NMeW]VF-{Amide}	[Met5;1'NMeW32]GpTx-1(1-34)	0.046	>5	4.3	0.10	95.0	43.0	0.5
694	{H}-DCLRMMRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Arg4;Met5]GpTx-1(1-34)	0.060	>5	>5	0.29	-	-	0.3
695	{H}-DCLGFMRKCIPDNDKCCRSNLVCSRTHKWCK[1'NMeW]VF-{Amide}	[Ser19;1'NMeW32]GpTx-1(1-34)	0.030	>5	0.88	0.030	29.1	28.9	1.0
696	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Leu6]GpTx-1(1-34)	0.27	>5	>5	0.75	-	-	0.4
697	{H}-DCLGAGRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Gly6]GpTx-1(1-34)	8.1	>5	>5	4.4	-	-	1.8
698	{H}-DCLGAYRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Tyr6]GpTx-1(1-34)	4.4	>5	>5	>5	-	-	-
699	{H}-DCLGA[1'NMeW]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;1'NMeW6]GpTx-1(1-34)	0.34	>5	>5	0.32	-	-	1.1
700	{H}-DCLGAMRKCDPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Asp10]GpTx-1(1-34)	0.74	35	>50	0.84	-	-	0.9
701	{H}-	[Ala5;Asp10;Glu12]Gp	0.97	43	>50	1.5	-	-	0.6

	DCLGAMRKCDPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	Tx-1(1-34)							
702	{H}-DCLGAFRKCDPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Asp10]GpTx-1(1-34)	0.72	43	>50	0.37	-	-	1.9
703	{H}-DCLGAFRKCIPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Glu12]GpTx-1(1-34)	0.61	45	15	0.20	23.9	73.9	3.1
704	{H}-DCLGVMRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Glu28]GpTx-1(1-34)	0.99	49	>50	>5	-	-	-
705	{H}-DCLG[Nva]MRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Glu28]GpTx-1(1-34)	0.43	33	>50	3.4	-	-	0.1
706	{H}-DCLG[2-Abu]MRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Glu28]GpTx-1(1-34)	1.4	>50	>50	>5	-	-	-
707	{H}-DCLG[2-Abu]LRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Leu6;Glu28]GpTx-1(1-34)	1.2	6	>50	>5	-	-	-
708	{H}-DCLG[Nva]LRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[Nva5;Leu6;Glu28]GpTx-1(1-34)	0.37	31	>50	2.8	-	-	0.1
709	{H}-DCLGVLRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[Val5;Leu6;Glu28]GpTx-1(1-34)	0.74	43	>50	4.8	-	-	0.2
710	{H}-DCLGVMRKCDPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Val5;Asp10]GpTx-1(1-34)	0.69	35	>50	1.3	-	-	0.5
711	{H}-DCLGVMRKCIPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Val5;Glu12]GpTx-1(1-34)	0.48	26	>50	0.75	-	-	0.6
712	{H}-DCLGVMRKCDPENDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Val5;Asp10;Glu12]GpTx-1(1-34)	0.46	34	>50	1.7	-	-	0.3
713	{H}-DCLGVMRKCIPDNDKCCRPNLVCS[Cit]THKWCKYVF-{Amide}	[Val5;Cit25]GpTx-1(1-34)	0.83	36	>50	4.2	-	-	0.2

714	{H}-DCLGTMRKCDPDNDKCCRPNLVCSRTHKWC KYVF-{Amide}	[Thr5;Asp10]GpTx-1(1-34)	1.6	48	>50	>5	-	-	-	-
715	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHGWCK YVF-{Amide}	[Ala5;Gly28]GpTx-1(1-34)	1.0	>50	>50	>5	-	-	-	-
716	{H}-D[2-Abu]LGAMRKCDPDNDKC[2-Abu]RPNLVCSRTHKWCKYVF-{Amide}	[2-Abu2,17;Ala5;Asp10]GpTx-1(1-34)	3.7	49	>50	>5	-	-	-	-
717	{H}-D[2-Abu]LG[Nva]LRKCIPDNDKC[2-Abu]RPNLVCSRTHEWCKYVF-{Amide}	[2-Abu2,17;Nva5;Leu6;Glu28]GpTx-1(1-34)	>5	>50	>50	>5	-	-	-	-
718	{H}-D[2-Abu]LG[2-Abu]LRKCIPDNDKC[2-Abu]RPNLVCSRTHEWCKYVF-{Amide}	[2-Abu2,5,17;Leu6;Glu28]GpTx-1(1-34)	4.3	>50	>50	>5	-	-	-	-
719	{H}-D[2-Abu]LGALRKCIPDNDKC[2-Abu]RPNLVCSRTHEWCKYVF-{Amide}	[2-Abu2,17;Ala5;Leu6;Glu28]GpTx-1(1-34)	4.3	>50	>50	>5	-	-	-	-
720	{H}-D[2-Abu]LGVLRKCIPDNDKC[2-Abu]RPNLVCSRTHEWCKYVF-{Amide}	[2-Abu2,17;Val5;Leu6;Glu28]GpTx-1(1-34)	>5	33	>50	>5	-	-	-	-
721	{H}-DCLGA[Nle]RKCIPDNDKCCRPNLVCSRTHKW CKYVF-{Amide}	[Ala5;Nle6]GpTx-1(1-34)	0.15	45	>50	0.41	-	-	-	0.4
722	{H}-DCLGA[Nle]RKCEPDNDKCCRPNLVCSRTHKW CKYVF-{Amide}	[Ala5;Nle6,Glu10]GpTx-1(1-34)	0.33	44	48	0.48	144.9	101.0	-	0.7
723	{H}-DCLGALRKCEPDNDKCCRPNLVCSRTHKWCK YVF-{Amide}	[Ala5;Leu6;Glu10]GpTx-1(1-34)	0.38	>50	>50	1.2	-	-	-	0.3
724	{H}-DCLGAFRKCEPDNDKCCRPNLVCSRTHKWCK YVF-{Amide}	[Ala5;Phe6;Glu10]GpTx-1(1-34)	0.33	36	41	0.32	109.5	130.1	-	1.2
725	{H}-DCLGA[Nle]RKCIPENDKCCRPNLVCSRTHKW CKYVF-{Amide}	[Ala5;Nle6,Glu12]GpTx-1(1-34)	0.38	47	>50	0.27	-	-	-	1.4
726	{H}-DCLGALRKCIPENDKCCRPNLVCSRTHKWCKY	[Ala5;Leu6;Glu12]GpTx-1(1-34)	0.35	>50	49	0.56	138.2	83.4		0.6

	VF-{Amide}								
727	{H}-DCLGA[Nle]RKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Nle6;Glu28]GpTx-1(1-34)	0.51	34	34	3.4	66.8	10.1	0.2
728	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Leu6;Glu28]GpTx-1(1-34)	1.6	43	41	5.6	26.7	6.3	0.2
729	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[Ala5;Phe6;Glu28]GpTx-1(1-34)	1.1	48	>50	1.8	-	-	0.6
730	{H}-DCLGA[Nle]RKCIPDNDKCCRPNLVCSATHKWCKYVF-{Amide}	[Ala5,25;Nle6]GpTx-1(1-34)	0.84	47	49	1.7	58.0	29.3	0.5
731	{H}-DCLGALRKCIPDNDKCCRPNLVCSATHKWCKYVF-{Amide}	[Ala5,25;Leu6]GpTx-1(1-34)	0.60	38	37	2.8	61.5	13.2	0.2
732	{H}-DCLGAFRKCIPDNDKCCRPNLVCSATHKWCKYVF-{Amide}	[Ala5,25;Phe6]GpTx-1(1-34)	0.29	>50	45	0.60	156.1	73.7	0.5
733	{H}-DCLGA[Nle]RKCIPDNDKCCRPNLVCSETHKWCKYVF-{Amide}	[Ala5;Nle6;Glu25]GpTx-1(1-34)	1.6	33	42	5.2	25.9	8.1	0.3
734	{H}-DCLGALRKCIPDNDKCCRPNLVCSETHKWCKYVF-{Amide}	[Ala5;Leu6;Glu25]GpTx-1(1-34)	1.8	41	>50	0.3	-	-	0.2
735	{H}-DCLGAFRKCIPDNDKCCRPNLVCSETHKWCKYVF-{Amide}	[Ala5;Phe6;Glu25]GpTx-1(1-34)	1.5	41	48	3.6	32.0	13.3	0.4
736	{H}-DCLGFFRKCIPDND[Pra]CCRPNLVCSRTHKWCKYVF-{Amide}	[Phe6,Pra15]GpTx-1(1-34)	>5	32.6	>50	>5	-	-	-
737	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHHWCKYVF-{Amide}	[Ala5;His28]GpTx-1(1-34)	0.40	19.2	46.6	1.6	117.3	28.7	0.2
738	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHSWCKYVF-{Amide}	[Ala5;Ser28]GpTx-1(1-34)	0.65	21.9	>50	1.8	-	-	0.4
739	{H}-	[Ala5;Gln28]GpTx-1(1-	0.63	20.5	46.0	2.2	72.5	20.5	0.3

	DCLGAMRKCIPDNDKCCRPNLVCSRTHQWCK YVF-{Amide}	34)							
740	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[3Pal] WCKYVF-{Amide}	[Ala5;3Pal28]GpTx-1(1-34)	1.5	31.1	47.6	>5	32.5	-	-
741	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[4-aminoF]WCKYVF-{Amide}	[Ala5;4-aminoF28]GpTx-1(1-34)	1.1	24.4	>50	2.3	-	-	0.5
742	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[K(Ac)] WCKYVF-{Amide}	[Ala5;K(Ac)28]GpTx-1(1-34)	1.1	22.7	32.7	2.5	30.5	13.1	0.4
743	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[SDMA]WCKYVF-{Amide}	[Ala5;SDMA28]GpTx-1(1-34)	0.22	26.5	46.5	1.1	213.8	43.1	0.2
744	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[hArg] WCKYVF-{Amide}	[Ala5;hArg28]GpTx-1(1-34)	0.47	39.7	>50	0.62	-	-	0.6
745	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[R(Me)] WCKYVF-{Amide}	[Ala5;R(Me)28]GpTx-1(1-34)	0.25	40.0	>50	0.50	-	-	0.5
746	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[Orn]W CKYVF-{Amide}	[Ala5;Orn28]GpTx-1(1-34)	0.29	20.7	>50	0.76	-	-	0.4
747	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[Dap]W CKYVF-{Amide}	[Ala5;Dap28]GpTx-1(1-34)	0.37	38.3	34.5	0.78	94.0	44.4	0.5
748	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[Cit]W CKYVF-{Amide}	[Ala5;Cit28]GpTx-1(1-34)	0.87	24.2	>50	2.7	-	-	0.3
749	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[HCit] WCKYVF-{Amide}	[Ala5;HCit28]GpTx-1(1-34)	0.79	20.3	46.4	2.3	58.6	20.1	0.3
750	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHDWCK YVF-{Amide}	[Asp28]GpTx-1(1-34)	0.73	37.9	49.6	0.77	67.8	64.1	0.9
751	{H}-DCLGGVRKCIPDNDKCCRPNLVCSRTHKWCK YVF-{Amide}	[Gly5;Val6]GpTx-1(1-34)	>5	25.5	49.3	>5	-	-	-

752	{H}-DCLGGIRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Gly5;Ile6]GpTx-1(1-34)	>5	25.4	44.7	>5	-	-	-
753	{H}-DCLG[2-Abu][Nle]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Abu5;Nle6]GpTx-1(1-34)	0.06	40.2	>50	0.16	-	-	0.4
754	{H}-DCLGGFRKCEPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Gly5;Phe6;Glu10]GpTx-1(1-34)	0.35	34.2	>50	0.33	-	-	1.1
755	{H}-DCLGGFRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[Gly5;Phe6;Glu28]GpTx-1(1-34)	>5	15.3	>50	>5	-	-	-
756	{4-Pen}-DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	4-Pen-[Ala5;Phe6;2-Abu13;Arg28]GpTx-1(1-34)	0.18	44.4	>50	0.26	-	-	0.7
757	{4-Pen}-DCLGAFRKCIPD[2-Abu]DKCCRPNLVCSRTHKWCKYVF-{Amide}	4-Pen-[Ala5;Phe6;2-Abu13]GpTx-1(1-34)	0.71	34.9	>50	0.28	-	-	2.5
758	{4-Pen}-DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRTHKWCKYVF-{Amide}	4-Pen-[2-Abu5,13;Leu6]GpTx-1(1-34)	0.46	32.7	23.7	0.69	51.8	34.5	0.7
759	{4-Pen}-DCLG[Nva]LRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	4-Pen-[Nva5;Leu6;2-Abu13;Arg28]GpTx-1(1-34)	0.10	46.2	28.0	0.23	270.9	121.0	0.4
760	{4-Pen}-DCLG[Nva]LRKCIPD[2-Abu]DKCCRPNLVCSRTHKWCKYVF-{Amide}	4-Pen-[Nva5;Leu6;2-Abu13]GpTx-1(1-34)	0.19	35.2	27.4	0.26	145.4	109.2	0.8
761	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[Guf]WCKYVF-{Amide}	[Ala5;Guf28]GpTx-1(1-34)	0.16	26.9	>50	0.63	-	-	0.2
762	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[Dab]WCKYVF-{Amide}	[Ala5;Dab28]GpTx-1(1-34)	0.32	23.3	>50	0.86	-	-	0.4
763	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTHQWCKYVF-{Amide}	[Gln28]GpTx-1(1-34)	0.19	22.7	>50	0.27	-	-	0.7
764	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHFWCKYVF-{Amide}	[Ala5;Phe28]GpTx-1(1-34)	4.1	41.4	>50	>5	-	-	-
765	{H}-	[Ala5;Tyr28]GpTx-1(1-	0.79	42.0	46.8	1.4	58.8	33.2	0.6

	DCLGAMRKCIPDNDKCCRPNLVCSRTHYWCK YVF-{Amide}	34)							
766	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHLWCK YVF-{Amide}	[Ala5;Leu28]GpTx-1(1-34)	1.1	49.3	36.9	2.7	33.4	13.7	0.4
767	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHNWCK YVF-{Amide}	[Ala5;Asn28]GpTx-1(1-34)	1.7	>50	43.8	3.2	25.6	13.6	0.5
768	{H}-DCLGAMRKCIPDNDKCCRPNLVCS[Cit]THKW CKYVF-{Amide}	[Ala5;Cit25]GpTx-1(1-34)	1.8	23.5	>50	3.2	-	-	0.6
769	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHDWCK YVF-{Amide}	[Ala5;Asp28]GpTx-1(1-34)	>5	39.0	>50	>5	-	-	-
770	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHMWCK YVF-{Amide}	[Ala5;Met28]GpTx-1(1-34)	1.0	45.4	>50	4.1	-	-	0.3
771	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTH[K(Me)] WCKYVF-{Amide}	[Ala5;K(Me)28]GpTx-1(1-34)	1.6	40.1	>50	1.8	-	-	0.9
772	{H}-DCLGFMRKCIPDNDKCCRPNLVCSRTH[pS]W CKYVF-{Amide}	[pS28]GpTx-1(1-34)	0.90	>50	>50	0.81	-	-	1.1
773	{H}-DCLGTMRKCDPENDKCCRPNLVCSRTHKWCK YVF-{Amide}	[Thr5;Asp10;Glu12]GpTx-1(1-34)	4.5	28.4	>50	3.4	-	-	1.3
774	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYEF-{Amide}	[1-Nal10;Glu33]GpTx-1(1-34)	0.30	28.3	12.7	0.53	42.8	24.2	0.6
775	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKEVF-{Amide}	[1-Nal10;Glu32]GpTx-1(1-34)	>5	28.6	21.3	>5	-	-	-
776	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCEYVF-{Amide}	[1-Nal10;Glu31]GpTx-1(1-34)	>5	26.8	28.5	>5	-	-	-
777	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYAF-{Amide}	[1-Nal10;Ala33]GpTx-1(1-34)	0.20	39.5	8.6	0.20	43.7	42.4	1.0

778	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKAVF-{Amide}	[1-Nal10;Ala32]GpTx-1(1-34)	0.51	35.0	15.8	0.46	31.0	36.2	1.2
779	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCAYVF-{Amide}	[1-Nal10;Ala31]GpTx-1(1-34)	>5	36.5	38.0	3.2	-	12.0	-
780	{H}-DCLGFMRKC[1-Nal]PDNDKCCRPNLVCSRTHEWCKYVF-{Amide}	[1-Nal10;Glu28]GpTx-1(1-34)	0.78	27.5	28.9	1.1	37.3	26.4	0.7
781	{H}-DCLGFMRKC[1-Nal]PDNDECCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal10;Glu15]GpTx-1(1-34)	0.93	34.3	24.8	1.1	26.6	21.7	0.8
782	{H}-DCLGFMREC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu8;1-Nal10]GpTx-1(1-34)	1.1	30.7	12.4	1.2	11.2	10.1	0.9
783	{H}-DCLEFMRKC[1-Nal]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Glu4;1-Nal10]GpTx-1(1-34)	1.3	29.1	18.5	2.0	14.1	9.1	0.6
784	{H}-[1-Nal]CLGFMRECIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal1;Glu8]GpTx-1(1-34)	1.0	32.0	26.0	0.96	25.9	29.0	1.1
785	{H}-[1-Nal]CLGFMEKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal1;Glu7]GpTx-1(1-34)	1.8	30.6	27.7	1.9	15.4	14.7	1.0
786	{H}-[1-Nal]CLGFERKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[1-Nal1;Glu6]GpTx-1(1-34)	>5	26.3	33.9	>5	-	-	-
787	{H}-DCLGAMRKCIPDNDKCCRPNLVCSREHKWCKYVF-{Amide}	[Ala5;Glu26]GpTx-1(1-34)	>5	27.3	24.9	>5	-	-	-
788	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTEKWCKYVF-{Amide}	[Ala5;Glu27]GpTx-1(1-34)	>5	29.7	27.1	>5	-	-	-
789	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCEYVF-{Amide}	[Ala5;Glu31]GpTx-1(1-34)	>5	31.8	21.5	>5	-	-	-
790	{H}-DCLGAMRKCIPDNDKCCRPNLVCSRTHKWCK	[Ala5]GpTx-1(1-34)-Glu	>5	28.5	25.5	>5	-	-	-

	YVFE-{Amide}								
791	{H}-DCLGA{METO1]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5,Met(O)6]GpTx-1 isomer1	>5	39.5	>50	>5	-	-	-
792	{H}-DCLGA[METO1]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5,Met(O)6]GpTx-1 isomer2	>5	49.8	43.0	>5	-	-	-
793	{H}-DCLGAFRKCIPD[Pra]DKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Pra13]GpTx-1(1-34)	0.53	28.6	12.3	0.47	23.0	26.4	1.1
794	{H}-DCLGAFRKCIPD[K(Ac-Pra)]DKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;K(Ac-Pra)13]GpTx-1(1-34)	0.89	37.8	>50	0.70	-	-	1.3
795	{H}-DCLGAFRKCIPD[K(Ac-Pra)]DKCCRPNLVCSRTHRWCKYVF-{Amide}	[Ala5;Phe6;K(Ac-Pra)13;Arg28]GpTx-1(1-34)	0.78	24.6	18.0	0.25	23.1	70.9	3.1
796	{H}-DCLGALRKCIPD[Pra]DKCCRPNLVCSRLHRWCKYVF-{Amide}	[Ala5;Leu6,26;Pra13;Arg28]GpTx-1(1-34)	0.22	36.4	>50	0.48	-	-	0.5
797	{H}-DCLG[2-Abu]LRKCIPD[Pra]DKCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Abu5;Leu6;Pra13]GpTx-1(1-34)	0.52	34.0	26.6	0.93	50.8	28.7	0.6
798	{H}-DCLGAFRKCEPD[Pra]DKCCRPNLVCSRLHRWCKYVF-{Amide}	[Ala5;Phe6;Glu10;Pra13;Leu26;Arg28]GpTx-1(1-34)	0.54	32.2	>50	0.66	-	-	1.0
799	{H}-DCLG[2-Abu]LRKCIPD[K(Ac-Pra)]DKCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Abu5;Leu6;K(Ac-Pra)13]GpTx-1(1-34)	0.75	28.1	48.5	0.70	65.1	69.4	1.1
800	{H}-DCLGALRKCEPD[Pra]DKCCRPNLVCSRLHRWCKYVF-{Amide}	[Ala5;Leu6,26;Glu10;Pra13;Arg28]GpTx-1(1-34)	0.70	>50	>50	1.4	-	-	0.5
801	{H}-DCLG[2-Abu]LRKCIPD[K(4-Pen)]DKCCRPNLVCSRTHRWCKYVF-{Amide}	[2-Abu5;Leu6;K(4-Pen)13;Arg28]GpTx-1(1-34)	0.55	39.7	>50	0.81	-	-	0.7
802	{H}-DCLGALRKCIP[Pra]NDKCCRPNLVCSRLHRWCKYVF-{Amide}	[Ala5;Leu6,26;Pra12;Arg28]GpTx-1(1-34)	0.26	>50	12.3	0.54	46.6	22.7	0.5
803	{H}-DCLGAFRKCIP[Pra]NDKCCRPNLVCSRLHRWCKYVF-{Amide}	[Ala5;Phe6;Pra12;Leu26;Arg28]GpTx-1(1-34)	0.13	36.5	2.5	0.12	19.9	20.7	1.0

