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(54) **CLOSTRIDIAL NEUROTOXIN
COMPOSITIONS AND MODIFIED
CLOSTRIDIAL NEUROTOXINS**

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14, 2004, now Pat. No. 7,491,799, which is a continu-

ation-in-part of application No. 10/163,106, filed on
Jun. 4, 2002, which is a continuation-in-part of appli-
cation No. 09/910,346, filed on Jul. 20, 2001, now
abandoned, which is a continuation-in-part of applica-
tion No. 09/620,840, filed on Jul. 21, 2000, now Pat.
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(52) **U.S. Cl.** **530/403**

(57) **ABSTRACT**

Natural and modified neurotoxins and isolated neurotoxin compositions are described. The neurotoxins may include one or more structural modifications, wherein the structural modification(s) alters the biological persistence, such as the biological half-life and/or a biological activity of the modified neurotoxin relative to an identical neurotoxin without the structural modification(s). In one embodiment, methods of making the modified neurotoxin include using recombinant techniques. In some embodiments, methods of using the modified neurotoxin to treat conditions include treating various disorders, neuromuscular ailments and pain.

FIG. 1.



FIG. 2.

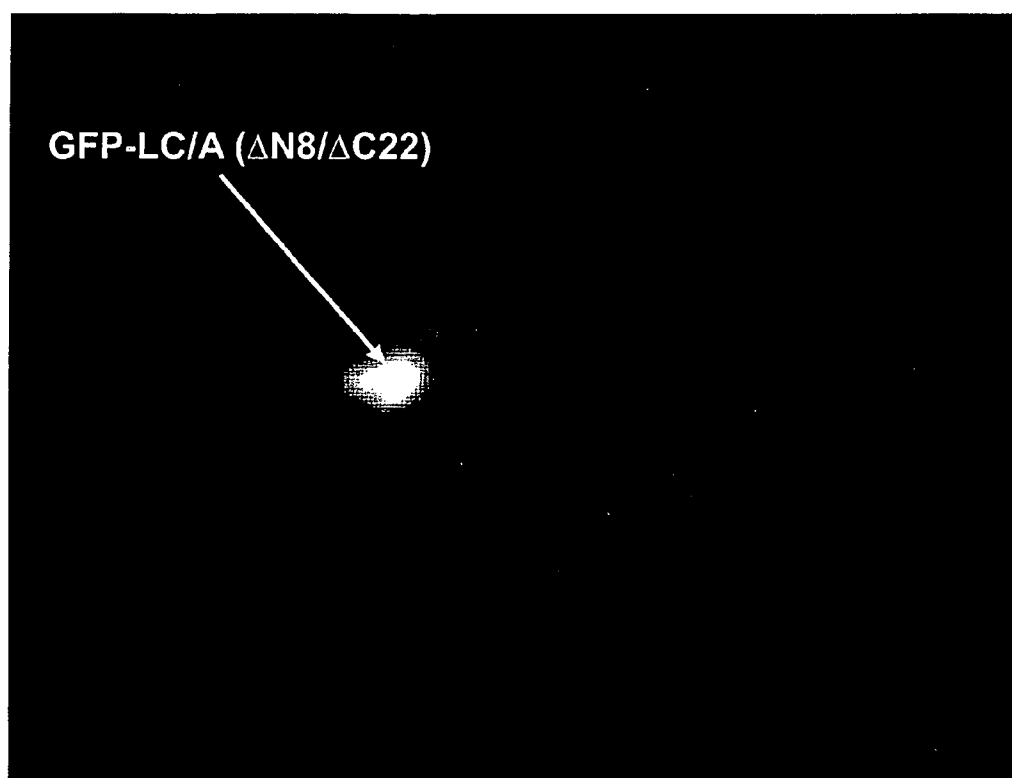


FIG. 3.

AN8
1 PFV NKQFN YKDPVNGVDIAYIKIPNAGQM QPVKAFKIHNKIWVIPERDTF
.....
51 TNPEEGDLNPPPEAKQVPVSYYDSTYLS TDNEKDN YLKGVTKL FERIYST
.....
101 DLGRMLLTSIVRGIPFWGGSTIDTELKV IDTNCINVIQPDGSRSEELNL
.....
151 VIIGPSADIIQFECKSFGHEVLNLRNGYGSTQYIRFSPDFTFGFEESLE
.....
201 VDTNPLLGAGKFATDPAVTLAHEL IHAGHRLYGIAINPNRVFKVNTNAYY
.....
251 EMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNKFKDIASTLNKAK
.....
301 SIVGTTASLQYMKNVFKEKYLLSEDTSGKFSVDKLFDKLYKMLTEIYTE
.....
351 DNFVKFFKVLNRKTYLNFDKAVKINIVPKVNYTIYDGFNLRNTNLAANF
.....
401 NGQNT EINN MNFTKLKNFTGLFEFYKLLCVRGIITSK
ΔC22
.....

FIG. 4.

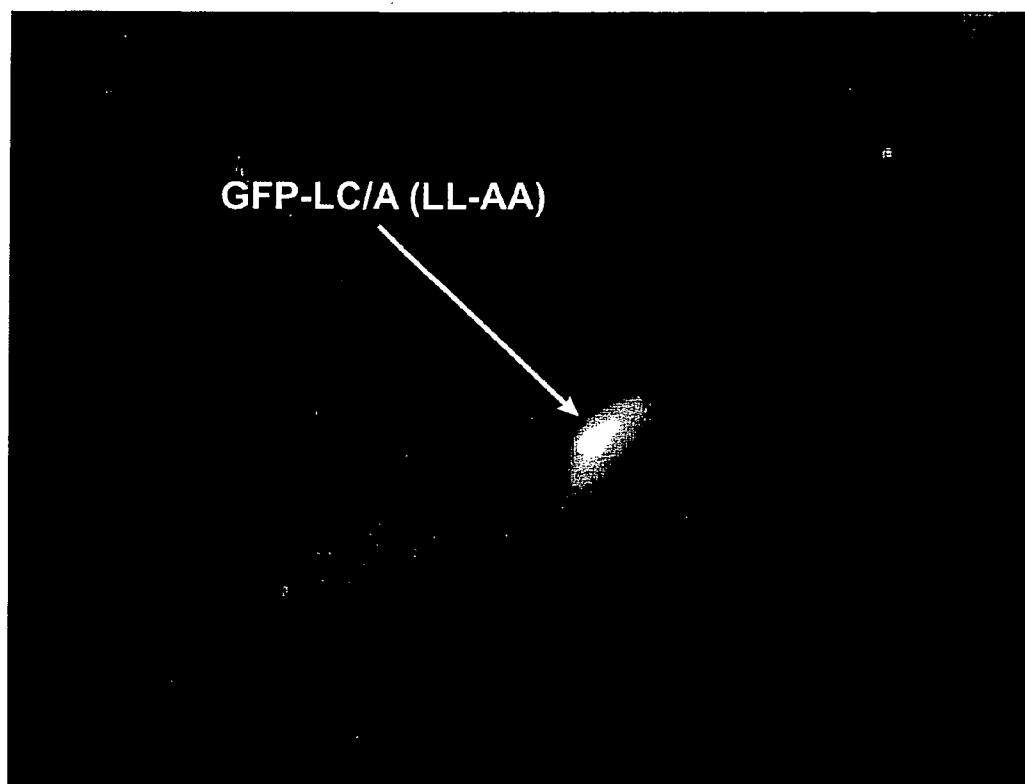


FIG. 5.

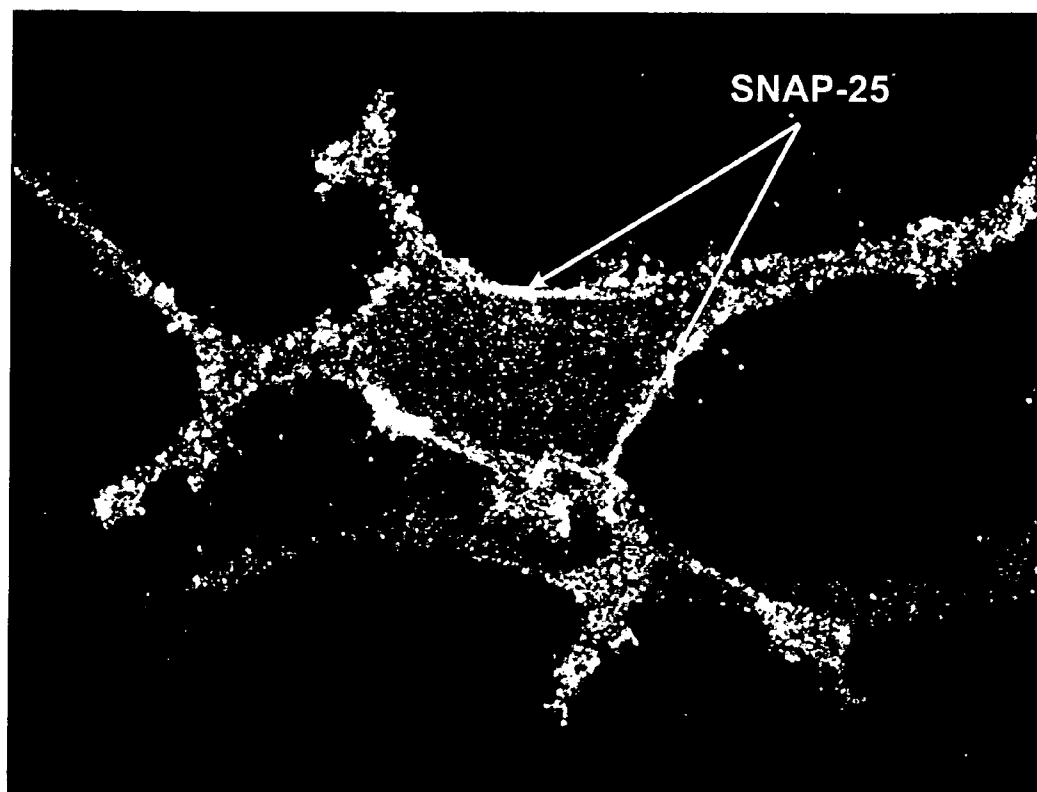


FIG. 6.

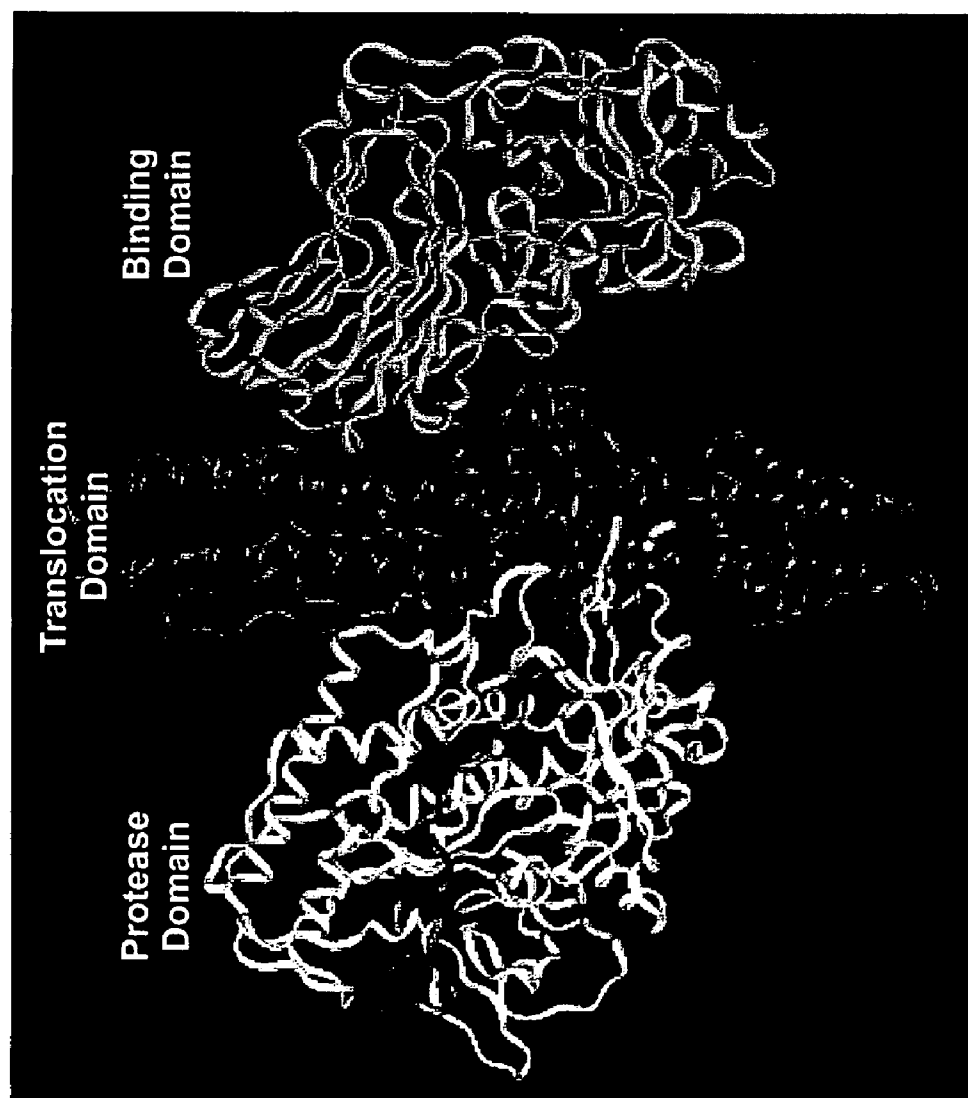


FIG. 7.

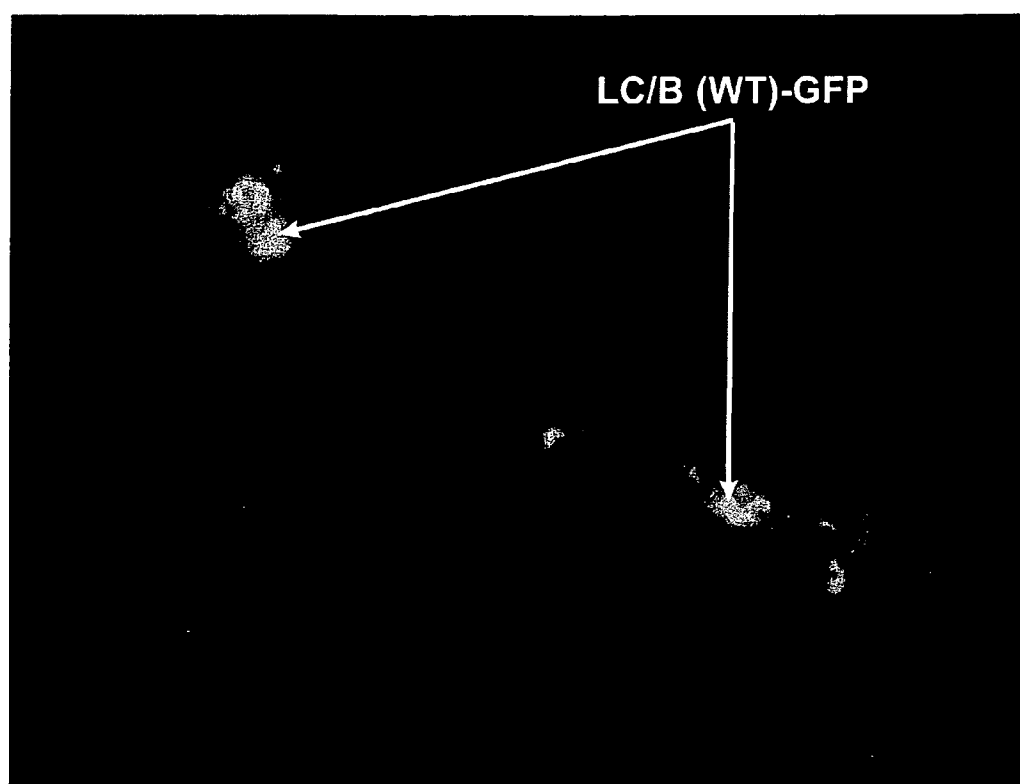


FIG. 8.

1 BoNT/A (Hall A) LC -PFVVKQFNFKDPVNGVDIAYIKIPNAGOMQPV-KAFKIHNKTIWIPERDITFNPEEGDLNPPPEAKQVPVSYYD 75
 BoNT/B (Danish I) LC MEVTINNENYNDPIDNNNIMMEPEFARGTGRIYKAFKIDRLWILPERYTFGYKPEDFNKSSGIFNRDVCYYD
 P NFNY DPI I I P KAFKI KWIIPER TF E YYD
 76 BoNT/A (Hall A) LC STYLSIDNEKDNYLKGVTKLFFERIVSTDLGRMLLITSTVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYR-SFE 150
 BoNT/B (Danish I) LC PDYLNNDKNIIFLQTMIKLFNRJKSKPLGEKLLLEMIINGIPYLGDRRVPLIEEFNTNIASVIVNKLISNPGEVER
 YL T K FL M KLF RI S LG LL II GI PF G I E I V E
 151 BoNT/A (Hall A) LC -----LNVITIGPSADIIQFCKSFGEHEVLNLTNRNGYGSTQYIPESPDFTFGFEESIEVDTNPLLGAGKFATDPA 225
 BoNT/B (Danish I) LC KKGIFANIIIFGPGPVLNENETIDIGIQNHFASTRGFGGIMQMKECEPEYVSVENNVQENKGIASIFNRRGYFSDPA
 NLII GP I E G SR GFG IKF PDF F E I F SDPA
 226 BoNT/A (Hall A) LC VTDAHELIIHAGRIYGTAINPNRVKVNNTNAYYEMSGLEVSEELRTFGGHDAKFTDSLOENEFRLYYYNKFKDI 300
 BoNT/B (Danish I) LC LIIMHELIIHVLHGLYGIKVD-DLPVINEKKFFMQSDTAIQAEELVTFGGQDPSIITPSTDKSIYDKVLQNERGL
 L L HELIH H LYGI I N FF S I EEL TFGG D I D N FK I
 301 BoNT/A (Hall A) LC ASTLNKAKSIVG-TTASLQYMKNVFKKYLLEDTSGKFSVDKCLKFDKLYKMTTEIYTEDNFVKFFKVLNKKTYL 375
 BoNT/B (Danish I) LC VDRLNKVLVCISDPNININIKKFKDKYKFVEDSEGKYSIDVESFDKLYKSLMFGFTETNIAENYKIKTRASYF
 LNK I IN KN FKDKY EDS GKFSID FDKLYK L FTE N FKI R SY
 376 BoNT/A (Hall A) LC NFDKAVFKIN-IVPKVNYTIYDGFNLRTNLAANFNQNTETNNMNFTKLKNFTGLFEFYKLLCVRGIITSK 447
 BoNT/B (Danish I) LC SDSLPPVKIKNLLDNEIYTIIEEGFENISDKDMEKEYRGONKALNKQAYEEIS--KEHLAVYKIQMCKSVK---
 KI IL YTI DGFINI L F GQN IN F I YKI K I

FIG. 9.

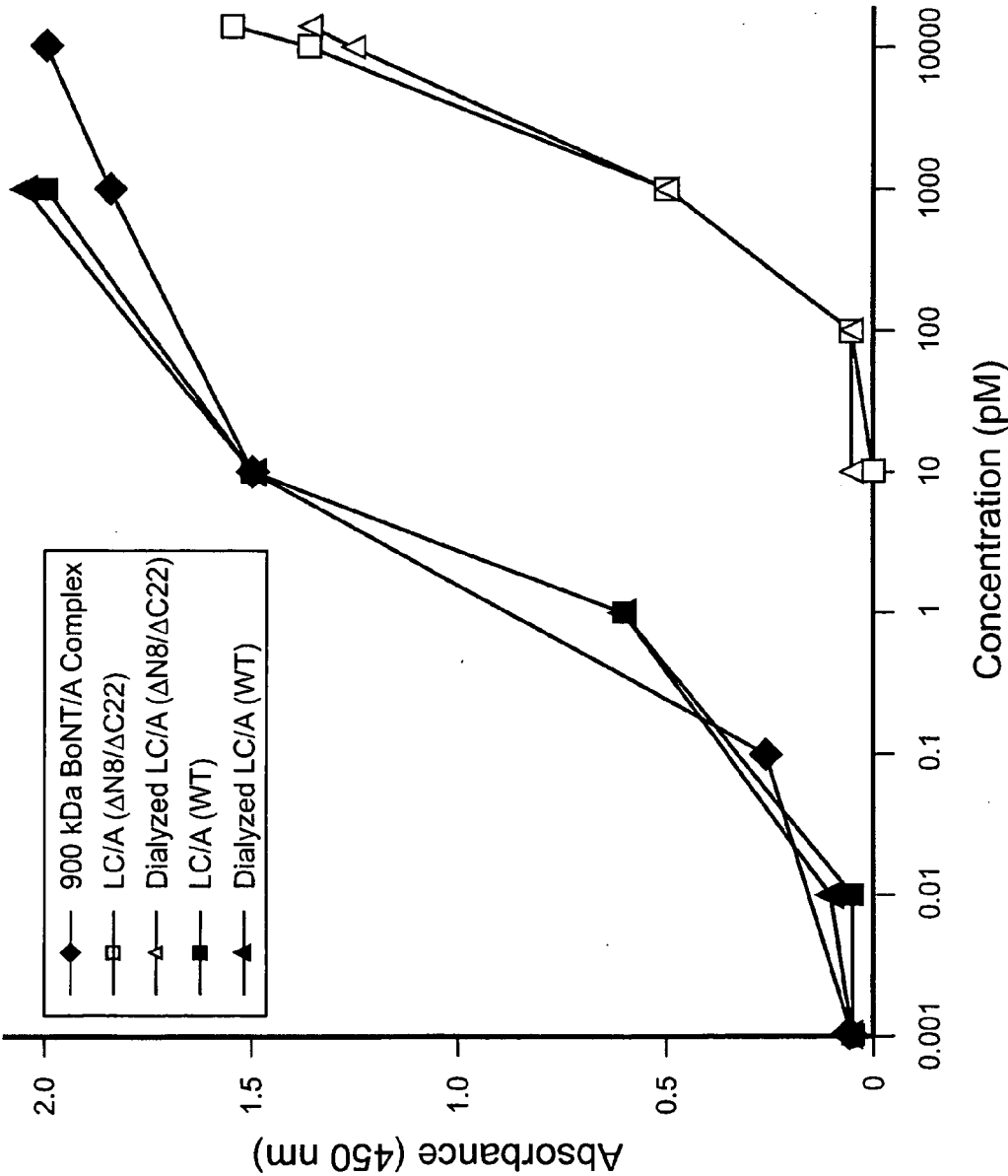


FIG. 10.

Amino Terminus

	6 x His	S-tag	Δ N8
LC/A (WT)			
LC/A (Δ N8/ Δ C22)	MHHHHHSSGLVPRGSGMKETAAAKFERQHMDSPDLGTDDDDKAM		PFV NKQFNYKDPV---
N-His-LC/A (WT)	MHHHHHSSGLVPRGSGMKETAAAKFERQHMDSPDLGTDDDDKAMGSFV NKQFNYKDPV---		

Carboxy Terminus

	Δ C22	6 x His
LC/A (WT)	---NFTKLKNFTGLFEFYKLLCVRGIITSK	
LC/A (Δ N8/ Δ C22)	---NFTKL-----TRAHHHHHH	
N-His-LC/A (WT)	---NFTKLKNFTGLFEFYKLLCVRGIITSK Leucine-based Motif	

FIG. 11.

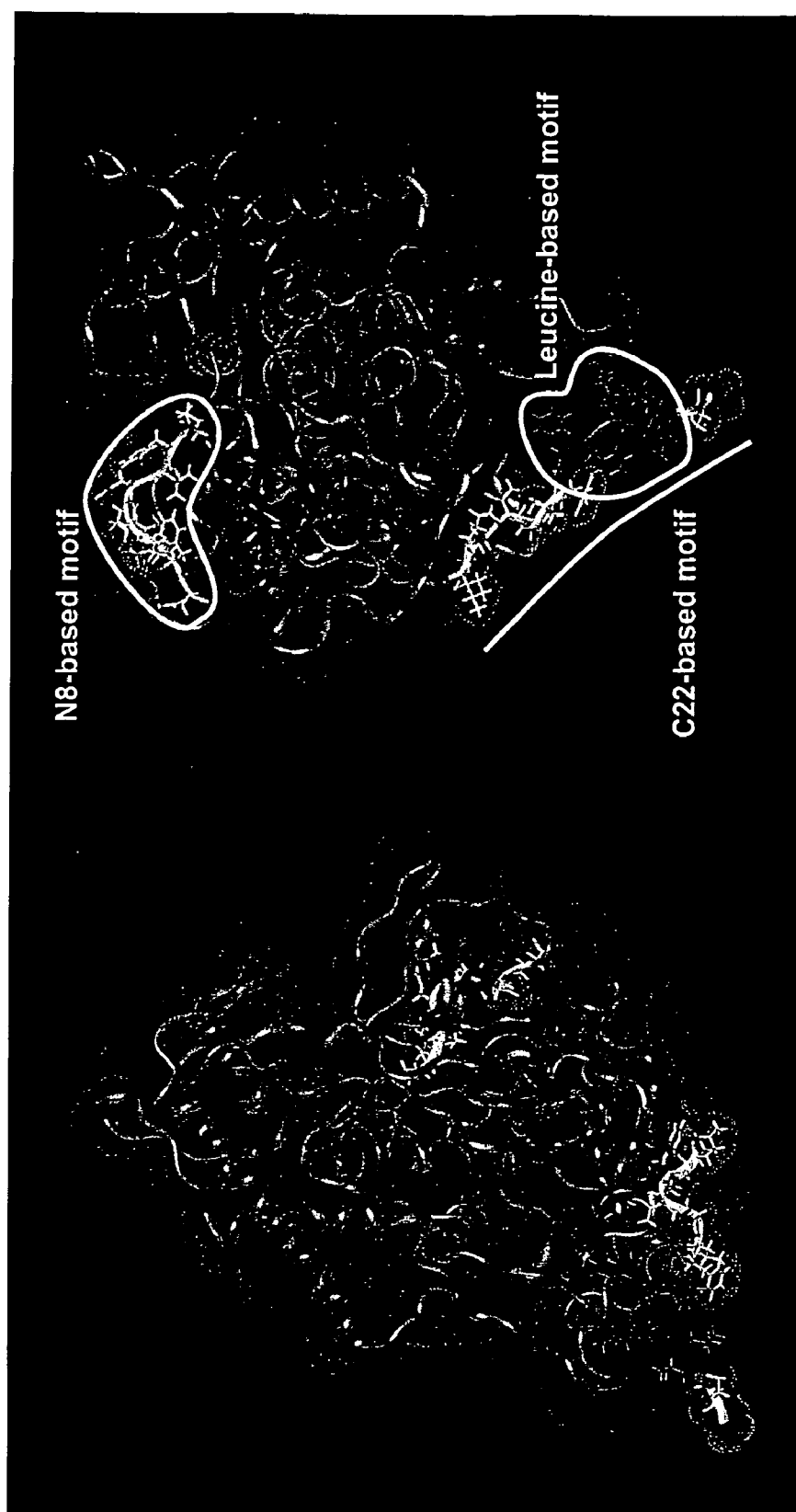


FIG. 12.

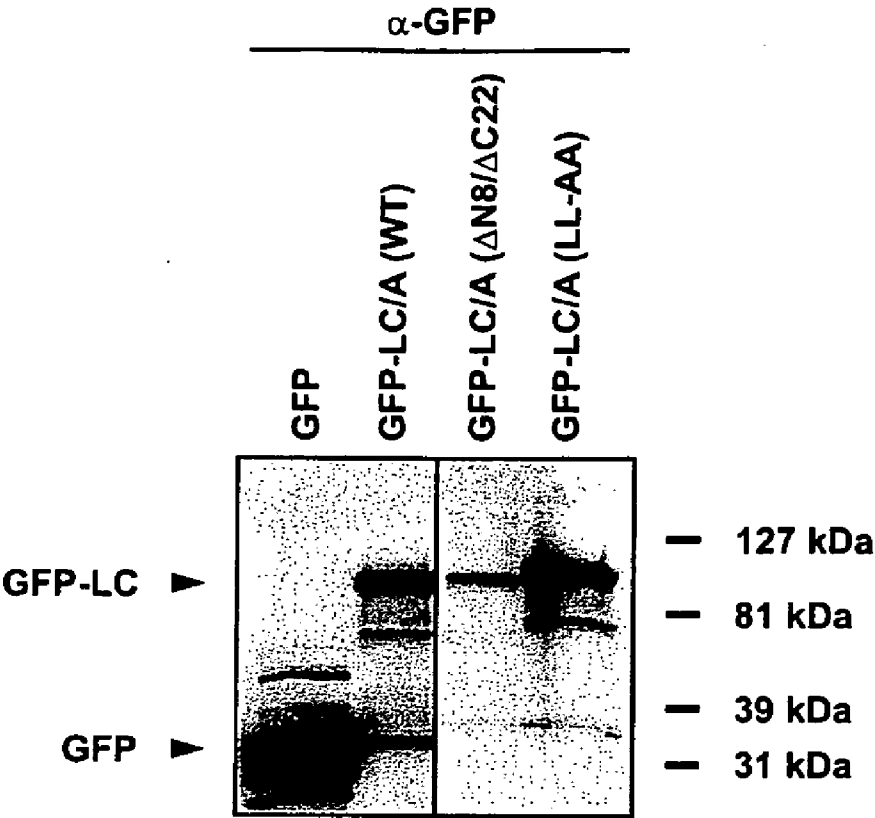


FIG. 13.

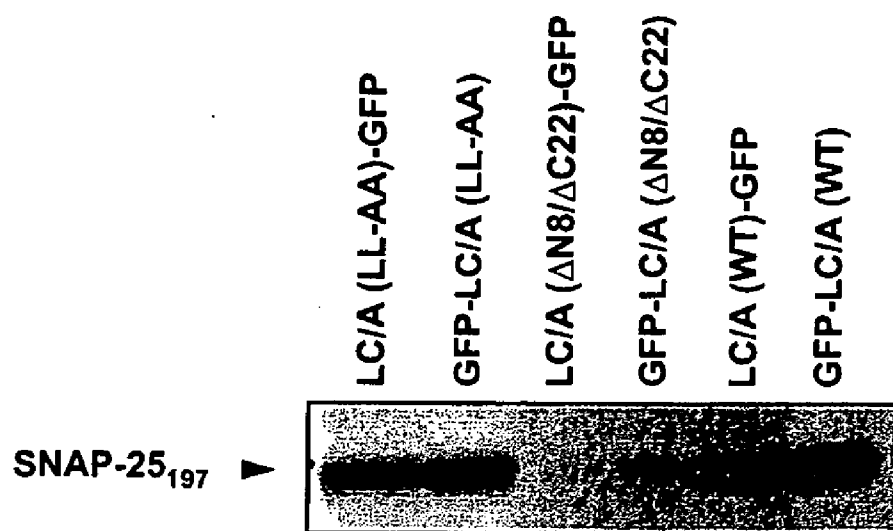


FIG. 14.

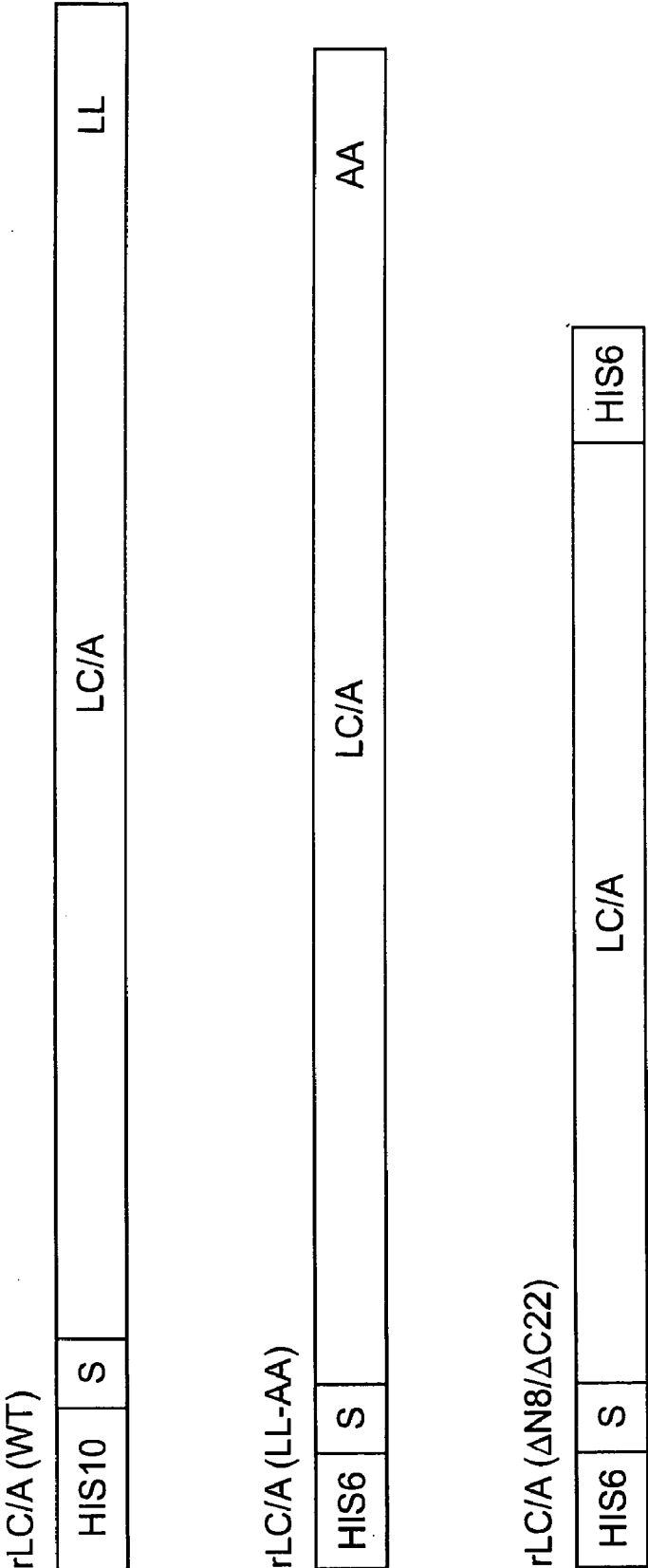


FIG. 15.

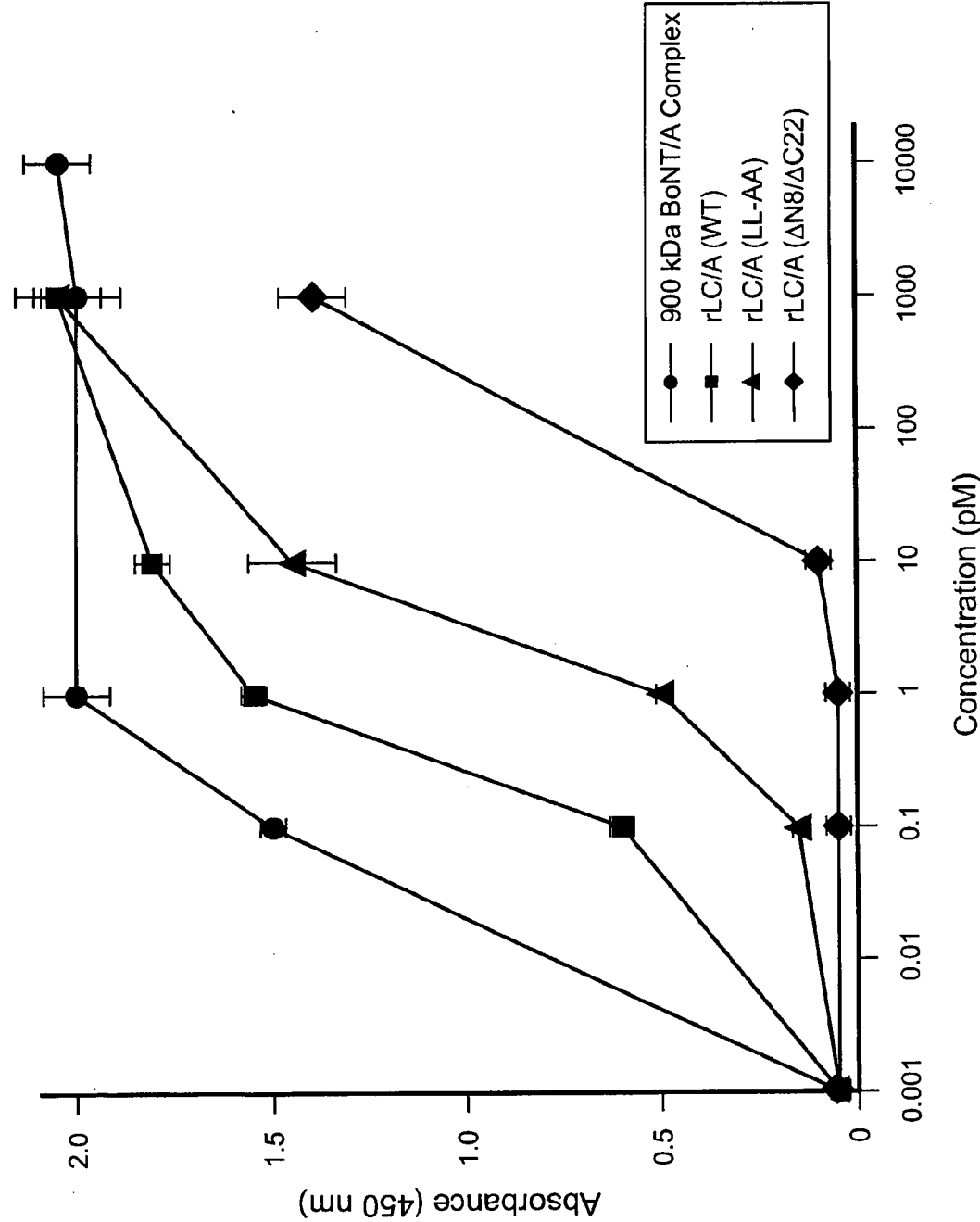


FIG. 16.

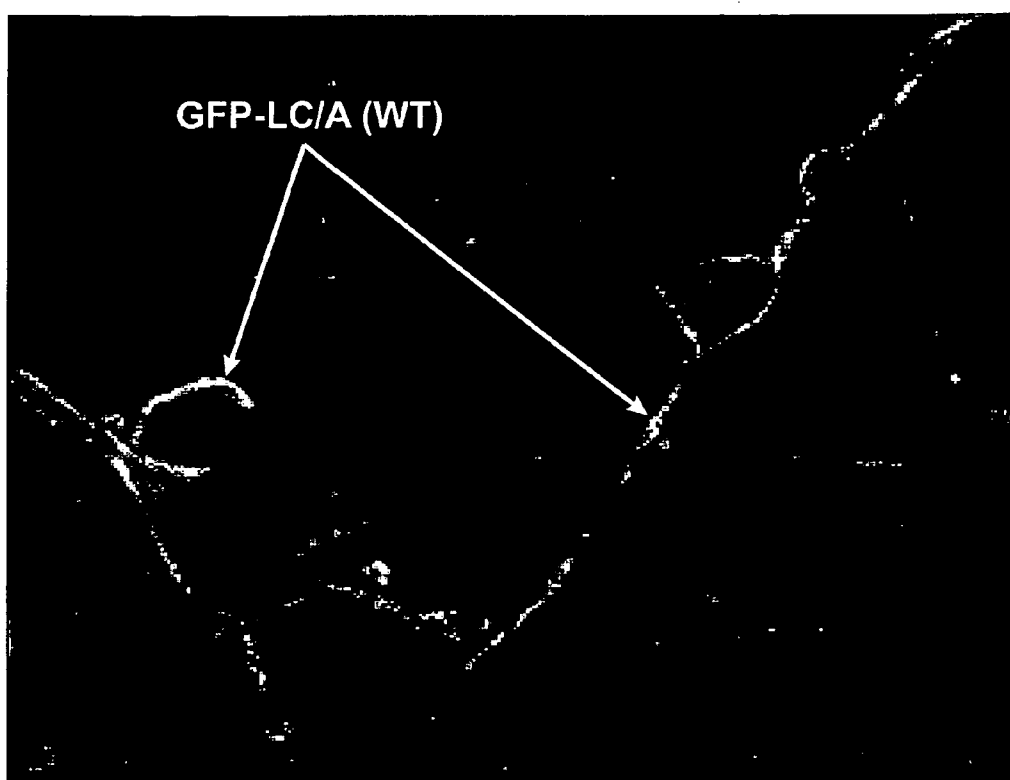


FIG. 17.