804	{H}-DCLG[2-Abu]FRKCIPD[K(4-Pen)]DKCCRPNLVCSRTHKWCKYVF-{Amide}	[2-Abu5;Phe6;K(4-Pen)13]GpTx-1(1-34)	0.50	>50	5.3	0.35	10.5	15.2	1.5
805	{H}-DCLG[Nva]LRKCIPD[K(4-Pen)]DKCCRPNLVCSRTHRWCKYVF-{Amide}	[Nva5;Leu6;K(4-Pen)13;Arg28]GpTx-1(1-34)	0.31	37.5	12.2	0.27	39.4	45.7	1.2
806	{H}-DCLG[Nva]LRKCIPD[K(4-Pen)]DKCCRPNLVCSRTHKWCKYVF-{Amide}	[Nva5;Leu6;K(4-Pen)13]GpTx-1(1-34)	0.29	34.2	8.3	0.39	28.9	21.5	0.7
807	{4-Pen}-DCLG[2-Abu]LRKCIPD[2-Abu]DKCCRPNLVCSRTHRWCKYVF-{Amide}	4-Pen-[2-Abu5,13;Leu6;Arg28]GpTx-1(1-34)	0.54	36.8	>50	0.90	-	-	0.6
808	{H}-DCLG[2-Abu]LRKCIPD[K(4-Pen)]DKCCRPNLVCSRTHEWCKYVF-{Amide}	[2-Abu5;Leu6;K(4-Pen)13;Glu28]GpTx-1(1-34)	1.8	>5	>5	4.1	-	-	0.4
809	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	[Ala5;Phe6;Arg28]GpTx-1(1-34)	0.3	>5	>5	0.3	-	-	1.0
810	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	[Ala5;Leu6;Arg28]GpTx-1(1-34)	0.2	>5	>5	0.2	-	-	1.0
811	{H}-GSDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	Gly-Ser-[Ala5;Phe6;Arg28]GpTx-1(1-34)	0.3	>5	>5	0.3	-	-	1.0
812	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{Amide}	Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)	0.2	>5	>5	0.2	-	-	1.0
813	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFW-{FreeAcid}	[Ala5;Phe6;Arg28]GpTx-1(1-34)-Trp-FreeAcid	>5	>5	>5	>5	-	-	-
814	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFW-{FreeAcid}	[Ala5;Leu6;Arg28]GpTx-1(1-34)-Trp-FreeAcid	0.6	>5	>5	0.6	-	-	1.0
815	{H}-GSDCLGAFRKCIPDNDKCCRPNLVCSRTHRWCKYVFW-{FreeAcid}	Gly-Ser-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Trp-FreeAcid	>5	>5	>5	>5	-	-	-
816	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVFW-{FreeAcid}	Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Trp-FreeAcid	>5	>5	>5	>5	-	-	-
817	{H}-	[Ala5;Phe6;Arg28]GpT	1.5	>5	>5	0.5	-	-	3.0

	DCLGAFRKCIPDNDKCCRPNLVCSRTHRWCK YVFF-{FreeAcid}	x-1(1-34)-Phe-FreeAcid							
818	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHRWCK YVFF-{FreeAcid}	[Ala5;Leu6;Arg28]GpT x-1(1-34)-Phe-FreeAcid	2.3	>5	>5	0.8	-	-	2.9
819	{H}-GSDCLGAFRKCIPDNDKCCRPNLVCSRTHRW CKYVFF-{FreeAcid}	Gly-Ser-[Ala5;Phe6;Arg28]GpT x-1(1-34)-Phe-FreeAcid	1.5	>5	>5	0.5	-	-	3.0
820	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRW CKYVFF-{FreeAcid}	Gly-Ser-[Ala5;Leu6;Arg28]GpT x-1(1-34)-Phe-FreeAcid	0.5	>5	>5	0.5	-	-	1.0
821	{H}-GSDCLGAFRKCIPDNDKCCRPNLVCSRTHRW CKYVF-{FreeAcid}	Gly-Ser-[Ala5;Phe6;Arg28]GpT x-1(1-34)-FreeAcid	3.2	>5	>5	3.2	-	-	1.0
822	{H}-GSDCLGALRKCIPDNDKCCRPNLVCSRTHRW CKYVF-{FreeAcid}	Gly-Ser-[Ala5;Leu6;Arg28]GpT x-1(1-34)-FreeAcid	3.7	>5	>5	3.7	-	-	1.0
823	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Phe6;Arg28]GpT x-1(1-34)-FreeAcid	3.4	>5	>5	3.4	-	-	1.0
824	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHAWCK YVF-{FreeAcid}	[Ala5,28;Phe6]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
825	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHDWCK YVF-{FreeAcid}	[Ala5;Phe6;Asp28]GpT x-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
826	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHEWCK YVF-{FreeAcid}	[Ala5;Phe6;Glu28]GpT x-1(1-34)-FreeAcid	>5	>5	>5	1.8	-	-	-
827	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHGWCK YVF-{FreeAcid}	[Ala5;Phe6;Gly28]GpT x-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
828	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHHWCK YVF-{FreeAcid}	[Ala5;Phe6;His28]GpT x-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
829	{H}-	[Ala5;Phe6]GpTx-1(1-	>5	>5	>5	2.3	-	-	-

	DCLGAFRKCIPDNDKCCRPNLVCSRTHKWCK YVF-{FreeAcid}	34)-FreeAcid							
830	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHLWCKY VF-{FreeAcid}	[Ala5;Phe6;Leu28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
831	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHMWCK YVF-{FreeAcid}	[Ala5;Phe6;Met28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	1.6	-	-	-
832	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHNWCK YVF-{FreeAcid}	[Ala5;Phe6;Asn28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	4.6	-	-	-
833	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHPWCK YVF-{FreeAcid}	[Ala5;Phe6;Pro28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
834	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHQWCK YVF-{FreeAcid}	[Ala5;Phe6;Gln28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	3.9	-	-	-
835	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHSWCK YVF-{FreeAcid}	[Ala5;Phe6;Ser28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
836	{H}-DCLGAFRKCIPDADKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5,13;Phe6;Arg28]GpTx-1(1-34)-FreeAcid	1.1	>5	>5	1.3	-	-	3.1
837	{H}-DCLGAFRKCIPDDDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Phe6;Asp13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	2.3	-	-	-
838	{H}-DCLGAFRKCIPDEDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Phe6;Glu13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	1.9	-	-	-
839	{H}-DCLGAFRKCIPDFDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Phe6,13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	1.2	-	-	-
840	{H}-DCLGAFRKCIPDGDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Phe6;Gly13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	1.5	-	-	-
841	{H}-DCLGAFRKCIPDHDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Phe6;His13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-

842	{H}-DCLGAFRKCIPDIDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Ile13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	3.0	-	-	-
843	{H}-DCLGAFRKCIPDKDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Lys13;Arg28]GpTx-1(1-34)-FreeAcid	3.6	2.8	>5	0.3	-	-	11.8
844	{H}-DCLGAFRKCIPDLDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Leu13;Arg28]GpTx-1(1-34)-FreeAcid	4.5	>5	>5	4.5	-	-	1.0
845	{H}-DCLGAFRKCIPDMDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Met13;Arg28]GpTx-1(1-34)-FreeAcid	4.7	>5	>5	0.8	-	-	5.8
846	{H}-DCLGAFRKCIPDPDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Pro13;Arg28]GpTx-1(1-34)-FreeAcid	2.9	>5	>5	2.9	-	-	1.0
847	{H}-DCLGAFRKCIPDQDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Gln13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	1.7	-	-	-
848	{H}-DCLGAFRKCIPDRDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Arg13,28]GpTx-1(1-34)-FreeAcid	4.5	>5	>5	0.6	-	-	7.1
849	{H}-DCLGAFRKCIPDSDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Ser13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	1.1	-	-	-
850	{H}-DCLGAFRKCIPDTDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Thr13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	1.3	-	-	-
851	{H}-DCLGAFRKCIPDVDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Val13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	1.7	-	-	-
852	{H}-DCLGAFRKCIPDWDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Phe6;Trp13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
853	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Leu6;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
854	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHDWCK	[Ala5;Leu6;Asp28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-

	YVF-{FreeAcid}								
855	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHEWCKYVF-{FreeAcid}	[Ala5;Leu6;Glu28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
856	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHLWCKYVF-{FreeAcid}	[Ala5;Leu6,28]GpTx-1(1-34)-FreeAcid	4.1	>5	>5	4.1	-	-	1.0
857	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHMWCKYVF-{FreeAcid}	[Ala5;Leu6;Met28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
858	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHQWCKYVF-{FreeAcid}	[Ala5;Leu6;Gln28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
859	{H}-DCLGALRKCIPDNDKCCRPNLVCSRTHSWCKYVF-{FreeAcid}	[Ala5;Leu6;Ser28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
860	{H}-DCLGALRKCIPDADKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5,13;Leu6;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	4.5	-	-	-
861	{H}-DCLGALRKCIPDDDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Leu6;Asp13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
862	{H}-DCLGALRKCIPDEDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Leu6;Glu13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
863	{H}-DCLGALRKCIPDFDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Leu6;Phe13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
864	{H}-DCLGALRKCIPDHDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Leu6;His13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	3.9	-	-	-
865	{H}-DCLGALRKCIPDIDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Leu6;Ile13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
866	{H}-DCLGALRKCIPDKDKCCRPNLVCSRTHRWCKYVF-{FreeAcid}	[Ala5;Leu6;Lys13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	2.3	-	-	-
867	{H}-	[Ala5;Leu6,13;Arg28]G	>5	>5	>5	4.9	-	-	-

	DCLGALRKCIPDLDKCCRPNLVCSRTHRWCKY VF-{FreeAcid}	pTx-1(1-34)-FreeAcid							
868	{H}-DCLGALRKCIPDMDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Leu6;Met13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
869	{H}-DCLGALRKCIPDQDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Leu6;Gln13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
870	{H}-DCLGALRKCIPDRDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Leu6;Arg13.28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	1.4	-	-	-
871	{H}-DCLGALRKCIPDSDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Leu6;Ser13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
872	{H}-DCLGALRKCIPDVDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Leu6;Val13;Arg28]GpTx-1(1-34)-FreeAcid	>5	>5	>5	>5	-	-	-
873	{H}-DCLGALRKCIPDYDKCCRPNLVCSRTHRWCK YVF-{FreeAcid}	[Ala5;Leu6;Tyr13;Arg28]GpTx-1(1-34)-FreeAcid	4.8	>5	>5	>5	-	-	-

Table 30. Electrophysiology by PatchXpress®

SEQ ID NO:	Designation	Nav1.3 Use IC50 (μM)	Nav1.4 Use IC50 (μM)	Nav1.5 Use IC50 (μM)	Nav1.7 Use IC50 (μM)	Nav1.4/ Nav1.3 Use	Nav1.5/ Nav1.3 Use	Nav1.4/ Nav1.7 Use	Nav1.5/ Nav1.7 Use	Nav1.3/ Nav1.7 Use
1	GpTx-1(1-34)	0.010	0.241	>10	0.005	24	>1000	48	>2000	2.0
528	Huwentoxin-IV	0.022	4.5	25.3	0.032	205	1150	141	791	0.7
529	Huwentoxin-I	0.905	24.89	>30	0.717	28	33	35	42	1.3
530	KIIIA	0.574	0.021		0.144	0	0	0	0	4.0
531	ProTxII	0.015	0.032	0.104	0.002	2	7	13	43	6.3
72	[Arg28]GpTx-1(1-34)	0.012	0.866	8.730	0.007	72	728	124	1247	1.7
22	[Ala5]GpTx-1(1-34)	0.129	4.460	>10	0.018	35	>78	248	>556	7.2
80	[1-Nal34]GpTx-1(1-34)	0.007	0.179	1.860	0.004	26	266	45	465	1.8
70	[Arg26]GpTx-1(1-34)	0.010	0.109	0.573	0.005	11	57	22	115	2.0
87	GpTx-1(1-34)-Trp	0.015	0.640	2.660	0.009	43	177	71	296	1.7
95	[Gln33]GpTx-1(1-34)	0.010	0.286	8.250	0.006	29	825	48	1375	1.7
77	[1-Nal1]GpTx-1(1-34)	0.066	0.439	7.6	0.023	7	115	19	330	2.9
78	[1-Nal10]GpTx-1(1-34)	0.039	0.402	12.91	0.005	10	331	80	2581	7.8
89	[Phe6]GpTx-1(1-34)	0.016	0.141	3.159	0.015	9	197	9	211	1.1
94	[Lys26;Thr27]GpTx-1(1-34)	0.016	0.462	1.393	0.004	29	87	116	348	4.0
121	[Leu26]GpTx-1(1-34)	0.023	0.508	5.008	0.003	22	218	169	1669	7.7
123	[Nle6]GpTx-1(1-34)	0.009	0.066	1.149	0.008	7	124	8	137	1.1

161	[1-Nal6]GpTx-1(1-34)	0.004	0.115	0.358	0.003	28	87	41	128	1.5
167	[1-Nal32]GpTx-1(1-34)	0.012	0.061	0.988	0.004	5	82	15	247	3.0
170	[Trp6]GpTx-1(1-34)	ND	0.234	3.674	0.022	--	--	10	164	0.0
177	[Trp22]GpTx-1(1-34)	ND	0.689	4.779	0.039	--	--	18	122	0.0
180	[Trp33]GpTx-1(1-34)	ND	0.096	2.350	0.018	--	--	6	134	0.0
33	[Glu33]GpTx-1(1-34)	0.052	2.753	>10	0.027	53	192	102	370	1.9
148	[Glu18]GpTx-1(1-34)	0.098	1.635	>10	0.018	17	>102	91	>556	5.4
242	[Bip5]GpTx-1(1-34)	0.003	0.103	2.077	0.062	34	692	2	34	0.05
243	[Cha5]GpTx-1(1-34)	0.007	0.126	3.389	0.003	18	484	42	1130	2.3
244	[Leu6]GpTx-1(1-34)	0.018	0.365	>10	0.026	20	556	14	385	0.7
245	[Cha6]GpTx-1(1-34)	0.002	0.092	2.678	0.003	46	1339	31	893	0.7
246	[1'NMeW32]GpTx-1(1-34)	0.018	0.154	6.849	0.006	9	381	26	1142	3.0
152	[Glu26]GpTx-1(1-34)	0.216	6.41	>10	0.052	30	46	123	192	4.2
174	[Trp18]GpTx-1(1-34)	0.042	1.46	>10	0.024	35	>238	61	>417	1.8
247	[pI-Phe5]GpTx-1(1-34)	0.090	1.1	>10	0.247	12	111	4	40	0.36
248	[Ile33]GpTx-1(1-34)	0.102	1.94	>10	0.037	19	98	52	270	2.8
249	[pI-Phe33]GpTx-1(1-34)	0.035	0.388	10.4	0.026	11	297	15	400	1.3
250	[1'NMeW33]GpTx-1(1-34)	0.037	0.396	9.54	0.054	11	258	7	177	0.7
251	[Arg28;1-Nal32]GpTx-1(1-34)	0.006	0.193	1.06	0.005	32	177	39	212	1.2
108	GpTx-1(2-34)	0.015	0.251	4.944	0.007	17	334	36	706	2.1
132	Ac-GpTx-1(1-34)	0.084	2.12	>10	0.013	25	>119	16.5	>769	6.5

252	[Ala5;Trp33]GpTx-1(1-34)	0.569	5.54	>10	0.034	10	>18	163	>294	16.7
253	[Ala5;Trp32]GpTx-1(1-34)	2.98	>10	>10	0.103	3	>3	97	>97	28.9
254	[Ala5;1-Nal32]GpTx-1(1-34)	0.122	2.8	>10	0.028	23	>82	100	>357	4.4
255	[Ala5;Leu26]GpTx-1(1-34)	0.47	>10	>10	0.049	21	>21	204	>204	9.6
256	[Ala5;1-Nal6]GpTx-1(1-34)	0.008	0.469	3.81	0.002	59	476	235	1905	4.0
257	[Ala5;Phe6]GpTx-1(1-34)	0.022	0.824	>10	0.012	37	>455	69	>833	1.8
22	[Ala5]GpTx-1(1-34)	0.158	1.114	>10	0.014	70	>63	795	>714	11.3
258	[Ala5;1-Nal33]GpTx-1(1-34)	0.201	2.95	>10	0.048	15	>50	61	>208	4.2
259	[Ala5;1-Nal10]GpTx-1(1-34)	0.482	>10	>10	0.097	21	>21	103	>103	5.0
260	[Ala5;Arg28]GpTx-1(1-34)	0.44	>10	>10	0.077	23	>23	130	>130	5.7
261	[Ala5;Trp6]GpTx-1(1-34)	0.081	6.11	>10	0.057	75	>123	107	>175	1.4
262	[Ala5;Phe6;Leu26;Arg28]GpTx-1(1-34)	0.008	1.895	>10	0.002	237	>1250	648	>5000	4.0
263	[Ala5;Phe6;Leu26]GpTx-1(1-34)	0.011	1.196	>10	0.004	109	>909	299	>2500	2.8
515	[Phe6; Atz(amino-PEG10)13]GpTx-1(1-34)	0.006	0.127	5.998	0.022	21	1000	6	273	0.3
590	[Phe6;Atz(20kDaPEG)13]GpTx-1(1-34)	0.232	7.98	>10	0.184	34	>43	43	>54	1.3
	[Phe6,Atz(2 kDa EtO-PEG*-	0.008	0.254	1.43	0.013	32	179	20	110	0.6

--	{[Phe6,Atz13*]GpTx-1(1-34)})13]GpTx-1(1-34); * = Et (Homodimeric Conjugate 1)									
--	[Phe6,Atz(EtO-PEG4*-{[Phe6,Atz13*]GpTx-1(1-34)})13]GpTx-1(1-34); * = Et (Homodimeric Conjugate 2)	0.046	0.299	0.863	0.019	7	19	16	45	2.4
19	[Glu3]GpTx-1(1-34)	-	3.81	>10	0.041	-	-	93	>244	-
21	[Ala3]GpTx-1(1-34)	-	0.569	>10	0.012	-	-	47	>833	-
63	[Arg4]GpTx-1(1-34)	-	0.165	5	0.003	-	-	55	1667	-
39	[Lys4]GpTx-1(1-34)	-	0.327	10.6	0.006	-	-	55	1767	-
265	[Gly5]GpTx-1(1-34)	-	12.8	>10	0.009	-	-	1422	>1111	-
88	[Ile5]GpTx-1(1-34)	-	2.12	>10	0.002	-	-	1060	>5000	-
268	[Met5]GpTx-1(1-34)	-	0.978	>10	0.002	-	-	489	>5000	-
272	[Val5]GpTx-1(1-34)	-	4.41	>10	0.018	-	-	245	>556	-

267	[Leu5]GpTx-1(1-34)	-	0.778	>10	0.007	-	-	111	>1429	-
649	[2-Abu5]GpTx-1(1-34)	-	>10	>10	0.083	-	-	>120	>120	-
650	[Nva5]GpTx-1(1-34)	-	4.26	>10	0.038	-	-	112	>263	-
657	[NMePhe5]GpTx-1(1-34)	-	0.727	>10	0.018	-	-	40	>556	-
678	[Tle5]GpTx-1(1-34)	-	4.819	>10	0.023	-	-	210	>435	-
683	[Cpg5]GpTx-1(1-34)	-	1.87	>10	0.005	-	-	374	>2000	-
684	[Chg5]GpTx-1(1-34)	-	1.749	>10	0.007	-	-	250	>1429	-
688	[NMeLeu5]GpTx-1(1-34)	-	8.47	>10	0.026	-	-	326	>385	-
286	[Tyr6]GpTx-1(1-34)	-	3.79	10	0.069	-	-	55	145	-
283	[Pro6]GpTx-1(1-34)	-	4.11	10	0.042	-	-	98	238	-
294	[2PAL6]GpTx-1(1-34)	-	2.94	10	0.042	-	-	70	238	-
296	[SDMA7]GpTx-1(1-34)	-	0.606	14	0.006	-	-	101	2333	-
145	[Glu7]GpTx-1(1-34)	-	>10	>10	0.098	-	-	>102	>102	-
295	[K(Me2)7]GpTx-1(1-34)	-	2.21	>10	0.02	-	-	111	>500	-

298	[K(Me2)8]GpTx-1(1-34)	-	0.884	>10	0.004	-	-	221	>2500	-
297	[SDMA8]GpTx-1(1-34)	-	0.57	>10	0.005	-	-	114	>2000	-
118	[Thr8]GpTx-1(1-34)	-	0.888	>10	0.009	-	-	99	>1111	-
119	[Asp10]GpTx-1(1-34)	-	2.45	>10	0.003	-	-	817	>3333	-
146	[Glu10]GpTx-1(1-34)	-	1.3	>10	0.002	-	-	650	>5000	-
90	[Asn10]GpTx-1(1-34)	-	0.749	>10	0.002	-	-	375	>5000	-
147	[Glu11]GpTx-1(1-34)	-	1.67	>10	0.002	-	-	835	>5000	-
163	[1-Nal13]GpTx-1(1-34)	-	0.291	7.33	0.002	-	-	146	3665	-
28	[Glu15]GpTx-1(1-34)	-	2.72	10	0.02	-	-	136	500	-
125	[2-Abu2,17]GpTx-1(1-34)	-	0.947	10	0.021	-	-	45	476	-
316	[2PAL18]GpTx-1(1-34)	-	1.57	13.7	0.003	-	-	523	4567	-
116	[Cit18]GpTx-1(1-34)	-	0.833	10	0.002	-	-	417	5000	-
49	[Lys18]GpTx-1(1-34)	-	0.58	16.4	0.002	-	-	290	8200	-
314	[K(Me2)18]GpTx-1(1-34)	-	0.774	10	0.005	-	-	155	2000	-

315	[SDMA18]GpTx-1(1-34)	-	0.593	10	0.006	-	-	99	1667	-
50	[Lys19]GpTx-1(1-34)	-	0.22	9.1	0.003	-	-	73	3033	-
331	[Tyr22]GpTx-1(1-34)	-	2.03	>10	0.018	-	-	113	>556	-
8	[Ala22]GpTx-1(1-34)	-	0.429	6.2	0.006	-	-	72	1033	-
334	[2PAL22]GpTx-1(1-34)	-	1.86	16	0.007	-	-	266	2286	-
117	[Cit25]GpTx-1(1-34)	-	1.86	>10	0.004	-	-	465	>2500	-
335	[K(Me2)25]GpTx-1(1-34)	-	0.764	13.3	0.008	-	-	96	1663	-
9	[Ala25]GpTx-1(1-34)	-	2.24	10	0.012	-	-	187	833	-
151	[Glu25]GpTx-1(1-34)	-	5.53	>10	0.028	-	-	198	>357	-
337	[His26]GpTx-1(1-34)	-	0.246	4.95	0.003	-	-	82	1650	-
350	[4CO2-F26]GpTx-1(1-34)	-	6.18	>10	0.065	-	-	95	>154	-
153	[Glu28]GpTx-1(1-34)	-	10.7	>10	0.026	-	-	412	>385	-
750	[Asp28]GpTx-1(1-34)	-	12.9	>10	0.015	-	-	860	>667	-
763	[Gln28]GpTx-1(1-34)	-	4.61	>10	0.004	-	-	1153	>2500	-

355	[K(Me2)28]GpTx-1(1-34)	-	1.43	8.74	0.011	-	-	130	795	-
79	[1-Nal29]GpTx-1(1-34)	-	5.92	>10	0.033	-	-	179	>303	-
129	[2-Nal29]GpTx-1(1-34)	-	7.37	>10	0.066	-	-	112	>152	-
384	[2PAL32]GpTx-1(1-34)	-	4.96	>10	0.035	-	-	142	>286	-
403	[4CO2-F33]GpTx-1(1-34)	-	0.742	>10	0.003	-	-	247	>3333	-
402	[2PAL33]GpTx-1(1-34)	-	0.277	3.46	0.01	-	-	28	346	-
696	[Ala5;Leu6]GpTx-1(1-34)	-	11.246	>10	0.03	-	-	375	>333	-
721	[Ala5;Nle6]GpTx-1(1-34)	-	2.828	>10	0.01	-	-	283	>1000	-
699	[Ala5;1'NMeW6]GpTx-1(1-34)	-	4.5	>10	0.051	-	-	88	>196	-
437	[Ala5;Glu29]GpTx-1(1-34)	-	>10	>10	>10	-	-	>1	>1	-
613	[3Pal5;Phe6]GpTx-1(1-34)	-	12.3	>10	0.063	-	-	195	>159	-
636	[2-Abu5;Leu6]GpTx-1(1-34)	-	3.211	>10	0.022	-	-	146	>455	-
635	[Aib5;Leu6]GpTx-1(1-34)	-	6.89	>10	0.02	-	-	345	>500	-
661	[Leu5,6]GpTx-1(1-34)	-	4.387	>10	0.011	-	-	399	>909	-

641	[Met5;Leu6]GpTx-1(1-34)	-	3.591	>10	0.27	-	-	13	>37	-
673	[NMeLeu5;Leu6]GpTx-1(1-34)	-	1.893	>10	0.012	-	-	158	>833	-
674	[NMePhe5;Leu6]GpTx-1(1-34)	-	1.232	11.26	0.012	-	-	103	938	-
672	[NMeVal5;Leu6]GpTx-1(1-34)	-	5.495	>10	0.05	-	-	110	>200	-
705	[Nva5;Glu28]GpTx-1(1-34)	-	>10	>10	0.056	-	-	>179	>179	-
637	[Nva5;Leu6]GpTx-1(1-34)	-	9.928	>10	0.083	-	-	120	>120	-
632	[Sar5;Phe6]GpTx-1(1-34)	-	2.4	>10	0.025	-	-	96	>400	-
617	[Ser5;Phe6]GpTx-1(1-34)	-	3.63	>10	0.024	-	-	151	>417	-
659	[Tle5;Leu6]GpTx-1(1-34)	-	5.862	>10	0.017	-	-	345	>588	-
644	[Val5;Leu6]GpTx-1(1-34)	-	6.666	>10	0.2	-	-	33	>50	-
692	[Ala5;1'NMeW32]GpTx-1(1-34)	-	2.81	>10	0.018	-	-	156	>556	-
694	[Arg4;Met5]GpTx-1(1-34)	-	1.127	13.222	0.029	-	-	39	456	-
620	[DiMeO-F5;Phe6]GpTx-1(1-34)	-	5.09	>10	0.033	-	-	154	>303	-

693	[Met5;1'NMeW32]GpTx-1(1-34)	-	1.43	14.799	0.007	-	-	204	2114	-
723	[Ala5;Leu6;Glu10]GpTx-1(1-34)	-	16.757	>10	0.03	-	-	559	>333	-
708	[Nva5;Leu6;Glu28]GpTx-1(1-34)	-	>10	>10	0.042	-	-	>238	>238	-
703	[Ala5;Phe6;Glu12]GpTx-1(1-34)	-	1.529	>10	0.028	-	-	55	>357	-
725	[Ala5;Nle6;Glu12]GpTx-1(1-34)	-	6.452	>10	0.023	-	-	281	>435	-
732	[Ala5,25;Phe6]GpTx-1(1-34)	-	7.788	>10	0.086	-	-	91	>116	-
809	[Ala5;Phe6;Arg28]GpTx-1(1-34)	-	3.29	>10	0.012	-	-	274	>833	-
810	[Ala5;Leu6;Arg28]GpTx-1(1-34)	-	6.89	>10	0.009	-	-	766	>1111	-
515	[Phe6; Atz(amino-PEG10)13]GpTx-1(1-34)	-	0.14	N.D.	0.003	-	-	47	-	-
516	[Phe6;Atz(amino-PEG10)22]GpTx-1(1-34)	-	0.422	N.D.	0.003	-	-	141	-	-
517	[Phe6;Atz(amino-PEG10)33]GpTx-1(1-34)	-	0.353	N.D.	0.027	-	-	13	-	-
526	[Phe6;Atz(amino-PEG10)15]GpTx-1(1-34)	-	0.179	N.D.	0.006	-	-	30	-	-
593	[Phe6,Atz(20kDa PEG)28]GpTx-1(1-34)	-	10	>10	0.733	-	-	14	>14	-

594	[Phe6,Atz(20kDa PEG)22]GpTx-1(1-34)	-	10	>10	0.728	-	-	14	>14	-
518	[Atz(amino-PEG10)1;Ala5;Phe6]GpTx-1(1-34)	-		N.D.	0.264	-	-	0	-	-
519	[Ala5;Phe6;Atz(amino-PEG10)12]GpTx-1(1-34)	-	0.463	N.D.	0.039	-	-	12	-	-
520	[Ala5;Phe6;Atz(amino-PEG10)13]GpTx-1(1-34)	-		N.D.	0.093	-	-	0	-	-
521	[Ala5;Phe6;Atz(amino-PEG10)33]GpTx-1(1-34)	-		N.D.	0.296	-	-	0	-	-
522	[Phe6;Atz(amino-PEG10)33;1-Nal34]GpTx-1(1-34)	-	0.097	N.D.	0.003	-	-	32	-	-
523	[Phe6;Leu26;Atz(amino-PEG10)33]GpTx-1(1-34)	-	0.209	N.D.	0.02	-	-	10	-	-
524	[Ala5;Phe6;Atz(amino-PEG10)15]GpTx-1(1-34)	-	0.85	N.D.	0.02	-	-	43	-	-
525	[Ala5;Phe6;Atz(amino-PEG10)22]GpTx-1(1-34)	-		N.D.	0.119	-	-	0	-	-
527	[Phe6:Atz(amino-PEG10)12;1-Nal34]GpTx-1(1-34)	-	0.108	N.D.	0.014	-	-	8	-	-
100	Ala-GpTx-1(1-34)	-	0.655	10	0.012	-	-	55	833	-
811	Gly-Ser-[Ala5;Phe6;Arg28]GpTx-1(1-34)	-	1.73	>10	0.011	-	-	157	>909	-

812	Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)	-	9.77	>10	0.012	-	-	814	>833	-
814	[Ala5;Leu6;Arg28]GpTx-1(1-34)-Trp-FreeAcid	-	>10	>10	0.05	-	-	>200	>200	-
817	Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-FreeAcid	-	7	>10	0.116	-	-	60	>86	-
819	Gly-Ser-[Ala5;Phe6;Arg28]GpTx-1(1-34)-Phe-FreeAcid	-	>7	>10	0.047	-	-	>149	>213	-
820	Gly-Ser-[Ala5;Leu6;Arg28]GpTx-1(1-34)-Phe-FreeAcid	-	>10	>10	0.056	-	-	>179	>179	-
414	GpTx-1(1-34)-2PAL	-	1.01	>10	0.027	-	-	37	>370	-
435	[Ala5;Glu28]GpTx-1(1-34)	-	>10	>10	0.614	-	-	>16	>16	-
761	[Ala5;Guf28]GpTx-1(1-34)	-	5.08	>10	0.005	-	-	1016	>2000	-
762	[Ala5;Dab28]GpTx-1(1-34)	-	13.7	>10	0.013	-	-	1054	>769	-
744	[Ala5;hArg28]GpTx-1(1-34)	-	>10	>10	0.014	-	-	>714	>714	-
749	[Ala5;HCit28]GpTx-1(1-34)	-	>10	>10	0.025	-	-	>400	>400	-
737	[Ala5;His28]GpTx-1(1-34)	-	>10	>10	0.026	-	-	>385	>385	-

748	[Ala5;Cit28]GpTx-1(1-34)	-	>10	>10	0.03	-	-	>333	>333	-
739	[Ala5;Gln28]GpTx-1(1-34)	-	>10	>10	0.037	-	-	>270	>270	-
743	[Ala5;SDMA28]GpTx-1(1-34)	-	>10	>10	0.041	-	-	>244	>244	-
738	[Ala5;Ser28]GpTx-1(1-34)	-	>10	>10	0.045	-	-	>222	>222	-
745	[Ala5;R(Me)28]GpTx-1(1-34)	-	>10	>10	0.051	-	-	>196	>196	-
746	[Ala5;Orn28]GpTx-1(1-34)	-	>10	>10	0.059	-	-	>169	>169	-
753	[2-Abu5;Nle6]GpTx-1(1-34)	-	0.94	>10	0.001	-	-	940	>10000	-
700	[Ala5;Asp10]GpTx-1(1-34)	-	>10	>10	0.05	-	-	>200	>200	-
704	[Val5;Glu28]GpTx-1(1-34)	-	>10	>10	0.029	-	-	>345	>345	-
709	[Val5;Leu6;Glu28]GpTx-1(1-34)	-	>10	>10	0.086	-	-	>116	>116	-
701	[Ala5;Asp10;Glu12]GpTx-1(1-34)	-	>10	>10	0.554	-	-	>18	>18	-
710	[Val5;Asp10]GpTx-1(1-34)	-	>10	>10	0.174	-	-	>57	>57	-
711	[Val5;Glu12]GpTx-1(1-34)	-	11.96	>10	0.074	-	-	162	>135	-
712	[Val5;Asp10;Glu12]GpTx-1(1-34)	-	>10	>10	0.116	-	-	>86	>86	-

713	[Val5;Cit25]GpTx-1(1-34)	-	>10	>10	0.028	-	-	>357	>357	-
702	[Ala5;Phe6;Asp10]GpTx-1(1-34)	-	6.08	>10	0.04	-	-	152	>250	-
722	[Ala5;Nle6;Glu10]GpTx-1(1-34)	-	>10	>10	0.096	-	-	>104	>104	-
724	[Ala5;Phe6;Glu10]GpTx-1(1-34)	-	11.07	>10	0.079	-	-	140	>127	-
726	[Ala5;Leu6;Glu12]GpTx-1(1-34)	-	12.3	>10	0.021	-	-	586	>476	-
727	[Ala5;Nle6;Glu28]GpTx-1(1-34)	-	>10	>10	0.08	-	-	>125	>125	-
--	[Ala5,Phe6,Atz(2 kDa EtO-PEG*-{[Ala5,Phe6,Atz13*, Leu26,Arg28]GpTx-1(1-34)})13,Leu26,Arg28]GpTx-1(1-34); * = Et (Homodimeric Conjugate 3)	-	2.2	19.2	0.091	-	-	24	211	-
1029	Biotin[long chain]-[2-Abu5,13;Leu6;Arg28]GpTx-1(1-34)	-	27.3	>10	0.011	-	-	2482	>909	-
1030	[Ala5;Phe6;Glu10;K(Biotin)13;Leu26;Arg28]GpTx-1(1-34)	-	7.13	>10	0.015	-	-	475	>667	-
--	Biotin-Ahx-[Ala5,Phe6,Atz(2 kDa EtO-PEG*-{Biotin}-Ahx-[Ala5,Phe6,Atz13*,L	-	3.43	>10	0.091	-	-	38	>110	-

	eu26,Arg28]GpTx-1(1-34))13,Leu26,Arg28]GpTx-1(1-34); * = Et (Homodimeric Conjugate 4)									
1032	DOTA-[Ala5]GpTx-1(1-34)	-	>10	>10	0.152	-	-	>66	>66	-
1033	[Ala5;Phe6;K(DOTA)13;Leu26;Arg28]GpTx-1(1-34)	-	13.1	>10	0.0275	-	-	476	>364	-
30	[Glu29]GpTx-1(1-34)	-	>10	>10	>10	-	-	-	-	-
22	[Ala5]GpTx-1(1-34)	-	10.426	>10	0.034	-	-	307	>294	-
22	[Ala5]GpTx-1(1-34)	-	10.392	>10	0.03	-	-	346	>333	-
153	[Glu28]GpTx-1	-	18.1	>10	0.0501	-	-	361	>200	-
809	[Ala5;Phe6;Arg28]GpTx-1(1-34)	-	3.29	>10	0.012	-	-	274	>833	-
810	[Ala5;Leu6;Arg28]GpTx-1(1-34)	-	6.89	>10	0.009	-	-	766	>1111	-
1034	[Ala5,Phe6,2-Abu13,Leu26,Arg28]GpTx-1(1-34)	-	7.26	>10	0.0047	-	-	1545	>2128	-
1035	[Ala5,Phe6,Glu10,2-Abu13,Leu26,Arg28]GpTx-1(1-34)	-	16.6	>10	0.0035	-	-	4743	>2857	-

1036	[Ala5,Leu6,2-Abu13,Leu26,Arg28]GpTx-1(1-34)	-	18	>10	0.0087	-	-	2069	>1149	-
640	[Ala5,Phe6,Pra13,Leu26,Arg28]GpTx-1(1-34)	-	4.029	>10	0.003	-	-	1343	>3333	-
798	[Ala5;Phe6;Glu10;Pra13;Leu26;Arg28]GpTx-1(1-34)	-	10.4	15.3	0.012	-	-	867	1275	-
796	[Ala5;Leu6,26;Pra13,Arg28]GpTx-1(1-34)	-	10.6	>10	0.009	-	-	1178	>1111	-
800	[Ala5;Leu6,26;Glu10,Pra13;Arg28]GpTx-1(1-34)	-	>10	>10	0.013	-	-	>769	>769	-
799	[2-Abu5;Leu6;K(Ac-Pra)13]GpTx-1(1-34)	-	4.66	>10	0.011	-	-	424	>909	-
801	[2-Abu5;Leu6;K(4-Pen)13;Arg28]GpTx-1(1-34)	-	5.71	>10	0.002	-	-	2855	>5000	-
807	4-Pen-[2-Abu5,13,Leu6;Arg28]GpTx-1(1-34)	-	7.55	>10	0.003	-	-	2517	>3333	-
756	4-Pen-[Ala5;Phe6;2-Abu13;Arg28]GpTx-1(1-34)	-	3.34	>10	0.004	-	-	835	>2500	-
794	[Ala5;Phe6;K(Ac-Pra)13]GpTx-1(1-34)	-	1.46	>10	0.011	-	-	133	>909	-
1037	[Ala5,Phe6,Atz(PEG 11-((2-hydroxyethyl)thio)acetamide)13,Leu26,Arg28]GpTx-1	-	5.07	>10	0.035	-	-	145	>286	-
1038	[Ala5,Phe6,Atz(PEG 3-(2-hydroxyethyl)thioacetamide)13,Leu26,Ar	-	1.8	>10	0.003	-	-	600	>3333	-

	g28]GpTx-1(1-34)									
1039	[Ala5;Phe6;Glu10;Atz(PEG11-((2-hydroxyethyl)thio)acetamide)13;Leu26;Arg28]GpTx-1(1-34)	-	>10	>10	0.021	-	-	>476	>476	-
1040	[Ala5;Phe6;Glu10;Atz(PEG3-((2-hydroxyethyl)thio)acetamide)13;Leu26;Arg28]GpTx-1(1-34)	-	5.95	>10	0.013	-	-	458	>769	-
1041	((2-Hydroxyethyl)thio)acetamide-NPEG11-triazole-[2-Abu5,13;Leu6;Arg28]GpTx-1(1-34)	-	>10	>10	0.087	-	-	>115	>115	-
1042	[2-Abu5,Leu6,K(ethyl-triazole-PEG11-((2-hydroxyethyl)thio)acetamide)13,Arg28]GpTx-1(1-34)	-	9.88	>10	0.018	-	-	549	>556	-
1043	[Ala5;Leu6,26;Atz(PEG11-((2-hydroxyethyl)thio)acetamide)13;Arg28]GpTx-1(1-34)	-	>10	>10	0.021	-	-	>476	>476	-
1044	[Ala5;Leu6,26;Glu10;Atz(PEG11-((2-hydroxyethyl)thio)acetamide)13;Arg28]GpTx-1(1-34)	-	>10	>10	0.054	-	-	>185	>185	-
1045	((2-hydroxyethyl)thio)acetamide-NPEG11-triazole-	-	9.65	>10	0.074	-	-	130	>135	-

	[Ala5,Phe6,2-Abu13,Arg28]GpTx-1(1-34)									
--	Fc-peptide Conjugate 1	-	2.88	>10	0.002	-	-	1440	>5000	-
--	Fc-peptide Conjugate 2	-	13.7	>10	0.08	-	-	171	>125	-
--	Immunoglobulin-peptide Conjugate 1	-	>10	>10	0.565	-	-	>18	>18	-
--	Immunoglobulin-peptide Conjugate 2	-	6.73	>10	0.026	-	-	259	>385	-
--	Fc-peptide Conjugate 1	-	>10	>10	0.694	-	-	14	>14	-
--	Fc-peptide Conjugate 2	-	15.2	>10	0.169	-	-	90	>59	-
--	Immunoglobulin-peptide Conjugate 1	-	>10	>10	0.716	-	-	>14	>14	-
--	Immunoglobulin-peptide Conjugate 2	-	7.51	>10	0.079	-	-	95	>127	-
--	Fc-peptide Conjugate 3	-	>10	>10	1.45	-	-	>7	>7	-
--	Fc-peptide Conjugate 4	-	>10	>10	0.474	-	-	>21	>21	-
--	Immunoglobulin-peptide Conjugate 3	-	>10	>10	0.077	-	-	>130	>130	-
--	Immunoglobulin-peptide Conjugate 4	-	>10	>10	0.126	-	-	>79	>79	-

--	Fc-peptide Conjugate 5	-	>10	>10	1.46	-	-	>7	>7	-
--	Fc-peptide Conjugate 6	-	>10	>10	0.264	-	-	>38	>38	-
--	Immunoglobulin-peptide Conjugate 5	-	>10	>10	0.927	-	-	>11	>11	-
--	Immunoglobulin-peptide Conjugate 6	-	>10	>10	0.271	-	-	>37	>37	-
--	Fc-peptide Conjugate 7	-	N.D.	N.D.	1.034	-	-	-	-	-
--	Fc-peptide Conjugate 8	-	>10	>10	0.473	-	-	>21	>21	-
--	Immunoglobulin-peptide Conjugate 7	-	7.87	>10	0.456	-	-	17	>22	-
--	Immunoglobulin-peptide Conjugate 8	-	0.607	9.24	0.148	-	-	4	62	-

Table 31. Electrophysiology by IonWorks® Quattro: comparison of GpTx-1 peptide analog PEG conjugates.