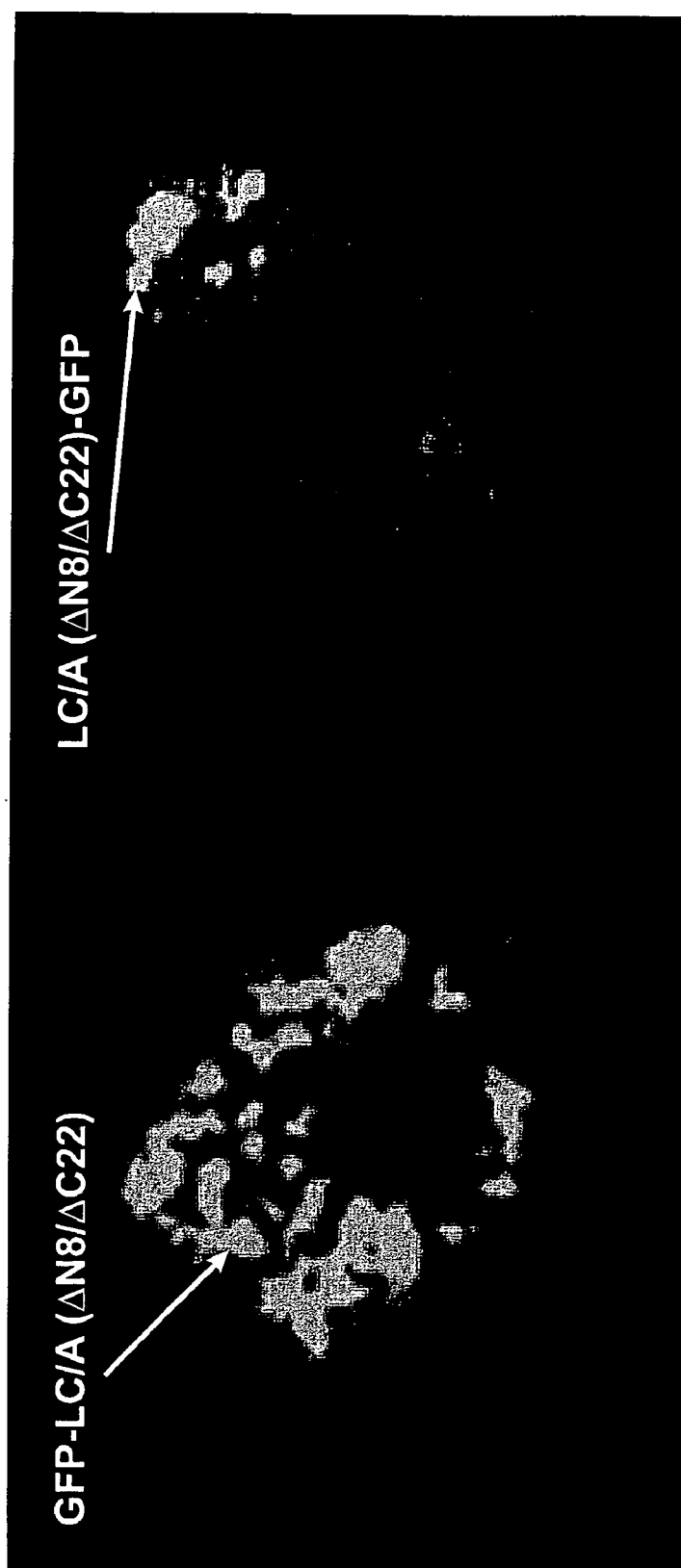


FIG. 18.

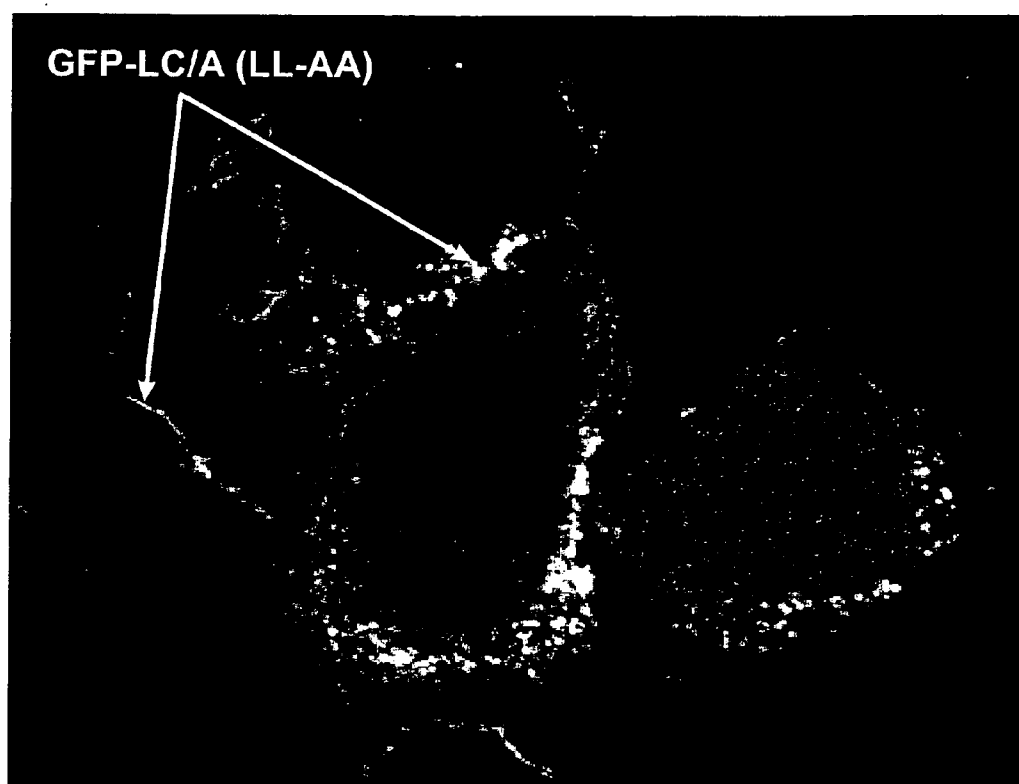


FIG. 19.

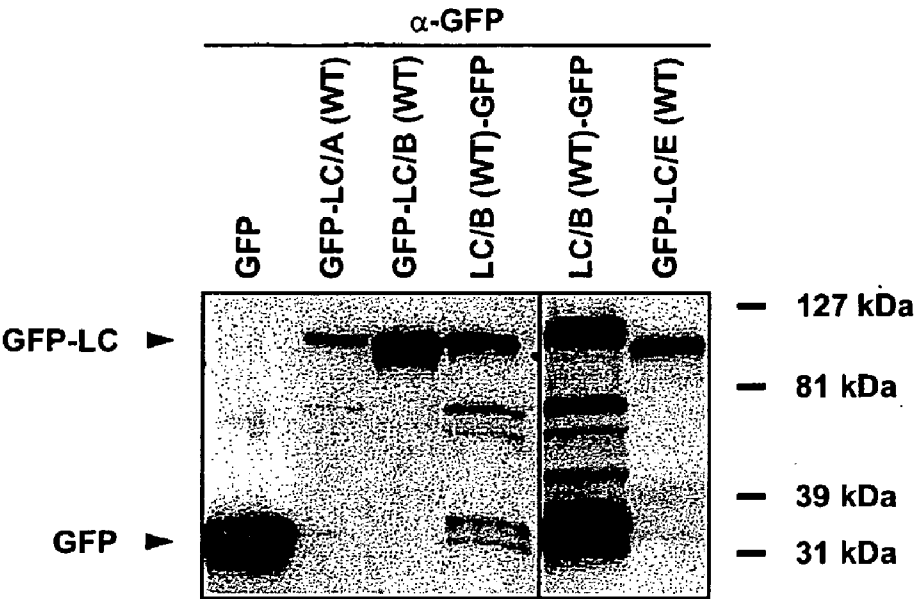


FIG. 20A.

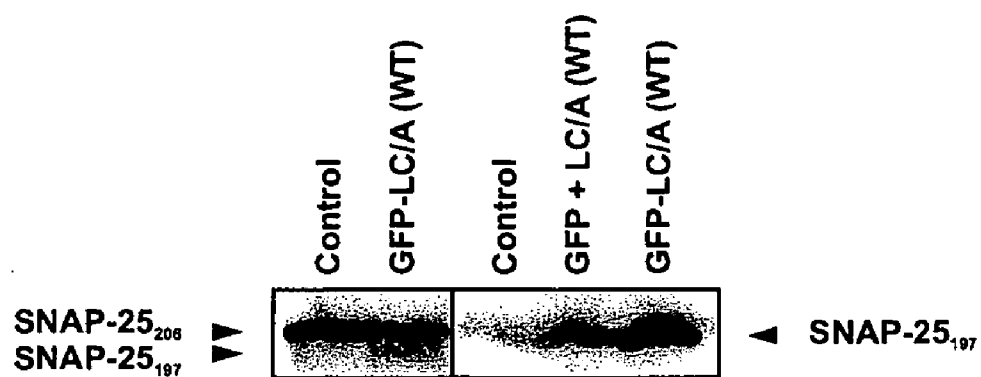


FIG. 20B.

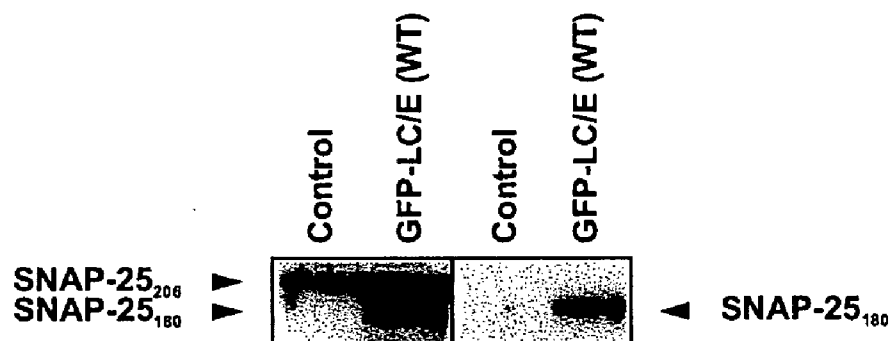


FIG. 21.

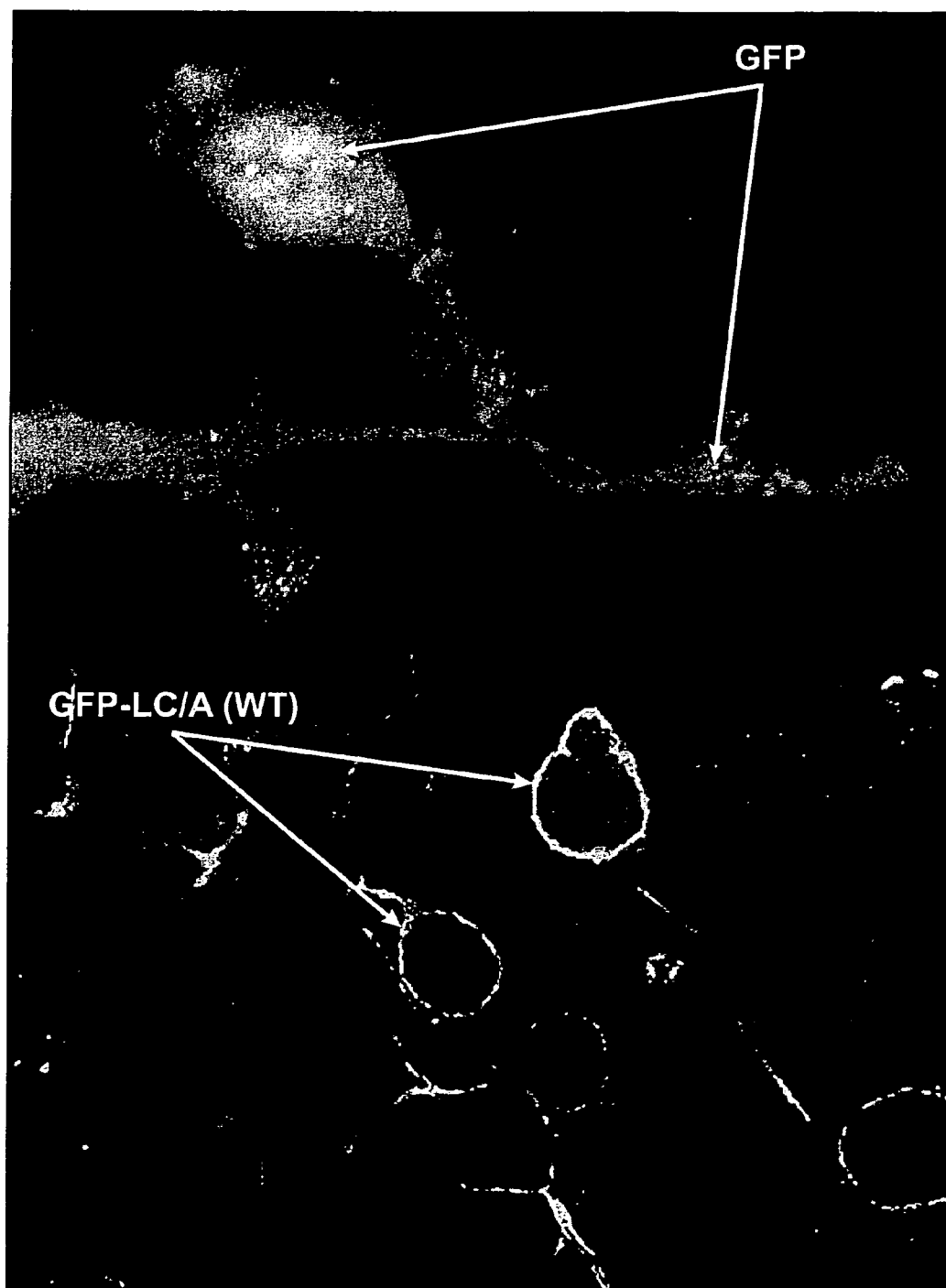


FIG. 22.

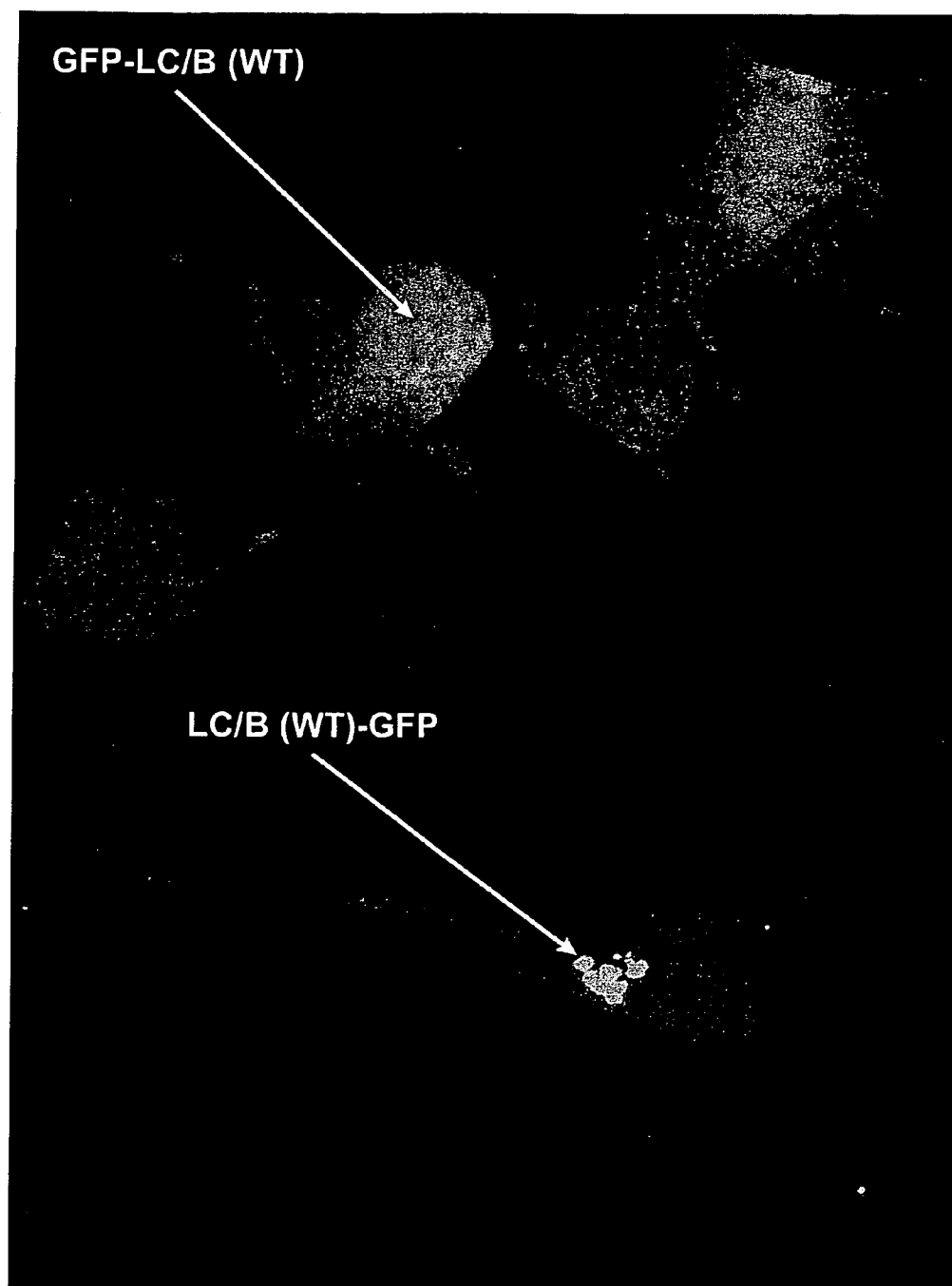


FIG. 23.

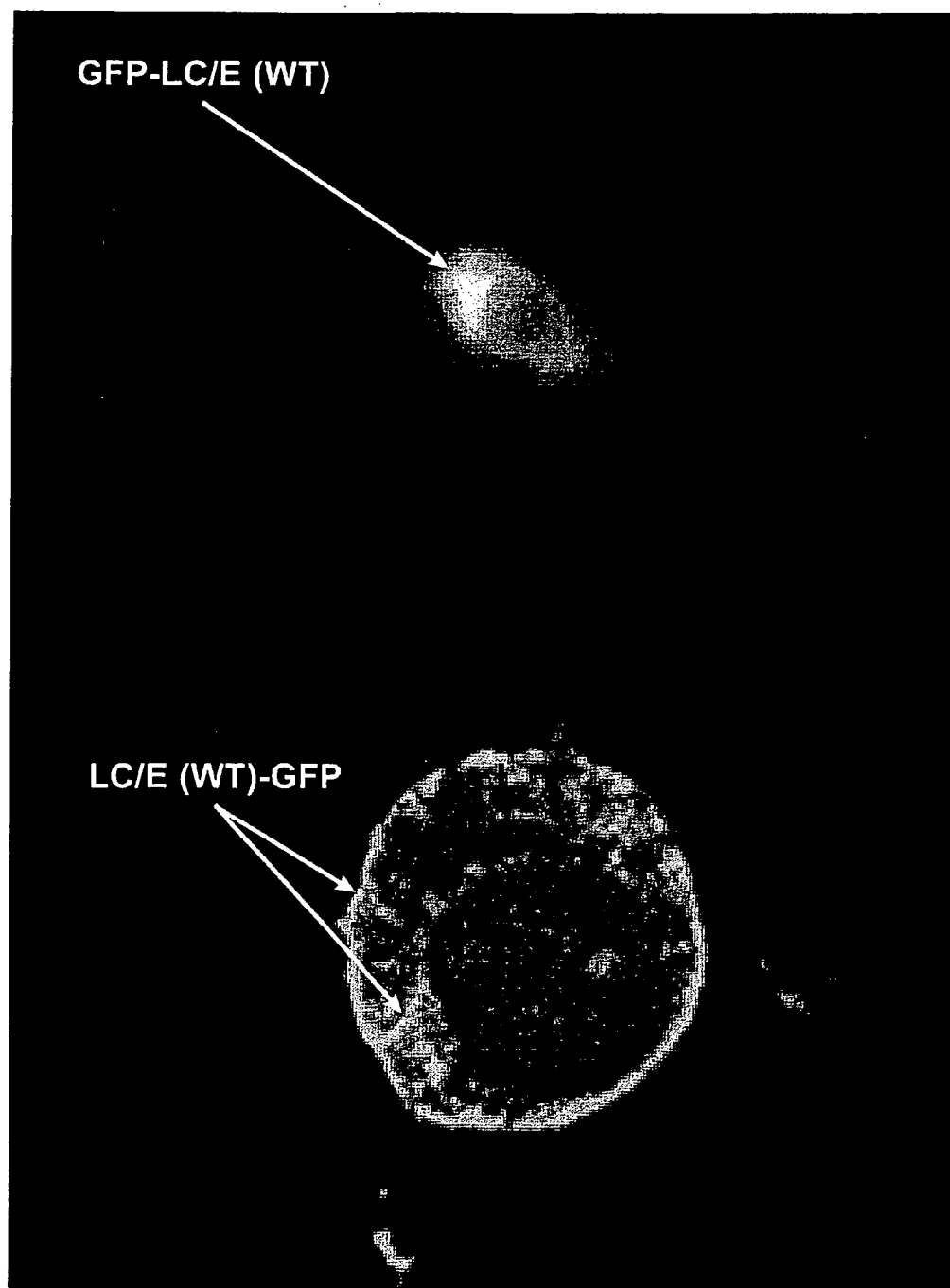


FIG. 24A.

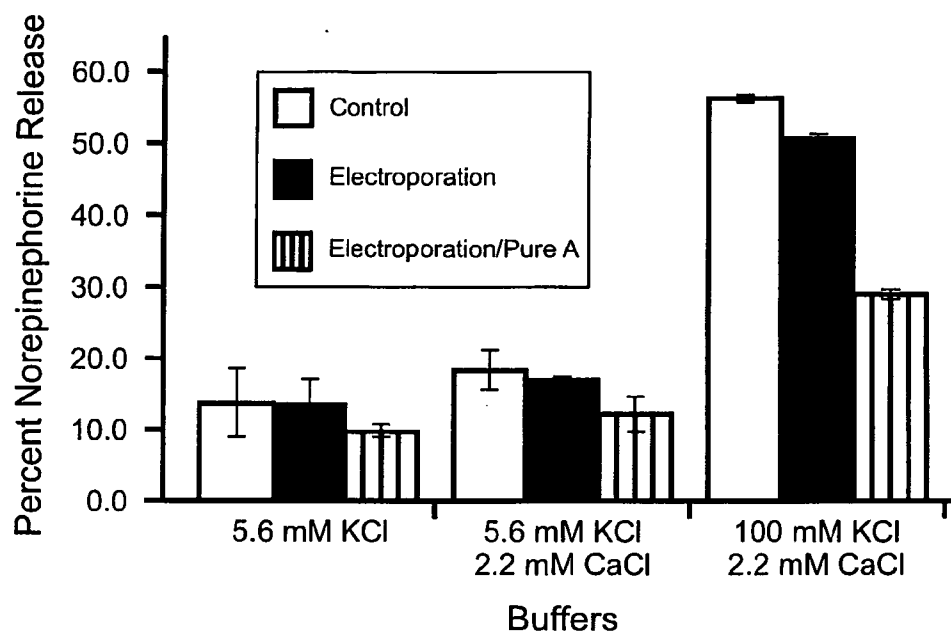
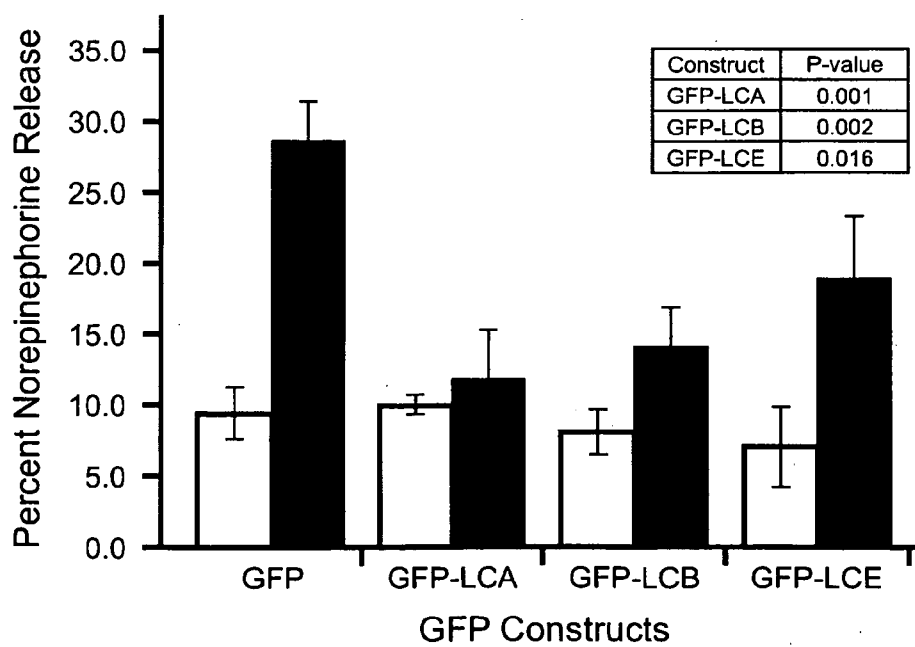


FIG. 24B.



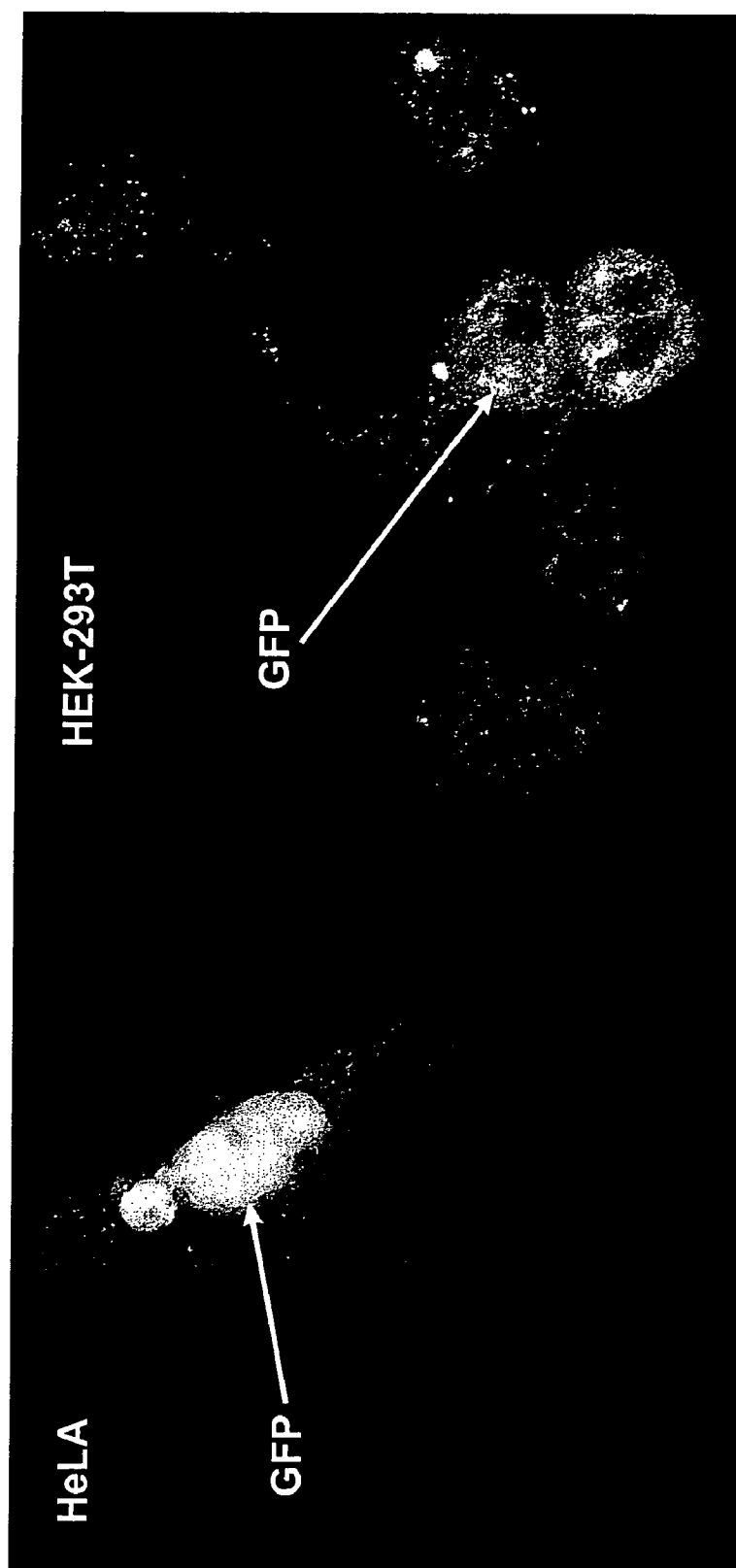
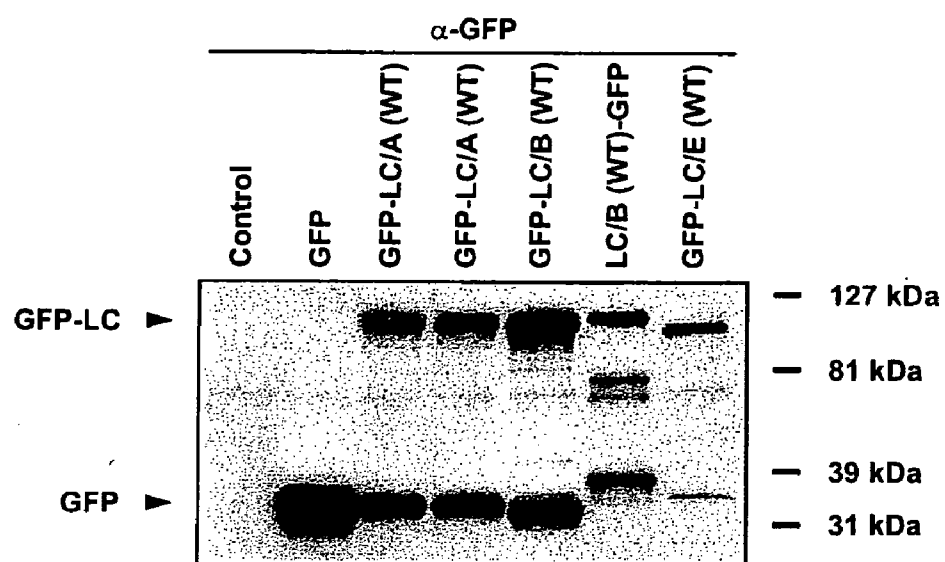


FIG. 25.

FIG. 26.



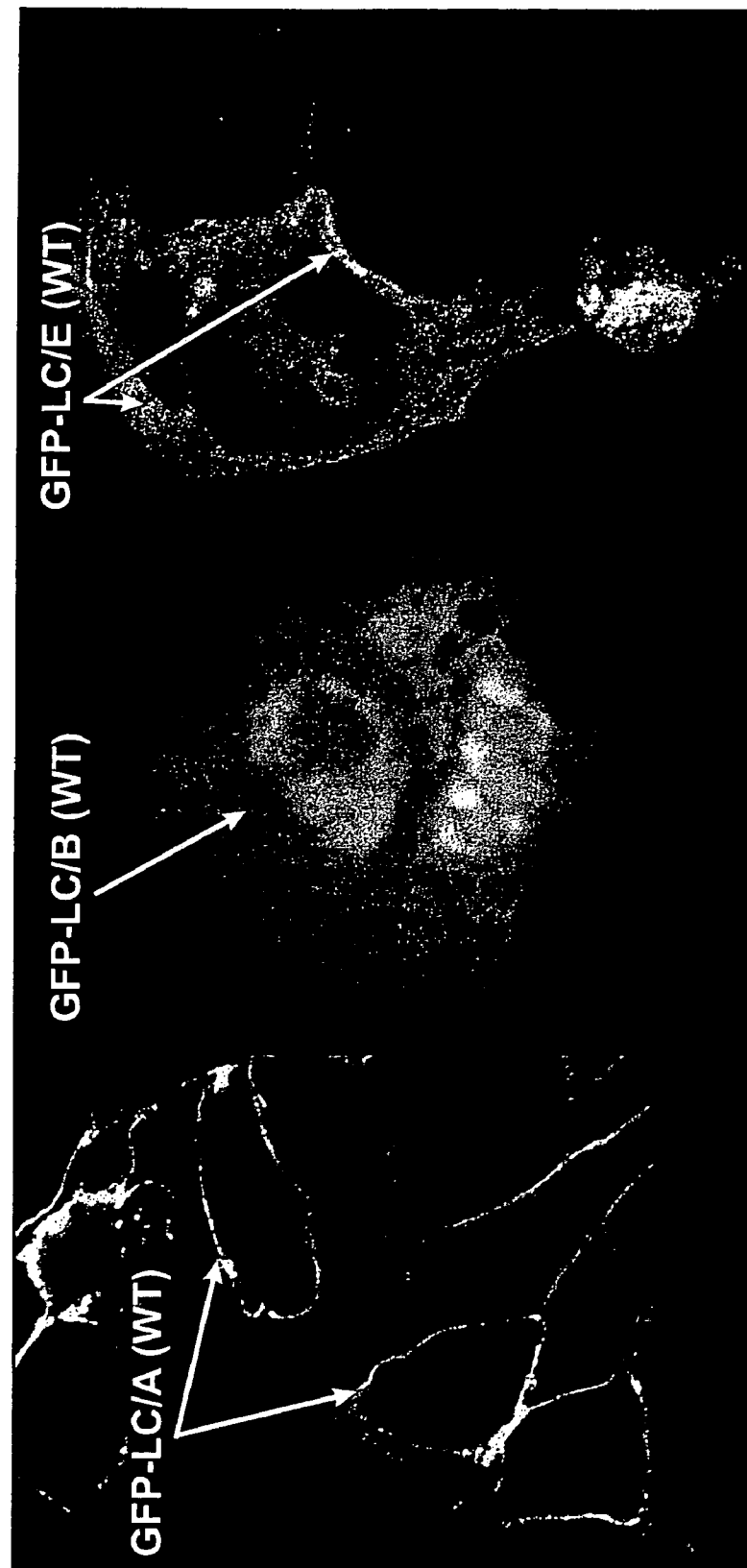


FIG. 27.

FIG. 28.

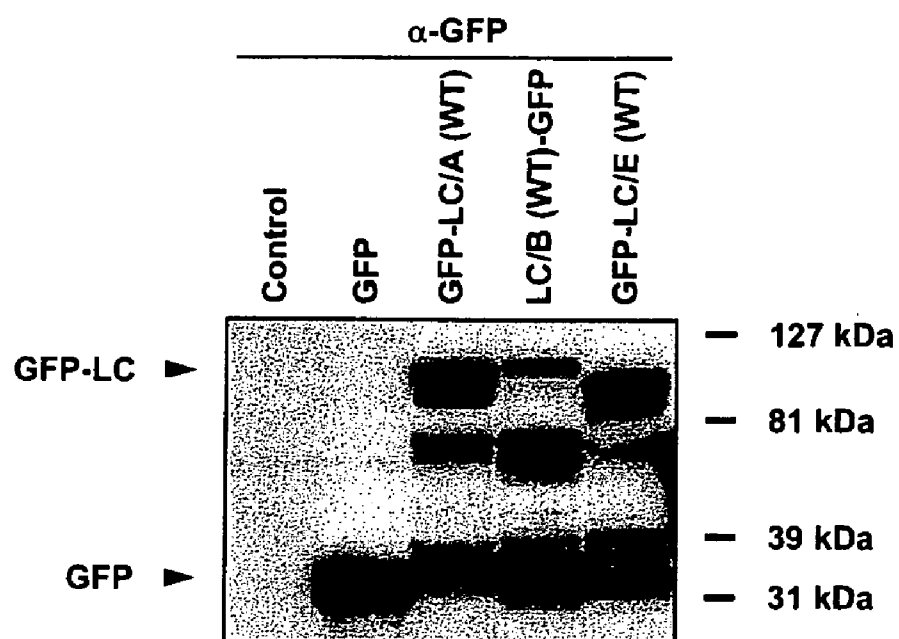


FIG. 29.

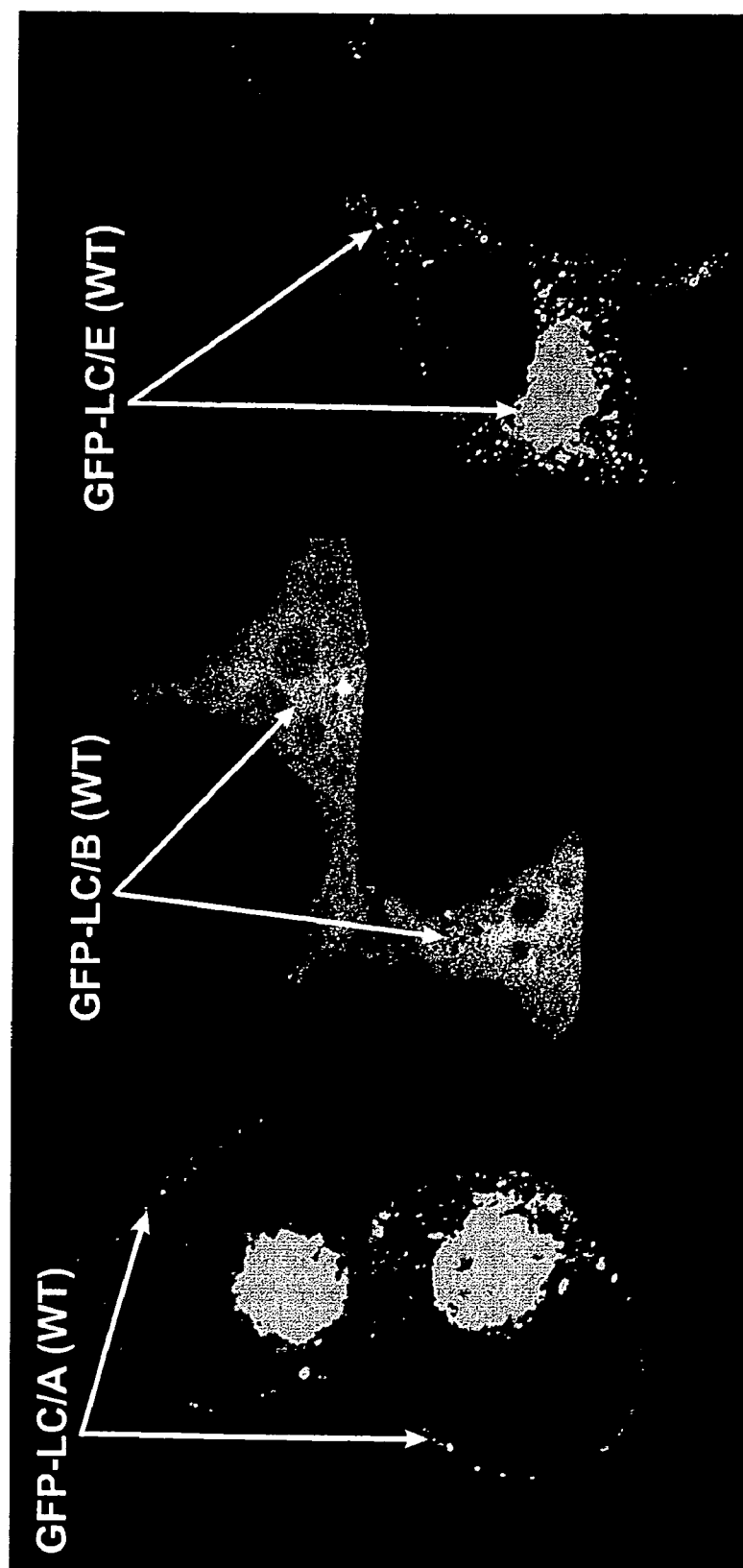


FIG. 30A.

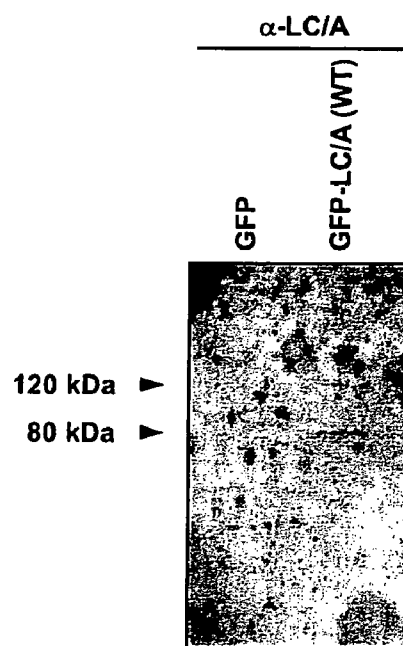


FIG. 30B.