SEQ ID NO:	Amino acid sequence	Designation	IWQ Use Nav1.7 (μM)	IWQ Use Nav1.5 (μM)	IWQ Use Nav1.4 (μM)	IWQ Use Nav1.3 (μM)	Nav1.4/Nav 1.7	Nav1.4/Nav 1.3	Nav1.7/Nav 1.3
532	{H}-[Atz(amino-PEG10)]DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	Atz(amino-PEG10)-[Phe6]GpTx1(1-34)	0.084	4.95	0.95	0.034	11.3	27.7	2.4
533	{H}-[Atz(amino-PEG10)]CLGFFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Atz(amino-PEG10)1;Phe6]GpTx1(1-34)	0.041	6.91	0.25	0.019	6.1	12.9	2.1
534	{H}-DCLG[Atz(amino-PEG10)]FRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Atz(amino-PEG10)5;Phe6]GpTx1(1-34)	16.257	14.9	8.9	16.793	0.5	0.5	1.0
535	{H}-DCLGF[Atz(amino-PEG10)]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Atz(amino-PEG10)6]GpTx1(1-34)	5.4	6.15	20.26	6.7	3.7	3.0	0.8
536	{H}-DCLGFFRKC[Atz(amino-PEG10)]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)10]GpTx1(1-34)	0.039	7.95	0.32	0.013	8.3	24.6	3.0
537	{H}-DCLGFFRKCI[Atz(amino-PEG10)]DNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)11]GpTx1(1-34)	0.136	8.02	1.10	0.056	8.1	19.6	2.4
538	{H}-DCLGFFRKCIP[Atz(amino-PEG10)]NDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)12]GpTx1(1-34)	0.050	6.31	0.16	0.016	3.2	9.8	3.1
515	{H}-DCLGFFRKCIPD[Atz(amino-PEG10)]DKCCRPNLVCSRTHKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)13]GpTx1(1-34)	0.025	4.710	0.400	0.010	16.2	39.5	2.4
526	{H}-DCLGFFRKCIPDND[Atz(amino-PEG10)]CCRPNLVCSRTHKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)15]GpTx1(1-34)	0.046	>5	1.177	0.024	25.8	50.1	1.9
539	{H}-DCLGFFRKCIPDNDKCCRP[Atz(amino-PEG10)]LVCSRTHKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)20]GpTx1(1-34)	0.538	8.9	5.6	0.250	10.4	22.4	2.1
540	{H}-DCLGFFRKCIPDNDKCCRPN[Atz(amino-PEG10)]VCSRTHKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)21]GpTx1(1-34)	0.763	11.4	12.0	0.587	15.8	20.5	1.3
516	{H}-DCLGFFRKCIPDNDKCCRPNL[Atz(amino-PEG10)]CSRTHKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)22]GpTx1(1-34)	0.111	7.9	1.1	0.059	10.1	19.1	1.9

541	{H}-DCLGFFRKCIPDNDKCCRPNLVC[Atz(amino-PEG10)]RTHKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)24]GpTx1(1-34)	1.738	6.2	8.9	0.701	5.1	12.7	2.5
542	{H}-DCLGFFRKCIPDNDKCCRPNLVCS[Atz(amino-PEG10)]THKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)25]GpTx1(1-34)	0.304	10.2	4.0	0.206	13.1	19.3	1.5
543	{H}-DCLGFFRKCIPDNDKCCRPNLVCSR[Atz(amino-PEG10)]HKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)26]GpTx1(1-34)	0.631	8.0	9.4	0.478	14.9	19.6	1.3
544	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRT[Atz(amino-PEG10)]KWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)27]GpTx1(1-34)	2.6	>5	>5	3.7	#####	#######	0.7
545	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTH[Atz(amino-PEG10)]WCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)28]GpTx1(1-34)	0.049	5.9	22.3	0.036	453.4	625.5	1.4
546	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHK[Atz(amino-PEG10)]CKYVF-{Amide}	[Phe6;Atz(amino-PEG10)29]GpTx1(1-34)	0.31	>5	>5	1.1	#####	#######	0.3
547	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCK[Atz(amino-PEG10)]VF-{Amide}	[Phe6;Atz(amino-PEG10)32]GpTx1(1-34)	5.0	>5	>5	>5	#####	#######	#####
517	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCKY[Atz(amino-PEG10)]F-{Amide}	[Phe6;Atz(amino-PEG10)33]GpTx1(1-34)	0.10	>5	1.1	0.032	10.3	33.5	3.3
548	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCKYV[Atz(amino-PEG10)]-{Amide}	[Phe6;Atz(amino-PEG10)34]GpTx1(1-34)	5.0	>5	>5	1.6	#####	#######	3.2
549	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCKYVF[Atz(amino-PEG10)]-{Amide}	[Phe6]GpTx1(1-34)-Atz(amino-PEG10)	0.36	>5	>5	0.12	#####	#######	3.0
550	{H}-[Atz(amino-PEG10)]DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCKYV[1-Nal]-{Amide}	Atz(amino-PEG10)-[Phe6;1-Nal34]GpTx1(1-34)	0.029	6.80	0.15	0.004			
551	{H}-[Atz(amino-PEG10)]CLGFFRKCIPDNDKCCRPNLVCSRTHKWCKYV[1-Nal]-{Amide}	[Atz(amino-PEG10)1;Phe6;1-Nal34]GpTx1(1-34)	0.039	4.3	0.36	0.014	9.2	24.9	2.7
552	{H}-DCLG[Atz(amino-PEG10)]FRKCIPDNDKCCRPNLVCSRTHKWCKYV[1-Nal]-{Amide}	[Atz(amino-PEG10)5;Phe6;1-Nal34]GpTx1(1-34)	4.6	>5	>5	2.5	#####	#######	1.8
553	{H}-DCLGF[Atz(amino-PEG10)]RKCIPDNDKCCRPNLVCSRTHKWCKYV[1-	[Atz(amino-PEG10)6;1-Nal34]GpTx1(1-34)	4.1	>5	>5	>5	#####	#######	#####

	Nal]-{Amide}											
554	{H}-DCLGFFRKC[Atz(amino-PEG10)]PDNDKCCRPNLVCSRTHKWCKYV[1-Nal]-{Amide}	[Phe6;Atz(amino-PEG10)10;1-Nal34]GpTx1(1-34)	0.058	8.61	0.14	0.015						
527	{H}-DCLGFFRKCIP[Atz(amino-PEG10)]NDKCCRPNLVCSRTHKWCKYV[1-Nal]-{Amide}	[Phe6;Atz(amino-PEG10)12;1-Nal34]GpTx1(1-34)	0.015	1.6	0.11	0.012	7.1	8.9				1.3
555	{H}-DCLGFFRKCIPDNDKCCRPNLVC[Atz(amino-PEG10)]RTHKWCKYV[1-Nal]-{Amide}	[Phe6;Atz(amino-PEG10)24;1-Nal34]GpTx1(1-34)	0.57	>5	>5	0.35	######	#########				1.6
556	{H}-DCLGFFRKCIPDNDKCCRPNLVCSR[Atz(amino-PEG10)]HKWCKYV[1-Nal]-{Amide}	[Phe6;Atz(amino-PEG10)26;1-Nal34]GpTx1(1-34)	0.32	>5	>5	0.32	######	#########				1.0
557	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRT[Atz(amino-PEG10)]KWCKYV[1-Nal]-{Amide}	[Phe6;Atz(amino-PEG10)27;1-Nal34]GpTx1(1-34)	0.90	>5	>5	0.82	######	#########				1.1
558	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHK[Atz(amino-PEG10)]CKYV[1-Nal]-{Amide}	[Phe6;Atz(amino-PEG10)29;1-Nal34]GpTx1(1-34)	0.093	>5	>5	0.14	######	#########				0.7
559	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCK[Atz(amino-PEG10)]V[1-Nal]-{Amide}	[Phe6;Atz(amino-PEG10)32;1-Nal34]GpTx1(1-34)	5.0	>5	>5	2.2	######	#########				2.3
522	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCKY[Atz(amino-PEG10)][1-Nal]-{Amide}	[Phe6;Atz(amino-PEG10)33;1-Nal34]GpTx1(1-34)	0.032	>5	0.39	0.014	12.0	27.3				2.3
560	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCKYV[1-Nal][Atz(amino-PEG10)]-{Amide}	[Phe6;1-Nal34]GpTx1(1-34)-Atz(amino-PEG10)	0.12	>5	2.2	0.037	18.3	58.3				3.2
561	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRTHKWCKYV[1-Nal]-{Amide}	[Phe6;1-Nal34]GpTx1(1-34)	0.011	2.2	0.17	0.007	14.7	23.5				1.6
562	{H}-[Atz(amino-PEG10)]DCLGAFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	Atz(amino-PEG10)-[Ala5;Phe6]GpTx1(1-34)	0.24	>5	2.8	0.14	11.9	20.7				1.7
518	{H}-[Atz(amino-PEG10)]CLGAFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Atz(amino-PEG10)1;Ala5;Phe6]GpTx1(1-34)	0.36	>5	>5	0.14	######	#########				2.5
563	{H}-DC[Atz(amino-	[Atz(amino-	0.20	>5	>5	0.072	######	#########				2.7

	PEG10)]GAFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	PEG10)3;Ala5;Phe6]GpTx1(1-34)							
564	{H}-DCL[Atz(amino-PEG10)]AFRKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Atz(amino-PEG10)4;Ala5;Phe6]GpTx1(1-34)	2.8	>5	>5	1.4	#####	######	2.0
565	{H}-DCLGA[Atz(amino-PEG10)]RKCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Atz(amino-PEG10)6]GpTx1(1-34)	5.0	>5	>5	>5	#####	######	#####
566	{H}-DCLGAF[Atz(amino-PEG10)]KCIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)7]GpTx1(1-34)	5.0	>5	>5	>5	#####	######	#####
567	{H}-DCLGAFR[Atz(amino-PEG10)]CIPDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)8]GpTx1(1-34)	2.3	>5	>5	1.4	#####	######	1.6
568	{H}-DCLGAFRKC[Atz(amino-PEG10)]PDNDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)10]GpTx1(1-34)	0.26	>5	>5	0.076	#####	######	3.5
519	{H}-DCLGAFRKCIP[Atz(amino-PEG10)]NDKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)12]GpTx1(1-34)	0.17	>5	1.5	0.088	8.7	16.8	1.9
520	{H}-DCLGAFRKCIPD[Atz(amino-PEG10)]DKCCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)13]GpTx1(1-34)	0.27	>5	>5	0.11	#####	######	2.5
524	{H}-DCLGAFRKCIPDND[Atz(amino-PEG10)]CCRPNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)15]GpTx1(1-34)	0.21	>5	3.7	0.089	17.5	41.2	2.3
569	{H}-DCLGAFRKCIPDNDKCC[Atz(amino-PEG10)]PNLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)18]GpTx1(1-34)	0.23	>5	>5	0.11	#####	######	2.2
570	{H}-DCLGAFRKCIPDNDKCCR[Atz(amino-PEG10)]NLVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)19]GpTx1(1-34)	0.64	>5	>5	0.52	#####	######	1.2
571	{H}-DCLGAFRKCIPDNDKCCRP[Atz(amino-PEG10)]LVCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)20]GpTx1(1-34)	5.0	>5	>5	4.0	#####	######	1.3
572	{H}-DCLGAFRKCIPDNDKCCRPN[Atz(amino-PEG10)]VCSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)21]GpTx1(1-34)	5.0	>5	>5	1.8	#####	######	2.8
525	{H}-DCLGAFRKCIPDNDKCCRPNL[Atz(amino-PEG10)]CSRTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)22]GpTx1(1-34)	0.66	>5	>5	0.23	#####	######	2.9
573	{H}-DCLGAFRKCIPDNDKCCRPNLVC[Atz(amino-PEG10)]RTHKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)24]GpTx1(1-34)	5.0	>5	>5	>5	#####	######	#####
574	{H}-DCLGAFRKCIPDNDKCCRPNLVCS[Atz(amino-PEG10)]THKWCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)25]GpTx1(1-34)	0.90	>5	>5	1.6	#####	######	0.6
575	{H}-	[Ala5;Phe6;Atz(amino-	5.0	>5	>5	>5	#####	######	#####

	DCLGAFRKCIPDNDKCCRPNLVCSRT[Atz(amino-PEG10)]KWCKYVF-{Amide}	PEG10)27]GpTx1(1-34)							
576	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTH[Atz(amino-PEG10)]WCKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)28]GpTx1(1-34)	1.7	>5	>5	1.7	#####	######	1.0
577	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHK[Atz(amino-PEG10)]CKYVF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)29]GpTx1(1-34)	5.0	>5	>5	>5	#####	######	#####
578	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHKWCK[Atz(amino-PEG10)]VF-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)32]GpTx1(1-34)	5.0	>5	>5	>5	#####	######	#####
521	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHKWCKY[Atz(amino-PEG10)]F-{Amide}	[Ala5;Phe6;Atz(amino-PEG10)33]GpTx1(1-34)	1.5	>5	>5	0.41	#####	######	3.7
579	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHKWCKYVF[Atz(amino-PEG10)]-{Amide}	[Ala5;Phe6]GpTx1(1-34)-Atz(amino-PEG10)	5.0	>5	>5	>5	#####	######	#####
580	{H}-DCLGAFRKCIPDNDKCCRPNLVCSRTHKWCKYVFW[Atz(amino-PEG10)]-{Amide}	[Ala5;Phe6]GpTx1(1-34)-Trp-Atz(amino-PEG10)	1.2	>5	>5	0.77	#####	######	1.6
581	{H}-[Atz(amino-PEG10)]CLGFFRKCIPDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	[Atz(amino-PEG10)1;Phe6;Leu26]GpTx1(1-34)	0.025	6.22	0.29	0.018			
582	{H}-DCLG[Atz(amino-PEG10)]FRKCIPDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	[Atz(amino-PEG10)5;Phe6;Leu26]GpTx1(1-34)	7.9	8.08	17.21	4.0			
583	{H}-DCLGF[Atz(amino-PEG10)]RKCIPDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	[Atz(amino-PEG10)6;Leu26]GpTx1(1-34)	7.4	8.36	20.91	5.8			
523	{H}-DCLGFFRKC[Atz(amino-PEG10)]PDNDKCCRPNLVCSRLHKWCKYVF-{Amide}	[Phe6;Atz(amino-PEG10)10;Leu26]GpTx1(1-34)	0.027	7.19	0.50	0.014			
584	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRLHK[Atz(amino-PEG10)]CKYVF-{Amide}	[Phe6;Leu26;Atz(amino-PEG10)29]GpTx1(1-34)	0.76	>5	>5	1.6	#####	######	0.5

585	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRLHKWCK[Atz(amino-PEG10)]VF-{Amide}	[Phe6;Leu26;Atz(amino-PEG10)32]GpTx1(1-34)	5.0	>5	>5	>5	#######	#########	######
586	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRLHKWCKY[Atz(amino-PEG10)]F-{Amide}	[Phe6;Leu26;Atz(amino-PEG10)33]GpTx1(1-34)	0.055	>5	1.8	0.026	33.1	69.6	2.1
587	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRLHKWCKYV[Atz(amino-PEG10)]-{Amide}	[Phe6;Leu26;Atz(amino-PEG10)34]GpTx1(1-34)	1.4	>5	>5	1.1	#######	#########	1.2
588	{H}-DCLGFFRKCIPDNDKCCRPNLVCSRLHKWCKYVF[Atz(amino-PEG10)]-{Amide}	[Phe6;Leu26]GpTx1(1-34)-Atz(amino-PEG10)	0.43	>5	>5	0.13	#######	#########	3.3

Table 32. Nav1.7 Use IC50 of conjugated GpTx-1 peptide analogs by PatchXpress®.

SEQ ID NO:	Designation	Nav1.7 Use IC50 (μM)
1	GpTx-1(1-34)	0.005
515	[Phe6;Atz(amino-PEG10)13]GpTx1(1-34)	0.022
515	[Phe6;Atz(amino-PEG10)13]GpTx1(1-34)	0.003
516	[Phe6;Atz(amino-PEG10)22]GpTx1(1-34)	0.003
517	[Phe6;Atz(amino-PEG10)33]GpTx1(1-34)	0.027
518	[Atz(amino-PEG10)1;Ala5;Phe6]GpTx1(1-34)	0.264
519	[Ala5;Phe6;Atz(amino-PEG10)12]GpTx1(1-34)	0.039
520	[Ala5;Phe6;Atz(amino-PEG10)13]GpTx1(1-34)	0.093
521	[Ala5;Phe6;Atz(amino-PEG10)33]GpTx1(1-34)	0.296
522	[Phe6;Atz(amino-PEG10)33;1-Nal34]GpTx1(1-34)	0.003
523	[Phe6;Leu26;Atz(amino-PEG10)33]GpTx1(1-34)	0.020
524	[Ala5;Phe6;Atz(amino-PEG10)15]GpTx1(1-34)	0.020
525	[Ala5;Phe6;Atz(amino-PEG10)22]GpTx1(1-34)	0.119
526	[Phe6;Atz(amino-PEG10)15]GpTx1(1-34)	0.006
527	[Phe6;Atz(amino-PEG10)12;1-Nal34]GpTx1(1-34)	0.014

[00469] Example 4: Plasma stability studies

[00470] The stability of GpTx-1 peptide and GpTx-1 peptide analogs were studied in human, rat and mouse plasmas. Peptide stock solutions were made from GpTx-1 peptide and GpTx-1 peptide analog reference standards in 50/50 (v/v) methanol/water and stored at -20 °C. 1 mg/mL peptide stock solutions were used to prepare 20 µg/mL peptide working solutions in HPLC grade water. The peptide working solutions were stored in a refrigerator at 2 to 8°C prior to use.

[00471] Stability samples were prepared by adding 225 µl plasma into the vials containing 25µl of 20 µg/mL peptide working solutions and were incubated at 37°C. The initial concentration was 2 µg/mL for each peptide in human, rat, or mouse plasma. 25 µl plasma samples at five time points (0, 2, 4, 8 and 24 hours) were aliquoted into the appropriate well of a 96-well plate, followed by the addition of 25 µl of internal standard solution (100 ng/mL, NAV peptide analog made in 50/50 methanol/water) and 100 µL of 0.1% formic acid and the samples were vortex mixed. An Oasis HLB µElution 96-well solid phase extraction plate was used to extract GpTx-1 or GpTx- peptide analog peptides from the pretreated plasma samples and the extracts were injected (10 µL) onto the LC-MS/MS system for analysis.

[00472] The LC-MS/MS consisted of an Acquity UPLC system (Waters, Milford, MA) coupled to a 5500 QTRAP mass spectrometer (AB Sciex, Toronto, Canada) with a Turbo IonSpray® ionization source. The analytical column was an Acquity UPLC BEH C_{18} 2.1 mm × 50 mm column. The mobile phases were 0.1% formic acid in acetonitrile/water (5/95, v/v, mobile phase A) and 0.1% formic acid in acetonitrile/water (95/5, v/v, mobile phase B). Data was collected and processed using AB Sciex Analyst® software (version 1.5).

[00473] The plasma stability of the tested peptides were derived from the peak area ratios corresponding to peptides and internal standard obtained from the LC-MS/MS analysis, all data were normalized to the value at 0-hr time point. Results are shown in Table 33, Table 34, and Table 35, below. GpTx-1 and GpTx-1 peptide analogs tested showed remarkable stability in human, mouse, and rat plasma, likely due to their compact, disulfide-stabilized structure.

Table 33. Stability of GpTx-1 and GpTx-1 peptide analogs in human plasma.

	% peptide remaining				
incubation time (hr)	GpTx-1(1-34); SEQ ID NO:1	[1-Nal10]GpTx-1(1-34); SEQ ID NO:78	[Ala5]GpTx-1(1-34); SEQ ID NO:22	GpTx-1(2-34); SEQ ID NO:108	Ac-GpTx-1(1-34); SEQ ID NO:132
0	100	100	100	100	100
2	102	99	105	107	100
4	101	93	99	92	104
8	98	97	101	91	101
24	93	82	105	82	97

Table 34. Stability of GpTx-1 and GpTx-1 peptide analogs in mouse plasma.

	% peptide remaining				
incubation time (hr)	GpTx-1(1-34); SEQ ID NO:1	[1-Nal10]GpTx-1(1-34); SEQ ID NO:78	[Ala5]GpTx-1(1-34); SEQ ID NO:22	GpTx-1(2-34); SEQ ID NO:108	Ac-GpTx-1(1-34); SEQ ID NO:132
0	100	100	100	100	100
2	103	98	106	100	105
4	105	92	107	95	103
8	97	92	105	87	103
24	93	88	99	81	106

Table 35. Stability of GpTx-1 and GpTx-1 peptide analogs in rat plasma.

	% peptide remaining	
incubation time (hr)	GpTx-1(1-34); SEQ ID NO:1	[1-Nal10]GpTx-1(1-34); SEQ ID NO:78
0	100	100
2	110	104
4	109	106
6	100	108
8	111	112
24	91	89

[00474] Example 5: PEGylated conjugates of GpTx-1 peptide analogs studies

[00475] To identify sites with GpTx-1 that could be modified with a half-life extending moiety, a set of positional analogs was prepared containing propargylglycine at each non-cysteine position. After folding, the alkyne-containing peptide was subjected to copper catalyzed 1,3-dipolar cycloaddition with a ~500 Da MW azido PEG to obtain the site-specifically PEGylated peptides with a triazole linkage, thus converting the propargylglycine or Pra residue in the sequence to a 3-(1,2,3-triazol-4-yl)alanine or Atz residue. Electrophysiological screening of this series of analogs (Table 30, Table 31, and Table 32, above) identified several positions within GpTx-1, including the N-terminus and positions 1, 10, 12, 13, 15, 22, 28, and 33 of SEQ ID NO:1, where a large chemical moiety could be introduced without significantly reducing potency at $Na_V1.7$ or $Na_V1.3$. In general, these locations tend to be on the hydrophilic surface of GpTx-1, away from or around the periphery the hydrophobic binding face. Having identified these positions, larger MW conjugates (20 kDa PEG; SEQ ID NO:590) and homodimeric constructs of [Phe6; Atz13]GpTx-1(1-34) (SEQ ID NO:591) or [Ala5;Phe6;Atz13]GpTx-1(1-34) (SEQ ID NO:1028) or Biotin-Ahx--[Ala5,Phe6,Atz13,Leu26,Arg28]GpTx-1(1-34) (SEQ ID NO:1031) were prepared (See, Figure 81A) and tested (See, Table 30, and Figures 46-58). Four of these homodimers, with different sized PEG linkers covalently linked to each of the two peptides at position 13 relative to the native GpTx-1 sequence (SEQ ID NO:1), were designated as follows (* = ethyl):

[00476] [Phe6,Atz(2 kDa EtO-PEG*-{[Phe6,Atz13*]GpTx-1(1-34)})13]GpTx-1(1-34) ("Homodimeric Conjugate 1") (See, Figure 81A);

[00477] [Phe6,Atz(500 Da EtO-PEG*-{[Phe6,Atz13*]GpTx-1(1-34)})13]GpTx-1(1-34) ("Homodimeric Conjugate 2");

[00478] [Ala5,Phe6,Atz(2 kDa EtO-PEG*-{[Ala5,Phe6,Atz13*,Leu26,Arg28]GpTx-1(1-34)})13,Leu26,Arg28]GpTx-1(1-34) ("Homodimeric Conjugate 3");

[00479] Biotin-Ahx-[Ala5,Phe6,Atz(2 kDa EtO-PEG*-{Biotin-Ahx-[Ala5,Phe6,Atz13*,Leu26,Arg28]GpTx-1(1-34)})13,Leu26,Arg28]GpTx-1(1-34) ("Homodimeric Conjugate 4").

[00480] Example 6: NMR structure determination of GpTx-1

[00481] The structure of GpTx-1 was obtained by high resolution NMR spectroscopy in water, pH ~3 and T=298 K. The data were collected on a Bruker Avance III 800 MHz spectrometer using standard 2D experiments. (See Wutchrich, NMR of Proteins and Nucleic Acids, John Wiley & Sons, Canada, (1986)). The structure was calculated from 500 NOE constraints (216 long-range), 45 dihedral angles constraints, 11 hydrogen-bond constraints and 3 disulfide-bond constraints, using Cyana 2.1 software. The final RMSD for the backbone atoms was 0.1±0.05 A and for all heavy atoms 0.74 ± 0.12 A. (See Figure 7 for the overlay of the 20 lowest energy conformations of the peptide backbone, Figure 8 for the overlay of the heavy atoms from the 20 lowest energy conformations of the peptide, and Figure 9 for a ribbon representation of the peptide backbone). The structure confirms the disulfide connectivity of the six cysteine residues as C_2—C_{17}, C_9—C_{23}, and C_{16}—C_{30} or a C1—C4, C2—C5, C3—C6 pattern, making GpTx-1 a member of the inhibitory cystine knot (ICK) family of peptides.

[00482] The folded structure of GpTx-1 (SEQ ID NO:1) is amphipathic in nature with a flat hydrophobic face on one side of the molecule and a hydrophilic (mostly cationic) face on the opposite side. The systematic analoging of GpTx-1, in particular the positional scanning with alanine and glutamic acid, identifies several residues as being critical for activity at $Na_V1.7$ and $Na_V1.3$. These residues, namely Phe5, Met6, His27, Trp29, Lys31, Tyr32, and Phe34, releative to SEQ ID NO:1, are clustered on the one face of GpTx-1. Residues 27 through 34 of SEQ ID NO:1 form a C-terminal β-strand, while Phe5 and Met6 are adjacent to that strand and form the remainder of this hydrophobic face. Since changes that alter the nature of this face disrupt activity against $Na_V1.7$ and $Na_V1.3$, this may be the portion of the molecule that interacts with the VGSCs at the binding interface. (See Figure10 and Figure 11).

[00483] Example 7: Preliminary pharmacokinetic determination in mice

[00484] Pharmacokinetic studies. Preliminary pharmacokinetic (PK) studies were conducted. One PK study was conducted with 7 week-old male CD-1 mice from Charles River Laboratories. The mice had catheters placed in the carotid artery by the vendor. [Ala5]GpTx-1 (SEQ ID NO:22) was dosed intravenously to 3 mice and subcutaneously to 3 mice. GpTx-1 (SEQ ID NO:1) was dosed subcutaneously to 3 mice. All doses were at 1 mg/kg and i.v. injections were made via the lateral tail vein. Blood samples for i.v.-dosed animals were taken at 3, 15, 30 min and 1, 2, 4, 6, 8, and 24 hours post dose, blood samples for s.c.-dose animals were

taken at 15, 30 min and 1, 2, 4, 6, 8, and 24 hours post dose. For each sample 15 μL of blood was collected via the carotid artery catheter and mixed in 35 μL of 0.1 M citrate buffer. Samples were then frozen at -80°C until analysis.

[00485] Another PK study was conducted with 7 week-old unmodified male CD-1 mice from Taconic. [Ala5]GpTx-1 (SEQ ID NO:22) was dosed to 12 mice at 1 mg/kg subcutaneously and to 12 mice at 1 mg/kg intravenously via the lateral tail vein. At 0.5, 1, 2, 4, 8 and 24 hours post-dose, 2 mice from each dose route were euthanized and blood samples and brains were collected. Brains were weighed and frozen at -80°C immediately. Blood samples were collected in EDTA-treated microtainers and centrifuged at 13000 rpm for 5 minutes, after which plasma was extracted and frozen at -80°C in a 96-well plate.

[00486] Another PK study was conducted with 7 week-old unmodified CD-1 mice from Taconic. [Ala5]GpTx-1 (SEQ ID NO:22) was dosed to 21 mice at 5 mg/kg subcutaneously. At 0.5, 1, 1.25, 1.5, 2, 3, and 4 hours post-dose, 3 mice were euthanized and blood samples and brains were collected. Brains were weighed and frozen at -80°C immediately. Blood samples were collected in EDTA-treated microtainers and centrifuged at 13000 rpm for 5 minutes, after which plasma was extracted and frozen at -80°C in a 96-well plate.

[00487] LC-MS/MS Analytical Procedure. Peptide stock solutions (1 mg/mL) were made from peptide reference standards in 50/50 (v/v) methanol/water and stored at -20 °C. 1 mg/mL peptide stock solutions were used to prepare 100 μg/mL peptide working solution in 50/50 (v/v) methanol/water. The peptide working solutions were stored in a refrigerator at 2 to 8°C.

[00488] Standard samples were prepared in citrate-buffered mouse blood (blood/0.1M citrate buffer, 30/70, v/v). Standards concentrations of 5, 10, 25, 50, 100, 250, 500 and 1000 ng/mL were prepared by serial dilution of a freshly prepared 5000 ng/mL solution in citrate-buffered mouse blood using the 100 μg/mL peptide working solution. 25 μl blood samples were aliquoted into the appropriate well of a 96-well plate, followed by the addition of 50 μl of internal standard solution (100 ng/mL, peptide analog made in 50/50 methanol/water) and 150 μL of 0.1M $ZnSO_4$ and the samples were vortex mixed for 5 min, then centrifuge for 10 min at 4000 rpm. Supernatant was then extracted using an Oasis HLB μElution 96-well solid phase extraction plate to extract peptides and the extracts were injected (10 μL) onto the LC-MS/MS system for analysis.

[00489] The LC-MS/MS consisted of an Acquity UPLC system (Waters, Milford, MA) coupled to a 5500 QTRAP mass spectrometer (AB Sciex, Toronto, Canada) with a Turbo IonSpray® ionization source. The analytical column was an Acquity UPLC BEH C_{18}

2.1 mm × 50 mm column. The mobile phases were 0.1% formic acid in acetonitrile/water (5/95, v/v, mobile phase A) and 0.1% formic acid in acetonitrile/water (95/5, v/v, mobile phase B). Data was collected and processed using AB Sciex Analyst® software (version 1.5).

[00490] The calibration curve was derived from the peak area ratios (peptide /internal standard) using $1/x^2$ weighted linear least-squares regression of the area ratio versus the concentration of the corresponding peptide standard. The regression equation from the calibration standards was used to back calculate the measured concentration for each standard and blood samples.

[00491] Results. In the pharmacokinetic studies, GpTx-1 (SEQ ID NO:1) was found to be lethal to the mice at 1 mg/kg and 0.5 mg/kg i.v. doses. A 1 mg/kg s.c. dose of GpTx-1 (SEQ ID NO:1) to mice was tolerated and showed measureable plasma concentrations for 1 h. (See, Figure 16). A 1 mg/kg i.v. dose of [Ala5]GpTx-1 (SEQ ID NO:22) was tolerated in mice with an approximate in vivo half-life of 15 min. (See, Figure 17A and Figure 17B). A 1 mg/kg s.c. dose of [Ala5]GpTx-1 (SEQ ID NO:22) also gave measurable exposure in blood. (See, Figure 17B). In another study, a 5 mg/kg s.c. dose yielded peptide concentrations in the plasma that were sustained at about 0.6 μM, 40-fold over the in vitro Nav1.7 IC_{50} by PatchXpress® (PX), for 3 h with a calculated t1/2 = 0.6 h, higher than the 1 mg/kg s.c. and i.v. doses and suitable for further in vivo testing. (See, Figure 17B).

[00492] Example 8: Ion channel counterscreens

[00493] Cardiac ion channel counterscreens (hERG and hNav1.5).

[00494] Cardiac ion channel counterscreens (hERG and hNav1.5) were conducted as described below, for which representative results are shown in Figures 18 and 19A-B.

[00495] Counterscreen against the cloned human Nav1.5 sodium channel using the PatchXpress® system.

[00496] Cell line. HEK293 cells stable transfected with human hNav1.5 were purchased from Cytomyx, Inc.

[00497] The extracellular (HB-PS) recording solution contained 70 mM NaCl, 67 mM N-methyl-D-glucamine, 4 mM KCl, 1.8 mM $CaCl_2$, 1 mM $MgCl_2$, 10 mM HEPES, 10 mM Glucose adjusted to pH 7.4 with HCl. The internal recording solution contained 130 mM CsF, 10 mM NaCl, 10 mM EGTA, 2 mM $MgCl_2$, 10 mM HEPES adjusted to pH 7.20 with CsOH. Stock solutions of reference standard or test articles were diluted into HB-PS prior to application. Test articles included either peptides or peptide conjugates described herein. A standardized step protocol was used to elicit ionic current through the hNav1.5 sodium channel. Cells are held at −80 mV. Onset and steady state block of hNav1.5 sodium current due to Test Article was measured using a pulse pattern with fixed amplitudes (conditioning prepulse: −120 mV for 50 ms; depolarizing test step to −30 mV for 20 ms) repeated at 10-s intervals. Currents were acquired at 10 kHz and filtered at 3 kHz, in episodic mode. When whole cell configuration was established, cells were washed for 3 minutes, followed by applying control vehicle for 5 minutes. The DataStable_PC function of the PatchXpress scripting utility with then allow the experiment to begin only when the baseline current was stable or an additional 5 minutes had elapsed. Then control and each concentration of test article was applied for 5 minutes. There were 3 additions for each concentration with 1-minute interval. To determine IC_{50}, Test Article at 1 μM, 3 μM, 10 μM and 30 μM was applied to cells cumulatively (without washout between test article concentrations; $n \geq 3$ where n = number of cells). Electrophysiological data acquisition was performed using PatchXpress Commander v1.4 (Molecular Devices, Sunnyvale, CA) and analyses was performed using DataXpress v2.04 (Molecular Devices, Sunnyvale, CA). The three peak inward currents before and after test article application were used to calculate the percentage of current inhibition at each concentration. Acceptance criteria for a good recording include: (1) seal resistance > 200 MΩ, (2) access resistance < 10 MΩ, (3) peak tail current > 200 pA, (4) leakage current < 25% of the peak tail current, (5) rundown < 2.5%/minute in control vehicle.

[00498] Counterscreens against the human IKr (hERG) potassium channel using the PatchXpress® system.

[00499] Cell culture. HEK293 cells stably expressing human ERG (hERG) potassium channel were purchased from Millipore (Cat. # CYL3039). Growth media for the HEK-hERG cells contains DMEM/F12 (Invitrogen # 11320), 1X Non Essential Amino Acid (Gibco # 11140), 10% Fetal Bovine Serum (Gibco # 16000) and 400 μg/ml geneticin (Gibco # 10131-027). Cells were maintained in culture at 37°C in a humidified 95% air, 5% CO_2 environment. Seeding density for a T75 Corning flask is four million cells, and a subcultivation ratio of 1:3 is performed twice weekly or whenever the cell density reaches 80% confluency. Cells are lifted from a T75 flask on the day of PatchXpress 7000A® experiments by using 0.05% trypsin-EDTA (Sigma) for 3 minutes at 37°C. They are then re-suspended in growth media for at least thirty minutes at 37°C in a humidified 95% air, 5% CO_2 atmosphere before loading onto the SealChip recording chambers (AVIVA Biosciences).

[00500] Electrophysiology Recording by PatchXpress® 7000A (Molecular Devices). The intracellular solution for whole cell patch clamp recordings contained (in mM) potassium chloride (70), potassium fluoride (60), magnesium chloride (2), ethylene glycol tetraacetic acid (EGTA, 11), magnesium adenosine triphosphate (5) and HEPES (10). The pH was adjusted to 7.2 with KOH, and the final osmolarity was set at 295 mOsm. The extracellular solution contains (in mM) sodium chloride (135), potassium chloride (4), magnesium chloride (1), calcium chloride (1.8), HEPES (10) and glucose (10). pH is adjusted to 7.4 with NaOH, and the final somolarity was set at 305 mOsm.

[00501] After achieving whole cell recording mode, cells are held at a holding potential of -80 mV. A voltage step to -50 mV from holding voltage of -80 mV for 500 msec is used to establish a baseline or reference point for the peak outward tail current measurement. This is followed by a depolarizing step to +30 mV for 2s to drive the channels to the inactivated state. A step back to -50 mV for 2s removes inactivation and thereby revealing the maximum peak outward tail current. Voltage steps are repeated once every 10 sec. Total hERG outward tail current is determined by the difference between the peak outward tail current at the repolarizing -50 mV step and the first baseline current at -50 mV prior to channel activation.

[00502] Test sample preparation. Test compounds (up to 10 μM), which included the peptides and peptide conjugates described herein, were serially diluted into the extracellular recording buffer containing 0.1% w/v bovine serum albumin (BSA) and subsequently transferred to glass perfusion reservoirs. Three μL of the serial dilutions were then transferred to nine hundred μL of assay buffer containing 0.1% w/v BSA in assay buffer.

[00503] PatchXpress® Procedure. Cumulative concentration response curve is generated from 4 concentrations (0.3, 1, 3, and 10 μM) for drug potency measurement. Each concentration of the test compound is added 3 times separated by 60 sec to ensure complete exchange of assay buffer in the recording chamber. There is a three minute wait time between subsequent additions. Prior to test compound addition, two glass vials containing assay buffer and vehicle control (0.3% DMSO) are used as controls (i.e., 1 x assay buffer, 1 x 0.3% DMSO, and 4 escalating concentrations of test compound).

[00504] Data Analysis. Outward hERG tail current from every successful whole cell recording must be visually inspected for quality. The general criteria for good quality recordings are: 1) holding current at -80 mV must not exceed 300 pA during the drug addition procedure, 2) peak outward tail current must be greater than 300 pA and 3) peak outward tail current does not change by greater than 2.5%/min during the eight minute control period in 0.3% DMSO. Potency estimates are generated by Protocol Engine (Amgen) using nonlinear mixed models to quantify the consistency of the assay from cell to cell and to provide an accurate measurement of drug potency over the population of the same cell type (Miu *et al.*, 2006, JALA 11:195).

[00505] Results of counterscreen for GpTx-1 (SEQ ID NO:1) and [Ala5]GpTx-1 (SEQ ID NO:22) against hERG are shown in Figure 18. Results of counterscreen for GpTx-1 (SEQ ID NO:1) and [Ala5]GpTx-1 (SEQ ID NO:22) against hNav1.5 are shown in Figures 19A and 19B.

[00506] Example 9: In vivo pain models

[00507] The compositions of the present invention can be tested in any relevant in vivo pain models. Examples include:

[00508] Tactile Allodynia- Von Frey Test. Von Frey filaments are used to assess mechanical sensitivity in rodents. Mice are placed on a wire mesh floor, enclosed in an individual testing chamber and allowed to acclimate until calm. Calibrated filaments of various bending forces are then applied to the paw of a mouse to measure the response to a non-noxious tactile (e.g., touch) stimulus. The pattern of responses and non-responses to the series of filaments determines the animal's mechanical threshold. This threshold is used as the endpoint of the assay.

[00509] Rat Neuropathic Pain Model. Male Sprague-Dawley rats (200 g) are anesthetized with isoflurane inhalant anesthesia and the left lumbar spinal nerves at the level of L5 and L6 are

tightly ligated (4-0 silk suture) distal to the dorsal root ganglion and prior to entrance into the sciatic nerve, as first described by Kim and Chung (An experimental model for peripheral neuropathy produced by segmental spinal nerve ligation in the rat. Pain 50:355-363, (1992)). The incisions are closed and the rats are allowed to recover. This procedure results in mechanical (tactile) allodynia in the left hind paw as assessed by recording the pressure at which the affected paw (ipsilateral to the site of nerve injury) is withdrawn from graded stimuli (von Frey filaments ranging from 4.0 to 148.1 mN) applied perpendicularly to the plantar surface of the paw (between the footpads) through wire-mesh observation cages. A paw withdrawal threshold (PWT) is determined by sequentially increasing and decreasing the stimulus strength and analyzing withdrawal data using a Dixon non-parametric test, as described by Chaplan, S.R., et al. (Quantitative assessment of tactile allodynia in the rat paw. J. Neurosci. Meth, 53:55-63 (1994)).

[00510] Rat CFA Inflammatory Pain Model. Male Sprague-Dawley rats (200 g) are injected in the left hindpaw with complete Freund's adjuvant (CFA). This procedure results in mechanical (tactile) and themal allodynia in the left hind paw as assessed by recording the pressure at which the affected paw is withdrawn from graded stimuli (von Frey filaments ranging from 4.0 to 148.1 mN) applied perpendicularly to the plantar surface of the paw (between the footpads) through wire-mesh observation cages or by applying radiant heat. PWT is determined by sequentially increasing and decreasing the stimulus strength and analyzing withdrawal data using a Dixon non-parametric test, as described by Chaplan et al. (1994). Rats are included in the study only if they do not exhibit motor dysfunction (e.g., paw dragging or dropping) or broken skin and their PWT is below 39.2 mN (equivalent to 4.0 g). At appropriate times after CFA injection rats are treated with test peptides and/or test vehicle-conjugated peptides (usually a screening dose of 60 mg/kg) or control solution (PBS or other vehicle) once by s.c. injection and PWT is determined. Average paw withdrawal threshold (PWT) was converted to percent of maximum possible effect (%MPE) using the following formula: %MPE = 100 * (PWT of treated rats – PWT of control rats)/(15-PWT of control rats). Thus, the cutoff value of 15 g (148.1 mN for mechanical allodynia) is equivalent to 100% of the MPE and the control response is equivalent to 0% MPE.

[00511] Preferred molecules of the present invention are expected to produce an antinociceptive effect with a PDwith appropriate exposures compared to IC_{50} on the target.

[00512] Mouse Formalin Pain Model Experimental Procedure. Formalin injection into a rodent paw evokes a well-studied form of pain quantitated by the number of times the animal flinches its paw. The pain following formalin injection comes in two characteristic phases: a first

phase lasts approximately ten minutes and likely corresponds to the immediate pain mediated by peripheral neurons. The second phase, beginning approximately ten minutes after formalin injection and lasting for another 30 to 40 minutes, corresponds to sensitization of neurons in the spinal cord and hyperactivity of peripheral pain-sensing neurons. Compounds represented in this application were tested to see if they reduce the number of flinches in phase II of the formalin response and so are potential analgesic drugs (Bregman H et al., "Identification of a potent, state-dependent inhibitor of Nav1.7 with oral efficacy in the formalin model of persistent pain." J Med Chem 54(13):4427-4445, 2011).

[00513] Male CD-1 mice (8-12 weeks of age, Harlan Laboratories, Frederick, MD) were used for all in vivo efficacy experiments. Animal subjects had free access to food (Teklad Global Soy Protein-Free Extruded Rodent Diet 2020X) and water and were maintained on a 12-h light/dark cycle for the entire duration of the study. All animals were housed on standard solid-bottomed caging with corn cob bedding in groups of 4 animals per cage. The animal colony was maintained at approximately 21°C and 60% humidity. All experiments were conducted in accordance with the International Association for the Study of Pain guidelines.

[00514] On test day, during or before acclimation, the animals were dosed with either an investigational compound or vehicle. Following dose administration, all mice (n=12) were conditioned to behavioral analysis chambers (dimensions: 10cm diameter, 14cm tall cylinder with lid on top of elevated glass) for 5 minutes prior to the formalin injection. Video cameras were set underneath for recording the mouse behavior (5 minute acclimation and 40 minute test session). At test time, mice were lightly restrained in a cloth glove and injected with 20uL of a 2% formalin solution into the dorsal surface of the left hind paw using an insulin syringe (U100, 0.3cc, 28-30G). Immediately following the formalin injection, animals were returned to the chamber and observed for 40 minutes. Paw lifting/licking behavior was recorded in 5 minute intervals after which ipsilateral and contralateral paw widths were measured. After study completion animals were immediately euthanized.

[00515] In the first mouse formalin pain model study, [Ala5]GpTx-1(1-34) (SEQ ID NO:22) was dosed at 5 mg/kg s.c. 1-hour pre-treatment with morphine at 1 mg/kg s.c. 30-min pre-treatment as the positive control. (See, Figure 59). The peptide had no effect in the first or acute phase (0-5 minutes post formalin injection). (See, Figure 60). The peptide significantly reduced the time spent lifting and/or licking the affected paw during the second phase (5-40 minutes post formalin injection) compared to vehicle (PBS). (See, Figure 61). In this experiment the 1 mg/kg s.c. dose of morphine used as a positive control did not significantly reduce pain response in the animals, and it was increased to 3 mg/kg in the following studies.

The terminal plasma exposure (peptide plasma concentrations at 45 min post formalin injection) for the peptide was 0.80 ± 0.21 μM. Neither the peptide nor the morphine positive control significantly reduced the paw edema caused by formalin injection relative to the vehicle (PBS). (See, Figure 62).

[00516] The mouse formalin pain model was repeated with 1-hour pre-treatment doses of 5, 1.67, and 0.5 mg/kg s.c. to determine the dose response of [Ala5]GpTx-1(1-34) (SEQ ID NO:22). (See, Figure 63). The peptide had no effect at any dose in the first phase (0-5 minutes post formalin injection). (See, Figure 64). The positive control, a 3 mg/kg s.c. dose of morphine, did significantly reduce the time spent lifting/licking the affected paw in the first phase. The 5 mg/kg s.c. dose of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) demonstrated a significant reduction of the time spent lifting/licking in the second phase of the study, as did the morphine positive control. (See, Figure 65). However, the lower peptide doses (1.67 and 0.5 mg/ kg s.c.) had no significant effect relative to the vehicle in the second phase. Terminal exposures (peptide plasma concentrations at 45 min post formalin injection) were0.58 ± 0.26 μM, 0.15 ± 0.05 μM, and 0.04 ± 0.2 μM for the 5.0, 1.67, and 0.5 mg/kg doses, respectively. Neither the peptide nor the morphine positive control significantly reduced the paw edema caused by formalin injection relative to the vehicle (PBS). (See, Figure 66). In the first two mouse formalin experiments, [Ala5]GpTx-1(1-34) (SEQ ID NO:22) demonstrated a significant reproducible reduction in paw lifting/licking at plasma concentratons between 0.60-0.80 μM. One other peptide was tested in the formalin pain model, [Glu29]GpTx-1(1-34) (SEQ ID NO:30). The substitution of glutamic acid for tryptophan at position 29 greatly reduces potency against Nav1.7, so [Glu29]GpTx-1 was prepared and tested as a negative control. A 5 mg/kg s.c. dose of [Glu29]GpTx-1 had no significant effect on the time spent lifting/licking in the formalin pain model in mice with a terminal mean peptide plasma concentration of 0.502 ± 0.271 μM, demonstrating that peptide Nav1.7 potency correlates with efficacy in the formalin pain model. (See, Figures 95-98).