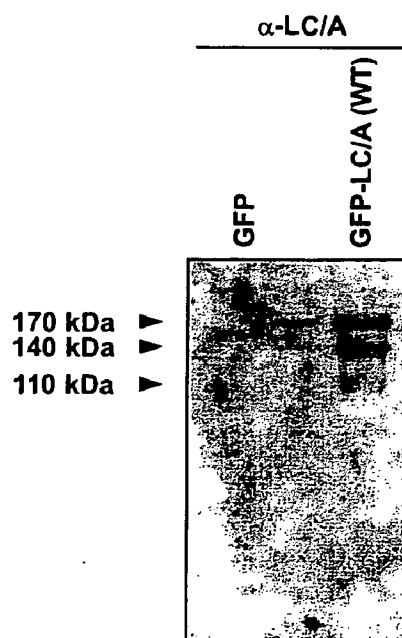


FIG. 31A.

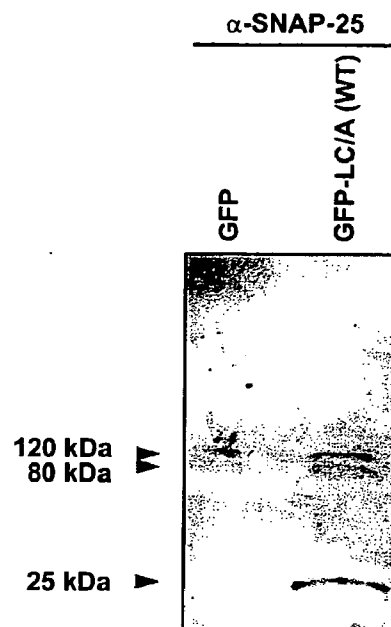


FIG. 31B.

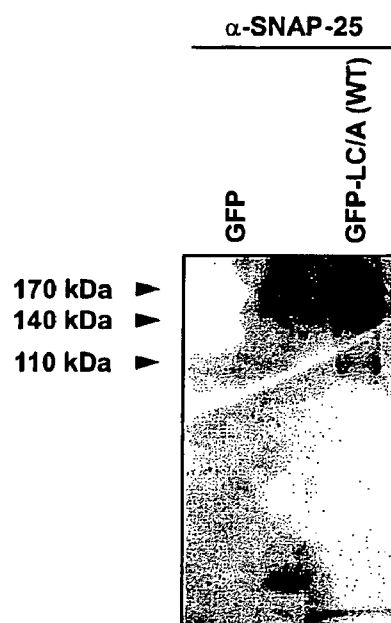


FIG. 32.

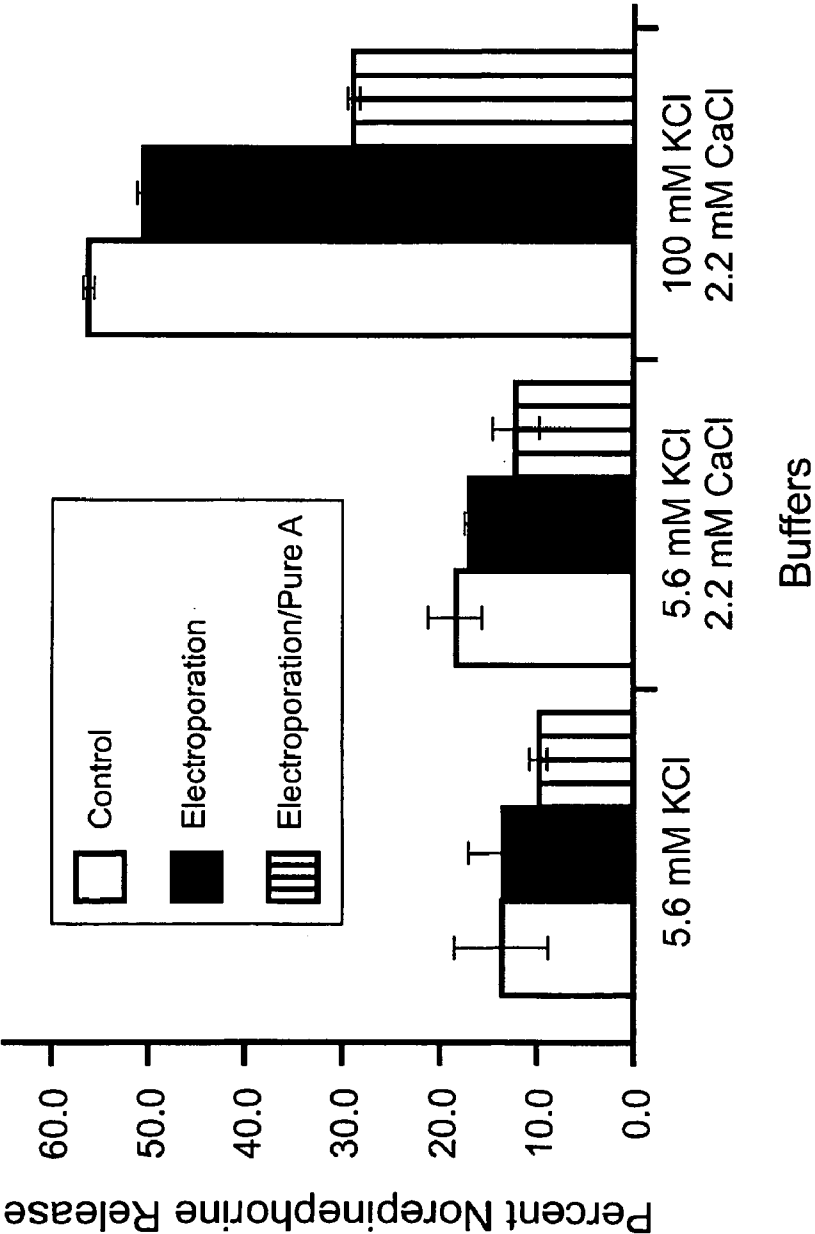


FIG. 33.

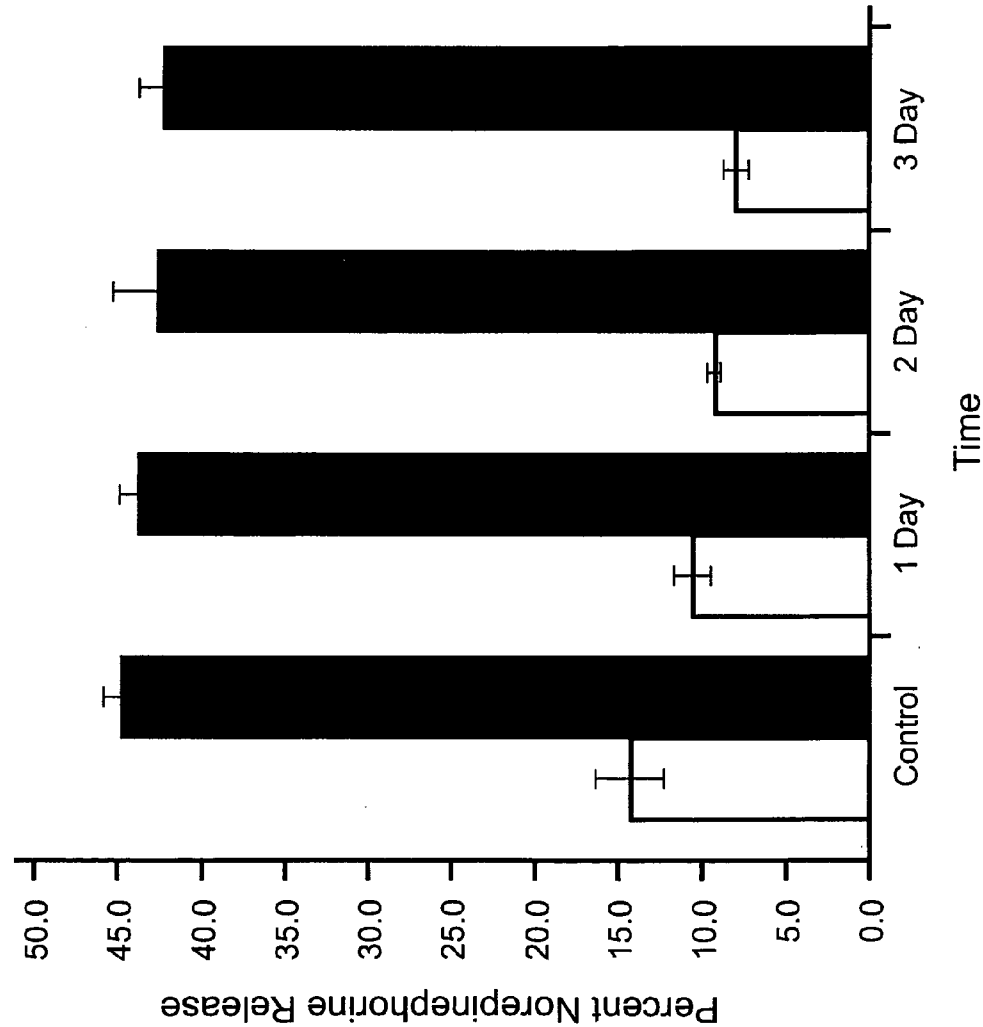


FIG. 34.

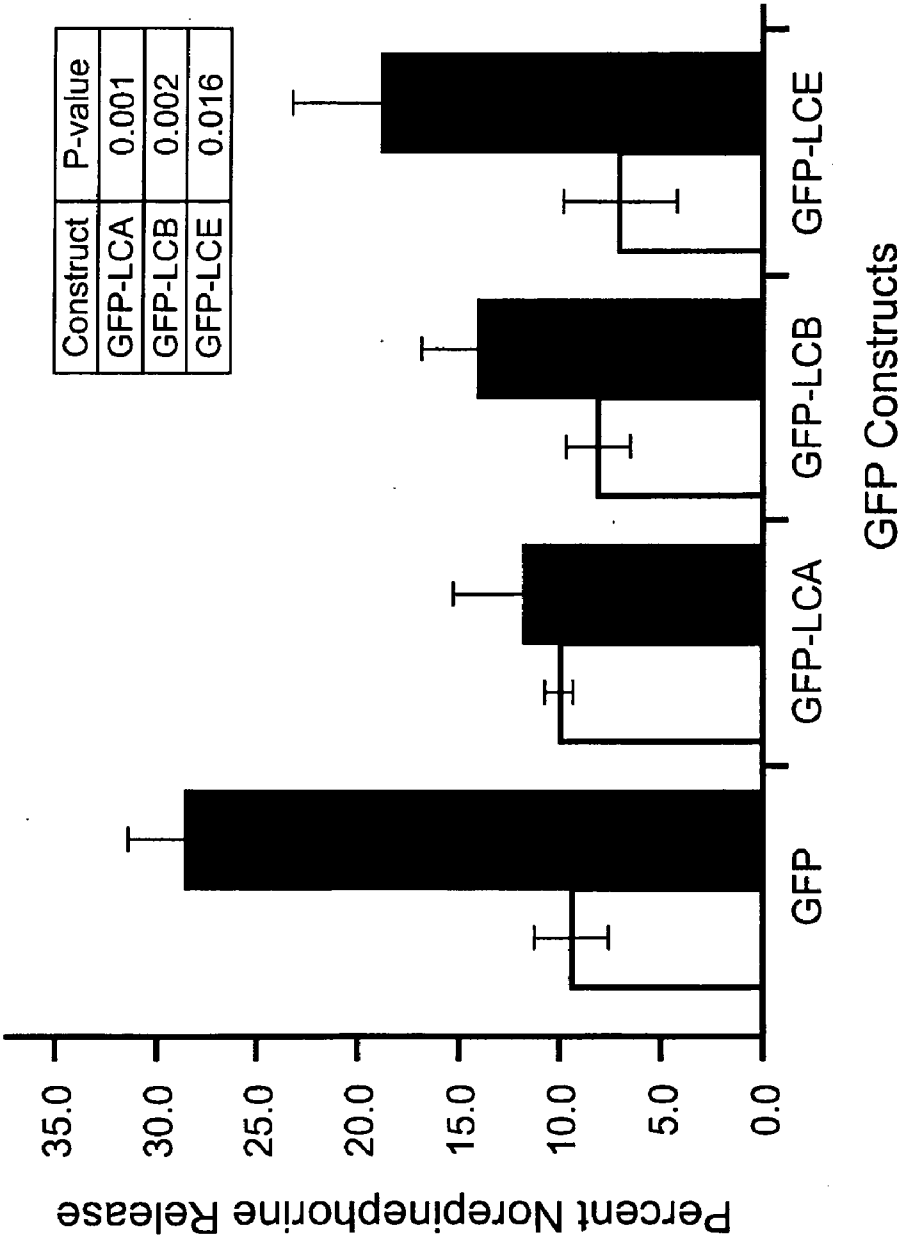


FIG. 35.

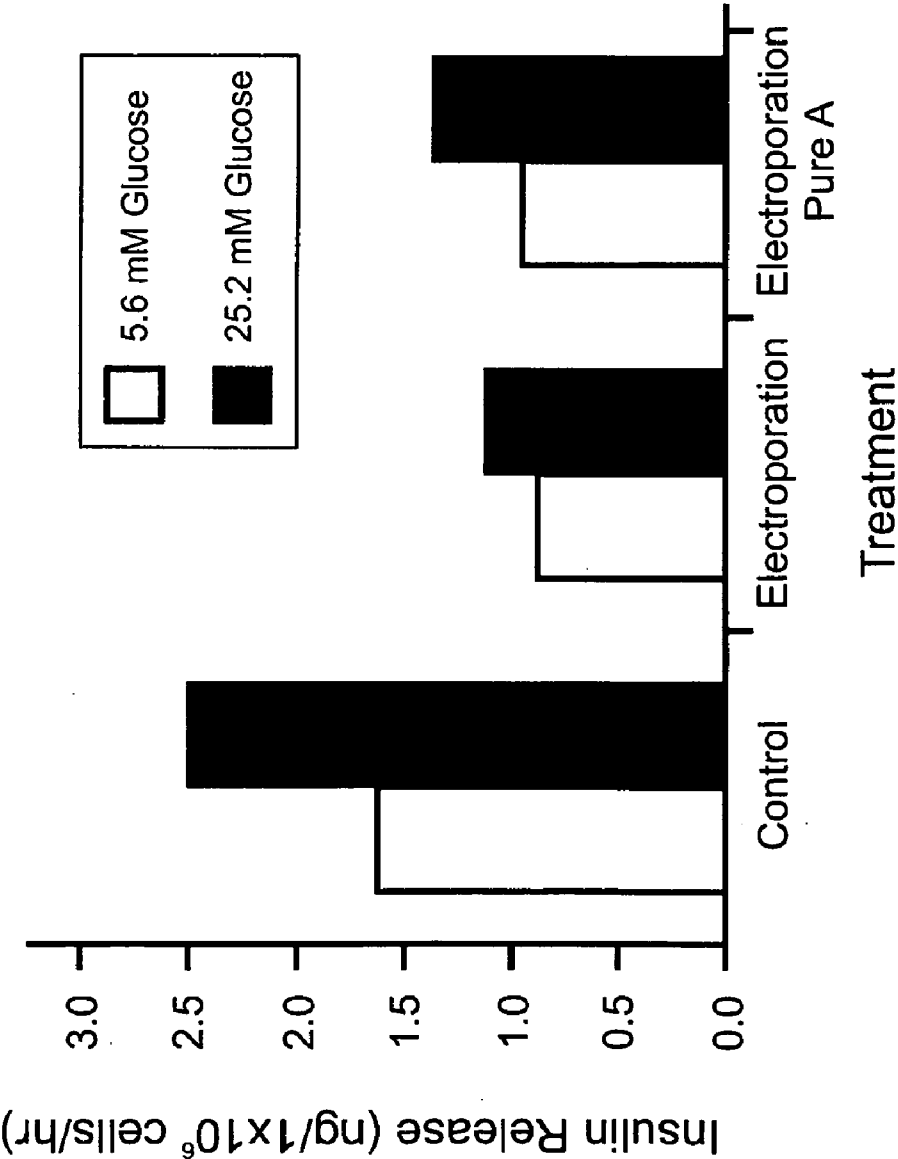


FIG. 36.

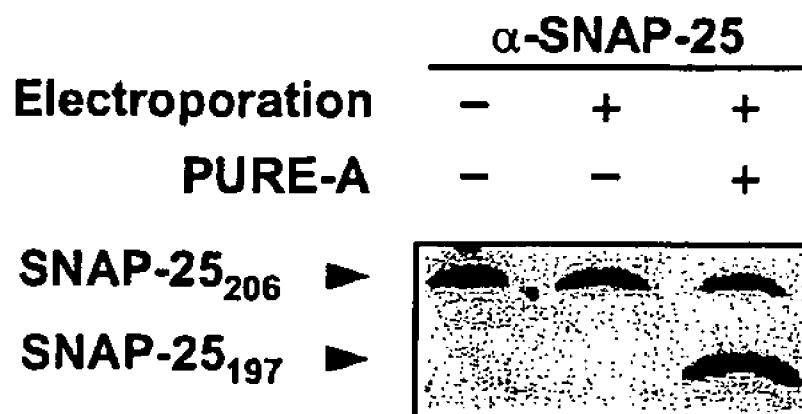
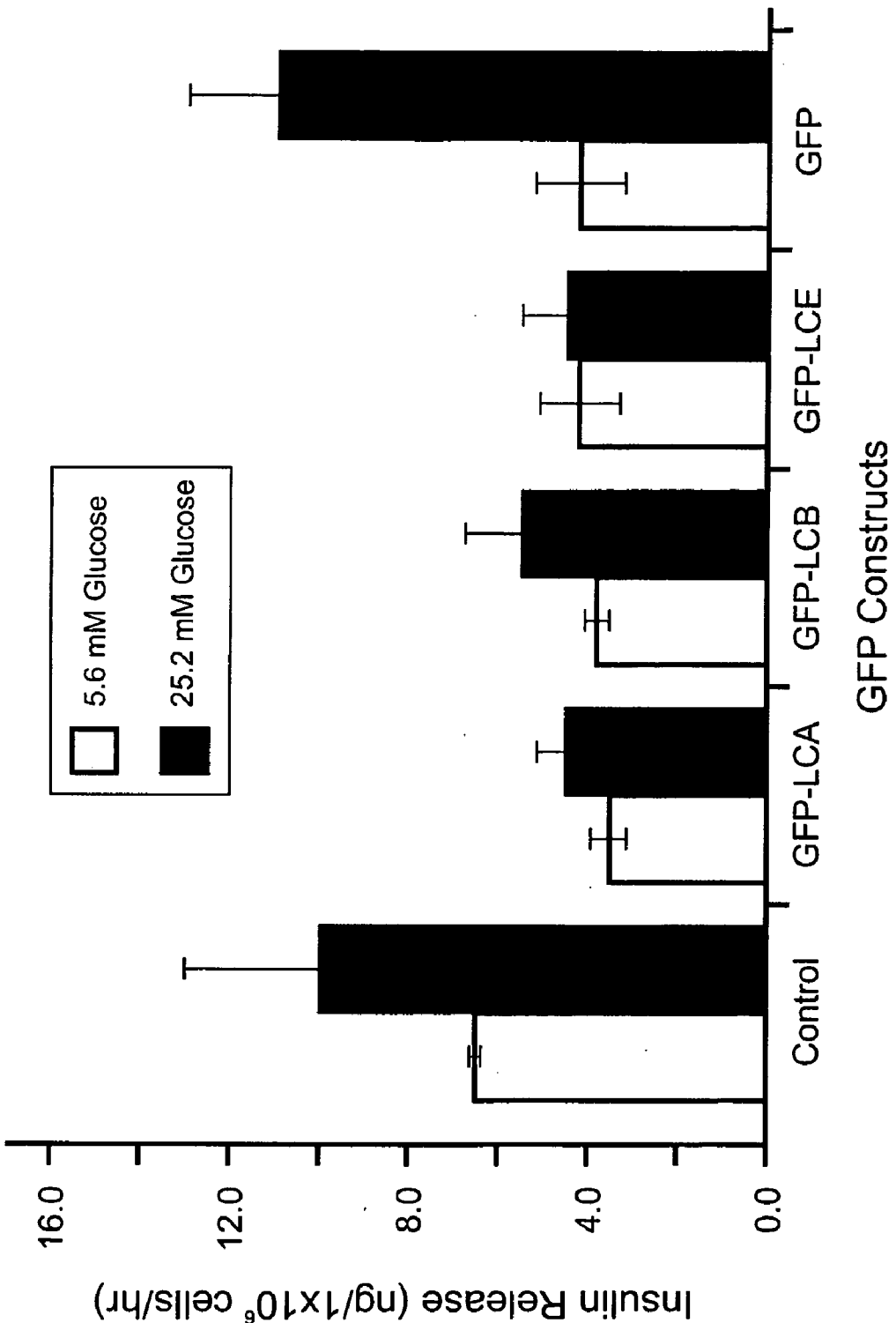


FIG. 37.



CLOSTRIDIAL NEUROTOXIN COMPOSITIONS AND MODIFIED CLOSTRIDIAL NEUROTOXINS

CROSS REFERENCE

[0001] This application is a divisional and claims priority pursuant to 35 U.S.C. 120 to U.S. patent application Ser. No. 10/757,077, filed Jan. 14, 2004, a continuation-in-part of U.S. patent application Ser. No. 10/163,106, filed Jun. 4, 2003, which is a continuation-in-part of U.S. patent application Ser. No. 09/910,346, filed Jul. 20, 2001, which is a continuation-in-part of U.S. patent application Ser. No. 09/620,840, filed Jul. 21, 2000, now U.S. Pat. No. 6,903,187. All prior applications are incorporated herein by reference in their entireties.

BACKGROUND

[0002] The present invention relates to modified neurotoxins, particularly modified Clostridial neurotoxins, and use thereof to treat various conditions including conditions that have been treated using naturally occurring botulinum toxins.

[0003] The present invention also relates to a composition comprising an isolated or purified botulinum toxin light chain (or a part thereof) and an intracellular structure, such as a component of a mammalian plasma membrane.

[0004] Botulinum toxin, for example, botulinum toxin type A, has been used in the treatment of numerous conditions including pain, skeletal muscle conditions, smooth muscle conditions and glandular conditions. Botulinum toxins are also used for cosmetic purposes.

[0005] Numerous examples exist for treatment using botulinum toxin. For examples of treating pain see Aoki, et al., U.S. Pat. No. 6,113,915 and Aoki, et al., U.S. Pat. No. 5,721, 215. For an example of treating a neuromuscular disorder, see U.S. Pat. No. 5,053,005, which suggests treating curvature of the juvenile spine, i.e., scoliosis, with an acetylcholine release inhibitor, preferably botulinum toxin A. For the treatment of strabismus with botulinum toxin type A, see Elston, J. S., et al., British Journal of Ophthalmology, 1985, 69, 718-724 and 891-896. For the treatment of blepharospasm with botulinum toxin type A, see Adenis, J. P., et al., J. Fr. Ophthalmol., 1990, 13 (5) at pages 259-264. For treating spasmodic and oromandibular dystonia torticollis, see Jankovic et al., Neurology, 1987, 37, 616-623. Spasmodic dysphonia has also been treated with botulinum toxin type A. See Blitzer et al., Ann. Otol. Rhino. Laryngol, 1985, 94, 591-594. Lingual dystonia was treated with botulinum toxin type A according to Brin et al., Adv. Neurol. (1987) 50, 599-608. Cohen et al., Neurology (1987) 37 (Suppl. 1), 123-4, discloses the treatment of writer's cramp with botulinum toxin type A.

[0006] It would be beneficial to have botulinum toxins with altered biological persistence and/or altered biological activity. For example, a botulinum toxin can be used to immobilize muscles and prevent limb movements after tendon surgery to facilitate recovery. It would be beneficial to have a botulinum toxin (such as a botulinum toxin type A) which exhibits a reduced period of biological persistence so that a patient can regain muscle use and mobility at about the time they recover from surgery. Furthermore, a botulinum toxin with an altered biological activity, such as an enhanced biological activity can have utility as a more efficient toxin (i.e. more potent per unit amount of toxin), so that less toxin can be used.

[0007] Additionally, there is a need for modified neurotoxins (such as modified Clostridial toxins) which can exhibit an enhanced period of biological persistence and modified neurotoxins (such as modified Clostridial toxins) with reduced biological persistence and/or biological activity and methods for preparing such toxins.

[0008] Furthermore, there is a need for an isolated composition comprising a botulinum toxin light chain component and an intracellular structure component wherein the structure component interacts with the light chain component in a manner effective to facilitate substrate proteolysis within a cell, since such a composition can have utility for research, diagnostic and therapeutic purposes.

DEFINITIONS

[0009] Before proceeding to describe the present invention, the following definitions are provided and apply herein.

[0010] "Heavy chain" means the heavy chain of a Clostridial neurotoxin. It has a molecular weight of about 100 kDa and can be referred to herein as Heavy chain or as H.

[0011] "H_N" means a fragment (having a molecular weight of about 50 kDa) derived from the Heavy chain of a Clostridial neurotoxin which is approximately equivalent to the amino terminal segment of the Heavy chain, or the portion corresponding to that fragment in the intact Heavy chain. It is believed to contain the portion of the natural or wild-type Clostridial neurotoxin involved in the translocation of the light chain across an intracellular endosomal membrane.

[0012] "H_C" means a fragment (about 50 kDa) derived from the Heavy chain of a Clostridial neurotoxin which is approximately equivalent to the carboxyl terminal segment of the Heavy chain, or the portion corresponding to that fragment in the intact Heavy chain. It is believed to be immunogenic and to contain the portion of the natural or wild-type Clostridial neurotoxin involved in high affinity binding to various neurons (including motor neurons), and other types of target cells.

[0013] "Light chain" means the light chain of a Clostridial neurotoxin. It has a molecular weight of about 50 kDa, and can be referred to as light chain, L or as the proteolytic domain (amino acid sequence) of a Clostridial neurotoxin. The light chain is believed to be effective as an inhibitor of exocytosis, including as an inhibitor of neurotransmitter (i.e. acetylcholine) release when the light chain is present in the cytoplasm of a target cell.

[0014] "Neurotoxin" means a molecule that is capable of interfering with the functions of a cell, including a neuron. The "neurotoxin" can be naturally occurring or man-made. The interfered with function can be exocytosis.

[0015] "Modified neurotoxin" means a neurotoxin which includes a structural modification. In other words, a "modified neurotoxin" is a neurotoxin which has been modified by a structural modification. The structural modification changes the biological persistence, such as the biological half-life (i.e. the duration of action of the neurotoxin) and/or the biological activity of the modified neurotoxin relative to the neurotoxin from which the modified neurotoxin is made or derived. The modified neurotoxin is structurally different from a naturally existing neurotoxin.

[0016] "Mutation" means a structural modification of a naturally occurring protein or nucleic acid sequence. For example, in the case of nucleic acid mutations, a mutation can be a deletion, addition or substitution of one or more nucleotides in the DNA sequence. In the case of a protein sequence

mutation, the mutation can be a deletion, addition or substitution of one or more amino acids in a protein sequence. For example, a specific amino acid comprising a protein sequence can be substituted for another amino acid, for example, an amino acid selected from a group which includes the amino acids alanine, asparagine, cysteine, aspartic acid, glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, leucine, methionine, proline, glutamine, arginine, serine, threonine, valine, tryptophan, tyrosine or any other natural or non-naturally occurring amino acid or chemically modified amino acids. Mutations to a protein sequence can be the result of mutations to DNA sequences that when transcribed, and the resulting mRNA translated, produce the mutated protein sequence. Mutations to a protein sequence can also be created by fusing a peptide sequence containing the desired mutation to a desired protein sequence.

[0017] "Structural modification" means any change to a neurotoxin that makes it physically or chemically different from an identical neurotoxin without the structural modification.

[0018] "Biological persistence" or "persistence" means the time duration of interference or influence caused by a neurotoxin or a modified neurotoxin with a cellular (such as a neuronal) function, including the temporal duration of an inhibition of exocytosis (such as exocytosis of neurotransmitter, for example, acetylcholine) from a cell, such as a neuron.

[0019] "Biological half-life" or "half-life" means the time that the concentration of a neurotoxin or a modified neurotoxin, preferably the active portion of the neurotoxin or modified neurotoxin, for example, the light chain of Clostridial toxins, is reduced to half of the original concentration in a mammalian cell, such as in a mammalian neuron.

[0020] "Biological activity" or "activity" means the amount of cellular exocytosis inhibited from a cell per unit of time, such as exocytosis of a neurotransmitter from a neuron.

[0021] "Target cell" means a cell (including a neuron) with a binding affinity for a neurotoxin or for a modified neurotoxin.

[0022] "PURE A" means a purified botulinum toxin type A, that is the 150 kDa toxin molecule.

SUMMARY

[0023] New structurally modified neurotoxins have been discovered. The present structurally modified neurotoxins can provide substantial benefits, for example, enhanced or decreased biological persistence and/or biological half-life and/or enhanced or decreased biological activity as compared to the unmodified neurotoxin.

[0024] In accordance with the present invention, there are provided structurally modified neurotoxins, which include a neurotoxin and a structural modification. The structural modification is effective to alter a biological persistence of the structurally modified neurotoxin relative to an identical neurotoxin without the structural modification. Also, the structurally modified neurotoxin is structurally different from a naturally existing neurotoxin.

[0025] The present invention also encompasses a modified neurotoxin comprising a neurotoxin with a structural modification, wherein said structural modification is effective to alter a biological activity of said modified neurotoxin relative to an identical neurotoxin without said structural modification, and wherein said modified neurotoxin is structurally different from a naturally existing neurotoxin. This structural modification can be effective to reduce exocytosis from a

target cell by more than the amount of the exocytosis reduced from the target cell by an identical neurotoxin without said structural modification. Alternately, the structural modification can be effective to reduce an exocytosis from a target cell by less than the amount of the exocytosis reduced from the cell by an identical neurotoxin without said structural modification. Significantly, the exocytosis can be exocytosis of a neurotransmitter and the modified neurotoxin can exhibit an altered biological activity without exhibiting an altered biological persistence. The structural modification can comprise a leucine-based motif. Additionally, the modified neurotoxin can exhibit an altered biological activity as well as an altered biological persistence. The present invention also includes the circumstances where: (a) the modified neurotoxin exhibits an increased biological activity as well as an increased biological persistence; (b) the modified neurotoxin exhibits an increased biological activity and a reduced biological persistence; (c) the modified neurotoxin exhibits a decreased biological activity and a decreased biological persistence, and; (d) the modified neurotoxin exhibits an decreased biological activity and an increased biological persistence.

[0026] Importantly, a unit amount (i.e. on a molar basis) of the modified neurotoxin can be more efficient to reduce an exocytosis from a cell than is a unit amount of the naturally existing neurotoxin. In other words, a unit amount of a modified neurotoxin, such as a modified botulinum toxin type A, can cleave its' intracellular substrate (SNAP) in a manner such that a greater inhibition of neurotransmitter exocytosis results (i.e. less neurotransmitter is released from the cell), as compared to the inhibition of neurotransmitter exocytosis exhibited by the naturally occurring neurotoxin.

[0027] Further in accordance with the present invention, are structurally modified neurotoxins, wherein a structural modification is effective to enhance a biological persistence of the modified neurotoxin. The enhanced biological persistence of the structurally modified neurotoxin can be due, at least in part, to an increased half-life and/or biological activity of the structurally modified neurotoxin.

[0028] Still further in accordance with the present invention, there are provided structurally modified neurotoxins wherein a biological persistence of the structurally modified neurotoxin is reduced relative to that of an identical neurotoxin without the structural modification. This reduction in biological persistence can be due, at least in part, to a decreased biological half-life and/or activity of the structurally modified neurotoxins.

[0029] Still further in accordance with the present invention, there are provided structurally modified neurotoxins wherein the structural modification comprises a number of amino acids. For example, the number of amino acids comprising the structural modification can be 1 or more amino acids, from 1 to about 22 amino acids, from 2 to about 10 amino acids, and from about 4 to about 7 amino acids.

[0030] In one embodiment, the structural modifications of the structurally modified neurotoxins can comprise an amino acid. The amino acid can comprise an R group containing a number of carbons. For example, the number of carbon atoms in the amino acid can be 1 or more, from 1 to about 20 carbons, from 1 to about 12 carbons, from 1 to about 9 carbons, from 2 to about 6 carbons, and about 4 carbons. R group as used in this application refers to amino acid side chains. For example, the R group for alanine is CH_3 , and, for example, the R group for serine is CH_2OH .

[0031] In some embodiments, there are provided structurally modified neurotoxins wherein the modification comprises an amino acid. The amino acid can comprise an R group which is substantially hydrocarbyl.

[0032] In still another embodiment, there are provided structurally modified neurotoxins wherein the structural modification comprises an amino acid. The amino acid further can comprise an R group that includes at least one heteroatom.

[0033] Further in accordance with the present invention, there are provided structurally modified neurotoxins wherein the structural modification comprises, for example, a leucine-based motif, a tyrosine-based motif, and/or an amino acid derivative. Examples of an amino acid derivative that can comprise a structurally modified neurotoxin are a myristylated amino acid, an N-glycosylated amino acid, and a phosphorylated amino acid. The phosphorylated amino acids can be phosphorylated by, for example, casein kinase II, protein kinase C, and tyrosine kinase.

[0034] Still further in accordance with the present invention, there are provided structurally modified neurotoxins which can include a structural modification. The neurotoxin can comprise three amino acid sequence regions. The first region can be effective as a cellular binding moiety. This binding moiety can be a binding moiety for a target cell, such as a neuron. The binding moiety can be the carboxyl terminus of a botulinum toxin heavy chain. It is well known that the carboxyl terminus of a botulinum toxin heavy chain can be effective to bind, for example, receptors found on certain cells, including certain nerve cells. In one embodiment, the carboxyl terminus binds to receptors found on a presynaptic membrane of a nerve cell. The second region can be effective to translocate a structurally modified neurotoxin, or a part of a structurally modified neurotoxin across an endosome membrane. The third region can be effective to inhibit exocytosis from a target cell. The inhibition of exocytosis can be inhibition of neurotransmitter release, such as acetylcholine from a presynaptic membrane. For example, it is well known that the botulinum toxin light chain is effective to inhibit, for example, acetylcholine (as well as other neurotransmitters) release from various neuronal and non-neuronal cells.

[0035] At least one of the first, second or third regions can be substantially derived from a Clostridial neurotoxin. The third region can include the structural modification. In addition, the modified neurotoxin can be structurally different from a naturally existing neurotoxin. Also, the structural modification can be effective to alter a biological persistence of the modified neurotoxin relative to an identical neurotoxin without the structural modification.

[0036] In one embodiment, there are provided structurally modified neurotoxins, wherein the neurotoxin can be botulinum serotype A, B, C₁, C₂, D, E, F, G, tetanus toxin and/or mixtures thereof.

[0037] In some embodiments, there are provided structurally modified neurotoxins where the third region can be derived from botulinum toxin serotype A. In addition, there are provided structurally modified neurotoxins wherein the third region cannot be derived from botulinum serotype A.

[0038] In still another embodiment, there are provided structurally modified neurotoxins wherein the structural modification includes a biological persistence enhancing component effective to enhance the biological persistence of the structurally modified neurotoxin. The enhancing of the

biological persistence can be at least in part due to an increase in biological half-life and/or activity of the structurally modified neurotoxin.

[0039] Further in accordance with the present invention, there are provided structurally modified neurotoxins comprising a biological persistence enhancing component, wherein the biological persistence enhancing component can comprise a leucine-based motif. The leucine-based motif can comprise a run of 7 amino acids, where a quintet of amino acids and a duplet of amino acids can comprise the leucine-based motif. The quintet of amino acids can define the amino terminal end of the leucine-based motif. The duplet of amino acids can define the carboxyl end of the leucine-based motif. There are provided structurally modified neurotoxins wherein the quintet of amino acids can comprise one or more acidic amino acids. For example, the acidic amino acid can be glutamate or aspartate. The quintet of amino acids can comprise a hydroxyl containing amino acid. The hydroxyl containing amino acid can be, for example, a serine, a threonine or a tyrosine. This hydroxyl containing amino acid can be phosphorylated. At least one amino acid comprising the duplet of amino acids can be a leucine, isoleucine, methionine, alanine, phenylalanine, tryptophan, valine or tyrosine. In addition, the duplet of amino acids in the leucine-based motif can be leucine-leucine, leucine-isoleucine, isoleucine-leucine or isoleucine-isoleucine, leucine-methionine. The leucine-based motif can be an amino acid sequence of phenylalanine-glutamate-phenylalanine-tyrosine-lysine-leucine-leucine.

[0040] In one embodiment, there are provided structurally modified neurotoxins wherein the modification can be a tyrosine-based motif. The tyrosine-based motif can comprise four amino acids. The amino acid at the N-terminal end of the tyrosine-based motif can be a tyrosine. The amino acid at the C-terminal end of the tyrosine-based motif can be a hydrophobic amino acid.

[0041] Further in accordance with the present invention, the third region can be derived from botulinum toxin serotype A or form one of the other botulinum toxin serotypes.

[0042] Still further in accordance with the present invention, there are provided structurally modified neurotoxins where the biological persistence of the structurally modified neurotoxin can be reduced relative to an identical neurotoxin without the structural modification. The reduced biological persistence can be in part due a decreased biological half-life and/or to a decrease biological activity of the neurotoxin.

[0043] In one embodiment, there are provided structurally modified neurotoxins, where the structural modification can include a leucine-based motif with a mutation of one or more amino acids comprising the leucine-based motif. The mutation can be a deletion or substitution of one or more amino acids of the leucine-based motif.

[0044] In some embodiments, there are provided structurally modified neurotoxins, where the structural modification includes a tyrosine-based motif with a mutation of one or more amino acids comprising the tyrosine-based motif. For example, the mutation can be a deletion or substitution of one or more amino acids of the tyrosine-based motif.

[0045] In still another embodiment, there are provided structurally modified neurotoxins, wherein the structural modification comprises an amino acid derivative with a mutation of the amino acid derivative or a mutation to a nucleotide or amino acid sequence which codes for the derivatization of the amino acid. For example, a deletion or substitution of

the derivatized amino acid or a nucleotide or amino acid sequence responsible for a derivatization of the derivatized amino acid. The amino acid derivative can be, for example, a myristylated amino acid, an N-glycosylated amino acid, or a phosphorylated amino acid. The phosphorylated amino acid can be produced by, for example, casein kinase II, protein kinase C or tyrosine kinase.

[0046] In one embodiment of the present invention, there are provided structurally modified neurotoxins, wherein the first, second and/or third regions of the structurally modified neurotoxins can be produced by recombinant DNA methodologies, i.e. produced recombinantly.

[0047] In some embodiments of the present invention, there are provided structurally modified neurotoxins, wherein the first, second and/or third region of the neurotoxin is isolated from a naturally existing Clostridial neurotoxin.

[0048] Another embodiment of the present invention provides a modified neurotoxin comprising a botulinum toxin (such as a botulinum toxin type A) which includes a structural modification which is effective to alter a biological persistence of the modified neurotoxin relative to an identical neurotoxin without the structural modification. The structural modification can comprise a deletion of amino acids 416 to 437 from a light chain of the neurotoxin of SEQ ID NO: 29.

[0049] In still another embodiment of the present invention there is provided a modified neurotoxin (such as a botulinum toxin type A) which includes a structural modification which is effective to alter a biological persistence of the modified neurotoxin relative to an identical neurotoxin without the structural modification. The structural modification can comprise a deletion of amino acids 1 to 8 from a light chain of the neurotoxin of SEQ ID NO: 29.

[0050] Still further in accordance with the present invention there is provided a modified neurotoxin, such as a botulinum toxin type A, which includes a structural modification which is effective to alter a biological persistence of the modified neurotoxin relative to an identical neurotoxin without the structural modification. The structural modification may comprise, for example, a deletion of 2 or more amino acids from 1 to 20 and a deletion of 2 or more amino acids from 398 to 437 from a light chain of the neurotoxin of SEQ ID NO: 29. In one embodiment, the structural modification comprises a deletion of amino acids 1 to 8 and 416 to 437 from a light chain of the neurotoxin of SEQ ID NO: 29. In some embodiments, the structural modification comprises a deletion of amino acids 1 to 9 and 416 to 437 from a light chain of the neurotoxin of SEQ ID NO: 29. With regard to deletion on either the 1-8 or 1-9 amino acids; after synthesis the initial Methionine (M) of, for example, BoNT/A is apparently post-translationally removed within Clostridia. Amino acids 1-8 do not include the initial Met residue. If one includes the initial Met residue, then amino acids 1-9 are removed. Of course a recombinant toxin would need a Met residue incorporated to start protein synthesis. It may or may not be removed following synthesis.