[00517] The mouse formalin pain model was repeated with 1-hour pre-treatment doses of 5, 3, and 1 mg/kg s.c. to further investigate the dose response of [Ala5]GpTx-1(1-34) (SEQ ID NO:22). (See, Figure 67). The peptide had no effect at any dose in the first phase (0-5 minutes post formalin injection). (See, Figure 68). The 5 mg/kg s.c. dose of peptide demonstrated a significant reduction of the time spent lifting/licking in the second phase of the study, as did the morphine positive control. However, the lower peptide doses did not show a reduction in lifting/licking behavior relative to the vehicle control in the second phase. The 1 mg/kg s.c. group was not significantly different from the vehicle control whereas the 3 mg/kg s.c. group appeared to significantly increase time spent lifting/licking. (See, Figure 69). Terminal

exposures (peptide plasma concentrations at 45 min post formalin injection) were 1.84 ± 0.18 μM, 0.53 ± 0.23 μM, and 0.20 ± 0.05 μM for the 5, 3, and 1 mg/kg doses, respectively. Neither the peptide nor the morphine positive control significantly reduced the paw edema caused by formalin injection relative to the vehicle (PBS). (See, Figure 70).

[00518] Mouse Open Field Analysis Experimental Protocol. To verify that efficacy in the formalin model produced by a test compound is not due to sedation or damage to the animal, compounds were also tested for their effects on the overall movement of animals (open-field testing). Naïve animals are administered test compound and placed in a novel environment, and the movements the animal undergoes during exploration of the novel environment are automatically recorded. Reductions in movement of 50% or more mean that efficacy in the formalin test cannot be ascribed to true analgesia.

[00519] Male CD-1 mice (8-12 weeks of age, Harlan Laboratories, Frederick, MD) were used for all in vivo efficacy experiments. Animal subjects had free access to food (Teklad Global Soy Protein-Free Extruded Rodent Diet 2020X) and water and were maintained on a 12-h light/dark cycle for the entire duration of the study. All animals were housed on standard solid-bottomed caging with corn cob bedding in groups of 4 animals per cage. The animal colony was maintained at approximately 21°C and 60% humidity. All experiments were conducted in accordance with the International Association for the Study of Pain guidelines.

[00520] On test day, animals were dosed with either an investigational compound or vehicle and given at least 30 minutes to acclimate to the testing room. Mice (N=8) were placed in a clean open field chamber (Kinder Scientific Photobeam Activity System) at the appropriate time after dose administration. The changes in overall animal movement were recorded on the system for 60 minutes under lights off conditions. The following parameters were evaluated: total basic movement, total rearing, total time rearing, and total fine movement.

[00521] Results of the open field analysis. [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at 3 mg/kg s.c. dose with a 1-hour pre-treatment time had no effect on the total basic movement, total fine movement, total rearing, or total time rearing in CD-1 mice. No doses of peptide significantly decreased exploratory behavior in relation to the vehicle control. However, at a 5 mg/kg s.c. dose with a 1-hour pre-treatment the peptide significantly reduced the total fine movement and total time rearing components of locomotor activity in CD-1 mice relative to the vehicle. Total basic movement and total rearing were also reduced. (See, Figures 71-74). Terminal exposures (peptide plasma concentrations at 2 h post peptide injection) were 1.79 ± 0.38 μM and 0.89 ± 0.33 μM for the 5 and 3 mg/kg s.c. doses, respectively. In this experiment, the 3 mg/kg dose, which had no significant effect on locomotor activity, resulted in a peptide

plasma concentration equivalent to those that had demonstrated reproducible efficacy in the formalin pain model. Higher peptide plasma concentrations (> 1.5 μM) resulted in significant effects on locomotor activity, as was demonstrated by a repeat open field analysis of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at a 5 mg/kg dose with a terminal exposure of 2.1 ± 0.47 μM. (See, Figures 99-102). Three other peptides were tested in the open field analysis: [Glu29]GpTx-1(1-34) (SEQ ID NO:30), [Glu28]GpTx-1(1-34) (SEQ ID NO:153), and [Ala5,Phe6,Glu10,2-Abu13,Leu26,Arg28]GpTx-1 (SEQ ID NO:1035). The substitution of glutamic acid for tryptophan at position 29 greatly reduces potency against Nav1.7, so [Glu29]GpTx-1 (SEQ ID NO:30) was prepared and tested as a negative control. A 5 mg/kg s.c. dose of [Glu29]GpTx-1 had no significant effect on the locomotor activity of mice in the open field analysis with a terminal mean peptide plasma concentration of 0.771 ± 0.272 μM. (See, Figures 103-106). A 5 mg/kg dose of [Glu28]GpTx-1(1-34) (SEQ ID NO:153) significantly reduced locomotor activity in the open field analysis with a terminal mean peptide plasma concentration of 1.28 ± 0.403 μM, similar to the result with the 5 mg/kg dose of [Ala5]GpTx-1 (SEQ ID NO:22). (See, Figures 107-110). A 5 mg/kg dose of [Ala5,Phe6,Glu10,2-Abu13,Leu26,Arg28]GpTx-1 (SEQ ID NO:1035) in the open field analysis resulted in moribund behavior or lethality in animals at a terminal mean peptide plasma concentraiton of 1.72 ± 0.313 μM.

[00522] Mouse Veratridine Pain Model Experimental Protocol. Veratridine is a nonselective activator of voltage-gated sodium ion channels (Hille B, Ion Channels of Excitable Membranes, Sinauer Associates, Sunderland MA 2001) that causes a painful flinching (paw licking and lifting or guarding) response when injected into the rodent paw. Accordingly, testing compounds like those of the present invention that are sodium channel inhibitors quantifies not only their effect on pain, but on pain caused by sodium channel activation. That is, effects of a test compound on veratridine-induced paw lifting and licking not only measures analgesic efficacy but the in vivo receptor occupancy of sodium channels.

[00523] Male CD-1 mice (8-12 weeks of age, Harlan Laboratories, Frederick, MD) were used for all in vivo efficacy experiments. Animal subjects had free access to food (Teklad Global Soy Protein-Free Extruded Rodent Diet 2020X) and water and were maintained on a 12-h light/dark cycle for the entire duration of the study. All animals were housed on standard solid-bottomed caging with corn cob bedding in groups of 4 animals per cage. The animal colony was maintained at approximately 21°C and 60% humidity. All experiments were conducted in accordance with the International Association for the Study of Pain guidelines.

[00524] On test day, during or before acclimation, the animals were dosed with either an investigational compound or vehicle. Following dose administration, all mice (n=12) were conditioned to behavioral analysis chambers (dimensions: 10cm diameter, 14cm tall cylinder with lid on top of elevated glass) for 5 minutes prior to the veratridine injection. Video cameras were set underneath for recording the mouse behavior (5 minute acclimation and 20 minute test session). At test time, mice were lightly restrained in a cloth glove and injected with 20uL of 1μg of veratridine (Sigma-Aldrich #V109) in 1% ethanol in phosphate buffered saline suspension into the dorsal surface of the left hind paw using an insulin syringe (U100, 0.3cc, 28-30G). Immediately following the veratridine injection, animals were returned to the chamber and observed for 20 minutes. Paw lifting/licking behavior was recorded in 5 minute intervals after which ipsilateral and contralateral paw widths were measured. After study completion animals were immediately euthanized.

[00525] In the first mouse veratridine pain model, [Ala5]GpTx-1(1-34) (SEQ ID NO:22) was dosed at 5 mg/kg s.c. with a 1-hour pre-treatment time, and mexiletine was dosed at a 30 mg/kg intraperitoneal ("i.p.") dose with a 30 minute pre-treatment time as a control. The anti-nociceptive effect was measured on the veratridine-induced (1 μg injection in the dorsal paw) spontaneous nociceptive behaviors in CD-1 mice. Overall there was a good paw lifting response from the vehicle group that was significantly reversed with mexiletine. At 5 mg/kg, [Ala5]GpTx-1(1-34) (SEQ ID NO:22) was unable to significantly reduce the lifting behavior. (See, Figure 75). There is no reduction of paw edema across all groups. (See, Figure 76). However, in examining the time course of the experiment the peptide did appear to have some effect during the 10-15 and 15-20 minute time bins. (See, Figure 77). Terminal exposure (peptide plasma concentration at 1.5 h post peptide injection) was 0.70 ± 0.10 μM for the 5 mg/kg dose.

[00526] In the repeat of the mouse veratridine pain model, [Ala5]GpTx-1(1-34) (SEQ ID NO:22) was dosed at 1 and 5 mg/kg s.c. with a 1-hour pre-treatment time, and mexiletine was dosed at a 30 mg/kg i.p. dose with a 30 minute pre-treatment time as a control. There was a robust paw lifting response from the vehicle group that was significantly reversed with mexiletine. At 1 and 5 mg/kg, [Ala5]GpTx-1(1-34) (SEQ ID NO:22) had no effect of the lifting behavior. (See, Figure 78). There was no reduction of paw edema in any of the groups. (See, Figure 79). The peptide doses had no significant effect throughout the time course of the experiment. (See, Figure 80). Terminal exposures (peptide plasma concentration at 1.5 h post peptide injection) were 0.72 ± 0.13 μM and 0.09 ± 0.05 μM for the 5 and 1 mg/kg doses, respectively.

[00527] The foregoing example of in vivo pain models for the screen of therapeutic embodiments of the inventive molecules are non-limiting. The skilled practitioner is aware of other relevant pain models.

[00528] Example 10: Preliminary Cardiac Safety Assessment

[00529] Isolated Perfused Rabbit Heart (Langendorff Preparation). The effects of [Ala5]GpTx-1(1-34) (SEQ ID NO:22) in the isolated perfused rabbit heart (Langendorff preparation) assay were determined as described below, for which results are shown below in Table 36 and Table 37.

Table 36. Effects of 1 μM [Ala5]GpTx-1(1-34) (SEQ ID NO:22) on electrocardiography intervals in the isolated perfused rabbit heart assay (Langendorff preparation). The peptide had no delaying effects on ventricular repolarization (QTc or JTc intervals). The peptide had no effects on heart rate (HR). The peptide also had no effects on ventricular depolarization and conduction (QRS and PR intervals). (Abbreviations: HR, heart rate; PR interval, time interval from onset of atrial depolarization (P wave) to onset of ventricular depolarization (QRS complex); QRS duration, time interval from onset to end of QRS complex, which is the duration of ventricular depolarization; QT interval, time interval from onset of QRS complex to end of T wave, which is the duration of ventricular depolarization and repolarization; QTc interval, QT interval corrected with HR; JT interval, the difference between QT interval and QRS duration (JT = QT – QRS), which is the duration of ventricular repolarization; and JTc interval, JT interval corrected with HR.)

STATISTICS (NORMALIZED VALUES), %

Mean

Treatment	HR	PR	QRS	QT	QTcF	JT	JTcF
1% BSA	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1uM SEQ ID NO:22	-0.18	-3.52	-1.55	-4.19	-4.22	-4.57	-4.60

Standard Deviation

Treatment	HR	PR	QRS	QT	QTcF	JT	JTcF
1% BSA	0.00	0.00	0.00	0.00	0.00	0.00	0.00
1uM SEQ ID NO:22	1.87	2.19	2.66	2.48	2.10	3.12	2.76

Table 37. Effects of 1 μM [Ala5]GpTx-1(1-34) (SEQ ID NO:22) on hemodynamic parameters in the isolated perfused rabbit heart assay (Langendorff preparation). The peptide had no effects on LV contractility (dP/dt+) and no effects on coronary blood flow (CF). The peptide had no direct effects on coronary vasculature. (Abbreviations: **LVSP**, left ventricular systolic pressure; **LVDP**, left ventricular diastolic pressure; **dP/dt+**, maximal rate of increase in LV pressure; **dP/dt-**, minimal rate of decrease in LV pressure; **LVDevP**, LV developed pressure, LVDevP = LVSP-LVDP; and **CF**, Coronary flow.)

LVP - Normalized Values (%)							
uM	LVSP, mean	LVDP, mean	dP/dt+, mean	dP/dt-, mean	Flow, mean	LVDevP	N
Baseline	1.64	0.92	1.72	2.60	0.04	1.69	4
1uM SEQ ID NO:22	-3.81	-3.16	-4.55	-2.90	0.29	-7.22	4
LVP Standard Deviation							
uM	LVSP, SD	LVDP, SD	dP/dt+, SD	dP/dt-, SD	Flow SD	LVDevP, SD	N
Baseline	2.13	0.40	1.61	3.65	0.45	2.51	4
1uM SEQ ID NO:22	1.41	2.15	2.72	0.95	2.09	1.10	4

[00530] Acquisition and Acclimatization. Six female New Zealand White rabbits, 14 – 22 weeks old and 2.5 – 3.5 kg were obtained from Harlan Laboratories. Upon receipt, rabbits were examined by veterinary personnel to ensure acceptable health status. Veterinary care was provided by the veterinarians and staff. Rabbits were acclimated for at least 7 days prior to use. Unhealthy rabbits were not used for the study.

[00531] Method of Identification. Each rabbit was assigned an identification number by the supplier. An ear tag containing the identification number was affixed to each rabbit by the supplier. This identification number was displayed on a cage card, along with the rabbit's date of arrival, date of birth, source, and sex. The identification numbers of the rabbits used in the study and their final weights were recorded in notebooks.Composition of Perfusion Medium. The perfusion medium consists of modified oxygenated Krebs-Henseleit buffer (37°C at the heart) composed of (mM): NaCl (120), KCl (4.7), $MgSO_4$ (1.2), KH_2PO_4 (1.2), d-glucose (11.1), $CaCl_2$ (1.8), $NaHCO_3$ (25), and Na-pyruvate (2.0). This perfusion

medium is constantly bubbled with 95% O_2/5% CO_2. For testing [Ala5]GpTx-1(1-34) (SEQ ID NO:22), 1% BSA was added in the buffer.

Anesthesia and Heart Removal. Each rabbit was anaesthetized with pentobarbital (50 mg/kg, IV; ear vein). Complete suppression of pain was assessed by pinching a paw (pedal withdrawal reflex). Rabbits were restrained in a rabbit cage restrainer while anesthesia induction was taking place to avoid injury to the animal and the investigator.

[00532] Exposing the heart: Once the animal was anesthetised the heart was excised. The diaphragm was accessed by a transabdominal incision and cut carefully to expose the thoracic cavity. The thorax was opened by a bilateral incision along the lower margin of the last to first ribs, the thoracic cage was then reflected over the animals head, exposing the heart. To remove the heart, the organ was cradled gently between the fingers to avoid injury and lifted slightly before incising the aorta, vena cava and pulmonary vessels.

[00533] Isolated Heart Preparation Perfused by Langendorff Apparatus. Hearts were rapidly removed, mounted on a Langendorff apparatus, and perfused with oxygenated Krebs-Henseleit buffer under constant pressure. Spontaneously beating (unpaced) hearts were included in the study if they exhibited acceptable and stable baseline values for each parameter (mechanical, heart rate, cardiac interval, etc) during the equilibration period. Perfusion buffer temperature was maintained ~ 37°C throughout the study period.

[00534] Experimental Plan. Each individual heart (N = 4 total) was equilibrated for approximately 30 to 60 minutes. Following this equilibration period, baseline measurements were collected for approximately 10 minutes in 1% BSA. After this period, hearts were exposed to [Ala5]GpTx-1(1-34) (SEQ ID NO:22) at 1 μM for 20 minutes. Cardiac parameters were measured continuously during the study using a computerized data acquisition system. (See Qu et al., BeKm-1, A Peptide Inhibitor of hERG potassium currents, prolongs QTc intervals in isolated rabbit heart, J. Pharmacol. Exp. Ther. (337):2-8 (2011) for details and validation studies.)

[00535] Electrocardiographic Measurements. Simultaneous 2-lead surface-contacted electrocardiograms were recorded with flexible unipolar electrodes placed on the heart, one over the epicardium of ventricles and the other over the epicardium of the left atria.

[00536] Hemodynamic Measurements. The latex balloon in the left ventricle (LV) was expanded with water to achieve a LVEDP of approximately 5-10 mmHg. The balloon was connected with tubing to a pressure transducer to measure LVEDP and LVSP. Coronary perfusion pressure (CPP) was measured with a pressure transducer connected to a side-arm port of the aortic block.

[00537] Data Analysis. For analysis, left ventricular pressure (LVP) and CPP were automatically performed with Notocord. Measurements from the final 30 sec of the equilibration period and each dose exposure period were evaluated and used to determine effects. Electrocardiograms (ECGs) were analyzed with EMKA ecgAUTO software (EMKA Technologies, Paris, France) and 1 minute consecutive ECG waveforms (30 seconds before the next event marker) were analyzed for HR, PR, QRS and QT intervals. Values from each individual heart were pooled to determine an average for each variable at individual concentrations. Average percent change of each variable between baseline and each concentration were also determined. For HR correction of QT intervals, Fridericia's equation was used ($QTcF=QT/RR^{1/3}$). Data are presented as average percent change of each variable between baseline and each concentration. A ≥ 10% change in HR, PR, QRS, QTc, and JTc and a ≥ 15% change in +dP/dt and CF are considered drug-related. All values are presented as mean ± S.D.

[00538] Results. At a 1 μM concentration, [Ala5]GpTx-1(1-34) (SEQ ID NO:22), had no effects in the isolated perfused rabbit heart assay (Langendorff preparation). The peptide had no delaying effects on ventricular repolarization (QTc or JTc intervals) and had no effects on heart rate. The peptide also had no effects on ventricular depolarization and conduction (QRS and PR intervals). The peptide had no effects on LV contractility (dP/dt+) and no effects on coronary blood flow (CF). The peptide had no direct effects on coronary vasculature.

Example 11: Site specific peptide conjugation

[00539] The following protocol was used to site-specifically conjugate toxin peptide analogs (see, Table 5A and Table 5B for toxin peptide analog amino acid sequences) to either a human immunoglobulin at a linkage site on the heavy chain (C273 of SEQ ID NO:3087) or on a human immunoglobulin Fc domain (at C52 of SEQ ID NO:3089).

[00540] Preparation of peptide-linker constructs. Alkyne-containing peptides were subjected to copper catalyzed 1,3-dipolar cycloaddition with azido-PEG bromoacetamides of two differing lengths to obtain the site-specifically PEGylated peptides with a triazole linkage, thus converting a propargylglycine or Pra residue in the sequence to a 3-(1,2,3-triazol-4-yl)alanine or Atz residue. (See, Figure 81B). Peptide containing either propargylglycine (Pra) at position 13 or 4-pentynoyl (4-Pen) at the N-terminus (7.4 mM in 6.7 mL water), azido-PEG11-bromoacetamide (150 mM, 0.964 mL in water), tris((1-benzyl-1H-1,2,3-triazol-4-

yl)methyl)amine (TBTA, 10 mM, 2.2 mL in DMSO), sodium ascorbate (50 mM, 10.1 mL in water), and copper (II) sulfate (35 mM, 2.9 mL in water) solutions were prepared fresh. Peptide and reagents were added in the following order to a 50 mL centrifuge tube to achieve the following final concentrations. Peptide stock solution (6.7 mL) was added for a final concentration of 3.7 mM, followed by addition of azido-PEG11-bromoacetamide (0.402 mL) for a final concentration of 4.5 mM. TBTA (0.603 mL) was added for a final concentration of 0.45 mM and mixed thoroughly. Sodium ascorbate (4.522 mL) was then added for a final concentration of 16.9 mM and mixed thoroughly. $CuSO_4$ (1.292 mL) was added for a final concentration of 3.4 mM. The solution was allowed to stand for 1 h at which time it was judged to be complete by LC-MS. To a 25mL SPE filter tube was added SP Sepharose High Performance as a slurry (8 mL) with a pipette. The gel was conditioned with wash buffer (50 mL 20 mM NaOAc, pH = 4.0), loaded with the peptide solution, washed (50 mL, 20 mM NaOAc, pH = 4.0 and 50 mL, 20 mM NaOAc, pH = 4.0, 0.1M NaCl), and eluted with 45 ml 1M NaCl, 20 mM NaOAc, pH = 4.0) into a 50 mL centrifuge tube. The product mixture was purified by loading onto a preparative HPLC column (Phenomenex Luna 5u C18(2) 100A AXIA, 250 x 30mm) at 30 mL/min using an Agilent prep loading pump. The column was was flushed for 10 min with 10% B. The column was attached to a prep HPLC (Agilent), and the peptide was eluted with a 10-40% B gradient over 60 min, followed by a 10 min flush and a 10 min equilibration. The fractions were analyzed by LC-MS, pooled, and lyophilized to afford pure peptide-linker construct for conjugation to IgG or Fc domain.

[00541] Antibody Preparation/Reduction. Anti-DNP mAb (E273C, hIgG1) (kappa/IgG1z) was concentrated to ~5mg/ml in reaction buffer (20mM sodium phosphate pH 6.8, 2mM EDTA).

[00542] The amino acid sequence of the human IgG heavy chain monomer that was used was the following (variable region is underlined; C273 linkage site is italicized and underlined):

[00543] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAP GKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARYNFNYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD

SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK//SEQ ID NO.: 3087.

[00544] The amino acid sequence of the human IgG kappa light chain monomer that was used was the following (variable region is underlined):

[00545] DIQMTQSPSSVSASVGDRVTITCRASQGISRRLAWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPFTFGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC// SEQ ID NO.: 3088.

[00546] The amino acid sequence of the human IgG1z Fc domain monomer that was used was the following (C52 linkage site is italicized and underlined):

[00547] DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDP*C*VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK//SEQ ID NO.: 3089.

Table 38. Immunoglobulin-peptide conjugates and Fc domain-peptide conjugates made. "Monovalent" conjugate molecules had one toxin peptide (i.e., peptide covalently conjugated via linker to one HC or Fc domain monomer in the molecule, but not to the other HC or Fc domain monomer) in the molecule; "Bivalent" conjugate molecules had two toxin peptides (i.e., one peptide covalently conjugated via linker to each HC or Fc domain monomer in the molecule). SEQ ID NOS:1046, 1047, and 1048 are as set forth in Table 5A.