[0051] For example, a native synthesized BoNT/A can comprise: MPFVNKQFNYKD (SEQ ID NO: 14), whereas a native processed BoNT/A can comprise PFVNKQFNYKD (SEQ ID NO: 15). Thus a proposed 8 amino acid deletion of SEQ ID NO: 27 would retain the YKD amino acid residues, while a recombinantly produced deletion would retain the amino acid residues NYKD at position numbers 9-12 of SEQ ID NO: 14.

[0052] Still further in accordance with the present invention, there is provided a modified botulinum toxin, such as a modified botulinum toxin type A, which includes a structural modification effective to alter a biological persistence of the modified neurotoxin relative to an identical neurotoxin without said structural modification. The structural modification can comprise a substitution of leucine at position 427 for an alanine and a substitution of leucine at position 428 for an alanine in a light chain of said neurotoxin of SEQ ID NO: 29.

[0053] Additionally, the scope of the present invention also includes methods for enhancing the biological persistence and/or for enhancing the biological activity of a neurotoxin. In these methods, a structural modification can be fused or added to the neurotoxin, for example, the structural modification can be a biological persistence enhancing component and/or a biological activity enhancing component. Examples of structural modifications that can be fused or added to the neurotoxin are a leucine-based motif, a tyrosine-based motif and an amino acid derivative. Examples of amino acid derivatives are a myristylated amino acid, an N-glycosylated amino acid, and a phosphorylated amino acid. An amino acid can be phosphorylated by, for example, protein kinase C, casein kinase II or tyrosine kinase.

[0054] Also in accordance with the present invention, there are provided methods for reducing the biological persistence and/or for reducing the biological activity of a neurotoxin. These methods can comprise a step of mutating an amino acid of the neurotoxin. For example, an amino acid of a leucine-based motif within the neurotoxin can be mutated. Also, for example, one or more amino acids within a tyrosine-based motif of the neurotoxin can be mutated. Also, for example, an amino acid derivative for DNA or amino acid sequence responsible for the derivatization of the amino acid can be mutated. The derivatized amino acid can be a myristylated amino acid, a N-glycosylated amino acid, or a phosphorylated amino acid. The phosphorylated amino acid can be produced by, for example, protein kinase C, casein kinase II and tyrosine kinase. These mutations can be, for example, amino acid deletions or amino acids substitutions.

[0055] The present invention also includes methods for treating a condition. The methods can comprise a step of administering an effective dose of a structurally modified neurotoxin to a mammal to treat a condition. The structurally modified neurotoxin can include a structural modification. The structural modification is effective to alter the biological persistence and/or the biological activity of the neurotoxin. These methods for treating a condition can utilize a neurotoxin that does not comprise a leucine-based motif. Also, these methods for treating a condition can utilize a neurotoxin, which includes a biological persistence enhancing component and/or a biological activity enhancing component. The biological persistence or activity enhancing component can comprise, for example, a tyrosine-based motif, a leucine-based motif or an amino acid derivative. The amino acid derivative can be, for example, a myristylated amino acid, an N-glycosylated amino acid or a phosphorylated amino acid. The phosphorylated amino acid can be produced by, for example, protein kinase C, casein kinase II or tyrosine kinase. The condition treated can be a neuromuscular disorder, an autonomic disorder or pain. The treatment of a neuromuscular disorder can comprise a step of locally administering an effective amount of a modified neurotoxin to a muscle or a group of muscles. A method for treating an autonomic disorder can comprise a step of locally adminis-

tering an effective amount of a modified neurotoxin to a gland or glands. A method for treating pain can comprise a step of administering an effective amount of a modified neurotoxin to the site of the pain. In addition, the treatment of pain can comprise a step of administering an effective amount of a modified neurotoxin to the spinal cord.

[0056] Still further in accordance with the present invention, there are provided compositions and methods for treating with modified neurotoxins conditions including spasmodic dysphonia, laryngeal dystonia, oromandibular dysphonia, lingual dystonia, cervical dystonia, focal hand dystonia, blepharospasm, strabismus, hemifacial spasm, eyelid disorder, cerebral palsy, focal spasticity, spasmodic colitis, neurogenic bladder, anismus, limb spasticity, tics, tremors, bruxism, anal fissure, achalasia, dysphagia, lacrimation, hyperhydrosis, excessive salivation, excessive gastrointestinal secretions, pain from muscle spasms, headache pain, brow furrows and skin wrinkles.

[0057] The present invention also provides for isolated compositions which include a botulinum toxin light chain component and an intracellular structure component. The structure component interacts with the light chain component in a manner effective to facilitate or alter substrate proteolysis within a cell. Such a composition can have utility for research, diagnostic and therapeutic purposes. It is believed that toxin light chain localization is important for maintenance of the intracellular activity of, at least, the LC of BoNT. Thus, it is believed that an intracellular localization is an important factor in the long biological half life of LC/A. For example, our invention indicates that LC/A may be localized to the intracellular plasma membrane. Our experiments indicate that the LC/A may not be actually inserted into the plasma membrane, but may be instead directly associated with proteins that reside at or near the plasma membrane.

[0058] Also provided are methods of producing an isolated composition comprising a botulinum toxin light chain component and an intracellular structure component wherein the structure component interacts with the light chain component in a manner effective to facilitate substrate proteolysis within a cell. The methods may include the steps of: 1) interacting a botulinum toxin light chain component with an intracellular structure component at conditions effective to facilitate proteolysis of a substrate within a cell; and 2) isolating the composition. Compositions which include a modified botulinum toxin light chain and a structure component may be isolated by these methods as well.

[0059] In one embodiment, the light chain component is a type A toxin light chain component and the intracellular structure component is a plasma membrane, for example a plasma membrane of a mammalian cell.

[0060] In some embodiments, the light chain component is a type B toxin light chain component and the intracellular structure includes a cytoplasm component. The cytoplasm component may include mitochondria, nucleus, endoplasmic reticulum, golgi apparatus, lysosomes or secretory vesicles or combination thereof. The cytoplasm component may include any portion of an organelle, for example, the membrane of an organelle. Further, the cytoplasm component may also include any substance which is included inside a cell. In one embodiment, the cytoplasm component is from a mammalian cell.

[0061] The structure component of the present invention may include a cell membrane. The cell membrane may be a plasma membrane, for example, a plasma membrane of a mammalian cell.

[0062] The structure component may include a protein complex. In one embodiment, the protein complex includes a light chain component. A protein complex may also include a substrate of the light chain. In one embodiment, the substrate is an intracellular component involved in exocytosis. For example, the substrate may be SNAP-25. A protein complex may be between about 100 kDa and about 1000 kDa or more. In one embodiment, the protein complex is between about 100 kDa and about 400 kDa. For example, the protein complex may be about 110 kDa, about 140 kDa or about 170 kDa.

[0063] Our invention also includes an isolated composition comprising a botulinum toxin light chain component and an intracellular structure component wherein the structure component interacts with the light chain component in a manner effective to facilitate substrate proteolysis within a cell, where the light chain component comprises a C-terminal portion of a botulinum toxin light chain. Thus, our invention encompasses what can be referred to as a "swapping of tails". For example our invention encompasses a chimeric toxin protein where the C-terminal tail of LC/A and LC/E are swapped or changed. Also included within the scope of our invention is a modified or chimeric toxin molecule wherein the N-terminus of the LC of one botulinum toxin serotype are swapped or exchanged for the N-terminus of the LC of another botulinum toxin serotype.

[0064] Without wishing to be bound by theory, it can be hypothesized that toxin LC localization can provide a protective role (i.e. protective from cellular proteases) and thereby provide the LC of, for example, BoNT/A with its extended duration of action.

[0065] It is conceivable that a modified toxin could be cytosolic with full enzymatic activity, and only the duration of action is modified. Our invention encompasses a cytoplasmic botulinum toxin light chain that does not interact with an intracellular structure component. For example, upon removal of the targeting sequence of BoNT/A it can accumulate in the cytosol and exhibit a shorter duration of action, and not interact with an intracellular structure component in a specific manner.

[0066] Thus, the presence of localizing signals and interaction with cellular partners can be important for sequestration of LC/A from cellular proteases. In this manner, sequestration or protection of the LC may be responsible for the long duration of action of BoNT/A by protection of the LC potentially extending the enzymatic activity beyond that of a LC lacking any localization or interacting signals.

[0067] In the present compositions, the light chain component may include the light chain of botulinum toxin type A, B, C, D, E, F or G or a portion thereof or a modified light chain thereof. In one embodiment, the light chain component comprises a C-terminal portion of a botulinum toxin light chain.

[0068] In one embodiment, a modified light chain is a light chain with an added biological activity- or biological persistence-enhancing component effective to enhance the proteolytic activity of the light chain. For example, the enhancing component may include a leucine based motif of SEQ ID No: 1.

[0069] In some embodiments, a modified light chain component is a light chain with a mutation to one or more amino acids included in the light chain to reduce the proteolytic

activity of the light chain. For example, the mutation may be in a biological activity/persistence enhancing component of the light chain, for example, in a leucine based motif of SEQ ID NO: 1.

[0070] Any combination of features described herein are included within the scope of the present invention provided that the features included in any such combination are not mutually inconsistent as will be apparent from the context, this specification, and the knowledge of one of ordinary skill in the art.

[0071] Additional advantages and aspects of the present invention are apparent in the following detailed description and claims.

BRIEF DESCRIPTION OF THE DRAWINGS

[0072] FIG. 1 shows localization of GFP-botulinum toxin A light chain in (nerve growth factor) NGF-differentiated live PC12 cells visualized on a fluorescence inverted microscope. The arrow indicates that GFP-botulinum toxin A light chain localizes to the plasma membrane.

[0073] FIG. 2 shows the localization of GFP-truncated botulinum toxin A light chain in NGF-differentiated live PC12 cells visualized on a fluorescence inverted microscope. The arrow indicates that GFP-truncated botulinum toxin A light chain localizes to punctate bodies inside the cytoplasm.

[0074] FIG. 3 shows the amino acid sequence for botulinum type A light chain. The amino acid sequence of SEQ ID NO: 29 shown, minus the underlined amino acids represents botulinum type A truncated light chain. The overline labeled $\Delta N8$ indicates the eight amino acids deleted from the amino terminus of the light chain, the overline labeled $\Delta C22$ indicates the 22 amino acids deleted from the carboxy terminus of the light chain. The double underline indicates the leucine-based motif and the dotted lines indicate tyrosine-based motifs.

[0075] FIG. 4 shows the localization of GFP-botulinum toxin A light chain with LL to AA mutation at position 427 and 428 in NGF-differentiated live PC12 cells visualized on a fluorescence inverted microscope. The arrow indicates that GFP-botulinum toxin A light chain with LL to AA mutation localizes to punctate bodies inside the cytoplasm.

[0076] FIG. 5 shows localization of fluorescently labeled anti-SNAP-25 visualized in horizontal confocal sections of staurosporine-differentiated PC12 cells.

[0077] FIG. 6 shows an x-ray crystallographic structure of botulinum toxin type A. The arrow indicates that SNAP-25 localizes to the plasma membrane.

[0078] FIG. 7 shows localization of GFP-botulinum type B neurotoxin light chain in NGF-differentiated live PC12 cells visualized on a fluorescence inverted microscope. The arrow indicates that GFP-botulinum toxin B light chain localizes to punctate bodies inside the cytoplasm.

[0079] FIG. 8 shows sequence alignment and consensus sequence for botulinum toxin type A Hall A light chain of SEQ ID NO: 29 and botulinum toxin type B Danish I light chain of SEQ ID NO: 30.

[0080] FIG. 9 is a graph which illustrates the results of an in vitro ELISA assay carried out by the inventors demonstrating that a truncated LC/A in vitro cleaves substrate at a slower rate or less efficiently than does non-truncated LC/A.

[0081] FIG. 10 shows a comparison of LC/A constructs expressed from *E. coli* for in vitro analysis. The LC/A (WT) sequences shown are amino acids 2-14 of SEQ ID NO: 29 (Amino terminus) and amino acids 412-438 of SEQ ID NO:

29 (Carboxyl Terminus). The LC/A ($\Delta N8/\Delta C22$) sequences shown are SEQ ID NO: 25 (Amino terminus) and SEQ ID NO: 26 (Carboxyl Terminus). The N-His LC/A (WT) sequences shown are SEQ ID NO: 148 (Amino terminus) and amino acids 412-438 of SEQ ID NO: 29 (Carboxyl Terminus).

[0082] FIG. 11 shows a ribbon diagram of LC/A with a Connolly surface overlay. The coordinates were extracted from the holotoxin x-ray structure (Protein Data Bank accession I.D. 3BTA) from Lacy et al., *Nat. Struct. Biol.*, 5, 898 (1998). Residues 1-430 are shown in the structure, the 8 C-terminal amino acids were not resolved in the holotoxin structure.

[0083] FIG. 12 shows the detection of GFP-LC fusion proteins expressed in differentiated PC12 cells by western blot.

[0084] FIG. 13 is a western blot showing GFP-LC activity.

[0085] FIG. 14 shows the *E. coli* recombinant constructs for expression of rLC/A and mutants.

[0086] FIG. 15 shows a SNAP-25 ELISA assay data showing in vitro activity of *E. coli* expressed rLC/A and mutants.

[0087] FIG. 16 shows localization of GFP-LC/A at the plasma membrane of PC12 cells by confocal microscopy. Images are from slices at approximately the middle of the cell.

[0088] FIG. 17 shows PC12 cells transfected with plasmids encoding GFP-LCA($\Delta N/\Delta C$) and LCA($\Delta N/\Delta C$)-GFP. The N- and C-terminal truncated form of LC/A may be localized to an internal structure or accumulated within the cell rather than at the plasma membrane. Confocal microscope images are taken from slices at approximately the middle of the cell.

[0089] FIG. 18 shows confocal images of GFP-LCA(LL-->AA) expressed in PC12 cells. This construct shows a mixed pattern of localization. Some cells seem to have protein localized to the plasma membrane as well as the cytosol, other cells have primarily cytosolic protein, while others are localized to near the plasma membrane, but in a much more diffuse manner than GFP-LC/A (similar to other reported dileucine mutants).

[0090] FIG. 19 shows the expression of transfected light chains in differentiated PC12 cells.

[0091] FIG. 20 shows activity assessed by western blot of the lysate of transfected cells. FIG. 20A shows the presence of the SNAP-25₁₉₇ BoNT/A cleavage product in lysates containing GFP-LCA and GFP+LCA, but not GFP alone. FIG. 20B shows the presence of the SNAP-25₁₈₀ BoNT/E cleavage product in lysates containing GFP-LCE, but not GFP alone.

[0092] FIG. 21 shows that light chain A localizes to the plasma membrane. The top panel shows that GFP alone exhibits a diffuse cytoplasmic localization. However, the bottom panel shows that GFP-botulinum toxin A light chain localizes to the plasma membrane.

[0093] FIG. 22 shows that light chain B localizes in the cytoplasm. The top panel shows that GFP-botulinum toxin B light chain exhibits a diffuse cytoplasmic localization. The bottom panel shows that botulinum toxin B light chain-GFP localizes to punctate bodies inside the cytoplasm.

[0094] FIG. 23 shows that Light Chain E also localizes primarily in the cytoplasm. The top panel shows that GFP-botulinum toxin E light chain exhibits a semi-diffuse cytoplasmic localization. The bottom panel shows that botulinum toxin B light chain-GFP exhibits a diffuse cytoplasmic localization.

[0095] FIG. 24 shows that expressed LCs inhibit exocytosis.

[0096] FIG. 25 shows localization of GFP in HeLa and HEK293T cells.

[0097] FIG. 26 shows detection of GFP-LC fusion proteins expressed in HeLa cells.

[0098] FIG. 27 shows localization of Light Chains in HeLa is similar to PC12 Cells. The panel on the left shows that GFP-botulinum toxin A light chain localizes to the plasma membrane. The middle panel shows that GFP-botulinum toxin B light chain exhibits a diffuse cytoplasmic localization. The panel on the right shows that GFP-botulinum toxin E light chain exhibits a semi-diffuse cytoplasmic localization.

[0099] FIG. 28 shows the detection of GFP-LC fusion proteins expressed in HEK 293T cells.

[0100] FIG. 29 shows HEK293T cells transfected with plasmids encoding GFP-LCA, GFP-LCE, GFP-LCB, and LCB-GFP. The panel on the left shows that GFP-botulinum toxin A light chain localizes to the plasma membrane. The middle panel shows that GFP-botulinum toxin B light chain exhibits a diffuse cytoplasmic localization. The panel on the right shows that GFP-botulinum toxin E light chain exhibits a semi-diffuse cytoplasmic localization.

[0101] FIG. 30 shows western blots probed with a polyclonal antibody to LCA to determine the size of the complex containing GFP-LCA. PC-12 cells were treated with DPBT prior to lysis and the samples were immunoprecipitated using a monoclonal antibody for GFP. The western blot of the samples separated under reducing conditions shows a 80 kDa protein corresponding to GFP-LCA (FIG. 30A). FIG. 30B shows the western blot of immunoprecipitated samples separated under non-reducing conditions leaving the cross linking agent uncleaved. Three different sized protein complexes containing GFP-LCA were detected. The 120 kDa protein is not completely defined. The 80 kDa protein is GFP-LCA.

[0102] FIG. 31 shows western Blots probed with a polyclonal antibody to SNAP-25 to determine if the immunoprecipitated protein complexes containing GFP-LCA (FIG. 30) also contain SNAP-25. FIG. 31A shows the western blot of the samples separated under reduced conditions. A 25 kDa protein is detected in the GFP-LCA sample corresponding to SNAP-25. FIG. 31B shows the western blot of samples separated under non-reducing conditions. The three protein bands detected with the antibody for SNAP-25 were detected with the antibody for LCA. These data indicate LCA forms a complex with SNAP-25 when transfected into PC-12 cells.

[0103] FIG. 32 is a graph showing the % of norepinephrine released from PC-12 cells when placed in buffers containing various concentrations of $\text{Ca}^{2+}/\text{K}^{+}$. The cells were untreated (control), electroporated, or electroporated in the presence of 500 nM PURE-A (electroporation/Pure A). Norepinephrine secretion was lower in PC-12 cells electroporated with 500 nM PURE-A. These results indicate an inhibition of PC-12 exocytosis caused by BoNT-A can be detected. The Y-axis shows the % of norepinephrine released.

[0104] FIG. 33 is a graph showing the % norepinephrine released from PC-12 cells exposed to 500 nM PURE A for up to three days. Exocytosis was measured in cells placed in buffer containing 100 mM KCl without (light shaded bar) or with 2.2 mM CaCl_2 (Dark Shaded Bar). Exposure to 500 nM PURE A for up to three days has no effect on exocytosis by PC-12 cells. The Y-axis shows the % of norepinephrine released.

[0105] FIG. 34 is a graph showing the % norepinephrine released from PC-12 cells transfected with various plasmid constructs containing GFP and light chain fusion proteins.

Exocytosis was measured in cells placed in buffer containing 100 mM KCl without (light shaded bar) or with 2.2 mM CaCl_2 (dark shaded bar). The constructs containing the light chain inhibited exocytosis when expressed in PC-12 cells. The Y-axis shows the % of norepinephrine released.

[0106] FIG. 35 is a graph showing the amount of insulin secreted by HIT-T15 cells placed in media containing high (25.2 mM) and low concentrations (5.6 mM) of glucose. The cells were untreated (control), electroporated, or electroporated in the presence of 500 nM PURE-A (electroporation/Pure A). PURE-A inhibited insulin secretion in electroporated HIT-T15 cells. The Y-axis shows the insulin released in ng/100,000 cells/hr.

[0107] FIG. 36 shows a western blot of a cell lysate of HIT-T15 cell treated with PURE A. The blot was probed with a polyclonal antibody for the cleaved SNAP-25 produced by BoNT-A (SNAP-25₁₉₇). The cells were untreated (control)-lane 1, electroporated-lane 2, or electroporated in the presence of 500 nM PURE-A (electroporation/Pure A)-lane 3.

[0108] FIG. 37 is a graph showing the amount of insulin released from HIT-T15 cells transfected with various plasmid constructs containing GFP and light chain fusion proteins. Exocytosis was measured in cells placed in media containing 5.6 mM glucose (light shaded bar) or 25.6 mM glucose (dark shaded bar). The constructs containing the light chain inhibited exocytosis when expressed in PC-12 cells. The Y-axis shows the insulin released in ng/1,000,000 cells/hr.

DETAILED DESCRIPTION

[0109] The present invention is based upon the discovery that the biological persistence and/or the biological activity of a neurotoxin can be altered by structurally modifying the neurotoxin. In other words, a modified neurotoxin with an altered biological persistence and/or biological activity can be formed from a neurotoxin containing or including a structural modification. In one embodiment, the structural modification includes the fusing of a biological persistence enhancing component to the primary structure of a neurotoxin to enhance its biological persistence. In a suitable embodiment, the biological persistence enhancing component is a leucine-based motif. Even more preferably, the biological half-life and/or the biological activity of the modified neurotoxin is enhanced by about 100%. Generally speaking, the modified neurotoxin has a biological persistence of about 20% to 300% more than an identical neurotoxin without the structural modification. That is, for example, the modified neurotoxin including the biological persistence enhancing component is able to cause a substantial inhibition of neurotransmitter release for example, acetylcholine from a nerve terminal for about 20% to about 300% longer than a neurotoxin that is not modified.

[0110] The present invention also includes within its scope a modified neurotoxin with a biological activity altered as compared to the biological activity of the native or unmodified neurotoxin. For example, the modified neurotoxin can exhibit a reduced or an enhanced inhibition of exocytosis (such as exocytosis of a neurotransmitter) from a target cell with or without any alteration in the biological persistence of the modified neurotoxin.

[0111] In a broad embodiment of the present invention, a leucine-based motif is a run of seven amino acids. The run is organized into two groups. The first five amino acids starting from the amino terminal of the leucine-based motif form a "quintet of amino acids." The two amino acids immediately

following the quintet of amino acids form a “duplet of amino acids.” In a suitable embodiment, the duplet of amino acids is located at the carboxyl terminal region of the leucine-based motif. In a suitable embodiment, the quintet of amino acids includes at least one acidic amino acid selected from a group consisting of a glutamate and an aspartate.

[0112] The duplet of amino acid includes at least one hydrophobic amino acid, for example leucine, isoleucine, methionine, alanine, phenylalanine, tryptophan, valine or tyrosine. Preferably, the duplet of amino acid is a leucine-leucine, a leucine-isoleucine, an isoleucine-leucine or an isoleucine-isoleucine, leucine-methionine. Even more preferably, the duplet is a leucine-leucine.

[0113] In one embodiment, the leucine-based motif is xDxxxLL (SEQ ID NO: 17), wherein x can be any amino acids. In another embodiment, the leucine-based motif is xExxxLL (SEQ ID NO: 18), wherein E is glutamic acid. In another embodiment, the duplet of amino acids can include an isoleucine or a methionine, forming xDxxxLI (SEQ ID NO: 19) or xDxxxLM (SEQ ID NO: 20), respectively. Additionally, the aspartic acid, D, can be replaced by a glutamic acid, E, to form xExxxLI (SEQ ID NO: 21), xExxxIL (SEQ ID NO: 22) and xExxxLM (SEQ ID NO: 23). In a preferred embodiment, the leucine-based motif is phenylalanine-glutamate-phenylalanine-tyrosine-lysine-leucine-leucine, SEQ ID NO: 1.

[0114] In some embodiments, the quintet of amino acids comprises at least one hydroxyl containing amino acid, for example, a serine, a threonine or a tyrosine. Preferably, the hydroxyl containing amino acid can be phosphorylated. More preferably, the hydroxyl containing amino acid is a serine which can be phosphorylated to allow for the binding of adapter proteins.

[0115] Although non-modified amino acids are provided as examples, a modified amino acid is also contemplated to be within the scope of this invention. For example, leucine-based motif can include a halogenated, preferably, fluorinated leucine.

[0116] Various leucine-based motif are found in various species. A list of possible leucine-based motif derived from the various species that can be used in accordance with this invention is shown in Table 1. This list is not intended to be limiting.

TABLE 1

Species	Sequence	SEQ ID NO:
Botulinum type A	FEFYKLL	1
Rat VMAT1	EEKRAIL	2
Rat VMAT2	EEKMAIL	3
Rat VACHT	SERDVLL	4
Rat δ	VDTQVLL	5
Mouse δ	AEVQALL	6
Frog γ/δ	SDKQNLL	7
Chicken γ/δ	SDRQNLI	8
Sheep δ	ADTQVLM	9
Human CD3 γ	SDKQTL	10

TABLE 1-continued

Species	Sequence	SEQ ID NO:
Human CD4	SQIKRLL	11
Human δ	ADTQALL	12
<i>S. cerevisiae</i> Vam3p	NEQSPLL	13

[0117] VMAT is vesicular monoamine transporter; VACHT is vesicular acetylcholine transporter and *S. cerevisiae* Vam3p is a yeast homologue of synaptobrevin. Italicized serine residues are potential sites of phosphorylation.

[0118] The modified neurotoxin can be formed from any neurotoxin. Also, the modified neurotoxin can be formed from a fragment of a neurotoxin, for example, a botulinum toxin with a portion of the light chain and/or heavy chain removed. Preferably, the neurotoxin used is a Clostridial neurotoxin. A Clostridial neurotoxin comprises a polypeptide having three amino acid sequence regions. The first amino acid sequence region can include a target cell (i.e. a neuron) binding moiety which is substantially completely derived from a neurotoxin selected from a group consisting of beratti toxin; butyricum toxin; tetanus toxin; botulinum type A, B, C₁, D, E, F, and G. Preferably, the first amino acid sequence region is derived from the carboxyl terminal region of a toxin heavy chain, H_C. Also, the first amino acid sequence region can comprise a targeting moiety which can comprise a molecule (such as an amino acid sequence) that can bind to a receptor, such as a cell surface protein or other biological component on a target cell.

[0119] The second amino acid sequence region is effective to translocate the polypeptide or a part thereof across an endosome membrane into the cytoplasm of a neuron. In one embodiment, the second amino acid sequence region of the polypeptide comprises an amine terminal of a heavy chain, H_N, derived from a neurotoxin selected from a group consisting of beratti toxin; butyricum toxin; tetanus toxin; botulinum type A, B, C₁, D, E, F, and G.

[0120] The third amino acid sequence region has therapeutic activity when it is released into the cytoplasm of a target cell, such as a neuron. In one embodiment, the third amino acid sequence region of the polypeptide comprises a toxin light chain, L, derived from a neurotoxin selected from a group consisting of beratti toxin; butyricum toxin; tetanus toxin; botulinum type A, B, C₁, D, E, F, and G.

[0121] The Clostridial neurotoxin can be a hybrid neurotoxin. For example, each of the neurotoxin's amino acid sequence regions can be derived from a different Clostridial neurotoxin serotype. For example, in one embodiment, the polypeptide comprises a first amino acid sequence region derived from the H_C of the tetanus toxin, a second amino acid sequence region derived from the H_N of botulinum type B, and a third amino acid sequence region derived from the light chain of botulinum serotype E. All other possible combinations are included within the scope of the present invention.

[0122] Alternatively, all three of the amino acid sequence regions of the Clostridial neurotoxin can be from the same species and same serotype. If all three amino acid sequence regions of the neurotoxin are from the same Clostridial neurotoxin species and serotype, the neurotoxin will be referred to by the species and serotype name. For example, a neurotoxin polypeptide can have its first, second and third amino

acid sequence regions derived from Botulinum type E. In which case, the neurotoxin is referred as Botulinum type E.

[0123] Additionally, each of the three amino acid sequence regions can be modified from the naturally occurring sequence from which they are derived. For example, the amino acid sequence region can have at least one or more amino acids added or deleted as compared to the naturally occurring sequence.

[0124] A biological persistence enhancing component or a biological activity enhancing component, for example a leucine-based motif, can be fused with any of the above described neurotoxins to form a modified neurotoxin with an enhanced biological persistence and/or an enhanced biological activity. "Fusing" as used in the context of this invention includes covalently adding to or covalently inserting in between a primary structure of a neurotoxin. For example, a biological persistence enhancing component and/or a biological activity enhancing component can be added to a Clostridial neurotoxin which does not have a leucine-based motif in its primary structure. In one embodiment, a leucine-based motif is fused with a hybrid neurotoxin, wherein the third amino acid sequence is derived from botulinum serotype A, B, C₁, C₂, D, E, F, or G. In some embodiments, the leucine-based motif is fused with a botulinum type E.

[0125] In some embodiments, a biological persistence enhancing component and/or a biological activity enhancing component is added to a neurotoxin by altering a cloned DNA sequence encoding the neurotoxin. For example, a DNA sequence encoding a biological persistence enhancing component and/or a biological activity enhancing component is added to a cloned DNA sequence encoding the neurotoxin into which the biological persistence enhancing component and/or a biological activity enhancing component is to be added. This can be done in a number of ways which are familiar to a molecular biologist of ordinary skill. For example, site directed mutagenesis or PCR cloning can be used to produce the desired change to the neurotoxin encoding DNA sequence. The DNA sequence can then be reintroduced into a native host strain. In the case of botulinum toxins the native host strain would be a *Clostridium botulinum* strain. Preferably, this host strain will be lacking the native botulinum toxin gene. In an alternative method, the altered DNA can be introduced into a heterologous host system such as *E. coli* or other prokaryotes, yeast, insect cell lines or mammalian cell lines. Once the altered DNA has been introduced into its host, the recombinant toxin containing the added biological persistence enhancing component and/or a biological activity enhancing component can be produced by, for example, standard fermentation methodologies.

[0126] Similarly, a biological persistence enhancing component can be removed from a neurotoxin. For example, site directed mutagenesis can be used to eliminate biological persistence enhancing components, for example, a leucine-based motif.

[0127] Standard molecular biology techniques that can be used to accomplish these and other genetic manipulations are found in Sambrook et al. (1989) which is incorporated in its entirety herein by reference.

[0128] In one embodiment, the leucine-based motif is fused with, or added to, the third amino acid sequence region of the neurotoxin. In a suitable embodiment, the leucine-based motif is fused with, or added to, the region towards the carboxylic terminal of the third amino acid sequence region. More preferably, the leucine-based motif is fused with, or

added to, the carboxylic terminal of the third region of a neurotoxin. Even more preferably, the leucine-based motif is fused with, or added to the carboxylic terminal of the third region of botulinum type E. The third amino acid sequence to which the leucine-based motif is fused or added can be a component of a hybrid or chimeric modified neurotoxin. For example, the leucine-based motif can be fused to or added to the third amino acid sequence region (or a part thereof) of one botulinum toxin type (i.e. a botulinum toxin type A), where the leucine-based motif-third amino acid sequence region has itself been fused to or conjugated to first and second amino acid sequence regions from another type (or types) of a botulinum toxin (such as botulinum toxin type B and/or E).

[0129] In some embodiments, a structural modification of a neurotoxin which has a pre-existing biological persistence enhancing component and/or a biological activity enhancing component, for example, a leucine-based motif includes deleting or substituting one or more amino acids of the leucine-based motif. In addition, a modified neurotoxin includes a structural modification which results in a neurotoxin with one or more amino acids deleted or substituted in the leucine-based motif. The removal or substitution of one or more amino acids from the preexisting leucine-based motif is effective to reduce the biological persistence and/or a biological activity of a modified neurotoxin. For example, the deletion or substitution of one or more amino acids of the leucine-based motif of botulinum type A reduces the biological half-life and/or the biological activity of the modified neurotoxin.

[0130] Amino acids that can be substituted for amino acids contained in a biological persistence enhancing component include alanine, asparagine, cysteine, aspartic acid, glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, leucine, methionine, proline, glutamine, arginine, serine, threonine, valine, tryptophan, tyrosine and other naturally occurring amino acids as well as non-standard amino acids.

[0131] In the present invention the native botulinum type A light chain has been shown to localize to differentiated PC12 cell membranes in a characteristic pattern. Biological persistence enhancing components are shown to substantially contribute to this localization.

[0132] The data of the present invention demonstrates that when the botulinum toxin type A light chain is truncated or when the leucine-based motif is mutated, the light chain substantially loses its ability to localize to the membrane in its characteristic pattern. Localization to the cellular membrane is believed to be a key factor in determining the biological persistence and/or the biological activity of a botulinum toxin. This is because localization to a cell membrane can protect the localized protein from intracellular protein degradation.

[0133] FIGS. 1 and 2 show that deletion of the leucine-based motif from the light chain of botulinum type A can change membrane localization of the type A light chain. FIG. 1 shows localization of GFP-light chain A fusion protein in differentiated PC12 cells. The GFP fusion proteins were produced and visualized in differentiated PC12 cells using methods well known to those skilled in the art, for example, as described in Galli et al (1998) Mol Biol Cell 9:1437-1448, incorporated in its entirety herein by reference; also, for example, as described in Martinez-Arca et al (2000) J Cell Biol 149:889-899, also incorporated in its entirety herein by reference. Localization of a GFP-truncated light chain A is shown in FIG. 2. Comparing FIGS. 1 and 2, it can be seen that the pattern of localization is completely altered by the dele-

tion of the N-terminus and C-terminus comprising the leucine-based motif. FIG. 3 shows the amino acid sequence of the botulinum type A light chain. The underlined amino acid sequences indicate the amino acids that were deleted in the truncated mutant. The leucine-based motif is indicated by the asterisked bracket.

[0134] Further studies have been done in the present invention to analyze the effect of specific amino acid substitutions within the leucine-based motif. For example, in one study both leucine residues contained in the leucine-based motif were substituted for alanine residues. FIG. 4 shows the fluorescent image of differentiated PC12 cells transfected with DNA encoding this di-leucine to di-alanine substituted GFP-botulinum A light chain. As can be seen, the substitution of alanine for leucine at positions 427 and 428 in the botulinum type A light chain substantially changes the localization characteristic of the light chain.

[0135] It is within the scope of this invention that a leucine-based motif, or any other persistence enhancing component and/or a biological activity enhancing component present on a light chain, can be used to protect the heavy chain as well. A random coil belt extends from the botulinum type A translocation domain and encircles the light chain. It is possible that this belt keeps the two subunits in proximity to each other inside the cell while the light chain is localized to the cell membrane. The structure of native botulinum toxin type A is shown in FIG. 6.

[0136] In addition, the data of the present invention shows that the leucine-based motif can be valuable in localizing the botulinum A toxin in close proximity to the SNAP-25 substrate within the cell. This can mean that the leucine-based motif is important not only for determining the half-life of the toxin but for determining the activity of the toxin as well. That is, the toxin will have a greater activity if it is maintained in close proximity to the SNAP-25 substrate inside the cell. FIG. 5 shows the localization of SNAP-25 in horizontal confocal sections of differentiated PC12 cells (from Martinez-Arca et al (2000) *J Cell Biol* 149:889-899). Similarity in the pattern of localization can be seen when comparing localization of botulinum type A light chain as seen in FIG. 1 to localization of SNAP-25 seen in FIG. 5.

[0137] The data of the present invention clearly shows that truncation of the light chain, thereby deleting the leucine-based motif, or amino acid substitution within the leucine-based motif substantially changes membrane localization of the botulinum type A light chain in nerve cells. In both truncation and substitution a percentage of the altered light chain can localize to the cell membrane in a pattern unlike that of the native type A light chain (see FIGS. 1, 2 and 4). This data supports the presence of biological persistence enhancing components other than a leucine-based motif such as tyrosine motifs and amino acid derivatives. Use of these other biological persistence enhancing components and/or a biological activity enhancing components in modified neurotoxins is also within the scope of the present invention.

[0138] Also within the scope of the present invention is more than one biological persistence enhancing component used in combination in a modified neurotoxin to alter biological persistence of the neurotoxin that is modified. The present invention also includes use of more than one biological activity enhancing or biological activity reducing components used in combination in a modified neurotoxin to alter the biological activity of the neurotoxin that is modified.

[0139] Tyrosine-based motifs are within the scope of the present invention as biological persistence and/or a biological activity altering components. Tyrosine-based motifs comprise the sequence Y-X-X-Hy (SEQ ID NO: 24), where Y is tyrosine, X is any amino acid and Hy is a hydrophobic amino acid. Tyrosine-based motifs can act in a manner that is similar to that of leucine-based motifs. In FIG. 3 some of tyrosine motifs found in the type A toxin light chain are bracketed (SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, and SEQ ID NO: 38). In addition, a tyrosine-based motif is found within the leucine-based motif which is indicated by an asterisked bracket in FIG. 3.

[0140] Also within the scope of the present invention are modified neurotoxins which comprise one or more biological persistence altering components and/or a biological activity enhancing components which occur naturally in both botulinum toxin types A and B.

[0141] FIG. 7 shows localization of GFP-botulinum type B neurotoxin light chain in live, differentiated PC12 cells. Localization of the type B light chain appears to be to an intracellular organelle. Similar localization pattern is seen for GFP-truncated botulinum type A shown in FIG. 2. Localization of a botulinum toxin, or botulinum toxin light chain, within the cell is believed to be a key factor in determining biological persistence and/or biological activity of the toxin. Therefore, these data appear to indicate that there are biological persistence altering component(s), and/or biological activity altering component(s), common to the type A and type B botulinum toxins. These, and other biological persistence altering components, and biological activity altering components, are contemplated for use in accordance with the present invention.

[0142] FIG. 8 shows a sequence alignment between type A and type B light chains isolated from strains type A Hall A (SEQ ID NO: 29) and type B Danish I (SEQ ID NO: 30) respectively. Light chains or heavy chains isolated from other strains of botulinum toxin types A and B can also be used for sequence comparison. The shaded amino acids represent amino acid identities, or matches, between the chains. Each of the shaded amino acids between amino acid position 10 and amino acid position 425 of the FIG. 8 consensus sequence, alone or in combination with any other shaded amino acid or amino acids, represents a biological persistence altering component that is within the scope of the present invention. For example, amino acids KAFK at positions 19 to 22 of SEQ ID NO: 29, LNK at positions 304 to 306 of SEQ ID NO: 29, L at position 228 of SEQ ID NO: 29 in combination with KL at positions 95 and 96 of SEQ ID NO: 29, FDKLYK at positions 346 to 351 of SEQ ID NO: 29, YL-T at positions 78 to 81 of SEQ ID NO: 29, YYD at positions 73 to 75 of SEQ ID NO: 29 in combination with YL at positions 78 and 79 of SEQ ID NO: 29 in combination with T at position 81 of SEQ ID NO: 29, F at position 297 of SEQ ID NO: 29 in combination with I at position 300 of SEQ ID NO: 29 in combination with KL at positions 95 and 96 of SEQ ID NO: 29 can be biological persistence altering components for use within the scope of this invention. In addition, conserved regions of charge, hydrophobicity, hydrophilicity and/or conserved secondary, tertiary, or quaternary structures that may be independent of conserved sequence are within the scope of the present invention.

[0143] Amino acid derivatives are also within the scope of the present invention as biological persistence enhancing

components and/or as biological activity enhancing components. Examples of amino acid derivatives that act to effect biological persistence and/or biological activity are phosphorylated amino acids. These amino acids include, for example, amino acids phosphorylated by tyrosine kinase, protein kinase C or casein kinase II. Other amino acid derivatives within the scope of the present invention as biological persistence enhancing components and/or as biological activity enhancing components are myristylated amino acids and N-glycosylated amino acids.

[0144] The present invention also contemplates compositions which include a botulinum light chain component interacting with a cellular structure component, for example, an intracellular structure component. The structure component may include lipid, carbohydrate, protein or nucleic acid or any combination thereof.

[0145] The structure component may include a cell membrane, for example, a plasma membrane. In certain embodiments, the structure component comprises all or part of one or more organelles, for example, the nucleus, endoplasmic reticulum, golgi apparatus, mitochondria, lysosomes or secretory vesicles or combinations thereof. The structure component may include any portion of an organelle, for example, the membrane of an organelle. The structure component may also include any substance which is included in the cytoplasm of a cell.

[0146] The structure component may include one or more proteins. In a suitable embodiment, the structure component includes one or more cellular proteins. One or more of these cellular proteins may be membrane associated proteins, for example, plasma membrane associated proteins. In one embodiment of the invention, the structure component includes adaptor proteins. Examples of adaptor proteins are AP-1, AP-2 and AP-3. Adaptor proteins and their characteristics are well known in the art and are discussed in, for example, Darsow et al., *J. Cell Bio.*, 142, 913 (1998) which is incorporated in its entirety herein by reference. The one or more proteins may also include the substrate which is cleaved by the proteolytic domain of a botulinum toxin light chain component. For example, a protein included in the structure component may be SNAP-25.

[0147] The interaction between the light chain of botulinum type A and the structure component may contribute to localization of the toxin in a certain pattern. Therefore, the interaction may act to facilitate proteolysis by, for example, increasing the biological persistence and/or biological activity of the light chain.

[0148] A botulinum toxin heavy chain or portion thereof may also be associated with the light chain component when the light chain is interacting with the structure component.

[0149] In one embodiment, a botulinum toxin light chain component, when interacting with the structure component in a cell, may localize in the cell in a particular pattern. For example, localization of a botulinum toxin type A light chain component may be in a punctate or spotted pattern. For example, a botulinum type A light chain component may be localized in a punctate pattern on a cell membrane, for example, a plasma membrane. Botulinum type B light chain may localize in the cytoplasm. Botulinum type E may localize to the plasma membrane but to a lesser degree than type A. Botulinum type E may also localize in the cytoplasm.

[0150] Methodologies to produce an isolated composition of the invention are available to those skilled in the art. For example, a composition may be isolated by isolating the

plasma membrane from a cell after introduction of a light chain component, for example, light chain A, into a cell. The light chain may be introduced into the cell by, for example, electroporation or by endocytosis. In the case of introduction into the cell by endocytosis, a heavy chain component may be included with the light chain component to facilitate the endocytosis, for example, receptor mediated endocytosis, of the light chain. In such preparation process, the heavy chain component may also be isolated and be included in the composition.

[0151] After introduction into the cell, the light chain component associates or interacts with the substrate component forming a composition. The composition may be isolated by purification of the light chain component-structure component from the cell. Standard purification techniques known to those skilled in the art may be used to isolate a membrane and/or membrane associated protein(s) which is included in the structure component which interacts with the light chain component. Examples of conventional techniques for isolation and purification of the light chain component/structure component include immunoprecipitation and/or membrane purification techniques.

[0152] The light chain component may be crosslinked to a portion of the structure component before isolation. The technical procedures for cross linking of biomolecules using agents such as DTBP are well known to those skilled in the art.

[0153] In some embodiments, a composition of the invention may be prepared by mixing together a purified or a partially purified light chain component and a purified or a partially purified intracellular structure component under conditions which are effective to form the composition. Conditions important in forming the composition may include pH, ionic concentration and temperature.

[0154] The botulinum toxin light chain component of a composition, may be a modified botulinum toxin light chain. Modifications may be mutations and/or deletions as described elsewhere herein.

[0155] A modified light chain component may include a light chain A modified to remove a leucine based motif or other structure(s) which contributes to localization of the type A light chain to the plasma membrane thereby resulting in a light chain with a reduced ability to localize to a plasma membrane. This may result in a reduction in the biological activity and/or biological persistence of the light chain A. The biological persistence and/or activity of the modified light chain may be about 10% to about 90% that of an unmodified type A light chain.

[0156] Another modified light chain component may include a light chain A modified by adding one or more leucine based motifs, or other structure(s) which contributes to localization of the type A light chain to the plasma membrane, thereby resulting in a light chain with an increased ability to localize to a plasma membrane. This may result in an increase in the biological activity and/or biological persistence of the light chain A. The biological persistence and/or activity of the modified light chain may be about 1.5 to about 5 times that of an unmodified type A light chain.

[0157] Another modified light chain component may include a light chain B modified by adding one or more leucine based motifs, or other structure(s) which contributes to localization of the type A light chain to the plasma membrane, thereby resulting in a type B light chain with an increased ability to localize to a plasma membrane. This may

result in an increase in the biological activity and/or biological persistence of the light chain A. The biological persistence and/or activity of the modified light chain may be about 1.5 to about 10 times that of an unmodified type B light chain.

[0158] A modified light chain component may include a light chain E modified by adding one or more leucine based motifs, or other structure(s) which contribute to localization of the type A light chain to the plasma membrane, thereby resulting in a light chain with an increased ability to localize to a plasma membrane. This may result in an increase in the biological activity and/or biological persistence of the light chain A. The biological persistence and/or activity of the modified light chain may be about 2 to about 20 times that of an unmodified type E light chain.

[0159] Compositions of the invention have many uses and applications, for example, in research science and medicine. Other uses and applications will be readily apparent to those skilled in the art.

[0160] In one broad aspect of the present invention, a method is provided for treating a condition using a modified neurotoxin. The conditions can include, for example, skeletal muscle conditions, smooth muscle conditions, pain and glandular conditions. The modified neurotoxin can also be used for cosmetics, for example, to treat brow furrows.

[0161] The neuromuscular disorders and conditions that can be treated with a modified neurotoxin include: for example, spasmodic dysphonia, laryngeal dystonia, oromandibular and lingual dystonia, cervical dystonia, focal hand dystonia, blepharospasm, strabismus, hemifacial spasm, eyelid disorders, spasmodic torticollis, cerebral palsy, focal spasticity and other voice disorders, spasmodic colitis, neurogenic bladder, anismus, limb spasticity, tics, tremors, bruxism, anal fissure, achalasia, dysphagia and other muscle tone disorders and other disorders characterized by involuntary movements of muscle groups can be treated using the present methods of administration. Other examples of conditions that can be treated using the present methods and compositions are lacrimation, hyperhydrosis, excessive salivation and excessive gastrointestinal secretions, as well as other secretory disorders. In addition, the present invention can be used to treat dermatological conditions, for example, reduction of brow furrows, reduction of skin wrinkles. The present invention can also be used in the treatment of sports injuries.

[0162] Borodic U.S. Pat. No. 5,053,005 discloses methods for treating juvenile spinal curvature, i.e. scoliosis, using botulinum type A. The disclosure of Borodic is incorporated in its entirety herein by reference. In one embodiment, using substantially similar methods as disclosed by Borodic, a modified neurotoxin can be administered to a mammal, preferably a human, to treat spinal curvature. In a suitable embodiment, a modified neurotoxin comprising botulinum type E fused with a leucine-based motif is administered. Even more preferably, a modified neurotoxin comprising botulinum type A-E with a leucine-based motif fused to the carboxyl terminal of its light chain is administered to the mammal, preferably a human, to treat spinal curvature.

[0163] In addition, the modified neurotoxin can be administered to treat other neuromuscular disorders using well known techniques that are commonly performed with botulinum type A. For example, the present invention can be used to treat pain, for example, headache pain, pain from muscle spasms and various forms of inflammatory pain. For example, Aoki U.S. Pat. No. 5,721,215 and Aoki U.S. Pat. No. 6,113,915 disclose methods of using botulinum toxin type A for

treating pain. The disclosure of these two patents is incorporated in its entirety herein by reference.

[0164] Autonomic nervous system disorders can also be treated with a modified neurotoxin. For example, glandular malfunctioning is an autonomic nervous system disorder. Glandular malfunctioning includes excessive sweating and excessive salivation. Respiratory malfunctioning is another example of an autonomic nervous system disorder. Respiratory malfunctioning includes chronic obstructive pulmonary disease and asthma. Sanders et al. disclose methods for treating the autonomic nervous system; for example, treating autonomic nervous system disorders such as excessive sweating, excessive salivation, asthma, etc., using naturally existing botulinum toxins. The disclosure of Sander et al. is incorporated in its entirety by reference herein. In one embodiment, substantially similar methods to that of Sanders et al. can be employed, but using a modified neurotoxin, to treat autonomic nervous system disorders such as the ones discussed above. For example, a modified neurotoxin can be locally applied to the nasal cavity of the mammal in an amount sufficient to degenerate cholinergic neurons of the autonomic nervous system that control the mucous secretion in the nasal cavity.

[0165] Pain that can be treated by a modified neurotoxin includes pain caused by muscle tension, or spasm, or pain that is not associated with muscle spasm. For example, Binder in U.S. Pat. No. 5,714,468 discloses that headache caused by vascular disturbances, muscular tension, neuralgia and neuropathy can be treated with a naturally occurring botulinum toxin, for example Botulinum type A. The disclosures of Binder are incorporated in its entirety herein by reference. In one embodiment, substantially similar methods to that of Binder can be employed, but using a modified neurotoxin, to treat headache, especially the ones caused by vascular disturbances, muscular tension, neuralgia and neuropathy. Pain caused by muscle spasm can also be treated by an administration of a modified neurotoxin. For example, a botulinum type E fused with a leucine-based motif, preferably at the carboxyl terminal of the botulinum type E light chain, can be administered intramuscularly at the pain/spasm location to alleviate pain.

[0166] Furthermore, a modified neurotoxin can be administered to a mammal to treat pain that is not associated with a muscular disorder, such as spasm. In one broad embodiment, methods of the present invention to treat non-spasm related pain include central administration or peripheral administration of the modified neurotoxin.

[0167] For example, Foster et al. in U.S. Pat. No. 5,989,545 discloses that a botulinum toxin conjugated with a targeting moiety can be administered centrally (intrathecally) to alleviate pain. The disclosures of Foster et al. are incorporated in its entirety by reference herein. In one embodiment, substantially similar methods to that of Foster et al. can be employed, but using the modified neurotoxin according to this invention, to treat pain. The pain to be treated can be an acute pain, or preferably, chronic pain.

[0168] An acute or chronic pain that is not associated with a muscle spasm can also be alleviated with a local, peripheral administration of the modified neurotoxin to an actual or a perceived pain location on the mammal. In one embodiment, the modified neurotoxin is administered subcutaneously at or near the location of pain, for example, at or near a cut. In some embodiments, the modified neurotoxin is administered intramuscularly at or near the location of pain, for example, at or

near a bruise location on the mammal. In some embodiments, the modified neurotoxin is injected directly into a joint of a mammal, for treating or alleviating pain caused by arthritic conditions. Also, frequent repeated injection or infusion of the modified neurotoxin to a peripheral pain location is within the scope of the present invention. However, given the long lasting therapeutic effects of the present invention, frequent injection or infusion of the neurotoxin can not be necessary. For example, practice of the present invention can provide an analgesic effect, per injection, for 2 months or longer, for example 27 months, in humans.

[0169] Without wishing to limit the invention to any mechanism or theory of operation, it is believed that when the modified neurotoxin is administered locally to a peripheral location, it inhibits the release of Neuro-substances, for example substance P, from the peripheral primary sensory terminal by inhibiting SNARE-dependent exocytosis. Since the release of substance P by the peripheral primary sensory terminal can cause or at least amplify pain transmission process, inhibition of its release at the peripheral primary sensory terminal will dampen the transmission of pain signals from reaching the brain.

[0170] In addition to having pharmacologic actions at the peripheral location, the modified neurotoxin of the present invention can also have inhibitory effects in the central nervous system, upon direct intrathecal administration, as set forth in U.S. Pat. No. 6,113,915, or upon peripheral administration, where presumably the modified toxin acts through retrograde transport via a primary sensory afferent. This hypothesis of retrograde axonal transport is supported by published data which shows that botulinum type A can be retrograde transported to the dorsal horn when the neurotoxin is injected peripherally. Thus, work by Weigand et al, *Naunyn-Schmiedeberg's Arch. Pharmacol.* 1976; 292, 161-165, and Habermann, *Naunyn-Schmiedeberg's Arch. Pharmacol.* 1974; 281, 47-56, showed that botulinum toxin is able to ascend to the spinal area by retrograde transport. As such, a modified neurotoxin, for example botulinum type A with one or more amino acids mutated from the leucine-based motif, injected at a peripheral location, for example intramuscularly, can be expected to be retrograde transported from the peripheral primary sensory terminal to a central region.

[0171] The amount of the modified neurotoxin administered can vary widely according to the particular disorder being treated, its severity and other various patient variables including size, weight, age, and responsiveness to therapy. Generally, the dose of modified neurotoxin to be administered will vary with the age, presenting condition and weight of the mammal, preferably a human, to be treated. The potency of the modified neurotoxin will also be considered.

[0172] Assuming a potency (for a botulinum toxin type A) which is substantially equivalent to $LD_{50}=2,730$ U in a human patient and an average person is 75 kg, a lethal dose (for a botulinum toxin type A) would be about 36 U/kg of a modified neurotoxin. Therefore, when a modified neurotoxin with such an LD_{50} is administered, it would be appropriate to administer less than 36 U/kg of the modified neurotoxin into human subjects. Preferably, about 0.01 U/kg to 30 U/kg of the modified neurotoxin is administered. More preferably, about 1 U/kg to about 15 U/kg of the modified neurotoxin is administered. Even more preferably, about 5 U/kg to about 10 U/kg modified neurotoxin is administered. Generally, the modified neurotoxin will be administered as a composition at a dosage that is proportionally equivalent to about 2.5 cc/100 U. Those of ordinary skill in the art will know, or can readily ascertain, how to adjust these dosages for neurotoxin of greater or lesser potency. It is known that botulinum toxin type B can be

administered at a level about fifty times higher than that used for a botulinum toxin type A for similar therapeutic effect. Thus, the units amounts set forth above can be multiplied by a factor of about fifty for a botulinum toxin type B.

[0173] Although examples of routes of administration and dosages are provided, the appropriate route of administration and dosage are generally determined on a case by case basis by the attending physician. Such determinations are routine to one of ordinary skill in the art (see for example, *Harrison's Principles of Internal Medicine* (1998), edited by Anthony Fauci et al., 14th edition, published by McGraw Hill). For example, the route and dosage for administration of a modified neurotoxin according to the present disclosed invention can be selected based upon criteria such as the solubility characteristics of the modified neurotoxin chosen as well as the types of disorder being treated.

[0174] The modified neurotoxin can be produced by chemically linking the leucine-based motif to a neurotoxin using conventional chemical methods well known in the art. For example, botulinum type E can be obtained by establishing and growing cultures of *Clostridium botulinum* in a fermenter, and then harvesting and purifying the fermented mixture in accordance with known procedures.

[0175] The modified neurotoxin can also be produced by recombinant techniques. Recombinant techniques are preferable for producing a neurotoxin having amino acid sequence regions from different Clostridial species or having modified amino acid sequence regions. Also, the recombinant technique is preferable in producing botulinum type A with the leucine-based motif being modified by deletion. The technique includes steps of obtaining genetic materials from natural sources, or synthetic sources, which have codes for a cellular binding moiety, an amino acid sequence effective to translocate the neurotoxin or a part thereof, and an amino acid sequence having therapeutic activity when released into a cytoplasm of a target cell, preferably a neuron. In a suitable embodiment, the genetic materials have codes for the biological persistence enhancing component, preferably the leucine-based motif, the H_C , the H_N and the light chain of the Clostridial neurotoxins and fragments thereof. The genetic constructs are incorporated into host cells for amplification by first fusing the genetic constructs with a cloning vectors, such as phages or plasmids. Then the cloning vectors are inserted into a host, for example, *Clostridium* sp., *E. coli* or other prokaryotes, yeast, insect cell line or mammalian cell lines. Following the expressions of the recombinant genes in host cells, the resultant proteins can be isolated using conventional techniques.

[0176] There are many advantages to producing these modified neurotoxins recombinantly. For example, to form a modified neurotoxin, a modifying fragment, or component must be attached or inserted into a neurotoxin. The production of neurotoxin from anaerobic *Clostridium* cultures is a cumbersome and time-consuming process including a multi-step purification protocol involving several protein precipitation steps and either prolonged and repeated crystallization of the toxin or several stages of column chromatography. Significantly, the high toxicity of the product dictates that the procedure must be performed under strict containment (BL-3). During the fermentation process, the folded single-chain neurotoxins are activated by endogenous Clostridial proteases through a process termed nicking to create a dichain. Sometimes, the process of nicking involves the removal of approximately 10 amino acid residues from the single-chain to create the dichain form in which the two chains remain covalently linked through the intrachain disulfide bond.

[0177] The nicked neurotoxin is much more active than the unnicked form. The amount and precise location of nicking varies with the serotypes of the bacteria producing the toxin. The differences in single-chain neurotoxin activation and, hence, the yield of nicked toxin, are due to variations in the serotype and amounts of proteolytic activity produced by a given strain. For example, greater than 99% of *Clostridial botulinum* serotype A single-chain neurotoxin is activated by the Hall A *Clostridial botulinum* strain, whereas serotype B and E strains produce toxins with lower amounts of activation (0 to 75% depending upon the fermentation time). Thus, the high toxicity of the mature neurotoxin plays a major part in the commercial manufacture of neurotoxins as therapeutic agents.

[0178] The degree of activation of engineered *Clostridial* toxins is, therefore, an important consideration for manufacture of these materials. It would be a major advantage if neurotoxins such as botulinum toxin and tetanus toxin could be expressed, recombinantly, in high yield in rapidly-growing bacteria (such as heterologous *E. coli* cells) as relatively non-toxic single-chains (or single chains having reduced toxic activity) which are safe, easy to isolate and simple to convert to the fully-active form.

[0179] With safety being a prime concern, previous work has concentrated on the expression in *E. coli* and purification of individual H and light chains of tetanus and botulinum toxins; these isolated chains are, by themselves, non-toxic; see Li et al., *Biochemistry* 33:7014-7020 (1994); Zhou et al., *Biochemistry* 34:15175-15181 (1995), hereby incorporated by reference herein. Following the separate production of these peptide chains and under strictly controlled conditions the H and light chains can be combined by oxidative disulphide linkage to form the neuromuscular di-chains.

EXAMPLES

[0180] The following non-limiting examples provide those of ordinary skill in the art with specific suitable methods to treat non-spasm related pain within the scope of the present invention and are not intended to limit the scope of the invention.

Example 1

Treatment of Pain Associated with Muscle Disorder

[0181] An unfortunate 36 year old woman has a 15 year history of temporomandibular joint disease and chronic pain along the masseter and temporalis muscles. Fifteen years prior to evaluation she noted increased immobility of the jaw associated with pain and jaw opening and closing and tenderness along each side of her face. The left side is originally thought to be worse than the right. She is diagnosed as having temporomandibular joint (TMJ) dysfunction with subluxation of the joint and is treated with surgical orthoplasty meniscusectomy and condyle resection.

[0182] She continues to have difficulty with opening and closing her jaw after the surgical procedures and for this reason, several years later, a surgical procedure to replace prosthetic joints on both sides is performed. After the surgical procedure progressive spasms and deviation of the jaw ensues. Further surgical revision is performed subsequent to the original operation to correct prosthetic joint loosening. The jaw continues to exhibit considerable pain and immobility after these surgical procedures. The TMJ remained tender as well as the muscle itself. There are tender points over the temporomandibular joint as well as increased tone in the entire muscle. She is diagnosed as having post-surgical myofascial pain syndrome and is injected with the modified neu-

rotoxin into the masseter and temporalis muscles; the modified neurotoxin is botulinum type E comprising a leucine-based motif. The particular dose as well as the frequency of administrations depends upon a variety of factors within the skill of the treating physician.

[0183] Several days after the injections she noted substantial improvement in her pain and reports that her jaw feels looser. This gradually improves over a 2 to 3 week period in which she notes increased ability to open the jaw and diminishing pain. The patient states that the pain is better than at any time in the last 4 years. The improved condition persists for up to 27 months after the original injection of the modified neurotoxin.

Example 2

Treatment of Pain Subsequent to Spinal Cord Injury

[0184] A patient, age 39, experiencing pain subsequent to spinal cord injury is treated by intrathecal administration, for example, by spinal tap or by catheterization (for infusion) to the spinal cord, with the modified neurotoxin; the modified neurotoxin is botulinum type E comprising a leucine-based motif. The particular toxin dose and site of injection, as well as the frequency of toxin administrations, depend upon a variety of factors within the skill of the treating physician, as previously set forth. Within about 1 to about 7 days after the modified neurotoxin administration, the patient's pain is substantially reduced. The pain alleviation persists for up to 27 months.

Example 3

Peripheral Administration of a Modified Neurotoxin to Treat "Shoulder-Hand Syndrome"

[0185] Pain in the shoulder, arm, and hand can develop, with muscular dystrophy, osteoporosis and fixation of joints. While most common after coronary insufficiency, this syndrome can occur with cervical osteoarthritis or localized shoulder disease, or after any prolonged illness that requires the patient to remain in bed.

[0186] A 46 year old woman presents a shoulder-hand syndrome type pain. The pain is particularly localized at the deltoid region. The patient is treated by a bolus injection of a modified neurotoxin subcutaneously to the shoulder; preferably the modified neurotoxin is botulinum type E comprising a leucine-based motif. The modified neurotoxin can also be, for example, modified botulinum type A, B, C1, C2, D, E, F or G which comprise a leucine-based motif. The particular dose as well as the frequency of administrations depends upon a variety of factors within the skill of the treating physician, as previously set forth. Within 1-7 days after modified neurotoxin administration the patient's pain is substantially alleviated. The duration of the pain alleviation is from about 7 to about 27 months.

Example 4

Peripheral Administration of a Modified Neurotoxin to Treat Posttherapeutic Neuralgia

[0187] Posttherapeutic neuralgia is one of the most intractable of chronic pain problems. Patients suffering this excruciatingly painful process often are elderly, have debilitating disease, and are not suitable for major interventional procedures. The diagnosis is readily made by the appearance of the healed lesions of herpes and by the patient's history. The pain is intense and emotionally distressing. Posttherapeutic neuralgia can occur anywhere, but is most often in the thorax.

[0188] A 76 year old man presents a posttherapeutic type pain. The pain is localized to the abdomen region. The patient is treated by a bolus injection of a modified neurotoxin intradermally to the abdomen; the modified neurotoxin is, for example, botulinum type A, B, C1, C2, D, E, F and/or G. The modified neurotoxin comprises a leucine-based motif and/or additional tyrosine-based motifs. The particular dose as well as the frequency of administration depends upon a variety of factors within the skill of the treating physician, as previously set forth. Within 1-7 days after modified neurotoxin administration the patient's pain is substantially alleviated. The duration of the pain alleviation is from about 7 to about 27 months.

Example 5

Peripheral Administration of a Modified Neurotoxin to Treat Nasopharyngeal Tumor Pain

[0189] These tumors, most often squamous cell carcinomas, are usually in the fossa of Rosenmuller and can invade the base of the skull. Pain in the face is common. It is constant, dull-aching in nature.

[0190] A 35 year old man presents a nasopharyngeal tumor type pain. Pain is found at the lower left cheek. The patient is treated by a bolus injection of a modified neurotoxin intramuscularly to the cheek, preferably the modified neurotoxin is botulinum type A, B, C1, C2, D, E, F or G comprising additional biological persistence enhancing amino acid derivatives, for example, tyrosine phosphorylations. The particular dose as well as the frequency of administrations depends upon a variety of factors within the skill of the treating physician. Within 1-7 days after modified neurotoxin administration the patient's pain is substantially alleviated. The duration of the pain alleviation is from about 7 to about 27 months.

Example 6

Peripheral Administration of a Modified Neurotoxin to Treat Inflammatory Pain

[0191] A patient, age 45, presents an inflammatory pain in the chest region. The patient is treated by a bolus injection of a modified neurotoxin intramuscularly to the chest, preferably the modified neurotoxin is botulinum type A, B, C1, C2, D, E, F or G comprising additional tyrosine-based motifs. The particular dose as well as the frequency of administrations depends upon a variety of factors within the skill of the treating physician, as previously set forth. Within 1-7 days after modified neurotoxin administration the patient's pain is substantially alleviated. The duration of the pain alleviation is from about 7 to about 27 months.

Example 7

Treatment of Excessive Sweating

[0192] A male, age 65, with excessive unilateral sweating is treated by administering a modified neurotoxin. The dose and frequency of administration depends upon degree of desired effect. Preferably, the modified neurotoxin is botulinum type A, B, C1, C2, D, E, F and/or G. The modified neurotoxins comprise a leucine-based motif. The administration is to the gland nerve plexus, ganglion, spinal cord or central nervous system. The specific site of administration is to be determined by the physician's knowledge of the anatomy and physiology

of the target glands and secretory cells. In addition, the appropriate spinal cord level or brain area can be injected with the toxin. The cessation of excessive sweating after the modified neurotoxin treatment is up to 27 months.

Example 8

Post Surgical Treatments

[0193] A female, age 22, presents a torn shoulder tendon and undergoes orthopedic surgery to repair the tendon. After the surgery, the patient is administered intramuscularly with a modified neurotoxin to the shoulder. The modified neurotoxin can be botulinum type A, B, C, D, E, F, and/or G wherein one or more amino acids of a biological persistence enhancing component are deleted from the toxin. For example, one or more leucine residues can be deleted from and/or mutated from the leucine-based motif in botulinum toxin serotype A. Alternatively, one or more amino acids of the leucine-based motif can be substituted for other amino acids. For example, the two leucines in the leucine-based motif can be substituted for alanines. The particular dose as well as the frequency of administrations depends upon a variety of factors within the skill of the treating physician. The specific site of administration is to be determined by the physician's knowledge of the anatomy and physiology of the muscles. The administered modified neurotoxin reduces movement of the arm to facilitate the recovery from the surgery. The effect of the modified neurotoxin is for about five weeks or less.

Example 9

Cloning, Expression and Purification of the Botulinum Neurotoxin Light Chain Gene

[0194] This example describes methods to clone and express a DNA nucleotide sequence encoding a botulinum toxin light chain and purify the resulting protein product. A DNA sequence encoding the botulinum toxin light chain can be amplified by PCR protocols which employ synthetic oligonucleotides having sequences corresponding to the 5' and 3' end regions of the light chain gene. Design of the primers can allow for the introduction of restriction sites, for example, Stu I and EcoR I restriction sites into the 5' and 3' ends of the botulinum toxin light chain gene PCR product. These restriction sites can be subsequently used to facilitate unidirectional subcloning of the amplification products. Additionally, these primers can introduce a stop codon at the C-terminus of the light chain coding sequence. Chromosomal DNA from *C. botulinum*, for example, strain HallA, can serve as a template in the amplification reaction.

[0195] The PCR amplification can be performed in a 0.1 mL volume containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM MgCl₂, 0.2 mM of each deoxynucleotide triphosphate (dNTP), 50 pmol of each primer, 200 ng of genomic DNA and 2.5 units of Taq DNA polymerase. The reaction mixture can be subjected to 35 cycles of denaturation (1 minute at 94° C.), annealing (2 minutes at 55° C.) and polymerization (2 minutes at 72° C.). Finally, the reaction can be extended for an additional 5 minutes at 72° C.

[0196] The PCR amplification product can be digested with for example, Stu I and EcoR I, to release the light chain encoding, cloned, PCR DNA fragment. This fragment can then be purified by, for example, agarose gel electrophoresis, and ligated into, for example, a Sma I and EcoR I digested pBluescript II SK phagemid. Bacterial transformants, for

example, *E. coli*, harboring this recombinant phagemid can be identified by standard procedures, such as blue/white screening. Clones comprising the light chain encoding DNA can be identified by DNA sequence analysis performed by standard methods. The cloned sequences can be confirmed by comparing the cloned sequences to published sequences for botulinum light chains, for example, Binz, et al., in *J. Biol. Chem.* 265, 9153 (1990), Thompson et al., in *Eur. J. Biochem.* 189, 73 (1990) and Minton, Clostridial Neurotoxins, The Molecular Pathogenesis of Tetanus and Botulism p. 161-191, Edited by C. Motecuccio (1995).

[0197] The light chain can be subcloned into an expression vector, for example, pMal-P2. pMal-P2 harbors the malE gene encoding MBP (maltose binding protein) which is controlled by a strongly inducible promoter, P_{tac} .

[0198] To verify expression of the botulinum toxin light chain, a well isolated bacterial colony harboring the light chain gene containing pMal-P2 can be used to inoculate L-broth containing 0.1 mg/ml ampicillin and 2% (w/v) glucose, and grown overnight with shaking at 30° C. The overnight cultures can be diluted 1:10 into fresh L-broth containing 0.1 mg/ml of ampicillin and incubated for 2 hours. Fusion protein expression can be induced by addition of IPTG to a final concentration of 0.1 mM. After an additional 4 hour incubation at 30° C., bacteria can be collected by centrifugation at 6,000×g for 10 minutes.

[0199] A small-scale SDS-PAGE analysis can confirm the presence of a 90 kDa protein band in samples derived from IPTG-induced bacteria. This MW would be consistent with the predicted size of a fusion protein having MBP (~40 kDa) and botulinum toxin light chain (~50 kDa) components.

[0200] The presence of the desired fusion proteins in IPTG-induced bacterial extracts can be confirmed by western blotting using the polyclonal anti-L chain probe described by Cenci di Bello et al., in *Eur. J. Biochem.* 219, 161 (1993). Reactive bands on PVDF membranes (Pharmacia; Milton Keynes, UK) can be visualized using an anti-rabbit immunoglobulin conjugated to horseradish peroxidase (BioRad; Hemel Hempstead, UK) and the ECL detection system (Amersham, UK). Western blotting results typically confirm the presence of the dominant fusion protein together with several faint bands corresponding to proteins of lower MW than the fully sized fusion protein. This observation suggests that limited degradation of the fusion protein occurred in the bacteria or during the isolation procedure.

[0201] To produce the subcloned light chain, pellets from 1 liter cultures of bacteria expressing the wild-type Botulinum neurotoxin light chain proteins can be resuspended in column buffer [10 mM Tris-HCl (pH 8.0), 200 mM NaCl, 1 mM EGTA and 1 mM DTT] containing 1 mM phenylmethanesulfonyl fluoride (PMSF) and 10 mM benzamidine, and lysed by sonication. The lysates can be cleared by centrifugation at 15,000×g for 15 minutes at 4° C. Supernatants can be applied to an amylose affinity column [2×10 cm, 30 ml resin] (New England BioLabs; Hitchin, UK). Unbound proteins can be washed from the resin with column buffer until the eluate is free of protein as judged by a stable absorbance reading at 280 nm. The bound MBP-L chain fusion protein can be subsequently eluted with column buffer containing 10 mM maltose. Fractions containing the fusion protein can be pooled and dialyzed against 20 mM Tris-HCl (pH 8.0) supplemented with 150 mM NaCl, 2 mM, CaCl₂ and 1 mM DTT for 72 hours at 4° C.

[0202] The MBP-L chain fusion proteins can be purified after release from the host bacteria. Release from the bacteria can be accomplished by enzymatically degrading or mechanically disrupting the bacterial cell membrane. Amylose affinity chromatography can be used for purification. Recombinant wild-type or mutant light chains can be separated from the sugar binding domains of the fusion proteins by site-specific cleavage with Factor Xa. This cleavage procedure typically yields free MBP, free light chains and a small amount of uncleaved fusion protein. While the resulting light chains present in such mixtures can be shown to possess the desired activities, an additional purification step can be employed. For example, the mixture of cleavage products can be applied to a second amylose affinity column which binds both the MBP and uncleaved fusion protein. Free light chains can be isolated in the flow through fraction.

Example 10

Reconstitution of Native Light Chain, Recombinant Wild-Type Light Chain with Purified Heavy Chain

[0203] Native heavy and light chains can be dissociated from a BoNT with 2 M urea, reduced with 100 mM DTT and then purified according to established chromatographic procedures. For example, Kozaki et al. (1981, *Japan J. Med. Sci. Biol.* 34, 61) and Maisey et al. (1988, *Eur. J. Biochem.* 177, 683). A purified heavy chain can be combined with an equimolar amount of either native light chain or a recombinant light chain. Reconstitution can be carried out by dialyzing the samples against a buffer consisting of 25 mM Tris (pH 8.0), 50 μM zinc acetate and 150 mM NaCl over 4 days at 4° C. Following dialysis, the association of the recombinant light chain and native heavy chain to form disulfide linked 150 kDa dichains is monitored by SDS-PAGE and/or quantified by densitometric scanning.

Example 11

Production of a Modified Neurotoxin with an Enhanced Biological Persistence

[0204] A modified neurotoxin can be produced by employing recombinant techniques in conjunction with conventional chemical techniques.

[0205] A neurotoxin chain, for example a botulinum light chain that is to be fused with a biological persistence enhancing component to form a modified neurotoxin can be produced recombinantly and purified as described in example 9.

[0206] The recombinant neurotoxin chain derived from the recombinant techniques can be covalently fused with (or coupled to) a biological persistence enhancing component, for example a leucine-based motif, a tyrosine-based motif and/or an amino acid derivative. Peptide sequences comprising biological persistence enhancing components can be synthesized by standard t-Boc/Fmoc technologies in solution or solid phase as is known to those skilled in the art. Similar synthesis techniques are also covered by the scope of this invention, for example, methodologies employed in Milton et al. (1992, *Biochemistry* 31, 8799-8809) and Swain et al. (1993, *Peptide Research* 6, 147-154). One or more synthesized biological persistence enhancing components can be fused to the light chain of botulinum type A, B, C1, C2, D, E, F or G at, for example, the carboxyl terminal end of the toxin. The fusion of the biological persistence enhancing components is achieved by chemical coupling using reagents and

techniques known to those skilled in the art, for example PDPH/EDAC and Traut's reagent chemistry.

[0207] Alternatively, a modified neurotoxin can be produced recombinantly without the step of fusing the biological persistence enhancing component to a recombinant botulinum toxin chain. For example, a recombinant neurotoxin chain, for example, a botulinum light chain, derived from the recombinant techniques of example 9 can be produced with a biological persistence enhancing component, for example a leucine-based motif, a tyrosine-based motif and/or an amino acid derivative. For example, one or more DNA sequences encoding biological persistence enhancing components can be added to the DNA sequence encoding the light chain of botulinum type A, B, C1, C2, D, E, F or G. This addition can be done by any number of methods used for site directed mutagenesis which are familiar to those skilled in the art.

[0208] The recombinant modified light chain containing the fused or added biological persistence enhancing component can be reconstituted with a heavy chain of a neurotoxin by the method described in example 10 thereby producing a complete modified neurotoxin.

[0209] The modified neurotoxins produced according to this example have an enhanced biological persistence. Preferably, the biological persistence is enhanced by about 20% to about 300% relative to an identical neurotoxin without the additional biological persistence enhancing component(s).

Example 12

Production of a Modified Neurotoxin with a Reduced Biological Persistence

[0210] A modified neurotoxin with a reduced biological persistence can be produced by employing recombinant techniques. For example, a botulinum light chain derived from the recombinant techniques of example 9 can be produced without a biological persistence enhancing component. For example, one or more leucine-based motifs, tyrosine-based motifs and/or amino acid derivatives can be mutated. For example, one or more DNA sequences encoding biological persistence enhancing components can be removed from the DNA sequence encoding the light chain of botulinum type A, B, C1, C2, D, E, F or G. For example, the DNA sequence encoding the leucine based motif can be removed from the DNA sequence encoding botulinum type A light chain. Removal of the DNA sequences can be done by any number of methods familiar to those skilled in the art.

[0211] The recombinant modified light chain with the deleted biological persistence enhancing component can be reconstituted with a heavy chain of a neurotoxin by the method described in example 10 thereby producing a complete modified neurotoxin.

[0212] The modified neurotoxin produced according to this example has a reduced biological persistence. Preferably, the biological persistence is reduced by about 20% to about 300% relative to an identical neurotoxin, for example botulinum type A, with the leucine-based motif.

[0213] Although the present invention has been described in detail with regard to certain suitable methods, other embodiments, versions, and modifications within the scope of the present invention are possible. For example, a wide variety of modified neurotoxins can be effectively used in the methods of the present invention in place of Clostridial neurotoxins. Also, the corresponding genetic codes, i.e. DNA sequence, to the modified neurotoxins are also considered to

be part of this invention. Additionally, the present invention includes peripheral administration methods wherein two or more modified neurotoxins, for example botulinum type E with a fused leucine-based motif and botulinum type B comprising a leucine-based motif, are administered concurrently or consecutively. While this invention has been described with respect to various specific examples and embodiments, it is to be understood that the invention is not limited thereto and that it can be variously practiced with the scope of the following claims.

Example 13

Production of a Modified Neurotoxin with a Reduced Biological Persistence

[0214] Localization to the cellular membrane is likely a key factor in determining the biological persistence of botulinum toxins. This is because localization to a cell membrane can protect the localized protein from intracellular protein degrading complexes.

[0215] It is well known and generally accepted that the biological persistence of botulinum type B neurotoxin is shorter than the biological persistence of botulinum type A neurotoxin. In this work, it was demonstrated that when the botulinum toxin type A light chain is truncated, which comprises removing the leucine-based motif, the light chain substantially loses its ability to localize to the cellular membrane in its characteristic pattern. In fact, truncated type A light chain localizes to the cellular membrane in a pattern similar to that of botulinum toxin type B light chain.

[0216] Therefore, it can be hypothesized that truncated botulinum type A has a reduced biological persistence and/or a reduced biological activity similar to that of botulinum toxin type B.

Example 14

Production of a Modified Neurotoxin with an Altered Biological Persistence

[0217] Localization to the cellular membrane is likely a key factor in determining the biological persistence of botulinum toxins. This is because localization to a cell membrane can protect the localized protein from intracellular protein degrading complexes.

[0218] In this work, it was demonstrated that when the botulinum toxin type A light chain is mutated, changing the two leucines at positions 427 and 428 to alanines (FIG. 3), the light chain substantially loses its ability to localize to the cellular membrane in its characteristic pattern.

[0219] From this data it can be concluded that the mutated botulinum type A has an altered biological persistence.

Example 15

In Vitro Cleavage of SNAP 25 by Truncated LC/A

[0220] As illustrated by FIG. 9, an in vitro ELISA assay was carried out by the inventors demonstrating that a truncated LC/A in vitro cleaves SNAP-25 substrate less efficiently than does non-truncated LC/A. The data displayed is not a measure of inhibition of exocytosis but a measure of the in vitro formation of SNAP-25 cleavage. The assay was carried out as follows:

[0221] Materials: BirA-SNAP25₁₂₈₋₂₀₆—this is a recombinant substrate for LC/A, consisting of a BirA signal sequence

fused to the N-terminus of residues 128-206 of SNAP25. This fusion construct was produced in *E. coli* and the BirA signal sequence was biotinylated by the *E. coli*. Microtiter plates were coated with streptavidin. The toxin used was BoNT/A complex or LC/A constructs. The primary antibody was anti-SNAP25₁₉₇ antibody. This antibody recognizes the C-terminus of SNAP25 following cleavage by Type A toxin (BirA-SNAP25₁₂₈₋₁₉₇). The secondary antibody was goat, anti-rabbit IgG conjugated to horseradish peroxidase. The ImmunoPure TMB substrate was from Pierce, a colorimetric substrate for horseradish peroxidase. The antibody that recognizes the cleaved product SNAP25₁₉₇ is specific for that cleaved product and does not recognize the full length uncleaved substrate SNAP25₂₀₆.

[0222] Method: BirA-SNAP25₁₂₈₋₂₀₆ was bound to streptavidin on a microtiter plate. To the plates were added serial dilutions of BoNT/A 900 kDa complex, His6-S-nativeLC/A, or His6-S-truncLC/A-His6. All toxin samples were pre-incubated with DTT (this is not required for the LC/A constructs, but they were treated the same as the BoNT/A complex). The toxin samples were incubated with the substrate for 90 minutes at 37° C. The toxin was removed and the bound substrate was incubated with anti-SNAP25₁₉₇ antibody. Unbound antibody was washed away and the plates were then incubated with the secondary antibody (anti-rabbit IgG conjugated to horseradish peroxidase). Unbound antibody was again washed away and a colorimetric assay for horseradish peroxidase was performed. The assay was quantified by reading the absorbance at 450 nm.

[0223] In other work by the inventors disclosed herein the light chain constructs that were expressed in the PC-12 cells were expressed directly in the PC-12 cells and do not contain any tags. The light chain constructs that have been expressed from *E. coli* for these in vitro assays contain affinity tags for purification purposes (these tags are not present on the proteins expressed in the PC-12 cells, as disclosed herein). The LC/A expressed in PC12 was the fusion protein GFP-LC/A. Between the GFP and the LC/A there is a set of Gly to separate both proteins.

[0224] An explanation of the various constructs follows:

[0225] Complex (red in the graph)—this is BoNT/A 900 kDa complex isolated from *C. botulinum*

[0226] Truncated LC/A—a construct lacking 8 amino acids at the N-terminus and 22 amino acids at the C-terminus. However, this construct does contain a 6-histidine and an S-tag at the N-terminus as well as a 6-histidine tag at the C-terminus.

[0227] Dialyzed Truncated LC/A—same as Truncated LC/A, but imidazole resulting from the purification has been removed.

[0228] Full LC/A (dark green in graph)—native LC/A construct (full-length), but containing the N-terminal 6-histidine and S-tag. Does not have the C-terminal 6-histidine.

[0229] Dialyzed Full LC/A (light green in graph)—same as Full LC/A, but imidazole resulting from the purification has been removed.