Designation	SEQ ID NO of toxin peptide	Linker and residue position of linkage on toxin peptide	SEQ ID NOS of immunoglobulin monomers in conjugated molecule	Monovalent or Bivalent
Fc-peptide Conjugate 1	1046	PEG11-(acetamidomethyl) linker at residue 13 sidechain	3089; 3089	Monovalent
Fc-peptide Conjugate 2	1046	PEG11-(acetamidomethyl) linker at residue 13 sidechain	3089; 3089	Bivalent
Immunoglobulin-peptide Conjugate 1	1046	PEG11-(acetamidomethyl) linker at residue 13 sidechain	3087; 3088; 3087; 3088	Monovalent
Immunoglobulin-peptide Conjugate 2	1046	PEG11-(acetamidomethyl) linker at residue 13 sidechain	3087; 3088; 3087; 3088	Bivalent
Fc-peptide Conjugate 3	1047	PEG11-(acetamidomethyl)	3089; 3089	Monovalent

		linker at residue 13 sidechain		
Fc-peptide Conjugate 4	1047	PEG11-(acetamidomethyl) linker at residue 13 sidechain	3089; 3089	Bivalent
Immunoglobulin-peptide Conjugate 3	1047	PEG11-(acetamidomethyl) linker at residue 13 sidechain	3087; 3088; 3087; 3088	Monovalent
Immunoglobulin-peptide Conjugate 4	1047	PEG11-(acetamidomethyl) linker at residue 13 sidechain	3087; 3088; 3087; 3088	Bivalent
Fc-peptide Conjugate 5	1048	acetamidomethyl-NPEG11-triazole linker at N-terminal	3089; 3089	Monovalent
Fc-peptide Conjugate 6	1048	acetamidomethyl-NPEG11-triazole linker at N-terminal	3089; 3089	Bivalent
Immunoglobulin-peptide Conjugate 5	1048	acetamidomethyl-NPEG11-triazole linker at N-terminal	3087; 3088; 3087; 3088	Monovalent
Immunoglobulin-peptide Conjugate 6	1048	acetamidomethyl-NPEG11-triazole linker at N-terminal	3087; 3088; 3087; 3088	Bivalent
Fc-peptide Conjugate 7	1046	PEG3-(acetamidomethyl) linker at residue 13 sidechain	3089; 3089	Monovalent
Fc-peptide Conjugate 8	1046	PEG3-(acetamidomethyl) linker at residue 13 sidechain	3089; 3089	Bivalent

Immunoglobulin-peptide Conjugate 7	1046	PEG3-(acetamidomethyl) linker at residue 13 sidechain	3087; 3088; 3087; 3088	Monovalent
Immunoglobulin-peptide Conjugate 8	1046	PEG3-(acetamidomethyl) linker at residue 13 sidechain	3087; 3088; 3087; 3088	Bivalent

[00548] Reduction of engineered cysteines was done by incubating mAb with a 1:1 molar ratio of TCEP to cysteine (2:1 TECP to mAb) at room temperature for 30 minutes. TCEP was removed using a Zeba spin desalting column (≥ 7 kD Pierce) equilibrated with reaction buffer. Large scale preps were concentrated to appropriate volume prior to loading using amicon ultra (10,000-30,000MWCO) centrifugal concentrators.

[00549] Peptide preparation. Lyophilized peptide-linker containing a bromoacetamide functionality was resuspended in water at 20mg/ml immediately prior to conjugation reaction.

[00550] Conjugation reaction. Peptide and reduced mAb were mixed at a 2.5:1 molar ratio of peptide to cysteine (5:1 peptide to mAb) in reaction buffer at mAb concentration of 5 mg/ml and incubated for 12-16 hours at 4°C. The engineered free cysteines in the immunoglobulin react with the bromoacetamide functionality in peptide-linker to form a site-specific immunoglobulin-peptide conjugate with a stable thioacetamide linkage. (See, Figure 81B and Figure 82). If one cysteine reacts, then the result is a monovalent immunoglobulin-peptide conjugate, and if both cysteines react, then the result is a bivalent immunoglobulin-peptide conjugate

[00551] Purification of conjugates. Following incubation, conjugation reaction was desalted to removed excess free peptide and loaded onto a HiTrap SP-HP column (GE Healthcare; 1ml column for preps <10mg, 5ml column for preps >10mg). Column was rinsed in 5 column volumes of 90% buffer A (10mM sodium phosphate pH 6.5, 5% ethanol) 10% buffer B (10mM sodium phosphate pH 6.5, 5% ethanol, 1M NaCl). Conjugates (see, Table 38) were eluted over a 20 column volume gradient from 10% buffer B to 70% buffer B. Unmodified mAb elutes first followed by monvalent imunoglobulin-peptide conjugate (1 peptide per mAb), followed by bivalent imunoglobulin-peptide conjugate (2 peptides per mAb). Higher order conjugates resulting from over reduction of the mAb elute later. (See, Figure 83 for mAb immunoglobulin-peptide conjugates and Figure 84 for Fc domain-peptide conjugates).

Following purification, conjugates were formulated into A5SU storage buffer (10 mM sodium acetate pH 5.0, 9% sucrose) and concentrated to 10mg/ml to be stored at -80°C.

[00552] Analysis of conjugates. Conjugates were run on reducing SDS-PAGE to confirm conjugation to heavy chain (increase in size by ~5kD) and non-reducing SDS-PAGE to confirm internal disulfides remained intact. (See, Figure 83 for mAb imunoglobulin-peptide conjugates and Figure 84 for Fc domain-peptide conjugates). Conjugates were run on analytical SEC to determine if aggregation was present (Superdex-200 10/300 column in 100mM sodium phosphate, 250mM NaCl, pH 6.8 with isocratic elution ~1 ml/min for 35 min). (See, Figure 85).

[00553] LC-MS-TOF analysis of conjugates. LC/MS spectrometry of peptide conjugates was recorded using an Agilent 6224 TOF LC/MS spectrometer with a non-reduced method. After calibration, a 5 µg intact sample was loaded onto a Zorbax 300SB C6 column (1 x 50 mm, 3.5 µm, Agilent Technologies) operation at 75°C with a flow rate of 50 µl/min. Peptide-conjugate was eluted from the column using a gradient of 90% n-propanol with 0.1% TFA (Buffer B) and 0.1% TFA in water (Buffer A). The gradient condition was 20% to 90 % buffer B in 14 min. (See, Figure 86 for bivalent mAb-peptide conjugate and Figure 87 for bivalent Fc domain-peptide conjugate). The MS spectra indicate the addition of two peptides to the immunoglobulin and immunoglobulin Fc domain, respectively. The presence of multiple peaks is due to the different glycosylation isoforms.

[00554] Specific Reaction Results. From 100 mg of Anti-DNP mAb (E273C, hIgG1) and 15 mg of peptide-linker contruct (SEQ ID NO:1062) were obtained 22 mg of bivalent conjugate (Immunoglobulin-Peptide Conjugate 2) and 11 mg of monovalent conjugate (Immunoglobulin-peptide Conjugate 1). Samples were concentrated to 10 mg/mL in A5SU buffer and stored as aliquots at -80°C.

[00555] Models of Peptide Conjugates. For illustrative purposes only, models of Fc-peptide Conjugate 1, Fc-peptide Conjugate 2, Immunoglobulin-peptide Conjugate 1, and Immunoglobulin-peptide Conjugate 2 were created (MOE; Chemical Computing Group: Montreal, Quebec, Canada, 2010). (See, Figures 88-91). A homology model of the anti-DNP mAb (E273C) hIgG1 (comprising immunoglobulin monomers SEQ ID NO:3087; SEQ ID NO:3088; SEQ ID NO:3087; SEQ ID NO:3088) and anti-DNP mAb (E52C) hIgG1 Fc domain (homodimer of SEQ ID NO:3089) was constructed from an immunoglobulin crystal structure (1HZH.pdb) using the program MOE (MOE; Chemical Computing Group: Montreal, Quebec, Canada, 2010). The sites of conjugation, Cys273 in the immunoglobulin and Cys52 in the immunoglobulin Fc domain, are indicated. The PEG11 linkers are depicted in an arbitrary conformation connecting the appropriate cysteine residue(s) in the immunoglobulin and immunoglobulin Fc domain to the

Atz13 residue(s) in the peptide(s). A homology model of the peptide (SEQ ID NO:1046) was constructed from the NMR structure of GpTx-1 (MOE; Chemical Computing Group: Montreal, Quebec, Canada, 2010) and is displayed in an arbitrary relative orientation to the immunoglobulin and immunoglobulin Fc domain. One or two peptides are shown to reflect the monovalent or bivalent nature of each peptide conjugate.

[00556] Example 12: Preliminary pharmacokinetics of peptide conjugates in mice

[00557] Pharmacokinetic (PK) studies of toxin peptide conjugates. A preliminary PK study was conducted with 7-week-old unmodified CD-1 mice from Taconic. Fc-P2 (Fc-Peptide Conjugate 2) or its control Fc (SEQ ID NO:1062) were dosed subcutaneously at 1 mg/kg or 10 mg/kg to four separate groups of twelve mice. In a separate cohort, Ab-P2 (Immunoglobulin-peptide Conjugate 2) or its control Ab (anti-DNP mAb (E273C, hIgG1; comprising immunoglobulin monomers SEQ ID NO:3087; SEQ ID NO:3088; SEQ ID NO:3087; SEQ ID NO:3088) were dosed subcutaneously at 1 mg/kg or 10 mg/kg to four separate groups of twelve mice. Subcutaneous injections were delivered at the nape of the neck. At 0.5, 1, 2, 4, 8 and 24 hours post-dose, 2 mice from each of the four dose routes were euthanized and blood samples and brains were collected. Brains were weighed and frozen at -80°C immediately. Blood samples were collected in EDTA-treated microtainers and centrifuged at 13000 rpm for 5 minutes, after which plasma was extracted and frozen at -80°C in a 96-well plate.

[00558] LC-MS/MS Analytical Procedure. Peptide conjugate (Immunoglobulin-Peptide Conjugate 2 or Fc-Peptide Conjugate 2) stock solutions (100 µg/mL) were made from conjugate reference standards in DPBS with 1% BSA and stored at -20 °C. Standard samples were prepared in mouse serum. Standards concentrations of 25, 50, 100, 250, 500, 1000, 2500, 5000 and 10,000 ng/mL were prepared by serial dilution of a freshly prepared 10,000 ng/mL solution in mouse serum using the 100 µg/mL peptide conjugate stock solutions. 25 µl serum samples were aliquoted into the appropriate well of a 96-well plate, followed by the addition of 25 µl of internal standard solution (1µg/mL, αDA-IgG2 uniformly labeled with [^{15}N, $^{13}C_6$]-Leu made in DPBS with 1% BSA). Plasma samples were then processed by immunoaffinity capture in 96-well plate format using magnetic beads immobilized with anti-human Fc mouse antibody, followed by trypsin digestion and solid phase extraction using an Oasis HLB µElution 96-well solid phase extraction plate to extract tryptic peptides, the extracts were injected (10 µL) onto the LC-MS/MS system for analysis.

[00559] The LC-MS/MS consisted of an Acquity UPLC system (Waters, Milford, MA) coupled to a 5500 QTRAP mass spectrometer (AB Sciex, Toronto, Canada) with a Turbo IonSpray® ionization source. The analytical column was an Acquity UPLC BEH C_{18} (100 x 2.1 mm, 1.7 um). The mobile phases were 0.1% formic acid in acetonitrile/water (5/95, v/v, mobile phase A) and 0.1% formic acid in acetonitrile/water (95/5, v/v, mobile phase B). N-terminal DCLGAFR (SEQ ID NO:1050) from peptide SEQ ID NO:1062 was used as surrogate peptide for peptide conjugate (Immunoglobulin-Peptide Conjugate 2 or Fc-Peptide Conjugate 2) quantitative analysis.

[00560] Data was collected and processed using AB Sciex Analyst® software (version 1.5).

[00561] The calibration curve was derived from the peak area ratios (peptide /internal standard) using $1/x^2$ weighted linear least-squares regression of the area ratio versus the concentration of the corresponding peptide conjugate standard. The regression equation from the calibration standards was used to back calculate the measured concentration for each standard and mouse serum samples.

[00562] Results of the preliminary PK studies showed that exposures for the peptide conjugates were slightly lower than for the unmodified IgG and Fc, respectively. (See, Figure 88 and Figure 89). In both cases, a 10 mg/kg s.c. dose resulted in plasma concentrations at or near the in vitro Nav1.7 IC_{50} of the respective peptide conjugates at 24 h. C_{max} for (Fc-Peptide Conjugate 2) was reached between 8 and 24 h, but Cmax for (Immunoglobulin-Peptide Conjugate 2) occurred at or after 24 h. An accurate n vivo $t_{1/2}$ was not able to be calculated due to the brevity of the experiment. Immunoglobulin-Peptide Conjugate 2 and Fc-Peptide Conjugate 2 were both tested in the open field analysis in mice at a 10 mg/kg s.c. dose with a 24 h pre-treatment time and had no significant effect on the locomotor activity of the animals. (See, Figures 111-114). Immunoglobulin-Peptide Conjugate 2 and Fc-Peptide Conjugate 2 were both tested in the formalin pain model in mice at a 10 mg/kg s.c. dose with a 24 h pre-treatment time and had no significant effect on the spent lifting/licked the affected paw during either the first or second phase of the study. (See, Figures 115-117). It is likely that the dose was not sufficient to cover the target in vivo and observe efficacy.

Abbreviations

Abbreviations used throughout this specification are as defined below, unless otherwise defined in specific circumstances.

Ac	acetyl (used to refer to acetylated residues)
AcBpa	acetylated p-benzoyl-L-phenylalanine
ACN	acetonitrile
AcOH	acetic acid
ADCC	antibody-dependent cellular cytotoxicity
Aib	aminoisobutyric acid
bA	beta-alanine
Bpa	p-benzoyl-L-phenylalanine
BrAc	bromoacetyl ($BrCH_2C(O)$
BSA	Bovine serum albumin
Bzl	Benzyl
Cap	Caproic acid
CBC	complete blood count
CNS	central nervous system
COPD	Chronic obstructive pulmonary disease
CTL	Cytotoxic T lymphocytes
DCC	Dicylcohexylcarbodiimide
Dde	1-(4,4-dimethyl-2,6-dioxo-cyclohexylidene)ethyl
DOPC	1,2-Dioleoyl-sn-Glycero-3-phosphocholine
DOPE	1,2-Dioleoyl-sn-Glycero-3-phosphoethanolamine
DPPC	1,2-Dipalmitoyl-sn-Glycero-3-phosphocholine
DRG	dorsal root ganglion
DSPC	1,2-Distearoyl-sn-Glycero-3-phosphocholine
DTT	Dithiothreitol
EAE	experimental autoimmune encephalomyelitis
ECL	enhanced chemiluminescence
ESI-MS	Electron spray ionization mass spectrometry
Et	ethyl
FACS	fluorescence-activated cell sorting
Fmoc	fluorenylmethoxycarbonyl
HOBt	1-Hydroxybenzotriazole
HPLC	high performance liquid chromatography
HSL	homoserine lactone
IB	inclusion bodies

IWQ	IonWorks® Quattro
KCa	calcium-activated potassium channel (including IKCa, BKCa, SKCa)
KLH	Keyhole Limpet Hemocyanin
Kv	voltage-gated potassium channel
Lau	Lauric acid
LPS	lipopolysaccharide
LYMPH	lymphocytes
MALDI-MS	Matrix-assisted laser desorption ionization mass spectrometry
Me	methyl
MeO	methoxy
MeOH	methanol
MHC	major histocompatibility complex
MMP	matrix metalloproteinase
MW	Molecular Weight
MWCO	Molecular Weight Cut Off
1-Nap	1-napthylalanine
Nav, Na_V	voltage-gated sodium channel
NEUT	neutrophils
Nle	norleucine
NMP	N-methyl-2-pyrrolidinone
OAc	acetate
PAGE	polyacrylamide gel electrophoresis
PBMC	peripheral blood mononuclear cell
PBS	Phosphate-buffered saline
Pbf	2,2,4,6,7-pendamethyldihydrobenzofuran-5-sulfonyl
PCR	polymerase chain reaction
PD	pharmacodynamic
Pec	pipecolic acid
PEG	Poly(ethylene glycol)
Pic	picolinic acid
PK	pharmacokinetic
PNS	peripheral nervous system
PX	PatchXpress®
pY	phosphotyrosine
RBS	ribosome binding site
RT	room temperature (25 °C)

Sar	sarcosine
SDS	sodium dodecyl sulfate
STK	serine-threonine kinases
t-Boc	tert-Butoxycarbonyl
tBu	tert-Butyl
TCR	T cell receptor
TFA	trifluoroacetic acid
TG	trigeminal ganglion
THF	thymic humoral factor
Trt	trityl
TTX	tetrodotoxin

CLAIMS

What is claimed:

1. An isolated polypeptide comprising the amino acid sequence of the formula:

$X_{aa}^{1}X_{aa}^{2}$ $Cys^{3}X_{aa}^{4}X_{aa}^{5}X_{aa}^{6}X_{aa}^{7}X_{aa}^{8}X_{aa}^{9}Cys^{10}X_{aa}^{11}X_{aa}^{12}X_{aa}^{13}X_{aa}^{14}Asp^{15}X_{aa}^{16}$ Cys^{17}

$Cys^{18}X_{aa}^{19}X_{aa}^{20}X_{aa}^{21}X_{aa}^{22}X_{aa}^{23}$ $Cys^{24}X_{aa}^{25}X_{aa}^{26}X_{aa}^{27}X_{aa}^{28}X_{aa}^{29}Trp^{30}$

$Cys^{31}Lys^{32}Tyr^{33}X_{aa}^{34}Phe^{35}X_{aa}^{36}X_{aa}^{37}X_{aa}^{38}$

or a pharmaceutically acceptable salt thereof,

wherein:

X_{aa}^{1} is absent and X_{aa}^{2} is any amino acid residue;

X_{aa}^{4} is an acidic, hydrophobic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{5} is a Gly, Ala, hydrophobic, or basic amino acid residue;

X_{aa}^{6} is a Gly, Ala, 2-Abu, 2-Aib, Ile, Leu, Val, Nle, or Nva;

X_{aa}^{7} is a Gly, Ala, aromatic, or hydrophobic amino acid residue;

X_{aa}^{8} is a basic, acidic, or neutral hydrophilic amino acid residue, or an Ala residue;

X_{aa}^{9} is a basic or neutral hydrophilic amino acid residue;

X_{aa}^{11} is any amino acid residue;

X_{aa}^{12} is a Pro, acidic, neutral, or hydrophobic amino acid residue;

X_{aa}^{13} is any amino acid residue;

X_{aa}^{14} is any amino acid residue;

X_{aa}^{16} is a basic, neutral hydrophilic, or acidic amino acid residue, or an Ala residue;

X_{aa}^{19} is any amino acid residue;

X_{aa}^{20} is a Pro, Gly, basic, or neutral hydrophilic residue;

X_{aa}^{21} is a basic, hydrophobic, or neutral hydrophilic amino acid residue;

X_{aa}^{22} is a hydrophobic or basic amino acid residue;

X_{aa}^{23} is a hydrophobic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{25} is a Ser, Ala, or a neutral hydrophilic amino acid residue;

X_{aa}^{26} is an Ala, acidic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{27} is an acidic, basic, neutral hydrophilic or hydrophobic residue;

X_{aa}^{28} is an aromatic or basic amino acid residue;

X_{aa}^{29} is an acidic, basic, or neutral hydrophilic amino acid residue;

X_{aa}^{34} is any amino acid residue;

each of X_{aa}^{36}, X_{aa}^{37}, and X_{aa}^{38} is independently absent or is independently a neutral, basic, or hydrophobic amino acid residue;

and wherein the isolated polypeptide selectively inhibits Nav1.7 sodium channels relative to Nav1.4 and Nav1.5 sodium channels.

2. The isolated polypeptide of Claim 1 wherein X_{aa}^4 is selected from Ala, Glu, Asp, Phe, Pro, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, cyclohexylglycine (Chg), cyclohexylalanine (Cha), glycine, norleucine, norvaline, 1-Nal, 2-Nal, 4-phenyl-phenylalanine (Bip), Gln, Asn, Ser, Thr, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, and Cit residues.

3. The isolated polypeptide of Claim 1, wherein X_{aa}^5 is selected from Ala, Phe, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, glycine, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

4. The isolated polypeptide of Claim 1, wherein X_{aa}^7 is selected from Gly, Ala, Phe, Ile, Leu, Met, Val, Trp, Tyr, norleucine, norvaline, Pro, 2-pyridinylalanine, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, and 4-phenyl-phenylalanine (Bip) residues.

5. The isolated polypeptide of Claim 1, wherein X_{aa}^8 is selected from Ala, Arg, Lys, His, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Ser, Thr, Asn, Gln, Cit, Asp, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, and Glu residues.

6. The isolated polypeptide of Claim 1, wherein X_{aa}^9 is selected from Ala, Pro, Met, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Gln, Asn, Ser, Thr, and Cit residues.

7. The isolated polypeptide of Claim 1, wherein X_{aa}^{11} is selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

8. The isolated polypeptide of Claim 1, wherein X_{aa}^{12} is selected from alanine, valine, leucine, isoleucine, proline, serine, threonine, aspartic acid, glutamatic acid, glycine, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, Cha, and 4-phenyl-phenylalanine (Bip), cyclohexylglycine (Chg), cyclohexylalanine (Cha), asparagine, glutamine, methionine, hydroxyproline, phenylalanine, tryptophan, and tyrosine.

9. The isolated polypeptide of Claim 1, wherein X_{aa}^{13} is selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

10. The isolated polypeptide of Claim 1, wherein X_{aa}^{14} is selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

11. The isolated polypeptide of Claim 1, wherein X_{aa}^{16} is selected from Ala, Pro, Met, Arg, Lys, His, Pra, Atz, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Gln, Asn, Ser, Thr, Cit, Asp, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, and Glu residues.

12. The isolated polypeptide of Claim 1, wherein X_{aa}^{19} is selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine,

N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

13. The isolated polypeptide of Claim 1, wherein X_{aa}^{20} is selected from Ala, Gly, Pro, Met, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Gln, Asn, Ser, Thr, and Cit residues.