[0230] To graphically depict these differences, FIG. 10 shows the very N-terminus and the very C-terminus of these constructs (the middle portion of the LC/A proteins is not shown). What is referred to as Wildtype corresponds to the native LC/A that the inventors had expressed directly in the PC-12 cells (this is construct that the inventors demonstrated activity with via Western blot analysis of the cleaved SNAP25

product). Truncated LC/A is the truncated light chain containing the His and S-tags. N-His-LC/A is what was referred to as Full LC/A in FIG. 9.

Example 16A

Intracellular Localization of Botulinum Toxin Type A Light Chain

[0231] The sequences of LC/A, LC/B, and LC/E were analyzed for the presence of localization signals. A putative dileucine motif was identified at the C-terminus of LC/A and was unique to that serotype. The role of the dileucine motif in LC/A activity as well as localization was investigated. The inventors found that a LC/A construct that lacks 8 N-terminal and 22 C-terminal amino acids (including the dileucine motif) retains minimal activity and is mislocalized when expressed in PC12 cells. The specific role of the dileucine motif was elucidated by generating a LL-->AA double mutant. The LL-->AA mutant has minimally reduced activity, but is mislocalized when expressed in PC12 cells. The mislocalization is similar to that recently reported for the LL-->AA mutant of VAMP4. Localization and activity data are reported, supporting the hypothesis that the dileucine motif is important for proper intracellular localization of LC/A.

[0232] Materials and Methods: LC from BoNT/A (Allergan Hall A), N- and C-terminal truncated LC/A, and double mutant LC/A (LL-->AA) were cloned into pQBI25 (Qbiogene) as both N- and C-terminal GFP fusion proteins: GFP-LCA, LCA-GFP; GFP-LCA(LL-->AA); LCA(LL-->AA)-GFP; GFP-LCA(ΔN/ΔC); LCA(ΔN/ΔC)-GFP.

[0233] Undifferentiated PC12 (rat pheochromocytoma) cells were transfected with Lipofectamine2000 (Invitrogen) and then were differentiated with NGF (Harlan).

[0234] Expression and integrity of the light chains were assessed by immuno-precipitation with a GFP monoclonal antibody (3E6, Qbiogene), followed by western blot with antibodies to GFP (pAb, Santa Cruz) or LCA (pAb, Allergan).

[0235] Catalytic activity of PC12 expressed LC-GFP fusion proteins was determined by western blot analysis with the following antibodies:

[0236] SMI-81 (Sternberger) and N-19 (Santa Cruz): Recognize full-length SNAP-25 as well as SNAP25₁₉₇

[0237] pAb SNAP25₁₉₇: Polyclonal antibody generated at Allergan

[0238] specific to the BoNT/A cleaved peptide.

[0239] In vitro activity of rLC's was determined by SNAP25 ELISA assay. Recombinant LC (rLC/A), truncated LC (trunLC/A(ΔN8/ΔC22)), and double mutant LC/A(LL-->AA) were cloned into pET-30(+) vectors containing polyHis affinity tags. The LC's were purified via Ni²⁺ affinity chromatography.

[0240] A biotinylated substrate corresponding to SNAP25 (134-206) was immobilized on a streptavidin-coated microtiter plate. The appropriate LC constructs and 900 kDa BoNT/A complex were added to substrate coated plates. Protease activity was determined by quantitating the formation of SNAP(134-197) with a pAb (Allergan) specific for the proteolysis product. The activity of 900 kDa BoNT/A complex was determined as a control.

[0241] Localization of the GFP fusions in paraformaldehyde fixed cells was determined by confocal microscopy (Leica). Cell slices from the middle of the cell are shown in the images.

[0242] FIG. 3 shows LC/A sequence with the 8 N-terminal and 22 C-terminal amino acids that were deleted in the LC/A (Δ N8/ Δ C22) construct underlined. The dileucine motif is bracketed from the top with an asterisk. The two leucine residues that were mutated to alanines are the two leucines in the dileucine motif. Mutation of LL-->AA has been demonstrated to disrupt appropriate trafficking and localization of membrane associated proteins.

[0243] FIG. 11 shows a ribbon diagram of LC/A with a Connolly surface overlay from Lacy et al., *Nat. Struct. Biol.*, 5, 898 (1998) which is incorporated in its entirety herein by reference. The N- and C-terminal regions of interest are yellow with amino acid side-chains included. The dileucine motif is red and the Zn²⁺ atom is a silver sphere. The structure was extracted from the holotoxin x-ray structure and includes residues 1-430 (the 17 C-terminal amino acids were not resolved in the structure).

[0244] FIGS. 12 and 13 show GFP-LC/A recombinant fusion constructs that are expressed and active when transfected in PC12 cells. FIG. 12 shows the detection of GFP-LC fusion proteins expressed in differentiated PC12 cells by western blot. GFP-LC Fusion Proteins Detected in PC12 Lysates. Lanes: G, GFP; LC, GFP-LC/A; AA, GFP-LC/A (LL-->AA); TA, GFP-LCA(Δ N8/ Δ C22). Expression and integrity of the fusion proteins was also assessed with a pAb to LCA.

[0245] FIG. 13 shows expressed LC's are Active Proteases. PC12 cells transfected with and expressing the appropriate GFP-LC fusion construct were collected and lysed. Activity was assessed by western blot using either antibodies specific to the cleaved product of LCA (SNAP25₁₉₇) or to the N-terminus of SNAP25 (recognizes both cleaved and uncleaved SNAP25). Truncated LC/A is expressed less efficiently and appears to be much less active than LCA. LCA(AA) appears to be slightly less active than LC/A in PC12 cells. N-19 (Santa Cruz) SMI-81 (Sternberger) are antibodies to N-terminus SNAP25₂₀₆.

[0246] FIGS. 14 and 15 show *E. coli* expression and in vitro activity of rLC/A and mutants. FIG. 14 shows *E. coli* expression of rLC/A and mutants. * corresponds to the minimal essential domain of LC/A reported in Kadkhodayan et al, *Prot. Exp. Purif.*, 19, 125 (2000) which is incorporated in its entirety herein by reference.

[0247] FIG. 15 shows a SNAP-25 ELISA assay showing in vitro activity of *E. coli* expressed rLC/A and mutants. SNAP25(134-206) was immobilized on a streptavidin-coated microtitre plate. The formation of SNAP-25(134-197) was

quantified with an Ab specific to that product. As a control 900 kDa BoNT/A complex was included. rLC/A(LL-->AA) is approximately 10 fold less active than rLC/A. Truncated LC/A is approximately 1000 fold less active than rLC/A.

[0248] FIG. 16 shows PC12 cells transfected with plasmids encoding GFP-LCA. Confocal images were captured at approximately the middle of the cell. Subcellular localization of the light chain in PC12 cells is shown. Localization of LC/A at the plasma membrane can clearly be observed. LCA-GFP displays the same localization pattern (data not shown).

[0249] FIG. 17 shows PC12 cells transfected with plasmids encoding GFP-LCA(Δ N/ Δ C) and LCA(Δ N/ Δ C)-GFP (data not shown). The N- and C-terminal truncated form of LC/A may be localized to an internal structure rather than at the plasma membrane.

[0250] FIG. 18 shows confocal images of GFP-LCA(LL-->AA) expressed in PC12 cells. Mutation to the dileucine motif disrupts LC/A localization of the plasma membrane. The dileucine mutant is localized in a more diffuse pattern than GFP-LCA. The localization pattern is similar to that seen for VAMP4 dileucine mutant as reported in Penden et al, *J. Biol. Chem.*, 276, 49183 (2001) which is incorporated in its entirety herein by reference.

[0251] The results shown in at least FIGS. 3 and 11 to 18 demonstrate that the presence of a dileucine motif is critical for the proper intracellular localization of LC/A and may be important for the long duration of action of BoNT/A.

[0252] Additional studies showed that a GFP-LCA construct with the eight amino acid residues of SEQ ID NO: 27 (PFVKNKQFN) deleted from the N-terminus (no C-terminus deletion) localized in PC12 cells a very similar pattern to the localization in PC12 cells of a truncated GFP-LCA construct with both the C and N terminus deletions.

[0253] Further studies showed that a GFP-LCA construct with the twenty two amino acid residues of SEQ ID NO: 28 (KNFTGLFEFYKLLCVRGIITSK) deleted from the C-terminus (no N-terminus deletion) localized in PC12 cells in a very similar manner to that of the GFP-LCA(LL-->AA) mutant.

[0254] A GFP-LCA construct with both the eight amino acid residues of SEQ ID NO: 27 (PFVKNKQFN) deleted from the N-terminus and the twenty two amino acid residues of SEQ ID NO: 28 (KNFTGLFEFYKLLCVRGIITSK) deleted from the C-terminus accumulated intracellularly.

Example 16B

[0255] The first 30 residues of the amino-terminus (N-term) and the last 50 residues of the carboxyl-terminal (C-term) of the amino acid sequences of botulinum toxin serotypes A through G light chains (LC) are shown in Table 2.

TABLE 2

Toxin	N-term (AAs 1-30) of LC	SEQ ID NO:	C-term (last 50 AAs) of LC	SEQ ID NO:
BoNT/A	MPFVKNKQFNYPVNGVDI AYIKIPNAGQM	39	GFNLRNTNLAANFNGQNT INNMFNFTKLNFTGLFEFY KLLCVRGIITSK	40
BoNT/B	MPVTINNFNYPNDPIDNDNI IMMEPPFARGT	41	YTIEEGFNISDKNMKEYR GQNKAINKQAYEEISKEHL AVYKIQMCKSVK	42

TABLE 2-continued

Toxin	N-term (AAs 1-30) of LC	SEQ ID NO:	C-term (last 50 AAs) of LC	SEQ ID NO:
BoNT/C ₁	MPITINNFNYSDPVDNKNILYLDTHLNTLA	43	NIPKSNLNLVFMGQNLNRN PALRKVNPNENMLYLFTKFC HKAIDGRSLYNK	44
BoNT/D	MTWPVKDFNYSDPVDNDNII LYLRIPQNKLI	45	YTIRDGFNLTKGFNIENS GQNIERNPALQKLSSSESVV DLFTKVCRLRLTK	46
BoNT/E	MPKINSFNYNDPVNDRTIL YIKPGGCQEFY	47	GYNINNLKVNFRGQANLNPRIITPITGRGLVKKIIRF CKNIVSVKGIRK	48
BoNT/F	MPVAINSFNYNDPVNDDTI LYMQIPYEES	49	TVSEGFNIGNLAVNNRGQS IKLNPKIIDSIPDKGLVEK IVKFCKSVIPRK	50
BoNT/G	MPVNIKNFNYNDPINNDII IMMEPFNDPGP	51	QNEGFNIASKNLKTEFNGQ NKAVNKEAYEEISLEHLVI YRIAMCKPVMYK	52

[0256] Alterations in the amino acid sequence of these serotypes can include amino acid substitutions, mutations, deletions, or various combinations of these alterations. Such alterations can be engineered in the first thirty amino acids (AAs) in the N-terminus of the light chain and/or the last fifty AAs in the C-terminus of the light chain using recombinant DNA technological methods that are standard in the art.

[0257] Examples of amino acid sequence substitutions include the replacement of one or more contiguous or non-contiguous amino acids in the first 30 amino acids of the N-terminus and/or the last 50 amino acids of the C-terminus of the light chain with an equal number and placement of amino acids that differ from the wild-type sequence. Substitutions can be conservative or non-conservative of the character of the amino acid. For example, the amino acid valine at a specific position in the wild-type sequence can be replaced with an alanine in the same position in the substituted sequence. Furthermore, basic residues such as arginine or lysine can be substituted for highly hydrophobic residues such as tryptophan. A proline or histidine residue may be substituted in order to form or disrupt a potentially important structural or catalytic element of the protein. Some examples of amino acid substitutions are indicated by bold underlined text in the sequences described in Table 3.

TABLE 3

Toxin	N-term (AAs 1-30) of LC	SEQ ID NO:	C-term (last 50 AAs) of LC	SEQ ID NO:
BoNT/A	MPF ANKQ FNYKDPVNGVD IAYIKIPNAGQM	53	GFNLRNTNLAANFNGQNT EINN MNRT KLKNFTGLFE FYKLLCVRGIITSK	54
BoNT/A	MPFVN KQFNK KDPVNGVD IAYIKIPNAGQM	55	GFNLRNTNLAANFNGQNT EINN MNFT KLKN AAG LFE FYKLLCVRGIITSK	56
BoNT/A	MPFVN KQFN KDPVNGVD IARIKIPNAGQM	57	GFNLRNTNLAAN HNG QNT EINN MNFT KLKNFTGLFE FYKLLCVRGIITSK	58
BoNT/A	MPFVN KHF FNYKDPVNGVD IAYIKIPNAGQM	59	GFNLRNTNLAANFNGQNT EINN MNFT KLKNFTGLFE FYKLL CARG IITSK	60

TABLE 3-continued

Toxin	N-term (AAs 1-30) of LC	SEQ ID NO:	C-term (last 50 AAs) of LC	SEQ ID NO:
BoNT/B	MPATINNFNYNDPIDNDN IIMMEPPFARGT	61	YTIEEGFNISDKNMGKEY RGQNKAINQAYEEISKE HLAVYKIRMCKSVK	62
BoNT/B	MPVTINNFNYNDPIDNDN IIA AE PPFARGT	63	YTIEEGFNISDKNMGKEY RGQNKAINQAYEEISKE HLAVRKIQMCKSVK	64
BoNT/B	MPVTINNF R NDPIDNDN IIMMEPPFARGT	65	YTIEEGFNISDKNMGKEY RGQNKAINQ AK EEISKE HLAVYKIQMCKSVK	66
BoNT/C ₁	MPITINNK NY SDPVDNKN ILYLDTHLNTLA	67	NIPKSNLNLVFMGQNLNRN NPALRKVNPNENMLYLFTK FCEKAIDGRSLRNK	68
BoNT/D	MTW PAK DFNYSD PAN DND ILYLRIPQNKLI	69	YTIRDGFNLTKGFNIEN SGQNIERNPALQKLSSSES VVDLFTK ACL RLTK	70
BoNT/E	MPKINSFNYND PAN DRTI LYIKPGGCQEFY	71	GYNINNLKVNFRGQANL NPRIITPITGRGHVKKII RFCKNIVSVKGIRK	72
BoNT/E	MPKINS R NYNDPVNDRTI LYIKPGGCQEFY	73	GYNINNLKVNFRGQANL NPRIITPITGRGLVKKII RFCK NAAS VKGIRK	74
BoNT/E	MPKINSFNYNDPVNDRTI LYIKPGGCQ EFR	75	GYNINNLKVNFRGQANL NPRIITPITGRGLVKKII RFCKNIV SA KIRK	76
BoNT/F	MP AA INSFNYNDPVNDDT ILYMQIPYEES	77	TVSEGFNIGNLAVNNRGQ SIKLNPKIIDSIPDKGLV EKIVKFCK SAI PRK	78
BoNT/G	MPVNIKN H NYNDPINND IIMMEPFNDPGP	79	QNEGFNIASKNLKTEFNG QNKAVNKEAYEEISLEHL VYRIAMCK PAM YK	80

[0258] Examples of amino acid sequence mutations include changes in the first 30 amino acids of the N-terminus and/or the last 50 amino acids of the C-terminus of the light

chain sequence such that one or several amino acids are added, substituted and/or deleted such that the identity, number and position of amino acids in the wild-type light chain sequence is not necessarily conserved in the mutated light chain sequence. Some examples of amino acid sequence mutations are described in Table 4, in which additions of amino acids are shown in bold underlined text, and deletions are indicated by dashes in the sequences shown.

TABLE 4

Toxin	N-term (AAs 1-30) of LC	SEQ ID C-term (last) NO: 50 AAs) of LC	SEQ ID NO:
BoNT/A	MPFVNKQFNYKDPVNGVD IAYIKIPH-----	81 GFNLRNTNLAANFNGQNT EINNMN AAAAAAAAA ----- -----CVRGIITSK	82
BoNT/A	M AAA ---NYKDPVNGVD IAYIKIPNAGQM	83 G KNLRNTNLAANFNGQNT EINNMNFTKLKNFTGLFE FYK-CVRGIITSK	84
BoNT/A	MPFVNKQFNYKDPVNGVD I AR ---NAGQM	85 GFNLRNTNLAA--- HNT EINNMNFTKLKNFTGLFE FYKLLCVRGIITSK	86
BoNT/A	MPKVNKQFN---VNGVD IAYIKIPNAGQM	87 GFNLRNTNLAANFNGQNT EINNMNFTKLKNFTGLFE FR -----TSK	88
BoNT/B	MPVTINNPNYNDPIDNDN II AAAAA ARGT	89 YTI PP GFNISDKNMGKEY RGQNKAINQAYEEISK EH-----	90
BoNT/B	M PA ---FNYNDPIDNDN IIMMEPPFARGT	91 YTIEEGFNISDKNMGKEY RGQNK AAAAA EEISKE HLAVYKIQMCKSVK	92
BoNT/B	MPVTINN NR ----- --MMEPPFARGT	93 YTIEEGFNISDKNMGKEY RGQNKAINQAY----- AAAAA IQMCKSVK	94
BoNT/C ₁	M-----SDPVDNKN ILYLDTHLNTLA	95 NIPKSNLNVLFMGQNLRSR NPALRKVNPNENML AAA --- -CHKAIDGRSLYNK	96
BoNT/D	M TR PKVD---DPVNDND ILYLRIPOQNKLI	97 YTIRDGFNLTNKGFNIE SGQNIERNPALQKL--- --DL PP KVCLRLTK	98
BoNT/E	MPKINS PP NYNDPVNDRT ILYIKPGGCQEFY	99 GYNINNLKVNFRGQANL NPRIITPITGRGLVK AA AA CKNIVSVKGIRK	100
BoNT/E	MPKINSFNYND PA AAAND RTILYIKPGGCQEFY	101 GYNINNLKVNFRGQANL NPRIITPITGRGLV--- H RFCKNIVSVKGIRK	102
BoNT/E	MPKINSFNYNDPVNDRTI L K IKPGGC K EFY	103 GYNINNLKVNFRGQANL NPRIITPITGRGL PP --- -----	104
BoNT/F	MP-----NYNDPVNDT ILYMQIPYEEKS	105 TVSEGFNIGNLAVNNRGQ SIKLNPKIIDSIPDK GAA AAAA ---CKSVIPRK	106
BoNT/G	MPVNI PP ---DPINDD IIMMEPPNDPGP	107 QNEGFNIASKNLKTEFNG QNKAVNKEA----- ----- AAAAAA	108

[0259] Examples of amino acid sequence deletions include the removal of one or more contiguous or non-contiguous amino acids from the first 30 amino acids of the N-terminus and/or the last 50 amino acids of the C-terminus of the light

chain sequence. Some examples of amino acid sequence deletions are indicated by dashes in the sequences shown in Table 5.

TABLE 5

Toxin	N-term (AAs 1-30) of LC	SEQ ID C-term (last) NO: 50 AAs) of LC	SEQ ID NO:
BoNT/A	M-----YKDPVNGVD IAYIKIPNAGQM	109 GFNLRNTNLAANFNGQNT EINNMNFTKLKNFTGLFE FYK-----	110
BoNT/A	MPFVNKQ-----VNGVD IAYIKIPNAGQM	111 GFNLRNTNLAANFNGQNT EINNMNFTKLK----- ---LLCVRGIITSK	112
BoNT/A	MPFVNKQFNYKDP----- -AYIKIPNAGQM	113 GFNLRNTNLAANFNGQNT EINNMN-----GLFE FYKLLCVRGIITSK	114
BoNT/A	MPFVNKQFNYKDPVNGVD IA-----	115 GFNLRN-----NT EINNMNFTKLKNFTGLFE FYKLLCVRGIITSK	116
BoNT/B	MPVTINNPNYNDPIDNDN IIMME-----	117 YTI-----ISDKNMGKEY RGQNKAINQAYEEISKE ELAVYKIQMCKSVK	118
BoNT/B	MPVTINNPNYND----- ---EPPFARGT	119 YTIEEGFNISD----- -GQNKAINQAYEEISKE HLAVYKIQMCKSVK	120
BoNT/B	MP-----NDPIDNDN IIMMEPPFARGT	121 YTIEEGFNISDKNMGKEY RGQNKAINQQA----- -----KIQMCKSVK	122
BoNT/C ₁	MPI-----SDPVDNKN ILYLDTHLNTLA	123 NIPKSNLNVLFMGQNLRSR NPALRKV-----K FCHKAIDGRSLYNK	124
BoNT/D	MTW-----VNDND ILYLRIPOQNKLI	125 YTIRDGFNLTNKGFNIE SGQNIERNPA----- --DLFTKVCLRLTK	126
BoNT/E	MP-----DPVNDRTI LYIKPGGCQEFY	127 GYNINNLKVNFRGQANL NPRIITPI----- RFCKNIVSVKGIRK	128
BoNT/E	MPKINSFNYN----- --IKPGGCQEFY	129 GYNINN-----GQANL NPRIITPITGRGLVKKII RFCKNIVSVKGIRK	130
BoNT/E	MPKINSFNYNDPVNDRTI LYIK-----	131 GYNINNLKVNFRGQANL NPRIITPITGRGLVKKII R-----KGIRK	132
BoNT/F	MPVAINSFNYNDPVNDT ILYMQIP-----	133 TVSEGFNIGNLAVNNRGQ SIKLNPKIIDSIPD----- ----KFCKSVIPRK	134
BoNT/G	M----- -----	135 QNEGFNIASKNLKTEFNG QNKAVNKEA----- ---RIAMCKPVMYK	135

Example 16C

[0260] In some embodiments of the present invention, the biological persistence and/or the enzymatic activity of a toxin can be altered by structurally modifying the toxin. In some embodiments, the structural modification includes the substitution, mutation or deletion of amino acids within the toxin. In a suitable embodiment, the structural modification includes a chimeric fusion construct in which a biological persistence-

enhancing component or an enzymatic activity-enhancing component may be fused to, swapped for, or incorporated within a terminal end of the light chain of a botulinum toxin. In some embodiments, the structural modification includes a chimeric fusion construct in which a biological persistence-reducing component or an enzymatic activity-reducing component may be fused to, swapped for, or incorporated within a terminal end of the light chain of a botulinum toxin. In a suitable embodiment, the persistence- or activity-enhancing or persistence- or activity-reducing component is an N-terminal region including the first 30 amino acids of a light chain of a botulinum toxin, or a C-terminal region including the last 50 amino acids of a light chain of a botulinum toxin. This biological persistence- or enzymatic activity-enhancing component or biological persistence- or enzymatic activity-reducing component is swapped for, fused to, or incorporated within an N- and/or C-terminus of a light chain of a botulinum toxin to enhance or reduce its biological persistence and/or enzymatic activity.

[0261] In some embodiments, the fusion of, addition to, or swapping of the N-terminal region of the light chain of BoNT/A into a chimeric construct results in an increase in biological persistence and/or enzymatic activity. In some embodiments, a substituted, mutated, or deleted N-terminal region of the light chain of BoNT/A within a chimeric construct results in a decrease in biological persistence and/or enzymatic activity. In some embodiments, the fusion of, addition to, or swapping of the C-terminal region of the light chain of BoNT/A into a chimeric construct results in an increase in biological persistence and/or enzymatic activity. In some embodiments, a substituted, mutated, or deleted C-terminal region of the light chain of BoNT/A within a chimeric construct results in a decrease in biological persistence and/or enzymatic activity.

[0262] Generally, it is suitable that the chimeric toxin has a biological persistence of about 20% to 300% greater than an identical toxin without the structural modification. The biological persistence of the chimeric toxin may be enhanced by about 100%. That is, for example, the modified botulinum neurotoxin including the biological persistence-enhancing component is able to cause a substantial inhibition of neurotransmitter release (for example, acetylcholine) from a nerve terminal for about 20% to about 300% longer than a neurotoxin without the structural modification.

[0263] Similarly, it is suitable that the chimeric botulinum toxin light chain has an altered enzymatic activity. For example, the chimeric toxin can exhibit a reduced or an enhanced inhibition of exocytosis (such as exocytosis of a neurotransmitter) from a target cell with or without any alteration in the biological persistence of the modified neurotoxin. Altered enzymatic activities include increased or decreased efficiency or potency, increased or decreased localization to the plasma membrane, increased or decreased substrate specificity, and/or increased or decreased rate of proteolysis of SNAP/SNARE proteins. An increase in enzymatic activity can be from 1.5 to 5 times greater than the biological activity of the native or unmodified light chain. For example, the chimeric botulinum neurotoxin including the enzymatic activity-enhancing component is able to cause a substantial inhibition of neurotransmitter release (for example, acetylcholine) from a nerve terminal due to an increased rate of proteolysis of the SNAP-25 substrate as compared to a neurotoxin without the structural modification.

[0264] It has been observed that a recombinant construct with both the eight amino acid residues of SEQ ID NO: 27 (PFVVKQFN) deleted from the N-terminus and the twenty-two amino acid residues of SEQ ID NO: 28 (KNFTGLFE-FYKLLCVRGIITSK) deleted from the C-terminus of the light chain of botulinum toxin A exhibits a reduced activity such that the effective concentration (EC_{50}) required to cleave the SNAP-25 substrate is nearly ten-fold greater than that of a similar construct with only the C-terminal twenty-two amino acid deletion (EC_{50} Δ N8 Δ C22=4663 pM vs. EC_{50} Δ C22=566 pM). The recombinant light chain of botulinum toxin A was used as a control (EC_{50} rLC/A=7 pM), and, therefore, as compared to the rLC/A construct, a 666-fold greater concentration of the Δ N8 Δ C22 construct is required. A recombinant light chain construct with the dileucine motif mutated to dialanine [rLC/A(LL-->AA)] also exhibits reduced activity (EC_{50} rLC/A(LL-->AA)=184 pM); however, the effective concentration of the Δ N8 Δ C22 construct is twenty-five fold greater than the rLC/A(LL-->AA) construct.

[0265] A modified light chain may include a light chain from botulinum toxins A, B, C1, D, E, F or G. One or multiple domains at the N- and/or C-terminus may be modified by addition, deletion or substitution. For example, a modified chimeric light chain component may include a light chain from BoNT/E modified by adding or replacing/substituting one or more N- and/or C-terminal end sequences derived from the BoNT/A light chain, thereby resulting in a chimeric BoNT/E-BoNT/A chimeric light chain with one or both terminal ends having one or more sequences which convey an increased or decreased ability to localize to a plasma membrane, increased or decreased biological persistence and/or an increased or decreased enzymatic activity.

[0266] A chimeric botulinum toxin can be constructed such that a C-terminal portion of the light chain of one botulinum toxin serotype replaces a similar C-terminal portion within the light chain of another botulinum toxin serotype. For example, the last twenty two amino acid residues bearing the dileucine motif from the C-terminus of the light chain of BoNT/A can replace the last twenty two amino acid residues of the C-terminus of the light chain of BoNT/E. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 136

MPKINSFNYNDPVNDRTILYIKPGGCQEFYKSFNIMKNIWIIPERNVIGT
 TPQDFHPPTSLKNGDSSYYDPNYLQSDDEEKDRFLKIVTKIFNRINNNLSG
 GILLEELS KANPYLGNDNTPDNQPHIGDASAVEIKFSNGSQDILLPNVII
 MGAEPDLFETNSSNISLRNNYMPSNHGFGSIAIVTFSPEYSFRFNDNSMN
 EFIQDPALTLMHელიSLHGLYGAKGITTKYTITQKQNPLITNIRGTNIE
 EFLTPGGTDLNII TSAQSNDIYTNLLADYKKIASKLSKVQVSNPLLPYK
 DVFEAKYGLDKDASGIYSVNINKFNDIFKKLYSFTFEDLATKQVKCRQT
 YIGQYKYPKLSNLLNDSIYNISEGYNINNLKVNFRGQANLNPIITPIT
GKNFTGLFEFYKLLCVRGIITSK

[0267] In the construct above, the majority of the amino acid sequence is derived from BoNT/E serotype, and the amino acids shown in bold underlined text are derived from the last twenty two amino acid residues of the C-terminus of the light chain of BoNT/A which bears the dileucine motif.

[0268] In a further example, the first thirty amino acid residues from the N-terminus of the light chain of BoNT/A can replace the first thirty amino acid residues of the N-terminus of the light chain of BoNT/B. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 137

MPFVNKQFNKDPVNGVDIA**YIKIPNAGQM**GRYYKAFKITDRIWIIPERY
TFGYKPEDFNKSSGIFNRDVCEYYDPDYLTNDKKNIFFQTLIKLFNRIK
SKPLGEKLEMIINGIPYLGDRRVPLEEFNTNIASVTVNKLISNPGEVER
KKGIFANLIIIFGPGPVLNENETIDIGIQNHASREGFGGIMQMFCPEYV
SVFNNVQENKGASIFNRRGYFSDPALILMHელიHVLHGLYGIKVDLPIV
PNEKKFFMQSTDTIQAEELYTFGGQDPSIISPSTDKSIYDKVLQNFGRIV
DRLNKVLVCISDPNININIKNFKDKYKFVEDSEGKYSIDVESFNKLYK
SLMLGFTEINIAENYKIKTRASYFSDSLPPVKIKNLLDNEIYTIIEGFNI
SDKNMGKEYRGQNKAINKQAYEEISKEHLAVYKIQMCKSVK

[0269] In the construct above, the majority of the amino acid sequence is derived from BoNT/B serotype, and the amino acids shown in bold underlined text are derived from the first thirty amino acid residues of the N-terminus of the light chain of BoNT/A.

[0270] Still further, the chimeric construct can have both N-terminal and the C-terminal replacements. For example, the first nine amino acid residues from the N-terminus of the light chain of BoNT/A can replace the first nine amino acid residues of the N-terminus of the light chain of BoNT/E. Additionally, in the same construct, the last twenty-two amino acid residues from the C-terminus of the light chain of BoNT/A can replace the last twenty-two amino acid residues from the C-terminus of the light chain of BoNT/E. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 138

MPFVNKQFNNDPVDNRTILYIKPGGCQEFYKSFNIMKNIWIIPERNVIGT
TPQDFHPPTSLKNGDSSYYDPNYLQSDDEEKDRFLKIVTKIFNRINNLSG
GILLEELSKANPYLGNDNTPDNQPHIGDASAVEIKFSNGSQDILLPNVII
MGAEPDLFETNSSNISLRNNYMPNSNHGFGSIAIVTFSPEYSFRFNDNSMN
EFIQDPALTLMHელიHLSLHGLYGAKGITTKYTITQKQNPLITNIRGTNIE
EFLTFGGTDLNIITSAQSNDIYTNLLADYKKIASKLSKVQVSNPLNPNYK
DVFEAKYGLDKDASGIYSVNINKFNIDFKKLYSFTEFDLATKFQVKCRQT
YIGQYKYFKLSNLLNDSIYINISEGYNNLNKVNFRGQANLNPRIITPIT
GKNFTGLFEFYKLLCVRGIITSK

[0271] In the construct above, the majority of the amino acid sequence is derived from BoNT/E serotype, and the amino acids shown in bold underlined text are derived from the first nine amino acid residues of the N-terminus and the last twenty-two amino acid residues of the C-terminus of the light chain of BoNT/A.

[0272] Similarly, the first nine amino acid residues from the N-terminus of the light chain of BoNT/A can replace the first nine amino acid residues of the N-terminus of the light chain

of BoNT/B. Additionally, in the same construct, the last twenty-two amino acid residues from the C-terminus of the light chain of BoNT/A can replace the last twenty-two amino acid residues from the C-terminus of the light chain of BoNT/B. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 139

MPFVNKQFNYNDPIDNDNIIMMEPPFARGTGYYKAFKITDRIWIIPERY
TFGYKPEDFNKSSGIFNRDVCEYYDPDYLTNDKKNIFFQTLIKLFNRIK
SKPLGEKLEMIINGIPYLGDRRVPLEEFNTNIASVTVNKLISNPGEVER
KKGIFANLIIIFGPGPVLNENETIDIGIQNHASREGFGGIMQMFCPEYV
SVFNNVQENKGASIFNRRGYFSDPALILMHელიHVLHGLYGIKVDLPIV
PNEKKFFMQSTDTIQAEELYTFGGQDPSIISPSTDKSIYDKVLQNFGRIV
DRLNKVLVCISDPNININIKNFKDKYKFVEDSEGKYSIDVESFNKLYK
SLMLGFTEINIAENYKIKTRASYFSDSLPPVKIKNLLDNEIYTIIEGFNI
SDKNMGKEYRGQNKAINKQKNFTGLFEFYKLLCVRGIITSK

[0273] In the construct above, the majority of the amino acid sequence is derived from BoNT/B serotype, and the amino acids shown in bold underlined text are derived from the first nine amino acid residues of the N-terminus and the last twenty-two amino acid residues of the C-terminus of the light chain of BoNT/A.

[0274] Furthermore, the first nine amino acid residues from the N-terminus of the light chain of BoNT/A can replace the first nine amino acid residues of the N-terminus of the light chain of BoNT/F. Additionally, in the same construct, the last twenty-two amino acid residues from the C-terminus of the light chain of BoNT/A can replace the last twenty-two amino acid residues from the C-terminus of the light chain of BoNT/F. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 140

MPFVNKQFNYNDPVDNDDTILYMQIPYEEKSKKYYKAFETMRNVWIIPERN
TIGTNPSPDFPPASLKNSSAYYDPNYLTDAEKDRYLKTTIKLFKRINS
NPAGKVLQEIISYAKPYLGNDHTPIDFSPVTRTTSVNIKLSTNVESML
LNLLVLGAGDPIDFESCCYPVRKLIDPDVYDPSNYGFGSINIVTFSPEYE
YTFNDISGGHNSSTESFIADPAISLAHელიHALHGLYGARGVTEETIEV
KQAPLMIAEKPIRLEEFLTFGGQDLNIITSAAMEKIYNNLLANYEKIATR
LSEVNSAPPEYDINEYKDYFQWKYGLDKNADGSYTVNENKFNIEYKKLYS
FTESDLANKFKVKCRNTYFIKYEFKVPNLLDDDIYTVSEGFNIGNLAVN
NRGQSIKLNPKIIDKNFTGLFEFYKLLCVRGIITSK

[0275] In the construct above, the majority of the amino acid sequence is derived from BoNT/F serotype, and the amino acids shown in bold underlined text are derived from the first nine amino acid residues of the N-terminus and the last twenty-two amino acid residues of the C-terminus of the light chain of BoNT/A.

[0276] In some embodiments, a light chain can be engineered such that one or more segments of the light chain of one or more toxin serotypes replace one or more segments of

equal or unequal length within the light chain of another toxin serotype. In a non-limiting example of this kind of chimeric construct, fifty amino acid residues from the N-terminus of the light chain of BoNT/A can replace eight amino acid residues of the N-terminus of the light chain of BoNT/B, resulting in a net gain of forty-two amino acids in length in the N-terminal region of the light chain chimera. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 141

MPFVNKQFNKYKDPVNGVDIAYIKIPNAGQMOPVKAFKIHNKIWIPIPERDT
FYNDPIDNDNIIMMEPPFARGTGRYYKAFKITDRIWIIPERYTFGYKPED
 FNKSSGIFNRDVCEYYDDYLDNTDKNIPFQTLLIKLFNRKSKPLGEKL
 LEMIINGIPYLGDRRVPLEEFNTNIASVTVNKLISNPGEVERKKGIFANL
 IIFGPGPVLNENETIDIGIQNHFAFSGREGFGGIMQMKFCPEYVSFVNNVQE
 NKGASIFNRRGYFSDPALILMHLEIHLVHLGLYGIKVDDLPIVPNEKKFFM
 QSTDITQAEELYTFGGQDPSIISPSTDKSIYDKVLQNFGRGIVDRNLNKVLV
 CISDPNININIIYKNKFKDKYKFVEDSEKYSIDVESFNKLYKSLMLGFTE
 INIAENYKIKTRASYFSDSLPPVKIKNLLDNEIYTIIEGFNISDKNMGKE
 YRGQNKAINKQAYEEISKEHLAVYKIQMCKSVK

[0277] In the construct above, the majority of the amino acid sequence is derived from BoNT/B serotype, and the amino acids shown in bold underlined text are derived from the first fifty amino acid residues of the N-terminus of the light chain of BoNT/A.

[0278] In a non-limiting example of this kind of chimeric construct, the last fifty amino acid residues from the C-terminus of the light chain of BoNT/A can replace fifteen amino acid residues within the C-terminus of the light chain of BoNT/E, resulting in a net gain of thirty-five amino acids in the C-terminal region of the light chain chimera. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 142

MPKINSFNYPNDPVNDRTILYIKPGGCQEFYKSFNIMKNIWIIPERNVIGT
 TPQDFHPPTSLKNGDSSYYDPNYLQSDDEEKDRFLKIVTKIFNRINNLSG
 GILLEELSKANPYLGNDNTPDNQPHIGDASAVEIKFSNGSQDILLPNVII
 MGAEPDLFETNSSNISLRNNYMPSNHGFGSIAIVTFSPEYSFRFNDNSMN
 EFIQDPALTLMHLEIHLHGLYGAKGITTQYITQKQNPITNIRGTNIE
 EFLTFGGTDLNIIITSAQSNDIYTNLLADYKKIASKLSKVQVSNPLNPKY
 DVFEAKYGLDKDASGIYSVNINKFNDIFKLYSFTFDLATKFQVKCRQT
 YIGQYKYFKLSNLLNDSIYNISEGYNINNLKVNFRGQANLNPIIT**PGF**
NLRNTNLAANFNGQNTTEINNMNFTKLKNFTGLFEFYKLLCVRGIITSKNI
 VSVKGIRK

[0279] In the construct above, the majority of the amino acid sequence is derived from BoNT/E serotype, and the amino acids shown in bold underlined text are derived from the last fifty amino acid residues of the C-terminus of the light chain of BoNT/A.

[0280] In a non-limiting example of this kind of chimeric construct, thirty amino acid residues from the N-terminus of the light chain of BoNT/A can replace ten amino acid residues of the N-terminus of the light chain of BoNT/E, resulting in a net gain of twenty amino acids in length in the N-terminal region of the chimera. Additionally, in the same construct, the last fifty amino acid residues from the C-terminus of the light chain of BoNT/A can replace the last fifty amino acid residues from the C-terminus of the light chain of BoNT/E. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 143

MPKINSFN**YMPFVNKQFNKYKDPVNGVDIAYIKIPNAGQM**YIKPGGCQEFY
 KSFNIMKNIWIIPERNVIGTTPQDFHPPTSLKNGDSSYYDPNYLQSDDEEK
 DRFLKIVTKIFNRINNLSGGILLEELSKANPYLGNDNTPDNQPHIGDAS
 AVEIKFSNGSQDILLPNVIMGAEPDLFETNSSNISLRNNYMPSNHGFGS
 IAIVTFSPEYSFRFNDNSMNEFIQDPALTLMHLEIHLHGLYGAKGITT
 YTITQKQNPITNIRGTNIEEFLTFGGTDLNIIITSAQSNDIYTNLLADYK
 KIASKLSKVQVSNPLNPKYDVFEAKYGLDKDASGIYSVNINKFNDIFKK
 LYSFTFDLATKFQVKCRQTYIGQYKYFKLSNLLNDSIYNI**SEGFNLRNT**
NLAANFNGQNTTEINNMNFTKLKNFTGLFEFYKLLCVRGIITSK

[0281] In the construct above, the majority of the amino acid sequence is derived from BoNT/E serotype, and the amino acids shown in bold underlined text are derived from the thirty amino acid residues of the N-terminus and the last fifty amino acid residues of the C-terminus of the light chain of BoNT/A.

[0282] In a non-limiting example of this kind of chimeric construct, thirty amino acid residues from the N-terminus of the light chain of BoNT/A can replace ten amino acid residues of the N-terminus of the light chain of BoNT/B, resulting in a net gain of twenty amino acids in length in the N-terminal region of the chimera. Additionally, in the same construct, the last fifty amino acid residues from the C-terminus of the light chain of BoNT/A can replace the last fifty amino acid residues from the C-terminus of the light chain of BoNT/B. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 144

MPVTINN**FNMPFVNKQFNKYKDPVNGVDIAYIKIPNAGQM**IMMEPPFARGT
 GRYYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRDVCEYYDDYLDN
 TNDKKNIPFQTLLIKLFNRKSKPLGEKLLLEMIINGIPYLGDRRVPLEEFN
 TNIASVTVNKLISNPGEVERKKGIFANLIIIFGPGPVLNENETIDIGIQNH
 FASREGFGGIMQMKFCPEYVSFVNNVQENKGASIFNRRGYFSDPALILMH
 ELIHLVHLGLYGIKVDDLPIVPNEKKFFMQSTDITQAEELYTFGGQDPSII
 SPSTDKSIYDKVLQNFGRGIVDRNLNKVLVCISDPNININIIYKNKFKDKYKF
 VEDSEKYSIDVESFNKLYKSLMLGFTEINIAENYKIKTRASYFSDSLPP
 VKIKNLLDNEI**GFNLRNTNLAANFNGQNTTEINNMNFTKLKNFTGLFEFYK**
LLCVRGIITSK

[0283] In the construct above, the majority of the amino acid sequence is derived from BoNT/B serotype, and the amino acids shown in bold underlined text are derived from the thirty amino acid residues of the N-terminus and the last fifty amino acid residues of the C-terminus of the light chain of BoNT/A.

[0284] In a non-limiting example of this kind of chimeric construct, thirty amino acid residues from the N-terminus of the light chain of BoNT/A can replace ten amino acid residues of the N-terminus of the light chain of BoNT/F, resulting in a net gain of twenty amino acids in length in the N-terminal region of the chimera. Additionally, in the same construct, the last fifty amino acid residues from the C-terminus of the light chain of BoNT/A can replace the last fifty amino acid residues from the C-terminus of the light chain of BoNT/F. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 145

MPVAINSFN**MPFVNKQFNKYKDPVNGVDIAYIKIPNAGQMLYMQIPYEEKS**
 KKKYKAFEMRNWVWIIPERNITGTNPSPDFPPASLKNKGSSAYYDPNYLT
 DAEKDRYLKTTIKLFPKRINSNPAGKVLQEIYAKPYLGNHDTPIDEFSP
 VTRTTSVNIKLSTNVESMLNLNLVLGAGPDIFESCCYPVRKLIDPDVVY
 DPSNYGFGSINIVTFSPEYEYTFNDISGGHNSSTESFIADPAISLAHELI
 HALHGLYGARGVTEETIEVKQAPLMIAEKPIRLEEFLTFGGQDLNIITS
 AMKEKIYNLLANYEKIATRLSEVNSAPPEYDINEYKDYFQWKYGLDKNA
 DGSYTVNENKFNEIYKKLYSFTESDLANKFKVKCRNTYFIKYEFLKVPNL
 LDDDIY**GFNLRNTNLAANFNQONTEINNMFNFKLNFTGLFEFYKLLCVR**
GIITSK

[0285] In the construct above, the majority of the amino acid sequence is derived from BoNT/F serotype, and the amino acids shown in bold underlined text are derived from the thirty amino acid residues of the N-terminus and the last fifty amino acid residues of the C-terminus of the light chain of BoNT/A.

[0286] In some embodiments, the swapped sequences can be derived from two different serotypes, resulting in a chimera with regions from three different serotypes in all. In this example, eight amino acid residues from the N-terminus of the light chain of BoNT/B can replace five amino acid residues of the N-terminus of the light chain of BoNT/E, resulting in a net gain of three amino acids in length in the N-terminal region of the chimera. Additionally, in the same construct, 30 amino acid residues including the dileucine repeat of the C-terminus of the light chain of BoNT/A can replace ten amino acid residues within the C-terminus of the light chain of BoNT/E, resulting in a net gain of 20 amino acids in the C-terminal region of the chimera. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 146

MPKINSFNNDP**VTINNFNY**DRITILYIKPGGCQEFYKSFNIMKNIWIIE
 RNVIGTTPQDFHPPTSLKNGDSSYYDPNYLQSDDEKDRFLKIVTKIFNRI
 NNNLSGGILLEELSKANPYLGNNDTPDNQFHIGDASAVEIKFSNGSQDIL

-continued

LPNVIIMGAEPDLFETNSSNISLRNNYMPSNHGFGSIAIVTFSPEYSFRF
 NDNSMNEFIQDPALTMHELIHSLHGLYGAKGITTYYTITQKQNPLITNI
 RGTNIEEFLTFGGTDLNIITSAQSNDIYTNLADYKKIASKLSKVQVSNP
 LLNPYKDVFEAKYGLDKDASGIYSVNINKFNDIFKKLYSFTEFDLATKQ
 VKCRQTYIGQYKYFKLSNLLNDSIYNISEGYNNLNKVNFRGQANLNPR
 IITPITGRGLVKKIIRFC**NNMFNFKLNFTGLFEFYKLLCVRGIITSK**

[0287] In the construct above, the majority of the amino acid sequence is derived from BoNT/E serotype, and the amino acids shown in bold italicized text are derived from eight amino acid residues of the N-terminus of the light chain of BoNT/B and thirty amino acid residues shown in bold underlined text are derived from thirty amino acid residues of the C-terminus of the light chain of BoNT/A.

[0288] In a non-limiting example, eight amino acid residues from the N-terminus of the light chain of BoNT/B can replace five amino acid residues of the N-terminus of the light chain of BoNT/F, resulting in a net gain of three amino acids in length in the N-terminal region of the chimera. Additionally, in the same construct, 30 amino acid residues including the dileucine repeat of the C-terminus of the light chain of BoNT/A can replace ten amino acid residues within the C-terminus of the light chain of BoNT/F, resulting in a net gain of 20 amino acids in the C-terminal region of the chimera. The amino acid sequence of the entire light chain of such a chimeric construct is shown below:

SEQ ID NO: 147

MPVAINSFNYND**VTINNFNY**TILYMQIPYEEKSKKKYKAFEMRNWVWIIP
 ERNTIGTNPSPDFPPASLKNKGSSAYYDPNYLTDAEKDRYLKTTIKLFPKR
 INSNPAGKVLQEIYAKPYLGNHDTPIDEFSPVTRTTSVNIKLSTNVES
 SMLNLNLVLGAGPDIFESCCYPVRKLIDPDVVYDPSNYGFGSINIVTFS
 EYEYTFNDISGGHNSSTESFIADPAISLAHELIHALHGLYGARGVTEET
 IEVKQAPLMIAEKPIRLEEFLTFGGQDLNIITSAMKEKIYNLLANYEKI
 ATRLSEVNSAPPEYDINEYKDYFQWKYGLDKNADGSYTVNENKFNEIYKK
 LYSFTESDLANKFKVKCRNTYFIKYEFLKVPNLDDDIYTVSEGFNIGNL
 AVNNRGQSICKLNPKIIDSIPDKGLVEK**NNMFNFKLNFTGLFEFYKLLCV**
RGIIITSKRK

[0289] In the construct above, the majority of the amino acid sequence is derived from BoNT/F serotype, and the amino acids shown in bold italicized text are derived from eight amino acid residues of the N-terminus of the light chain of BoNT/B and thirty amino acid residues shown in bold underlined text are derived from thirty amino acid residues of the C-terminus of the light chain of BoNT/A.

Example 16D

[0290] The invention also provides for a light chain of a botulinum toxin B, C1, D, E, F or G comprising about the first 30 amino acids from the N-terminus of the light chain of botulinum toxin type A and about the last 50 amino acids from the C-terminus of the light chain of botulinum toxin type A.

The first 30 amino acids of the N-terminus of type A here may be all or part, for example 2-16 contiguous or non contiguous amino acids, of the 30 amino acids. The last 50 amino acids here may be all or part, for example 5-43 contiguous or non-contiguous, amino acids of the 50 amino acids.

[0291] In some embodiments, such a light chain comprises about the first 20 amino acids from the N-terminus of the light chain of botulinum toxin type A and about the last 30 amino acids from the C-terminus of the light chain of botulinum toxin type A. The first 20 amino acids of the N-terminus of type A here may be all or part, for example 2-16 contiguous or non contiguous amino acids, of the 20 amino acids. The last 30 amino acids here may be all or part, for example 5-23 contiguous or non-contiguous, amino acids of the 30 amino acids.

[0292] In some embodiments, such a light chain comprises about the first 4 to 8, e.g. the first 8, amino acids from the N-terminus of the light chain of botulinum toxin type A and about the last 7 to 22, e.g. the last 22, amino acids from the C-terminus of the light chain of botulinum toxin type A. The first 8 amino acids of the N-terminus of type A here may be all or part, for example 2-7 contiguous or non contiguous amino acids, of the 7 amino acids. The last 22 amino acids here may be all or part, for example 5-16 contiguous or non-contiguous, amino acids of the 20 amino acids.

[0293] In some embodiments, the inclusion of about the first 30 amino acids from the N-terminus and about the last 50 amino acids from the C-terminus of the light chain of type A replaces one or more amino acids at the N- and C-termini, respectively, of the light chain of botulinum toxin type B, C1, D, E, F or G. The first 30 amino acids of the N-terminus of type A here may be all or part, for example 2-16 contiguous or non contiguous amino acids, of the 30 amino acids. The last 50 amino acids here may be all or part, for example 5-43 contiguous or non-contiguous, amino acids of the 50 amino acids.

[0294] In some embodiments, the inclusion of about the 20 amino acids from the N-terminus and about the 30 amino acids from the C-terminus of the light chain of type A replaces one or more amino acids at the N- and C-termini, respectively, of the light chain of botulinum toxin type B, C1, D, E, F or G. The first 20 amino acids of the N-terminus of type A here may be all or part, for example 2-16 contiguous or non contiguous amino acids, of the 20 amino acids. The last 30 amino acids here may be all or part, for example 5-23 contiguous or non-contiguous, amino acids of the 30 amino acids.

[0295] In some embodiments, the inclusion of about the first 4 to 8, for example the first 8, amino acids from the N-terminus and about the last 7 to 22, for example the last 22, amino acids from the C-terminus of the light chain of type A replaces one or more amino acids at the N- and C-termini, respectively, of the light chain of botulinum toxin type B, C1, D, E, F or G. The first 8 amino acids of the N-terminus of type A here may be all or part, for example 2-7 contiguous or non contiguous amino acids, of the 7 amino acids. The last 22 amino acids here may be all or part, for example 5-16 contiguous or non-contiguous, amino acids of the 20 amino acids.

[0296] The invention also provides for a modified botulinum toxin comprising the light chain of described herein, including the ones described in Example 16D.

Example 17

Intracellular Localization of Botulinum Toxin Types A, B and E Light Chains in Neuronal and Non-Neuronal Cells

[0297] Clostridial neurotoxins inhibit neurotransmission by cleavage of a SNARE protein; each serotype has a distinct therapeutic profile regarding efficacy, safety, and duration of action (BoNT/A>BoNT/B>>BoNT/E). After the toxin is internalised, the catalytic light chain (LC) translocates into the cytosol and cleaves one of the SNARE proteins. Differences in subcellular localization may influence the pharmacology of different serotypes. Constructs were generated encoding the LC from serotypes A, B and E fused with green fluorescent protein (GFP) at N- or C-terminus and transfected them into PC12 cells that were differentiated after transfection. Expression and catalytic activity of LC's were assessed by western blotting. Confocal microscopy reveals that GFP-LCA and LCA-GFP are localized in a punctate pattern on the plasma membrane and neurites, (very similar to the localization of GFP-SNAP-25). GFP-LCE and LCE-GFP are dispersed in the cytoplasm but their localization is markedly different from that of GFP alone. GFP-LCB is also cytosolic but different from GFP-LCE, while LCB-GFP is located in an internal structure. Localization data demonstrated that LCB-GFP is accumulated intracellularly (i.e. "localized" to the cytosol) and Western blot analysis demonstrated that this protein construct is being degraded in PC12 cells.

[0298] Thus, the LCB-GFP was noted to be in an extremely bright and presumably high concentration of LCB-GFP in a tight area and it was not cytosolic (was not diffuse throughout the cytosol). It may be that the LCB-GFP was, for example, retained in the ER (as is the case for some misfolded proteins), in a protein degradation path/organelle, or in an aggregation and precipitation within the cell (i.e. in an aggresome).

The inventors have shown that this pattern of localization is not unique to neuronal cells. Two non-neuronal cell lines: HeLa (adenocarcinoma of cervix) and HEK293T (human embryonic kidney) were transfected with the above described constructs. The various GFP-LC constructs expressed in HeLa cells displayed very similar patterns of localization for all serotypes, compared to those expressed in PC12 cells. Expression of the GFP-LC constructs in HEK293T cells resulted in a mixed patterns of localization with several constructs having similarities to LCB-GFP. Western blot analysis of the expressed proteins demonstrated that all the LC's were being degraded in HEK293T cells.

Materials and Methods:

[0299] The Light Chain genes from BoNT/A (Allergan Hall A), BoNT/B (NCTC 7273 Beans) and BoNT/E (NCTC 11219) were amplified from genomic DNA by PCR. The genes were cloned into pQBI25 plasmids (Qbiogene) as fusion proteins with GFP at the N-terminus or separately at the C-terminus:

[0300] GFP-LCA (GLCA), LCA-GFP; GFP-LCB (GLCB), LCB-GFP (LCBG); GFP-LCE (GLCE), LCE-GFP (LCEG)

[0301] The cell lines used for transfection were:

[0302] PC12: rat pheochromocytoma (chromaffin cells). NGF induces properties of sympathetic neurons.

[0303] HeLa cells: adenocarcinoma of cervix. Epithelial, non-secretory, no SNAP25, no VAMP-2.

[0304] HEK293T cells: primary human embryonal kidney transformed with SV40. No SNAP25, no VAMP-2 expression

[0305] Cell lines were transfected using Lipofectamine2000 (Invitrogen). PC12 cells were transfected under undifferentiated conditions and were differentiated afterwards with NGF (Harlan). Plasmids expressing GFP alone were used as a control in all experiments.

[0306] Expression and integrity of the transfected GFP-Light Chain fusions was assessed by immunoprecipitation using a GFP monoclonal antibody (3E6, Qbiogene), followed by western blot with antibodies probing for GFP (PolyAb, Santa Cruz) or LCA (PolyAb generated at Allergan).

[0307] Catalytic activity of the expressed Light Chain fusion proteins was determined by western blot using the following antibodies:

[0308] SMI-81 (Sternberger) and N-19 (Santa Cruz): Recognize cleaved (BoNT/A and BoNT/E) and full length SNAP25.

[0309] PolyAb SNAP25₁₉₇: Polyclonal antibody generated at Allergan, specific to the BoNT/A cleaved peptide.

[0310] PolyAb SNAP25₁₈₀: Polyclonal antibody generated at Allergan, specific to the BoNT/E cleaved peptide.

[0311] Localization of the Light Chains was determined by confocal microscopy (Leica). Cell slices were taken at several positions in the transfected cells. Slices with the focal point at the middle of the cell are shown.

[0312] Inhibition of exocytosis as a result of expressing GFP-LCs was assessed by quantitation of ³H-noradrenaline release induced by K⁺/Ca²⁺ stimulation.

[0313] Cells were loaded for 4 hours with ³H-noradrenaline at 0.042 mM in culture media, and then washed 3× with PBS. Exocytosis was induced with K⁺ in a Ca²⁺ containing buffer.

[0314] FIGS. 19 and 20 show the expression and activity of light chains in differentiated PC12 cells.

[0315] FIG. 19 shows the detection of GFP-LC fusion proteins expressed in differentiated PC12 cells. LCB-GFP is degraded in PC12 cells but not GFP-LCB. Expression and integrity of GFP-LCA was also assessed by probing with polyclonal antibody to LCA.

[0316] FIG. 20 shows Western blots of lysates from cells transfected with GFP, GFP-LCA, GFP-LCE, and GFP+LCA (each gene transfected separately, not a fusion construct). Activity of the light chains was assessed by probing with specific antibodies for the LCA and LCE cleaved products of SNAP25, and to the N-terminus of SNAP25 (recognizes both the cleaved and full-length SNAP25). The data shows that the expressed light chains are active proteases. Antibodies to SNAP-25₁₉₇ and SNAP-25₁₈₀ were produced at Allergan. Subcellular localization of light chains in PC12 cells is shown in FIGS. 21 to 23.

[0317] FIG. 21 shows that GFP-fused light chain A localizes to the plasma membrane. PC12 cells were transfected with plasmids encoding GFP and full length GFP-LCA. Images were taken in a confocal microscope, with the focal plane at the middle of the cell. A clear localization at the plasma membrane can be observed. LCA-GFP displayed the same plasma membrane localization pattern.

[0318] FIG. 22 shows that light chain B localizes in the cytoplasm. PC12 cells were transfected with plasmids encoding LCB-GFP and GFP-LCB. A different localization pattern was observed dependent on fusion of GFP to the N- or C-terminus of LCB. The localization pattern observed for LCB-GFP is likely due to degradation of the protein. GFP-LCB localizes to the cytoplasm.

[0319] FIG. 23 shows that Light Chain E also localizes primarily in the cytoplasm. PC12 cells expressing GFP-fusions of LCE do not extend neurites even in the presence of NGF. PC 12 cells were transfected with plasmids encoding GFP-LCE and LCE-GFP. The localization of LCE is cytoplasmic for both fusion proteins. Despite treatment with NGF, transfected cells were round, with very few neurites.

[0320] FIG. 24 shows that expressed LCs inhibit exocytosis in PC12 cells. Exocytosis was measured in undifferentiated PC12 cells expressing GFP, GFP-LCA, GFP-LCB, and GFP-LCE that were selected for 3 days with G418. Release of ³H-noradrenaline was induced by incubating the cells with 100 mM K⁺ in the presence of Ca²⁺. Inhibition of exocytosis was observed in cells expressing the light chains. FIG. 24A shows norepinephrine release by PC12 cells electroporated with PURE A. The Y-axis represents % norepinephrine release. FIG. 24B shows the percentage of ³H norepinephrine released by non-differentiated PC12 cells transfected with various GFP constructs. The Y-axis represents % norepinephrine release.

[0321] FIG. 25 shows localization of GFP in HeLa and HEK293T cells. HeLa and HEK293T cells were transfected with a plasmid encoding the Green Fluorescent Protein (GFP). GFP fluorescence can be detected throughout the entire cell, including the nuclei (middle of cell).

[0322] FIGS. 26 and 27 show subcellular localization of GFP light chain fusions in HeLa cells.

[0323] FIG. 26 shows detection of GFP-LC fusion proteins expressed in HeLa cells, by probing Western blots with an antibody for GFP. This was accomplished by immunoprecipitation with a monoclonal antibody against GFP, followed with Western blot analysis probing for GFP with a polyclonal antibody. In this cell line, LCB-GFP but not GFP-LCB is degraded, similar to PC12 cells. Expression and integrity of GFP-LCA was also assessed by probing with a polyclonal antibody to LCA. [Top: IP GFP(3E2)/WB GFP (PolyAb); Bottom: IP GFP(3E2)/WB LCA (PolyAb)].

[0324] FIG. 27 shows that localization of GFP-fused Light Chains expressed in HeLa cells is similar to PC12 Cells. HeLa cells were transfected with plasmids encoding GFP-LCA, GFP-LCE, GFP-LCB, and LCB-GFP. The pattern of localization for all Light Chains is similar to that observed in PC12 cells. Confocal images were acquired with the focal plane at the middle of the cells.

[0325] FIGS. 28 and 29 show subcellular localization of GFP light chain fusions in HEK293T cells. FIG. 28 shows the detection of GFP-LC fusion proteins expressed in HEK 293T cells. The fusion proteins were immunoprecipitated with a monoclonal antibody for GFP and the Western blots were probed with a polyclonal antibody for GFP. IP: GFP(3E2)/WB: GFP (PolyAb) The Western blot analysis revealed that all GFP-LC fusion proteins are being degraded in HEK293T cells.

[0326] FIG. 29 shows localization of the GFP fusion proteins in HEK293T cells transfected with plasmids encoding GFP-LCA, GFP-LCE, GFP-LCB, and LCB-GFP. The pattern of localization for all Light Chains is mixed with some resemblance to PC12 and HeLa cells but with accumulation of fluorescence intracellularly. The GFP-LC fusion proteins seem to accumulate similarly in all cell types when it is degraded. Western blots revealed that all GFP-LC fusion proteins are degraded in HEK293T cells. Accumulation of the fusion proteins within the cells appears to be indicative of protein degradation.

[0327] The data shown in FIG. 19-29 demonstrates at least that: the Light Chain of BoNT serotypes A, B and E displays a different subcellular localization; GFP-LCA, GFP-LCB, and GFP-LCE fusion proteins expressed in differentiated PC12 cells display protease activity and inhibit exocytosis; LCA localizes near the plasma membrane of PC12 and HeLa cells. Localization in HEK293T cells is different, probably due to degradation; LCE localizes to the cytoplasm in PC12 and HeLa cells; LCB-GFP is degraded in all cell types; GFP-LCB has a cytoplasmic localization; and localization of the Light Chains is similar in both neuronal and non-neuronal exocytic cells (PC12 and HeLa cells, respectively), suggesting that the signal(s) for subcellular localization are contained within the Light Chain sequences.

[0328] Localization of the light chains from different serotypes of botulinum toxin may play a role in the therapeutic profile and duration of action of the neurotoxins.

Example 18

Botulinum Toxin Light Chain Constructs and Light Chain-Intracellular Structure Compositions

[0329] Recombinant plasmids have been constructed to yield fusion proteins containing the green fluorescent protein attached to the light chain of botulinum neurotoxin (BoNT). These constructs are designated GFP-LCA, GFP-LCB, and GFP-LCE depending on the serotype of the constituent light chain. These light chains are metalloproteases that cleave a specific protein of the SNARE complex in neuronal cells inhibiting neurotransmitter release. Specifically, LCA and LCE cleave SNAP-25 and LCB cleaves VAMP2.

[0330] The inventors have shown that the protein product GFP-LCA localizes to the cytoplasmic side of the plasma membrane when expressed in PC-12 cells. The basis for membrane localization and identification of the compartment within the plasma membrane where the LCA resides was completed by identifying the proteins interacting with or in close proximity to GFP-LCA.

[0331] The inventors have also determined that the proteins expressed from the GFP-light chain constructs are active proteases with the ability to cleave specific SNARE proteins. The inventors also have demonstrated that these fusion proteins can inhibit exocytosis when expressed in secretory cell lines containing SNAP-25 and VAMP-2.

Methods:

[0332] Crosslinking Studies: PC-12 cells were transfected with the plasmid containing either GFP-LCA (experimental group) or GFP (control group) and differentiated with neuronal growth factor (NGF). The cells were treated with a primary amine reactive crosslinking agent and subsequently lysed using T-X-100. The protein crosslinking agent, DTBP, is a reducible 11.9 Å chain, which can be cleaved by strong reducing agents such as DTT. DTBP is also water-soluble and membrane permeable.

[0333] The GFP-LCA was immunoprecipitated using a monoclonal antibody to GFP. The goal was to precipitate the GFP-LCA along with any interacting proteins attached via the cross-linking reagent. (This method can be used to prepare an isolated composition made up of a botulinum toxin light chain component and an intracellular structure component [the interacting proteins]. It is believed that the intracellular structure component interacts with the light chain component in a manner effective to facilitate substrate (SNARE) proteolysis within a cell.) These samples were subjected to SDS-PAGE under reduced and non-reduced conditions and blotted to PVDF. The blots were subsequently probed with

antibodies specific for LCA and the SNARE protein SNAP-25. The antibodies used to probe are listed in the table below.

Antibody Target	Source	Type (polyclonal or monoclonal)
LCA	Allergan	Polyclonal
SNAP-25 (recognizes cleaved and uncleaved)	AB-CAM	Polyclonal

Results:

[0334] Crosslinking Studies: SNAP-25 immuno-precipitates with GFP-LCA suggesting these proteins form a complex when GFP-LCA is expressed in PC-12 cells. The inventors have also found that other SNARE type proteins immuno-precipitate with this complex when the cells are treated with a protein cross-linking agent prior to lysis. The inventors show the total size of the complex containing GFP-LCA and SNAP-25 using the cross-linking reagent.

[0335] FIG. 30 shows a western blot of GFP immuno-precipitated from cells transfected with GFP (lane 1) or GFP-LCA (lane 2). The cells were treated with a crosslinking agent DTBP prior to lysis. The samples were subjected to SDS-PAGE (4-15% polyacrilamide), blotted onto a PVDF membrane, and probed with an antibody for LCA. The samples are analyzed under reduced (FIG. 30A) and non-reduced (FIG. 30B) conditions. The crosslinking agent used in this study remains uncleaved in the non-reduced conditions. FIG. 30A shows that an 80 kDa protein is immuno-precipitated from PC-12 cells transfected with GFP-LCA, which correlates with the size of GFP-LCA. FIG. 30B shows three different protein complexes containing GFP-LCA are detected in the non-reduced sample with sizes of 110, 140 and 170 kDa. There were no protein bands larger than 170 kDa and nothing was detected in the wells of the gel. This result indicates sizes of the cellular complexes that contain GFP-LCA.

[0336] The blot from FIG. 30 was reprobed using a polyclonal antibody for SNAP-25 (FIG. 31). FIG. 31A shows a 25 kDa protein was detected in the reduced sample, which corresponds to the size of SNAP-25. This data confirms that SNAP-25 is immunoprecipitated with GFP-LCA. FIG. 31B shows the blot of the non-reduced samples, and the higher molecular weight proteins containing GFP-LCA were also detected using an antibody for SNAP-25. These data suggest GFP-LCA is in a complex that contains SNAP-25 when expressed in PC-12 cells.

Example 19

Proteins Expressed From the GFP-Light Chain Constructs Can Inhibit Exocytosis When Expressed in Secretory Cell Lines

[0337] The inventors have determined that the proteins expressed from the GFP-light chain constructs are active proteases with the ability to cleave specific SNARE proteins. In this example, the inventors also have demonstrated that these fusion proteins can inhibit exocytosis when expressed in secretory cell lines containing SNAP-25 and VAMP-2.

Methods:

[0338] Exocytosis Assay Exocytosis was measured using undifferentiated PC-12 cells exposed to tritium labeled norepinephrine (noradrenaline—Amersham). The labeled PC-12 cells were exposed to solutions containing various concen-

trations of potassium chloride and calcium chloride. The goal was to depolarize the PC-12 cells with potassium chloride and induce exocytosis via vesicle fusion with the plasma membrane with calcium chloride. The treated cells and the buffer containing the secreted ^3H -noradrenaline were collected separately and scintillation counted. Exocytosis was determined by calculating the percent norepinephrine released based on the formula below: $\% \text{ label released} = 100 * (\text{number of dpm in buffer}) / (\text{number of dpm in cell} + \text{number of dpm in buffer})$

[0339] Exocytosis was also analyzed using HIT-T15 cells, a hamster pancreatic cell line. This cell line is induced to secrete insulin when placed in media containing high glucose concentrations. HIT-T15 cells express SNAP-25 and their ability to secrete insulin is sensitive to treatment with BoNT-A. Insulin secretion was measured in HIT-T15 cells by placing the cells in DMEM containing high glucose (25 mM) or low glucose (5.6 mM). After 1 hour incubation at 37° C., the secretion media is collected and the amount of insulin secreted is determined using an insulin ELISA (APLCO diagnostics). Exocytosis is expressed as the amount of insulin secreted per 1×10^5 cells per hour.

Results:

[0340] Exocytosis Assay: The inventors have demonstrated that the GFP-light chain construct produce active enzymes capable of inhibiting exocytosis when expressed in exocytotic cells.

[0341] The primary set of experiments was completed with PC-12 cells. The inventors detected a decrease in exocytosis by PC-12 cells treated with BoNT-A (FIG. 32). The cells were either untreated (control) or permeabilized via electroporation in the presence or absence of 500 nM PURE A (purified botulinum toxin). First, analysis of the data reveals the percent norepinephrine released is significantly higher by PC-12 cells exposed to buffer containing a high concentration of potassium chloride (100 mM). It also appears the amount of ^3H -norepinephrine secreted is lower in the PC-12 cells treated with 500 nM PURE A compared with untreated cells. This is expected as PURE A cleaves SNAP-25 causing an inhibition of exocytosis. These data confirm that an effect of BoNT-A treatment on PC-12 cells can be measured using this assay.

[0342] PC-12 cells are not known to express the receptor necessary for BoNT-A binding and uptake. This was confirmed as follows. Exocytosis in PC-12 cells exposed to 500 nM exogenous PURE A was measured for up to three days. Exocytosis was induced by placing cells in buffer containing 100 mM potassium chloride with or without 2.2 mM calcium chloride. Cells placed in buffer containing 2.2 mM calcium chloride released a higher amount of norepinephrine. These results indicate exocytosis can be induced when PC-12 cells are placed in a buffer containing a high concentration of potassium chloride supplemented with calcium chloride. The

results in FIG. 33 also show no difference in exocytosis by cells exposed to exogenous 500 nM PURE A and untreated cells. These data confirm reported results that PC-12 cells do not contain the necessary receptor for the uptake of exogenous BoNT-A.

[0343] FIG. 34 shows the measurement of exocytosis by PC-12 cells transfected with plasmids containing the various GFP-light chain constructs. The cells containing the plasmid were selected by adding G418 to the growth media for three days. The data from the exocytosis assay shows the expressed fusion proteins inhibit ^3H -norepinephrine release by PC-12 cells placed in 100 mM KCl and 2.2 mM CaCl_2 . The inventors have shown that the GFP-LCA and GFP-LCE fusion proteins cleave SNAP-25₂₀₆ into SNAP-25₁₉₇ and SNAP-25₁₈₀, respectively. These data suggest the fusion proteins obtained from the expression of the plasmid constructs are active proteases that can inhibit exocytosis of PC-12 cells

[0344] A hamster pancreatic cell line, HIT-T15, was also used to determine if active enzymes are produced by the various GFP-light chain constructs. This is a non-neuronal cell line that secretes insulin when placed in media containing high concentrations of glucose. These cells contain SNAP-25 and their ability to secrete insulin has been shown to be sensitive to BoNT-A. The inventors confirmed that these cells secrete insulin in response to glucose, and this exocytosis is inhibited by BoNT-A. FIG. 35 shows the insulin secretion by HIT-T15 cells in response to high levels of glucose. The amount of insulin secreted by these cells is greater when placed in media containing high concentrations of glucose. FIG. 35 also shows insulin secretion is inhibited in HIT-T15 cells electroporated in the presence of 500 nM BoNT-A. The lysates from the cells treated with BoNT-A were found to contain the cleaved SNAP-25 produced by BoNT-A when analyzed via Western blots (FIG. 36). These data suggest insulin secretion in HIT-T15 is inhibited by BoNT-A cleavage of SNAP-25.

[0345] FIG. 37 shows the measurement of insulin released by HIT-T15 cells transfected with plasmids containing the various GFP-light chain fusion proteins. There was a decrease in the amount of insulin secreted by cells transfected with the plasmids containing light chain constructs when compared with untransfected cells and cells transfected with the plasmid containing GFP. This inhibition was especially seen when the cells were placed in media containing high concentrations of glucose. These data provide additional evidence the constructs produce active forms of the botulinum neurotoxin light chain.

[0346] While this invention has been described with respect to various specific examples and embodiments, it is to be understood that the invention is not limited thereto and that it can be variously practiced with the scope of the following claims. All articles, references, publications, and patents set forth above are incorporated herein by reference in their entirety.

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

-continued

Thr	Asn	Asp	Lys	Lys	Asn	Ile	Phe	Leu	Gln	Thr	Met	Ile	Lys	Leu	Phe	85	90	95
Asn	Arg	Ile	Lys	Ser	Lys	Pro	Leu	Gly	Glu	Lys	Leu	Leu	Glu	Met	Ile	100	105	110
Ile	Asn	Gly	Ile	Pro	Tyr	Leu	Gly	Asp	Arg	Arg	Val	Pro	Leu	Glu	Glu	115	120	125
Phe	Asn	Thr	Asn	Ile	Ala	Ser	Val	Thr	Val	Asn	Lys	Leu	Ile	Ser	Asn	130	135	140
Pro	Gly	Glu	Val	Glu	Arg	Lys	Lys	Gly	Ile	Phe	Ala	Asn	Leu	Ile	Ile	145	150	155
Phe	Gly	Pro	Gly	Pro	Val	Leu	Asn	Glu	Asn	Glu	Thr	Ile	Asp	Ile	Gly	165	170	175
Ile	Gln	Asn	His	Phe	Ala	Ser	Arg	Glu	Gly	Phe	Gly	Gly	Ile	Met	Gln	180	185	190
Met	Lys	Phe	Cys	Pro	Glu	Tyr	Val	Ser	Val	Phe	Asn	Asn	Val	Gln	Glu	195	200	205
Asn	Lys	Gly	Ala	Ser	Ile	Phe	Asn	Arg	Arg	Gly	Tyr	Phe	Ser	Asp	Pro	210	215	220
Ala	Leu	Ile	Leu	Met	His	Glu	Leu	Ile	His	Val	Leu	His	Gly	Leu	Tyr	225	230	235
Gly	Ile	Lys	Val	Asp	Asp	Leu	Pro	Ile	Val	Pro	Asn	Glu	Lys	Lys	Phe	245	250	255
Phe	Met	Gln	Ser	Thr	Asp	Ala	Ile	Gln	Ala	Glu	Glu	Leu	Tyr	Thr	Phe	260	265	270
Gly	Gly	Gln	Asp	Pro	Ser	Ile	Ile	Thr	Pro	Ser	Thr	Asp	Lys	Ser	Ile	275	280	285
Tyr	Asp	Lys	Val	Leu	Gln	Asn	Phe	Arg	Gly	Ile	Val	Asp	Arg	Leu	Asn	290	295	300
Lys	Val	Leu	Val	Cys	Ile	Ser	Asp	Pro	Asn	Ile	Asn	Ile	Asn	Ile	Tyr	305	310	315
Lys	Asn	Lys	Phe	Lys	Asp	Lys	Tyr	Lys	Phe	Val	Glu	Asp	Ser	Glu	Gly	325	330	335
Lys	Tyr	Ser	Ile	Asp	Val	Glu	Ser	Phe	Asp	Lys	Leu	Tyr	Lys	Ser	Leu	340	345	350
Met	Phe	Gly	Phe	Thr	Glu	Thr	Asn	Ile	Ala	Glu	Asn	Tyr	Lys	Ile	Lys	355	360	365
Thr	Arg	Ala	Ser	Tyr	Phe	Ser	Asp	Ser	Leu	Pro	Pro	Val	Lys	Ile	Lys	370	375	380
Asn	Leu	Leu	Asp	Asn	Glu	Ile	Tyr	Thr	Ile	Glu	Glu	Gly	Phe	Asn	Ile	385	390	395
Ser	Asp	Lys	Asp	Met	Glu	Lys	Glu	Tyr	Arg	Gly	Gln	Asn	Lys	Ala	Ile	405	410	415
Asn	Lys	Gln	Ala	Tyr	Glu	Glu	Ile	Ser	Lys	Glu	His	Leu	Ala	Val	Tyr	420	425	430
Lys	Ile	Gln	Met	Cys	Lys	Ser	Val	Lys								435	440	

<210> SEQ ID NO 31

<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype A

<220> FEATURE:

<221> NAME/KEY: PHOSPHORYLATION

-continued

<222> LOCATION: (1)...(4)
<223> OTHER INFORMATION: Tyrosine-based motif

<400> SEQUENCE: 31

Tyr Ile Lys Ile
1

<210> SEQ ID NO 32
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: PHOSPHORYLATION
<222> LOCATION: (1)...(4)
<223> OTHER INFORMATION: Tyrosine-based motif

<400> SEQUENCE: 32

Tyr Asp Ser Thr
1

<210> SEQ ID NO 33
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: PHOSPHORYLATION
<222> LOCATION: (1)...(4)
<223> OTHER INFORMATION: Tyrosine-based motif

<400> SEQUENCE: 33

Tyr Gly Ser Thr
1

<210> SEQ ID NO 34
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: PHOSPHORYLATION
<222> LOCATION: (1)...(4)
<223> OTHER INFORMATION: Tyrosine-based motif

<400> SEQUENCE: 34

Tyr Asn Lys Phe
1

<210> SEQ ID NO 35
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: PHOSPHORYLATION
<222> LOCATION: (1)...(4)
<223> OTHER INFORMATION: Tyrosine-based motif

<400> SEQUENCE: 35

Tyr Met Lys Asn
1

<210> SEQ ID NO 36
<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: PHOSPHORYLATION
<222> LOCATION: (1)...(4)

-continued

<223> OTHER INFORMATION: Tyrosine-based motif

<400> SEQUENCE: 36

Tyr Leu Asn Phe
1

<210> SEQ ID NO 37

<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype A

<220> FEATURE:

<221> NAME/KEY: PHOSPHORYLATION

<222> LOCATION: (1)...(4)

<223> OTHER INFORMATION: Tyrosine-based motif

<400> SEQUENCE: 37

Tyr Asp Gly Phe
1

<210> SEQ ID NO 38

<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype A

<220> FEATURE:

<221> NAME/KEY: PHOSPHORYLATION

<222> LOCATION: (1)...(4)

<223> OTHER INFORMATION: Tyrosine-based motif

<400> SEQUENCE: 38

Tyr Lys Leu Leu
1

<210> SEQ ID NO 39

<211> LENGTH: 30

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype A

<220> FEATURE:

<221> NAME/KEY: DOMAIN

<222> LOCATION: (1)...(30)

<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain

<400> SEQUENCE: 39

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
1 5 10 15Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met
20 25 30

<210> SEQ ID NO 40

<211> LENGTH: 50

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype A

<220> FEATURE:

<221> NAME/KEY: DOMAIN

<222> LOCATION: (1)...(50)

<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain

<400> SEQUENCE: 40

Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln
1 5 10 15Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr
20 25 30Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr
35 40 45

-continued

Ser Lys
50

<210> SEQ ID NO 41
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype B
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (13)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain

<400> SEQUENCE: 41

Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn
1 5 10 15

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

<210> SEQ ID NO 42
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype B
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain

<400> SEQUENCE: 42

Tyr Thr Ile Glu Glu Gly Phe Asn Ile Ser Asp Lys Asn Met Gly Lys
1 5 10 15

Glu Tyr Arg Gly Gln Asn Lys Ala Ile Asn Lys Gln Ala Tyr Glu Glu
20 25 30

Ile Ser Lys Glu His Leu Ala Val Tyr Lys Ile Gln Met Cys Lys Ser
35 40 45

Val Lys
50

<210> SEQ ID NO 43
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype C1
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain

<400> SEQUENCE: 43

Met Pro Ile Thr Ile Asn Asn Phe Asn Tyr Ser Asp Pro Val Asp Asn
1 5 10 15

Lys Asn Ile Leu Tyr Leu Asp Thr His Leu Asn Thr Leu Ala
20 25 30

<210> SEQ ID NO 44
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype C1
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain

<400> SEQUENCE: 44

Asn Ile Pro Lys Ser Asn Leu Asn Val Leu Phe Met Gly Gln Asn Leu

-continued

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1           5           10          15
Ser Arg Asn Pro Ala Leu Arg Lys Val Asn Pro Glu Asn Met Leu Tyr
          20          25          30

Leu Phe Thr Lys Phe Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr
          35          40          45

Asn Lys
  50

<210> SEQ ID NO 45
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype D
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain

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<400> SEQUENCE: 45

```

Met Thr Trp Pro Val Lys Asp Phe Asn Tyr Ser Asp Pro Val Asn Asp
1           5           10          15

Asn Asp Ile Leu Tyr Leu Arg Ile Pro Gln Asn Lys Leu Ile
          20          25          30

```

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<210> SEQ ID NO 46
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype D
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain

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<400> SEQUENCE: 46

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Tyr Thr Ile Arg Asp Gly Phe Asn Leu Thr Asn Lys Gly Phe Asn Ile
1           5           10          15

Glu Asn Ser Gly Gln Asn Ile Glu Arg Asn Pro Ala Leu Gln Lys Leu
          20          25          30

Ser Ser Glu Ser Val Val Asp Leu Phe Thr Lys Val Cys Leu Arg Leu
          35          40          45

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Thr Lys
  50

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<210> SEQ ID NO 47
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acid of light chain