14. The isolated polypeptide of Claim 1, wherein X_{aa}^{21} is selected from Ala, Phe, Pro, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, cyclohexylglycine (Chg), cyclohexylalanine (Cha), glycine, norleucine, norvaline, 1-Nal, 2-Nal, 4-phenyl-phenylalanine (Bip), Gln, Asn, Ser, Thr, and Cit residues.

15. The isolated polypeptide of Claim 1, wherein X_{aa}^{22} is selected from Ala, Phe, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, glycine, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

16. The isolated polypeptide of Claim 1, wherein X_{aa}^{23} is selected from Ala, Phe, Pro, Ile, Leu, Met, Val, Trp, Tyr, Arg, Lys, His, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, cyclohexylglycine (Chg), cyclohexylalanine (Cha), glycine, norleucine, norvaline, 1-Nal, 2-Nal, 4-phenyl-phenylalanine (Bip), Gln, Asn, Ser, Thr, and Cit residues.

17. The isolated polypeptide of Claim 1, wherein X_{aa}^{25} is selected from Ala, Gly Pro, Met, Gln, Asn, Ser, Thr, and Cit residues.

18. The isolated polypeptide of Claim 1, wherein X_{aa}^{26} is selected from Ala, Pro, Met, Arg, Lys, His, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, glycine, Glu, Asp, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, Gln, Asn, Ser, Thr, and Cit residues.

19. The isolated polypeptide of Claim 1, wherein X_{aa}^{27} is selected from Thr, Leu, Ile, Val, Ser, Met, Gln, Asn, Phe, Tyr, Trp, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 4-phenyl-phenylalanine (Bip), Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Asp, Glu, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, and Gly residues.

20. The isolated polypeptide of Claim 1, wherein X_{aa}^{28} is selected from Phe, Trp, Tyr, Arg, Lys, His, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, 1-Nal, 2-Nal, 2-pyridyl-alanine, 3-pyridyl-alanine, 4-pyridyl-alanine, 4-piperidinyl-alanine, and 4-phenyl-phenylalanine (Bip) residues.

21. The isolated polypeptide of Claim 1, wherein X_{aa}^{29} is selected from Ala, Asp, Glu, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, Phe, Gly, His, Lys, Asn, Pro, Gln, Arg, Ser, Thr, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, and Dab residues.

22. The isolated polypeptide of Claim 1, wherein X_{aa}^{34} is selected from Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, 2-pyridyl-alanine, 3-pyridyl-alanine, 4-carboxy-phenylalanine, and 4-phenyl-phenylalanine (Bip) residues.

23. The isolated polypeptide of Claim 1, wherein each of X_{aa}^{36} , X_{aa}^{37}, and X_{aa}^{38} is independently absent or is independently selected from Ala, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), and 4-phenyl-phenylalanine (Bip) residues.

24. The isolated polypeptide of Claim 1, wherein the carboxy-terminal residue is amidated.

25. The isolated polypeptide of Claim 1, wherein the isolated polypeptide comprises the amino acid sequence of the formula:

Asp-Cys-Leu-Gly-Xaa^{5}-Xaa^{6}-Arg-Lys-Cys-Xaa^{10}-Pro-Asp-Xaa^{13}-Asp-Lys-Cys-Cys-Arg-Pro-Asn-Leu-Val-Cys-Ser-Arg-Xaa^{26}-His-Xaa^{28}-Trp-Cys-Lys-Tyr-Val-Phe, wherein:

Xaa^{5} is a Gly, Ala, 2-Abu, 2-Aib, Ile, Leu, Val, Nle, or Nva residue;

Xaa^{6} is a Gly, Ala, Phe, Ile, Leu, Met, Val, Trp, Tyr, norleucine, norvaline, Pro, 2-pyridinylalanine, 1-Nal, 2-Nal, 1'NMe-Trp, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 2-chloro-phenylalanine, 4-chloro-phenylalanine, 3,4-dichlorophenylalanine, 4-trifluoromethyl-phenylalanine, or 4-phenyl-phenylalanine (Bip) residue;

Xaa^{10} is a Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), or 4-phenyl-phenylalanine (Bip) residue;

Xaa^{13} is a Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, norleucine, norvaline, 2-Abu, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), or 4-phenyl-phenylalanine (Bip) residue;

Xaa^{26} is a Thr, Leu, Ile, Val, Ser, Met, Gln, Asn, Phe, Tyr, Trp, norleucine, norvaline, 1-Nal, 2-Nal, cyclohexylglycine (Chg), cyclohexylalanine (Cha), 4-phenyl-phenylalanine (Bip), Arg, Lys, His, homolysine, ornithine, arginine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, Dab, Asp, Glu, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, or Gly residue; and

Xaa^{28} is a Ala, Asp, Glu, phosphoserine, phosphotyrosine, gamma-carboxyglutamic acid, Phe, Gly, His, Lys, Asn, Pro, Gln, Arg, Ser, Thr, Tyr, Pra, Atz, homolysine, ornithine, N-methyl-arginine, ω-aminoarginine, ω-methyl-arginine, 1-methyl-histidine, 3-methyl-histidine, homoarginine, N-methyl-lysine, N-ε-methyl lysine, or Dab residue.

26. The isolated polypeptide of Claim 25, wherein Xaa^{5} is Ala.

27. The isolated polypeptide of Claim 25 or Claim 26, wherein Xaa^{6} is Phe or Leu.

28. The isolated polypeptide of Claim 27, wherein Xaa^{10} is Glu.

29. The isolated polypeptide of any one of Claims 25 to 28, wherein Xaa^{13} is Atz.

30. The isolated polypeptide of any one of Claims 25 to 29, wherein Xaa^{26} is Leu.

31. The isolated polypeptide of any one of Claims 25 to 30, wherein Xaa^{28} is Arg.

32. The isolated polypeptide of Claim 1, wherein $X_{aa}{}^{6}$ is Ala.

33. The isolated polypeptide of Claim 32, wherein $X_{aa}{}^{27}$ is Glu.

34. The isolated polypeptide of Claim 32, wherein $X_{aa}{}^{29}$ is Asp, Glu, or Gln.

35. The isolated polypeptide of Claim 32, comprising an amino acid sequence selected from SEQ ID NOS: 22, 252, 255-263, 419-429, 435, 436, 438, 439, 518-521, 524, 525, 562-576, 579, 580, 602, 691, 696-703, 715, 721-735, 737-749, 756, 757, 761, 762, 764-771, 787, 788, 790-796, 798, 800, 802, 803, 809-812, 1028, 1030-1040, 1043-1047, 1062-1065, and 1068-1070.

36. The isolated polypeptide of Claim 32, comprising an amino acid sequence selected from SEQ ID NOS: 1082, 1096, 1110, 1124, 1135, 1146, 1157, 1165, 1173, 1181, 1192, 1203, 1214, 1222, 1230, 1238, 1249, 1260, 1271, 1279, 1287, 1295, 1306, 1317, 1328, 1336, 1344, 1352, 1360, 1368, 1376, 1384, 1392, 1400, 1408, 1416, 1424, 1432, 1440, 1448, 1456, 1464, 1472, 1480, 1488, 1496, 1504, 1512, 1520, 1528, 1536, 1544, 1552, 1560, 1568, 1576, 1584, 1592, 1600, 1608, 1616, 1624, 1632, 1640, 1658, 1672, 1686, 1700, 1711, 1722, 1733, 1741, 1749, 1757, 1768, 1779, 1790, 1798, 1806, 1814, 1825, 1836, 1847, 1855, 1863, 1871, 1882, 1893, 1904, 1912, 1920, 1928, 1936, 1944, 1952, 1960, 1968, 1976, 1984, 1992, 2000, 2008, 2016, 2024, 2032, 2040, 2048, 2056, 2064, 2072, 2080, 2088, 2096, 2104, 2112, 2120, 2128, 2136, 2144, 2152, 2160, 2168, 2176, 2184, 2192, 2200, 2208, 2216, 2234, 2248, 2262, 2276, 2287, 2298, 2309, 2317, 2325, 2333, 2344, 2355, 2366,

2374, 2382, 2390, 2401, 2412, 2423, 2431, 2439, 2447, 2458, 2469, 2480, 2488, 2496, 2504, 2512, 2520, 2528, 2536, 2544, 2552, 2560, 2568, 2576, 2584, 2592, 2600, 2608, 2616, 2624, 2632, 2640, 2648, 2656, 2664, 2672, 2680, 2688, 2696, 2704, 2712, 2720, 2728, 2736, 2744, 2752, 2760, 2768, 2776, 2784, 2792, 2808, 2822, 2833, 2844, 2855, 2863, 2871, 2879, 2890, 2901, 2912, 2920, 2928, 2936, 2944, 2952, 2960, 2968, 2976, 2984, 2992, 3000, 3008, 3016, 3024, 3032, 3040, 3048, 3056, 3064, 3072, and 3080.

37. The isolated polypeptide of Claim 32, comprising an amino acid sequence selected from SEQ ID NOS: 597-601 and 813-1027.

38. The isolated polypeptide of Claim 1, wherein X_{aa}^{6} is Gly.

39. The isolated polypeptide of Claim 38, wherein X_{aa}^{27} is Glu.

40. The isolated polypeptide of Claim 38, wherein X_{aa}^{29} is Asp, Glu, or Gln.

41. The isolated polypeptide of Claim 38, comprising an amino acid sequence selected from SEQ ID NOS: 265, 751, 752, 754, 755, 1081, 1095, 1109, 1123, 1134, 1145, 1156, 1164, 1172, 1180, 1191, 1202, 1213, 1221, 1229, 1237, 1248, 1259, 1270, 1278, 1286, 1294, 1305, 1316, 1327, 1335, 1343, 1351, 1359, 1367, 1375, 1383, 1391, 1399, 1407, 1415, 1423, 1431, 1439, 1447, 1455, 1463, 1471, 1479, 1487, 1495, 1503, 1511, 1519, 1527, 1535, 1543, 1551, 1559, 1567, 1575, 1583, 1591, 1599, 1607, 1615, 1623, 1631, 1639, 1657, 1671, 1685, 1699, 1710, 1721, 1732, 1740, 1748, 1756, 1767, 1778, 1789, 1797, 1805, 1813, 1824, 1835, 1846, 1854, 1862, 1870, 1881, 1892, 1903, 1911, 1919, 1927, 1935, 1943, 1951, 1959, 1967, 1975, 1983, 1991, 1999, 2007, 2015, 2023, 2031, 2039, 2047, 2055, 2063, 2071, 2079, 2087, 2095, 2103, 2111, 2119, 2127, 2135, 2143, 2151, 2159, 2167, 2175, 2183, 2191, 2199, 2207, 2215, 2233, 2247, 2261, 2275, 2286, 2297, 2308, 2316, 2324, 2332, 2343, 2354, 2365, 2373, 2381, 2389, 2400, 2411, 2422, 2430, 2438, 2446, 2457, 2468, 2479, 2487, 2495, 2503, 2511, 2519, 2527, 2535, 2543, 2551, 2559, 2567, 2575, 2583, 2591, 2599, 2607, 2615, 2623, 2631, 2639, 2647, 2655, 2663, 2671, 2679, 2687, 2695, 2703, 2711, 2719, 2727, 2735, 2743, 2751, 2759, 2767, 2775, 2783, 2791, 2807, 2821, 2832, 2843, 2854, 2862, 2870, 2878, 2889, 2900, 2911, 2919, 2927, 2935, 2943, 2951, 2959, 2967, 2975, 2983, 2991, 2999, 3007, 3015, 3023, 3031, 3039, 3047, 3055, 3063, 3071, and 3079.

42. The isolated polypeptide of Claim 1, wherein X_{aa}^{6} is 2-Abu.

43. The isolated polypeptide of Claim 42, wherein X_{aa}^{27} is Glu.

44. The isolated polypeptide of Claim 42, wherein X_{aa}^{29} is Asp, Glu, or Gln.

45. The isolated polypeptide of Claim 42, comprising an amino acid sequence selected from SEQ ID NOS: 605, 636, 649, 706, 707, 753, 758, 797, 799, 801, 804, 807, 808, 1029, 1041, 1042, 1048, 1066, 1067, 1083, 1097, 1111, 1125, 1136, 1147, 1158, 1166, 1174, 1182, 1193, 1204, 1215, 1223, 1231, 1239, 1250, 1261, 1272, 1280, 1288, 1296, 1307, 1318, 1329, 1337, 1345, 1353, 1361, 1369, 1377, 1385, 1393, 1401, 1409, 1417, 1425, 1433, 1441, 1449, 1457, 1465, 1473, 1481, 1489, 1497, 1505, 1513, 1521, 1529, 1537, 1545, 1553, 1561, 1569, 1577, 1585, 1593, 1601, 1609, 1617, 1625, 1633, 1641, 1659, 1673, 1687, 1701, 1712, 1723, 1734, 1742, 1750, 1758, 1769, 1780, 1791, 1799, 1807, 1815, 1826, 1837, 1848, 1856, 1864, 1872, 1883, 1894, 1905, 1913, 1921, 1929, 1937, 1945, 1953, 1961, 1969, 1977, 1985, 1993, 2001, 2009, 2017, 2025, 2033, 2041, 2049, 2057, 2065, 2073, 2081, 2089, 2097, 2105, 2113, 2121, 2129, 2137, 2145, 2153, 2161, 2169, 2177, 2185, 2193, 2201, 2209, 2217, 2235, 2249, 2263, 2277, 2288, 2299, 2310, 2318, 2326, 2334, 2345, 2356, 2367, 2375, 2383, 2391, 2402, 2413, 2424, 2432, 2440, 2448, 2459, 2470, 2481, 2489, 2497, 2505, 2513, 2521, 2529, 2537, 2545, 2553, 2561, 2569, 2577, 2585, 2593, 2601, 2609, 2617, 2625, 2633, 2641, 2649, 2657, 2665, 2673, 2681, 2689, 2697, 2705, 2713, 2721, 2729, 2737, 2745, 2753, 2761, 2769, 2777, 2785, 2793, 2809, 2823, 2834, 2845, 2856, 2864, 2872, 2880, 2891, 2902, 2913, 2921, 2929, 2937, 2945, 2953, 2961, 2969, 2977, 2985, 2993, 3001, 3009, 3017, 3025, 3033, 3041, 3049, 3057, 3065, 3073, and 3081.

46. The isolated polypeptide of Claim 1, wherein X_{aa}^{6} is Nle.

47. The isolated polypeptide of Claim 46, wherein X_{aa}^{27} is Glu.

48. The isolated polypeptide of Claim 46, wherein X_{aa}^{29} is Asp, Glu, or Gln.

49. The isolated polypeptide of Claim 46, comprising an amino acid sequence selected from SEQ ID NOS: 607, 638, 651, 1085, 1099, 1113, 1127, 1138, 1149, 1160, 1168, 1176, 1184, 1195, 1206, 1217, 1225, 1233, 1241, 1252, 1263, 1274, 1282, 1290, 1298, 1309, 1320, 1331, 1339, 1347, 1355, 1363, 1371, 1379, 1387, 1395, 1403, 1411, 1419, 1427, 1435, 1443, 1451, 1459, 1467, 1475, 1483, 1491, 1499, 1507, 1515, 1523, 1531, 1539, 1547, 1555, 1563, 1571, 1579, 1587, 1595, 1603, 1611, 1619, 1627, 1635, 1643, 1661, 1675, 1689, 1703, 1714, 1725, 1736, 1744, 1752, 1760, 1771,

1782, 1793, 1801, 1809, 1817, 1828, 1839, 1850, 1858, 1866, 1874, 1885, 1896, 1907, 1915, 1923, 1931, 1939, 1947, 1955, 1963, 1971, 1979, 1987, 1995, 2003, 2011, 2019, 2027, 2035, 2043, 2051, 2059, 2067, 2075, 2083, 2091, 2099, 2107, 2115, 2123, 2131, 2139, 2147, 2155, 2163, 2171, 2179, 2187, 2195, 2203, 2211, 2219, 2237, 2251, 2265, 2279, 2290, 2301, 2312, 2320, 2328, 2336, 2347, 2358, 2369, 2377, 2385, 2393, 2404, 2415, 2426, 2434, 2442, 2450, 2461, 2472, 2483, 2491, 2499, 2507, 2515, 2523, 2531, 2539, 2547, 2555, 2563, 2571, 2579, 2587, 2595, 2603, 2611, 2619, 2627, 2635, 2643, 2651, 2659, 2667, 2675, 2683, 2691, 2699, 2707, 2715, 2723, 2731, 2739, 2747, 2755, 2763, 2771, 2779, 2787, 2795, 2811, 2825, 2836, 2847, 2858, 2866, 2874, 2882, 2893, 2904, 2915, 2923, 2931, 2939, 2947, 2955, 2963, 2971, 2979, 2987, 2995, 3003, 3011, 3019, 3027, 3035, 3043, 3051, 3059, 3067, 3075, and 3083.

50. The isolated polypeptide of Claim 1, wherein X_{aa}^{6} is Nva.

51. The isolated polypeptide of Claim 50, wherein X_{aa}^{27} is Glu.

52. The isolated polypeptide of Claim 50, wherein X_{aa}^{29} is Asp, Glu, or Gln.

53. The isolated polypeptide of Claim 50, comprising an amino acid sequence selected from SEQ ID NOS: 606, 637, 650, 705, 708, 759, 760, 805, 806, 1084, 1098, 1112, 1126, 1137, 1148, 1159, 1167, 1175, 1183, 1194, 1205, 1216, 1224, 1232, 1240, 1251, 1262, 1273, 1281, 1289, 1297, 1308, 1319, 1330, 1338, 1346, 1354, 1362, 1370, 1378, 1386, 1394, 1402, 1410, 1418, 1426, 1434, 1442, 1450, 1458, 1466, 1474, 1482, 1490, 1498, 1506, 1514, 1522, 1530, 1538, 1546, 1554, 1562, 1570, 1578, 1586, 1594, 1602, 1610, 1618, 1626, 1634, 1642, 1660, 1674, 1688, 1702, 1713, 1724, 1735, 1743, 1751, 1759, 1770, 1781, 1792, 1800, 1808, 1816, 1827, 1838, 1849, 1857, 1865, 1873, 1884, 1895, 1906, 1914, 1922, 1930, 1938, 1946, 1954, 1962, 1970, 1978, 1986, 1994, 2002, 2010, 2018, 2026, 2034, 2042, 2050, 2058, 2066, 2074, 2082, 2090, 2098, 2106, 2114, 2122, 2130, 2138, 2146, 2154, 2162, 2170, 2178, 2186, 2194, 2202, 2210, 2218, 2236, 2250, 2264, 2278, 2289, 2300, 2311, 2319, 2327, 2335, 2346, 2357, 2368, 2376, 2384, 2392, 2403, 2414, 2425, 2433, 2441, 2449, 2460, 2471, 2482, 2490, 2498, 2506, 2514, 2522, 2530, 2538, 2546, 2554, 2562, 2570, 2578, 2586, 2594, 2602, 2610, 2618, 2626, 2634, 2642, 2650, 2658, 2666, 2674, 2682, 2690, 2698, 2706, 2714, 2722, 2730, 2738, 2746, 2754, 2762, 2770, 2778, 2786, 2794, 2810, 2824, 2835, 2846, 2857, 2865, 2873, 2881, 2892, 2903, 2914, 2922, 2930, 2938, 2946, 2954, 2962, 2970, 2978, 2986, 2994, 3002, 3010, 3018, 3026, 3034, 3042, 3050, 3058, 3066, 3074, and 3082.

54. The isolated polypeptide of Claim 1, comprising an amino acid sequence selected from SEQ ID NOS: 22, 262, 640, 1028, 1031, 1035, and 1046-1048.

55. The isolated polypeptide of Claim 1 or Claim 25, wherein the polypeptide is covalently linked to a half-life extending moiety.

56. The isolated polypeptide of Claim 55, wherein the half-life extending moiety is polyethylene glycol of molecular weight of about 1000 Da to about 100000 Da, an IgG Fc domain, a transthyretin, or a human serum albumin.

57. The isolated polypeptide of Claim 55, wherein the half-life extending moiety comprises a human immunoglobulin or a human immunoglobulin Fc domain, or both.

58. The isolated polypeptide of Claim 57, wherein the isolated polypeptide is covalently linked to an immunoglobulin or immunoglobulin Fc domain to form a monovalent immunoglobulin-peptide or Fc-peptide conjugate.

59. The isolated polypeptide of Claim 57, wherein two copies of the isolated polypeptide are covalently linked to an immunoglobulin or immunoglobulin Fc domain to form a bivalent immunoglobulin-peptide or Fc-peptide conjugate.

60. A pharmaceutical composition, comprising the isolated polypeptide of any of Claims 1 to 59, and a pharmaceutically acceptable carrier.

61. Use of a prophylactically effective amount of the isolated polypeptide of any one of Claims 1 to 59 in the manufacture of a medicament for preventing pain.

62. Use of a therapeutically effective amount of the isolated polypeptide of any one of Claims 1 to 59 in the manufacture of a medicament for treating pain.

63. The use of Claim 62, wherein the pain is chronic pain, acute pain, or persistent pain.

64. The use of Claim 63, wherein the chronic pain is associated with cancer, chemotherapy, osteoarthritis, fibromyalgia, primary erythromelalgia, post-herpetic neuralgia, painful diabetic neuropathy, idiopathic painful neuropathy, neuromas, paroxysmal extreme pain disorder, migraine, trigeminal neuralgia, orofacial pain, cluster headaches, complex regional pain syndrome (CRPS), failed back surgery syndrome, sciatica, interstitial cystitis, pelvic pain, lower back pain, inflammation-induced pain, or joint pain.

65. The use of Claim 63, wherein the acute or persistent pain is associated with trauma, burn, or surgery.

66. The isolated polypeptide of Claim 1, wherein X_{aa}^{29} is an acidic or neutral hydrophilic residue.

67. The isolated polypeptide of Claim 66, wherein X_{aa}^{29} is selected from Ala, Asp, Glu, Gly, Asn, Gln, Ser, Thr, phosphoserine, phosphotyrosine, and gamma-carboxyglutamic acid residues.