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<400> SEQUENCE: 47

```

Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp Arg
1           5           10          15

Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe Tyr
          20          25          30

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<210> SEQ ID NO 48
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E

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-continued

<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain

<400> SEQUENCE: 48

Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe Arg Gly Gln Asn Ala
1 5 10 15
Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr Gly Arg Gly Leu Val
20 25 30
Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val Ser Val Lys Gly Ile
35 40 45
Arg Lys
50

<210> SEQ ID NO 49
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype F
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain

<400> SEQUENCE: 49

Met Pro Val Ala Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp
1 5 10 15
Asp Thr Ile Leu Tyr Met Gln Ile Pro Tyr Glu Glu Lys Ser
20 25 30

<210> SEQ ID NO 50
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype F
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain

<400> SEQUENCE: 50

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

<210> SEQ ID NO 51
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype G
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain

<400> SEQUENCE: 51

Met Pro Val Asn Ile Lys Asn Phe Asn Tyr Asn Asp Pro Ile Asn Asn
1 5 10 15

-continued

Asp Asp Ile Ile Met Met Glu Pro Phe Asn Asp Pro Gly Pro
 20 25 30

<210> SEQ ID NO 52
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype G
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(50)
 <223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain

<400> SEQUENCE: 52

Gln Asn Glu Gly Phe Asn Ile Ala Ser Lys Asn Leu Lys Thr Glu Phe
 1 5 10 15

Asn Gly Gln Asn Lys Ala Val Asn Lys Glu Ala Tyr Glu Glu Ile Ser
 20 25 30

Leu Glu His Leu Val Ile Tyr Arg Ile Ala Met Cys Lys Pro Val Met
 35 40 45

Tyr Lys
 50

<210> SEQ ID NO 53
 <211> LENGTH: 30
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype A
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(30)
 <223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (4)...(4)
 <223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 53

Met Pro Phe Ala Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
 1 5 10 15

Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met
 20 25 30

<210> SEQ ID NO 54
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype A
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(50)
 <223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (25)...(25)
 <223> OTHER INFORMATION: Arginine substitution

<400> SEQUENCE: 54

Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln
 1 5 10 15

Asn Thr Glu Ile Asn Asn Met Asn Arg Thr Lys Leu Lys Asn Phe Thr
 20 25 30

Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr
 35 40 45

Ser Lys
 50

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<210> SEQ ID NO 55
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (10)...(10)
<223> OTHER INFORMATION: Lysine substitution

<400> SEQUENCE: 55

Met Pro Phe Val Asn Lys Gln Phe Asn Lys Lys Asp Pro Val Asn Gly
1 5 10 15

Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met
20 25 30

<210> SEQ ID NO 56
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (31)...(31)
<223> OTHER INFORMATION: Alanine substitution
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (32)...(32)
<223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 56

Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln
1 5 10 15

Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Ala Ala
20 25 30

Gly Leu Phe Glu Phe Tyr Lys Leu Cys Val Arg Gly Ile Ile Thr
35 40 45

Ser Lys
50

<210> SEQ ID NO 57
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (21)...(21)
<223> OTHER INFORMATION: Arginine substitution

<400> SEQUENCE: 57

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
1 5 10 15

Val Asp Ile Ala Arg Ile Lys Ile Pro Asn Ala Gly Gln Met
20 25 30

-continued

<210> SEQ ID NO 58
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13)...(13)
<223> OTHER INFORMATION: Histidine substitution

<400> SEQUENCE: 58

Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn His Asn Gly Gln
1 5 10 15
Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr
20 25 30
Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr
35 40 45
Ser Lys
50

<210> SEQ ID NO 59
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Histidine substitution

<400> SEQUENCE: 59

Met Pro Phe Val Asn Lys His Phe Asn Tyr Lys Asp Pro Val Asn Gly
1 5 10 15
Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met
20 25 30

<210> SEQ ID NO 60
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (43)...(43)
<223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 60

Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln
1 5 10 15
Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr
20 25 30
Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Ala Arg Gly Ile Ile Thr
35 40 45

-continued

Ser Lys
50

<210> SEQ ID NO 61
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype B
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (3)...(3)
<223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 61

Met Pro Ala Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn
1 5 10 15

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

<210> SEQ ID NO 62
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype B
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (44)...(44)
<223> OTHER INFORMATION: Arginine substitution

<400> SEQUENCE: 62

Tyr Thr Ile Glu Glu Gly Phe Asn Ile Ser Asp Lys Asn Met Gly Lys
1 5 10 15

Glu Tyr Arg Gly Gln Asn Lys Ala Ile Asn Lys Gln Ala Tyr Glu Glu
20 25 30

Ile Ser Lys Glu His Leu Ala Val Tyr Lys Ile Arg Met Cys Lys Ser
35 40 45

Val Lys
50

<210> SEQ ID NO 63
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype B
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (21)...(21)
<223> OTHER INFORMATION: Alanine substitution
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (22)...(22)
<223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 63

Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn
1 5 10 15

-continued

Asp Asn Ile Ile Ala Ala Glu Pro Pro Phe Ala Arg Gly Thr
20 25 30

<210> SEQ ID NO 64
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype B
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(50)
 <223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (41)...(41)
 <223> OTHER INFORMATION: Arginine substitution
 <400> SEQUENCE: 64

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

<210> SEQ ID NO 65
 <211> LENGTH: 30
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype B
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(30)
 <223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (10)...(10)
 <223> OTHER INFORMATION: Arginine substitution
 <400> SEQUENCE: 65

Met Pro Val Thr Ile Asn Asn Phe Asn Arg Asn Asp Pro Ile Asp Asn
1 5 10 15
 Asp Asn Ile Ile Met Met Glu Pro Pro Phe Ala Arg Gly Thr
20 25 30

<210> SEQ ID NO 66
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype B
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(50)
 <223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (30)...(30)
 <223> OTHER INFORMATION: Lysine substitution
 <400> SEQUENCE: 66

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

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35	40	45
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Val Lys
50

<210> SEQ ID NO 67
 <211> LENGTH: 30
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype C1
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(30)
 <223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (8)...(8)
 <223> OTHER INFORMATION: Lysine substitution

<400> SEQUENCE: 67

Met	Pro	Ile	Thr	Ile	Asn	Asn	Lys	Asn	Tyr	Ser	Asp	Pro	Val	Asp	Asn
1				5					10					15	

Lys	Asn	Ile	Leu	Tyr	Leu	Asp	Thr	His	Leu	Asn	Thr	Leu	Ala
	20				25							30	

<210> SEQ ID NO 68
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype C1
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(50)
 <223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (48)...(48)
 <223> OTHER INFORMATION: Arginine substitution

<400> SEQUENCE: 68

Asn	Ile	Pro	Lys	Ser	Asn	Leu	Asn	Val	Leu	Phe	Met	Gly	Gln	Asn	Leu
1			5						10					15	

Ser	Arg	Asn	Pro	Ala	Leu	Arg	Lys	Val	Asn	Pro	Glu	Asn	Met	Leu	Tyr
	20					25						30			

Leu	Phe	Thr	Lys	Phe	Cys	His	Lys	Ala	Ile	Asp	Gly	Arg	Ser	Leu	Arg
	35					40					45				

Asn Lys
50

<210> SEQ ID NO 69
 <211> LENGTH: 30
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype D
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(30)
 <223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (5)...(5)
 <223> OTHER INFORMATION: Alanine substitution
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (14)...(14)
 <223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 69

Met	Thr	Trp	Pro	Ala	Lys	Asp	Phe	Asn	Tyr	Ser	Asp	Pro	Ala	Asn	Asp
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1           5           10          15
Asn Asp Ile Leu Tyr Leu Arg Ile Pro Gln Asn Lys Leu Ile
      20             25             30

<210> SEQ ID NO 70
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype D
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (44)...(44)
<223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 70

Tyr Thr Ile Arg Asp Gly Phe Asn Leu Thr Asn Lys Gly Phe Asn Ile
1           5           10          15

Glu Asn Ser Gly Gln Asn Ile Glu Arg Asn Pro Ala Leu Gln Lys Leu
      20             25             30

Ser Ser Glu Ser Val Val Asp Leu Phe Thr Lys Ala Cys Leu Arg Leu
      35             40             45

Thr Lys
      50

<210> SEQ ID NO 71
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (13)...(13)
<223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 71

Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Ala Asn Asp Arg
1           5           10          15

Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe Tyr
      20             25             30

<210> SEQ ID NO 72
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (31)...(31)
<223> OTHER INFORMATION: Histidine substitution

<400> SEQUENCE: 72

Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe Arg Gly Gln Asn Ala
1           5           10          15

Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr Gly Arg Gly His Val
      20             25             30

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Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val Ser Val Lys Gly Ile
35 40 45

Arg Lys
50

<210> SEQ ID NO 73
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (7)...(7)
<223> OTHER INFORMATION: Arginine substitution

<400> SEQUENCE: 73

Met Pro Lys Ile Asn Ser Arg Asn Tyr Asn Asp Pro Val Asn Asp Arg
1 5 10 15

Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe Tyr
20 25 30

<210> SEQ ID NO 74
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (42)...(42)
<223> OTHER INFORMATION: Alanine substitution
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (43)...(43)
<223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 74

Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe Arg Gly Gln Asn Ala
1 5 10 15

Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr Gly Arg Gly Leu Val
20 25 30

Lys Lys Ile Ile Arg Phe Cys Lys Asn Ala Ala Ser Val Lys Gly Ile
35 40 45

Arg Lys
50

<210> SEQ ID NO 75
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (30)...(30)
<223> OTHER INFORMATION: Arginine substitution

<400> SEQUENCE: 75

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Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp Arg
1 5 10 15

Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe Arg
20 25 30

<210> SEQ ID NO 76
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (45)...(45)
<223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 76

Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe Arg Gly Gln Asn Ala
1 5 10 15

Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr Gly Arg Gly Leu Val
20 25 30

Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val Ser Ala Lys Gly Ile
35 40 45

Arg Lys
50

<210> SEQ ID NO 77
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype F
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(30)
<223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (3)...(3)
<223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 77

Met Pro Ala Ala Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp
1 5 10 15

Asp Thr Ile Leu Tyr Met Gln Ile Pro Tyr Glu Glu Lys Ser
20 25 30

<210> SEQ ID NO 78
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype F
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (46)...(46)
<223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 78

Thr Val Ser Glu Gly Phe Asn Ile Gly Asn Leu Ala Val Asn Asn Arg
1 5 10 15

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Gly Gln Ser Ile Lys Leu Asn Pro Lys Ile Ile Asp Ser Ile Pro Asp
 20 25 30

Lys Gly Leu Val Glu Lys Ile Val Lys Phe Cys Lys Ser Ala Ile Pro
 35 40 45

Arg Lys
 50

<210> SEQ ID NO 79
 <211> LENGTH: 30
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype G
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(30)
 <223> OTHER INFORMATION: Amino terminal 30 amino acids of light chain
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (8)...(8)
 <223> OTHER INFORMATION: Histidine substitution

<400> SEQUENCE: 79

Met Pro Val Asn Ile Lys Asn His Asn Tyr Asn Asp Pro Ile Asn Asn
 1 5 10 15

Asp Asp Ile Ile Met Met Glu Pro Phe Asn Asp Pro Gly Pro
 20 25 30

<210> SEQ ID NO 80
 <211> LENGTH: 50
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype G
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(50)
 <223> OTHER INFORMATION: Carboxyl terminal 50 amino acids of light chain
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (47)...(47)
 <223> OTHER INFORMATION: Alanine substitution

<400> SEQUENCE: 80

Gln Asn Glu Gly Phe Asn Ile Ala Ser Lys Asn Leu Lys Thr Glu Phe
 1 5 10 15

Asn Gly Gln Asn Lys Ala Val Asn Lys Glu Ala Tyr Glu Glu Ile Ser
 20 25 30

Leu Glu His Leu Val Ile Tyr Arg Ile Ala Met Cys Lys Pro Ala Met
 35 40 45

Tyr Lys
 50

<210> SEQ ID NO 81
 <211> LENGTH: 26
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype A
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(26)
 <223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 81

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
 1 5 10 15

Val Asp Ile Ala Tyr Ile Lys Ile Pro His
 20 25

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<210> SEQ ID NO 82
<211> LENGTH: 43
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(43)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 82

Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln
1 5 10 15

Asn Thr Glu Ile Asn Asn Met Asn Ala Ala Ala Ala Ala Ala Ala Ala
20 25 30

Ala Ala Cys Val Arg Gly Ile Ile Thr Ser Lys
35 40

<210> SEQ ID NO 83
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(26)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 83

Met Ala Ala Ala Asn Tyr Lys Asp Pro Val Asn Gly Val Asp Ile Ala
1 5 10 15

Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met
20 25

<210> SEQ ID NO 84
<211> LENGTH: 48
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(48)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 84

Gly Lys Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln
1 5 10 15

Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr
20 25 30

Gly Leu Phe Glu Phe Tyr Lys Cys Val Arg Gly Ile Ile Thr Ser Lys
35 40 45

<210> SEQ ID NO 85
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(26)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 85

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly

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1	5	10	15
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Val Asp Ile Ala Arg Asn Ala Gly Gln Met
 20 25

<210> SEQ ID NO 86
 <211> LENGTH: 46
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype A
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(46)
 <223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 86

Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala His Asn Thr Glu Ile
1 5 10 15

Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr Gly Leu Phe Glu
20 25 30

Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr Ser Lys
35 40 45

<210> SEQ ID NO 87
 <211> LENGTH: 26
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype A
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(26)
 <223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 87

Met Pro Lys Val Asn Lys Gln Phe Asn Val Asn Gly Val Asp Ile Ala
1 5 10 15

Tyr Ile Lys Ile Pro Asn Ala Gly Gln Met
20 25

<210> SEQ ID NO 88
 <211> LENGTH: 42
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype A
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(42)
 <223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 88

Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln
1 5 10 15

Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr
20 25 30

Gly Leu Phe Glu Phe Arg Arg Thr Ser Lys
35 40

<210> SEQ ID NO 89
 <211> LENGTH: 30
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype B
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(30)
 <223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

-continued

<400> SEQUENCE: 89

Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn
1 5 10 15

Asp Asn Ile Ile Ala Ala Ala Ala Ala Ala Arg Gly Thr
20 25 30

<210> SEQ ID NO 90

<211> LENGTH: 37

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype B

<220> FEATURE:

<221> NAME/KEY: VARIANT

<222> LOCATION: (1)...(37)

<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 90

Tyr Thr Ile Pro Pro Gly Phe Asn Ile Ser Asp Lys Asn Met Gly Lys
1 5 10 15

Glu Tyr Arg Gly Gln Asn Lys Ala Ile Asn Lys Gln Ala Tyr Glu Glu
20 25 30

Ile Ser Lys Glu His
35

<210> SEQ ID NO 91

<211> LENGTH: 26

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype B

<220> FEATURE:

<221> NAME/KEY: VARIANT

<222> LOCATION: (1)...(26)

<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 91

Met Pro Ala Phe Asn Tyr Asn Asp Pro Ile Asp Asn Asp Asn Ile Ile
1 5 10 15

Met Met Glu Pro Pro Phe Ala Arg Gly Thr
20 25

<210> SEQ ID NO 92

<211> LENGTH: 50

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype B

<220> FEATURE:

<221> NAME/KEY: VARIANT

<222> LOCATION: (1)...(50)

<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 92

Tyr Thr Ile Glu Glu Gly Phe Asn Ile Ser Asp Lys Asn Met Gly Lys
1 5 10 15

Glu Tyr Arg Gly Gln Asn Lys Ala Ala Ala Ala Ala Ala Glu Glu
20 25 30

Ile Ser Lys Glu His Leu Ala Val Tyr Lys Ile Gln Met Cys Lys Ser
35 40 45

Val Lys
50

<210> SEQ ID NO 93

-continued

<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype B
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(20)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 93

Met Pro Val Thr Ile Asn Asn Phe Asn Arg Met Met Glu Pro Pro Phe
1 5 10 15
Ala Arg Gly Thr
20

<210> SEQ ID NO 94
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype B
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(44)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 94

Tyr Thr Ile Glu Glu Gly Phe Asn Ile Ser Asp Lys Asn Met Gly Lys
1 5 10 15
Glu Tyr Arg Gly Gln Asn Lys Ala Ile Asn Lys Gln Ala Tyr Ala Ala
20 25 30
Ala Ala Ala Ala Ile Gln Met Cys Lys Ser Val Lys
35 40

<210> SEQ ID NO 95
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype C1
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(21)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 95

Met Ser Asp Pro Val Asp Asn Lys Asn Ile Leu Tyr Leu Asp Thr His
1 5 10 15
Leu Asn Thr Leu Ala
20

<210> SEQ ID NO 96
<211> LENGTH: 47
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype C1
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(47)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 96

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

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35	40	45
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<210> SEQ ID NO 97
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype D
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(26)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 97

Met	Thr	Arg	Pro	Val	Lys	Asp	Asp	Pro	Val	Asn	Asp	Asn	Asp	Ile	Leu
1				5					10					15	
Tyr	Leu	Arg	Ile	Pro	Gln	Asn	Lys	Leu	Ile						
			20					25							

<210> SEQ ID NO 98
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype D
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(44)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 98

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

<210> SEQ ID NO 99
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(31)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 99

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

<210> SEQ ID NO 100
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(50)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 100

Gly	Tyr	Asn	Ile	Asn	Asn	Leu	Lys	Val	Asn	Phe	Arg	Gly	Gln	Asn	Ala
1				5					10					15	

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Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr Gly Arg Gly Leu Val
 20 25 30

Lys Lys Ala Ala Ala Ala Cys Lys Asn Ile Val Ser Val Lys Gly Ile
 35 40 45

Arg Lys
 50

<210> SEQ ID NO 101
 <211> LENGTH: 33
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype E
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(33)
 <223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 101

Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Ala Ala Ala Ala
 1 5 10 15

Asn Asp Arg Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe
 20 25 30

Tyr

<210> SEQ ID NO 102
 <211> LENGTH: 47
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype E
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(47)
 <223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 102

Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe Arg Gly Gln Asn Ala
 1 5 10 15

Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr Gly Arg Gly Leu Val
 20 25 30

His Arg Phe Cys Lys Asn Ile Val Ser Val Lys Gly Ile Arg Lys
 35 40 45

<210> SEQ ID NO 103
 <211> LENGTH: 30
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype E
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(30)
 <223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 103

Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp Arg
 1 5 10 15

Thr Ile Leu Lys Ile Lys Pro Gly Gly Cys Lys Glu Phe Tyr
 20 25 30

<210> SEQ ID NO 104
 <211> LENGTH: 33
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype E
 <220> FEATURE:
 <221> NAME/KEY: VARIANT

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<222> LOCATION: (1)...(33)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of
LC

<400> SEQUENCE: 104

Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe Arg Gly Gln Asn Ala
1 5 10 15

Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr Gly Arg Gly Leu Pro
20 25 30

Pro

<210> SEQ ID NO 105
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype F
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(24)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 105

Met Pro Asn Tyr Asn Asp Pro Val Asn Asp Asp Thr Ile Leu Tyr Met
1 5 10 15

Gln Ile Pro Tyr Glu Glu Lys Ser
20

<210> SEQ ID NO 106
<211> LENGTH: 48
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype F
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(48)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of
LC

<400> SEQUENCE: 106

Thr Val Ser Glu Gly Phe Asn Ile Gly Asn Leu Ala Val Asn Asn Arg
1 5 10 15

Gly Gln Ser Ile Lys Leu Asn Pro Lys Ile Ile Asp Ser Ile Pro Asp
20 25 30

Lys Gly Ala Ala Ala Ala Ala Ala Cys Lys Ser Val Ile Pro Arg Lys
35 40 45

<210> SEQ ID NO 107
<211> LENGTH: 26
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype G
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(26)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 107

Met Pro Val Asn Ile Pro Pro Asp Pro Ile Asn Asn Asp Asp Ile Ile
1 5 10 15

Met Met Glu Pro Phe Asn Asp Pro Gly Pro
20 25

<210> SEQ ID NO 108
<211> LENGTH: 35
<212> TYPE: PRT

-continued

<213> ORGANISM: Clostridium botulinum serotype G
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(35)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 108

Gln Asn Glu Gly Phe Asn Ile Ala Ser Lys Asn Leu Lys Thr Glu Phe
1 5 10 15

Asn Gly Gln Asn Lys Ala Val Asn Lys Glu Ala Tyr Ala Ala Ala Ala
20 25 30

Ala Ala Ala
35

<210> SEQ ID NO 109
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(22)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 109

Met Tyr Lys Asp Pro Val Asn Gly Val Asp Ile Ala Tyr Ile Lys Ile
1 5 10 15

Pro Asn Ala Gly Gln Met
20

<210> SEQ ID NO 110
<211> LENGTH: 39
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(39)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 110

Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln
1 5 10 15

Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr
20 25 30

Gly Leu Phe Glu Phe Tyr Lys
35

<210> SEQ ID NO 111
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(24)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 111

Met Pro Phe Val Asn Lys Gln Val Asn Gly Val Asp Ile Ala Tyr Ile
1 5 10 15

Lys Ile Pro Asn Ala Gly Gln Met
20

-continued

<210> SEQ ID NO 112
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(40)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 112

Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln
1 5 10 15
Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Leu Leu Cys
 20 25 30
Val Arg Gly Ile Ile Thr Ser Lys
 35 40

<210> SEQ ID NO 113
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(24)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 113

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Ala Tyr Ile
1 5 10 15
Lys Ile Pro Asn Ala Gly Gln Met
 20

<210> SEQ ID NO 114
<211> LENGTH: 42
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(42)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 114

Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln
1 5 10 15
Asn Thr Glu Ile Asn Asn Met Asn Gly Leu Phe Glu Phe Tyr Lys Leu
 20 25 30
Leu Cys Val Arg Gly Ile Ile Thr Ser Lys
 35 40

<210> SEQ ID NO 115
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(20)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 115

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly
1 5 10 15

-continued

Val Asp Ile Ala
20

<210> SEQ ID NO 116
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype A
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(40)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 116

Gly Phe Asn Leu Arg Asn Asn Thr Glu Ile Asn Asn Met Asn Phe Thr
1 5 10 15

Lys Leu Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys
20 25 30

Val Arg Gly Ile Ile Thr Ser Lys
35 40

<210> SEQ ID NO 117
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype B
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(23)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 117

Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn
1 5 10 15

Asp Asn Ile Ile Met Met Glu
20

<210> SEQ ID NO 118
<211> LENGTH: 45
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype B
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(45)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 118

Tyr Thr Ile Ile Ser Asp Lys Asn Met Gly Lys Glu Tyr Arg Gly Gln
1 5 10 15

Asn Lys Ala Ile Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His
20 25 30

Leu Ala Val Tyr Lys Ile Gln Met Cys Lys Ser Val Lys
35 40 45

<210> SEQ ID NO 119
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype B
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(20)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

-continued

<400> SEQUENCE: 119

Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Glu Pro Pro Phe
1 5 10 15

Ala Arg Gly Thr
20

<210> SEQ ID NO 120

<211> LENGTH: 42

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype B

<220> FEATURE:

<221> NAME/KEY: VARIANT

<222> LOCATION: (1)...(42)

<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 120

Tyr Thr Ile Glu Glu Gly Phe Asn Ile Ser Asp Gly Gln Asn Lys Ala
1 5 10 15

Ile Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His Leu Ala Val
20 25 30

Tyr Lys Ile Gln Met Cys Lys Ser Val Lys
35 40

<210> SEQ ID NO 121

<211> LENGTH: 22

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype B

<220> FEATURE:

<221> NAME/KEY: VARIANT

<222> LOCATION: (1)...(22)

<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 121

Met Pro Asn Asp Pro Ile Asp Asn Asp Asn Ile Ile Met Met Glu Pro
1 5 10 15

Pro Phe Ala Arg Gly Thr
20

<210> SEQ ID NO 122

<211> LENGTH: 38

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype B

<220> FEATURE:

<221> NAME/KEY: VARIANT

<222> LOCATION: (1)...(38)

<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 122

Tyr Thr Ile Glu Glu Gly Phe Asn Ile Ser Asp Lys Asn Met Gly Lys
1 5 10 15

Glu Tyr Arg Gly Gln Asn Lys Ala Ile Asn Lys Gln Ala Lys Ile Gln
20 25 30

Met Cys Lys Ser Val Lys
35

<210> SEQ ID NO 123

<211> LENGTH: 23

<212> TYPE: PRT

<213> ORGANISM: Clostridium botulinum serotype C1

<220> FEATURE:

-continued

<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(23)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 123

Met Pro Ile Ser Asp Pro Val Asp Asn Lys Asn Ile Leu Tyr Leu Asp
1 5 10 15

Thr His Leu Asn Thr Leu Ala
20

<210> SEQ ID NO 124
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype C1
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(40)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 124

Asn Ile Pro Lys Ser Asn Leu Asn Val Leu Phe Met Gly Gln Asn Leu
1 5 10 15

Ser Arg Asn Pro Ala Leu Arg Lys Val Lys Phe Cys His Lys Ala Ile
20 25 30

Asp Gly Arg Ser Leu Tyr Asn Lys
35 40

<210> SEQ ID NO 125
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype D
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(20)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 125

Met Thr Trp Val Asn Asp Asn Asp Ile Leu Tyr Leu Arg Ile Pro Gln
1 5 10 15

Asn Lys Leu Ile
20

<210> SEQ ID NO 126
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype D
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(40)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 126

Tyr Thr Ile Arg Asp Gly Phe Asn Leu Thr Asn Lys Gly Phe Asn Ile
1 5 10 15

Glu Asn Ser Gly Gln Asn Ile Glu Arg Asn Pro Ala Asp Leu Phe Thr
20 25 30

Lys Val Cys Leu Arg Leu Thr Lys
35 40

<210> SEQ ID NO 127

-continued

<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(22)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 127

Met Pro Asp Pro Val Asn Asp Arg Thr Ile Leu Tyr Ile Lys Pro Gly
1 5 10 15

Gly Cys Gln Glu Phe Tyr
 20

<210> SEQ ID NO 128
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(40)
<223> OTHER INFORMATION:
Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 128

Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe Arg Gly Gln Asn Ala
1 5 10 15

Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Arg Phe Cys Lys Asn Ile
 20 25 30

Val Ser Val Lys Gly Ile Arg Lys
 35 40

<210> SEQ ID NO 129
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(20)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC

<400> SEQUENCE: 129

Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Ile Lys Pro Gly Gly Cys
1 5 10 15

Gln Glu Phe Tyr
 20

<210> SEQ ID NO 130
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(44)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of
LC

<400> SEQUENCE: 130

Gly Tyr Asn Ile Asn Asn Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile
1 5 10 15

Ile Thr Pro Ile Thr Gly Arg Gly Leu Val Lys Lys Ile Ile Arg Phe
 20 25 30

Cys Lys Asn Ile Val Ser Val Lys Gly Ile Arg Lys

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<400> SEQUENCE: 131

Thr Ile Leu Tyr Ile Lys
20

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<210> SEQ ID NO 132
<211> LENGTH: 42
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype E
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(42)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of
I.C
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<400> SEQUENCE: 132

Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr Gly Arg Gly Leu Val
20 25 30

Lys Lys Ile Ile Arg Lys Gly Ile Arg Lys
35 40

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<210> SEQ ID NO 133
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype F
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(25)
<223> OTHER INFORMATION: Variant of amino-terminal 30 amino acids of LC
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<400> SEQUENCE: 133

Asp Thr Ile Leu Tyr Met Gln Ile Pro
20 25

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<210> SEQ ID NO 134
<211> LENGTH: 42
<212> TYPE: PRT
<213> ORGANISM: Clostridium botulinum serotype F
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(42)
<223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of
LC
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<400> SEQUENCE: 134

Thr Val Ser Glu Gly Phe Asn Ile Gly Asn Leu Ala Val Asn Asn Arg
1 5 10 15

-continued

Gly Gln Ser Ile Lys Leu Asn Pro Lys Ile Ile Asp Ser Ile Pro Asp
20 25 30

Lys Phe Cys Lys Ser Val Ile Pro Arg Lys
35 40

<210> SEQ ID NO 135
 <211> LENGTH: 38
 <212> TYPE: PRT
 <213> ORGANISM: Clostridium botulinum serotype G
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(38)
 <223> OTHER INFORMATION: Variant of carboxyl-terminal 50 amino acids of LC

<400> SEQUENCE: 135

Gln Asn Glu Gly Phe Asn Ile Ala Ser Lys Asn Leu Lys Thr Glu Phe
1 5 10 15

Asn Gly Gln Asn Lys Ala Val Asn Lys Glu Ala Arg Ile Ala Met Cys
20 25 30

Lys Pro Val Met Tyr Lys
35

<210> SEQ ID NO 136
 <211> LENGTH: 423
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(423)
 <223> OTHER INFORMATION: BoNT/A-BoNT/E chimeric LC

<400> SEQUENCE: 136

Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp Arg
1 5 10 15

Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe Tyr Lys Ser
20 25 30

Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile
35 40 45

Gly Thr Thr Pro Gln Asp Phe His Pro Pro Thr Ser Leu Lys Asn Gly
50 55 60

Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Glu Glu Lys
65 70 75 80

Asp Arg Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asn
85 90 95

Asn Leu Ser Gly Gly Ile Leu Leu Glu Glu Leu Ser Lys Ala Asn Pro
100 105 110

Tyr Leu Gly Asn Asp Asn Thr Pro Asp Asn Gln Phe His Ile Gly Asp
115 120 125

Ala Ser Ala Val Glu Ile Lys Phe Ser Asn Gly Ser Gln Asp Ile Leu
130 135 140

Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr
145 150 155 160

Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His
165 170 175

Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe
180 185 190

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Arg Phe Asn Asp Asn Ser Met Asn Glu Phe Ile Gln Asp Pro Ala Leu
   195                               200                               205
Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala
   210                               215                               220
Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys Gln Asn Pro Leu
  225                               230                               235                               240
Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe Leu Thr Phe Gly
                               245                               250                               255
Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser Asn Asp Ile Tyr
                               260                               265                               270
Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser Lys Leu Ser Lys
   275                               280                               285
Val Gln Val Ser Asn Pro Leu Leu Asn Pro Tyr Lys Asp Val Phe Glu
   290                               295                               300
Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn
  305                               310                               315                               320
Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr Ser Phe Thr Glu
                               325                               330                               335
Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg Gln Thr Tyr Ile
   340                               345                               350
Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu Asn Asp Ser Ile
   355                               360                               365
Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe
   370                               375                               380
Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr
  385                               390                               395                               400
Gly Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val
   405                               410                               415
Arg Gly Ile Ile Thr Ser Lys
   420

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<210> SEQ ID NO 137
<211> LENGTH: 441
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(441)
<223> OTHER INFORMATION: BoNT/A-BoNT/B chimeric LC

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<400> SEQUENCE: 137

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

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100				105				110										
Ile	Asn	Gly	115	Ile	Pro	Tyr	120	Gly	Asp	Arg	125	Arg	Val	Pro	Leu	Glu	Glu	
Phe	Asn	Thr	130	Asn	Ile	Ala	135	Ser	Val	Thr	140	Val	Asn	Lys	Leu	Ile	Ser	Asn
Pro	Gly	Glu	145	Val	Glu	Arg	150	Lys	Lys	Gly	155	Ile	Phe	Ala	Asn	Leu	Ile	Ile
Phe	Gly	Pro	165	Gly	Pro	Val	170	Leu	Asn	Glu	175	Asn	Glu	Thr	Ile	Asp	Ile	Gly
Ile	Gln	Asn	180	His	Phe	Ala	185	Ser	Arg	Glu	190	Gly	Phe	Gly	Gly	Ile	Met	Gln
Met	Lys	Phe	195	Cys	Pro	Glu	200	Tyr	Val	Ser	205	Val	Phe	Asn	Asn	Val	Gln	Glu
Asn	Lys	Gly	210	Ala	Ser	Ile	215	Phe	Asn	Arg	220	Arg	Gly	Tyr	Phe	Ser	Asp	Pro
Ala	Leu	Ile	225	Leu	Met	His	230	Glu	Leu	Ile	235	His	Val	Leu	His	Gly	Leu	Tyr
Gly	Ile	Lys	245	Val	Asp	Asp	250	Leu	Pro	Ile	255	Val	Pro	Asn	Glu	Lys	Lys	Phe
Phe	Met	Gln	260	Ser	Thr	Asp	265	Thr	Ile	Gln	270	Ala	Glu	Glu	Leu	Tyr	Thr	Phe
Gly	Gly	Gln	275	Asp	Pro	Ser	280	Ile	Ile	Ser	285	Pro	Ser	Thr	Asp	Lys	Ser	Ile
Tyr	Asp	Lys	290	Val	Leu	Gln	295	Asn	Phe	Arg	300	Gly	Ile	Val	Asp	Arg	Leu	Asn
Lys	Val	Leu	305	Val	Cys	Ile	310	Ser	Asp	Pro	315	Asn	Ile	Asn	Ile	Asn	Ile	Tyr
Lys	Asn	Lys	325	Phe	Lys	Asp	330	Lys	Tyr	Lys	335	Phe	Val	Glu	Asp	Ser	Glu	Gly
Lys	Tyr	Ser	340	Ile	Asp	Val	345	Glu	Ser	Phe	350	Asn	Lys	Leu	Tyr	Lys	Ser	Leu
Met	Leu	Gly	355	Phe	Thr	Glu	360	Ile	Asn	Ile	365	Ala	Glu	Asn	Tyr	Lys	Ile	Lys
Thr	Arg	Ala	370	Ser	Tyr	Phe	375	Ser	Asp	Ser	380	Leu	Pro	Pro	Val	Lys	Ile	Lys
Asn	Leu	Leu	385	Asp	Asn	Glu	390	Ile	Tyr	Thr	395	Ile	Glu	Glu	Gly	Phe	Asn	Ile
Ser	Asp	Lys	405	Asn	Met	Gly	410	Lys	Glu	Tyr	415	Arg	Gly	Gln	Asn	Lys	Ala	Ile
Asn	Lys	Gln	420	Ala	Tyr	Glu	425	Glu	Ile	Ser	430	Lys	Glu	His	Leu	Ala	Val	Tyr
Lys	Ile	Gln	435	Met	Cys	Lys	440	Ser	Val	Lys								

<210> SEQ ID NO 138

<211> LENGTH: 423

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<221> NAME/KEY: DOMAIN

<222> LOCATION: (1)...(423)

<223> OTHER INFORMATION: BoNT/A-BoNT/E chimeric LC

<400> SEQUENCE: 138

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Met	Pro	Phe	Val	Asn	Lys	Gln	Phe	Asn	Asn	Asp	Pro	Val	Asn	Asp	Arg
1				5					10					15	
Thr	Ile	Leu	Tyr	Ile	Lys	Pro	Gly	Gly	Cys	Gln	Glu	Phe	Tyr	Lys	Ser
			20					25					30		
Phe	Asn	Ile	Met	Lys	Asn	Ile	Trp	Ile	Ile	Pro	Glu	Arg	Asn	Val	Ile
		35					40					45			
Gly	Thr	Thr	Pro	Gln	Asp	Phe	His	Pro	Pro	Thr	Ser	Leu	Lys	Asn	Gly
	50					55					60				
Asp	Ser	Ser	Tyr	Tyr	Asp	Pro	Asn	Tyr	Leu	Gln	Ser	Asp	Glu	Glu	Lys
65					70					75					80
Asp	Arg	Phe	Leu	Lys	Ile	Val	Thr	Lys	Ile	Phe	Asn	Arg	Ile	Asn	Asn
			85						90					95	
Asn	Leu	Ser	Gly	Gly	Ile	Leu	Leu	Glu	Glu	Leu	Ser	Lys	Ala	Asn	Pro
		100						105					110		
Tyr	Leu	Gly	Asn	Asp	Asn	Thr	Pro	Asp	Asn	Gln	Phe	His	Ile	Gly	Asp
	115					120						125			
Ala	Ser	Ala	Val	Glu	Ile	Lys	Phe	Ser	Asn	Gly	Ser	Gln	Asp	Ile	Leu
	130					135					140				
Leu	Pro	Asn	Val	Ile	Ile	Met	Gly	Ala	Glu	Pro	Asp	Leu	Phe	Glu	Thr
145				150						155					160
Asn	Ser	Ser	Asn	Ile	Ser	Leu	Arg	Asn	Asn	Tyr	Met	Pro	Ser	Asn	His
			165						170					175	
Gly	Phe	Gly	Ser	Ile	Ala	Ile	Val	Thr	Phe	Ser	Pro	Glu	Tyr	Ser	Phe
		180						185					190		
Arg	Phe	Asn	Asp	Asn	Ser	Met	Asn	Glu	Phe	Ile	Gln	Asp	Pro	Ala	Leu
	195					200						205			
Thr	Leu	Met	His	Glu	Leu	Ile	His	Ser	Leu	His	Gly	Leu	Tyr	Gly	Ala
	210					215					220				
Lys	Gly	Ile	Thr	Thr	Lys	Tyr	Thr	Ile	Thr	Gln	Lys	Gln	Asn	Pro	Leu
225					230					235					240
Ile	Thr	Asn	Ile	Arg	Gly	Thr	Asn	Ile	Glu	Glu	Phe	Leu	Thr	Phe	Gly
			245						250					255	
Gly	Thr	Asp	Leu	Asn	Ile	Ile	Thr	Ser	Ala	Gln	Ser	Asn	Asp	Ile	Tyr
		260						265					270		
Thr	Asn	Leu	Leu	Ala	Asp	Tyr	Lys	Lys	Ile	Ala	Ser	Lys	Leu	Ser	Lys
	275						280					285			
Val	Gln	Val	Ser	Asn	Pro	Leu	Leu	Asn	Pro	Tyr	Lys	Asp	Val	Phe	Glu
	290					295					300				
Ala	Lys	Tyr	Gly	Leu	Asp	Lys	Asp	Ala	Ser	Gly	Ile	Tyr	Ser	Val	Asn
305					310					315					320
Ile	Asn	Lys	Phe	Asn	Asp	Ile	Phe	Lys	Lys	Leu	Tyr	Ser	Phe	Thr	Glu
			325						330					335	
Phe	Asp	Leu	Ala	Thr	Lys	Phe	Gln	Val	Lys	Cys	Arg	Gln	Thr	Tyr	Ile
		340						345					350		
Gly	Gln	Tyr	Lys	Tyr	Phe	Lys	Leu	Ser	Asn	Leu	Leu	Asn	Asp	Ser	Ile
	355						360					365			
Tyr	Asn	Ile	Ser	Glu	Gly	Tyr	Asn	Ile	Asn	Asn	Leu	Lys	Val	Asn	Phe
	370					375					380				
Arg	Gly	Gln	Asn	Ala	Asn	Leu	Asn	Pro	Arg	Ile	Ile	Thr	Pro	Ile	Thr
385					390					395					400

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Gly Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val
 405 410 415

Arg Gly Ile Ile Thr Ser Lys
 420

<210> SEQ ID NO 139

<211> LENGTH: 441

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<221> NAME/KEY: DOMAIN

<222> LOCATION: (1)...(441)

<223> OTHER INFORMATION: BoNT/A-BoNT/B chimeric LC

<400> SEQUENCE: 139

Met Pro Phe Val Asn Lys Gln Phe Asn Tyr Asn Asp Pro Ile Asp Asn
 1 5 10 15

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

Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu
 35 40 45

Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly
 50 55 60

Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn
 65 70 75 80

Thr Asn Asp Lys Lys Asn Ile Phe Phe Gln Thr Leu Ile Lys Leu Phe
 85 90 95

Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile
 100 105 110

Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu
 115 120 125

Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn
 130 135 140

Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile
 145 150 155 160

Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly
 165 170 175

Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln
 180 185 190

Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu
 195 200 205

Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro
 210 215 220

Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr
 225 230 235 240

Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe
 245 250 255

Phe Met Gln Ser Thr Asp Thr Ile Gln Ala Glu Glu Leu Tyr Thr Phe
 260 265 270

Gly Gly Gln Asp Pro Ser Ile Ile Ser Pro Ser Thr Asp Lys Ser Ile
 275 280 285

Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val Asp Arg Leu Asn
 290 295 300

Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr

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<210> SEQ ID NO 140
<211> LENGTH: 436
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(436)
<223> OTHER INFORMATION: BoNT/A-BoNT/F chimeric LC

<400> SEQUENCE: 140
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Met	Pro	Phe	Val	Asn	Lys	Gln	Phe	Asn	Tyr	Asn	Asp	Pro	Val	Asn	Asp
1				5					10					15	
Asp	Thr	Ile	Leu	Tyr	Met	Gln	Ile	Pro	Tyr	Glu	Glu	Lys	Ser	Lys	Lys
			20					25					30		
Tyr	Tyr	Lys	Ala	Phe	Glu	Ile	Met	Arg	Asn	Val	Trp	Ile	Ile	Pro	Glu
		35					40					45			
Arg	Asn	Thr	Ile	Gly	Thr	Asn	Pro	Ser	Asp	Phe	Asp	Pro	Pro	Ala	Ser
	50					55					60				
Leu	Lys	Asn	Gly	Ser	Ser	Ala	Tyr	Tyr	Asp	Pro	Asn	Tyr	Leu	Thr	Thr
65					70				75					80	
Asp	Ala	Glu	Lys	Asp	Arg	Tyr	Leu	Lys	Thr	Thr	Ile	Lys	Leu	Phe	Lys
			85					90						95	
Arg	Ile	Asn	Ser	Asn	Pro	Ala	Gly	Lys	Val	Leu	Leu	Gln	Glu	Ile	Ser
		100						105					110		
Tyr	Ala	Lys	Pro	Tyr	Leu	Gly	Asn	Asp	His	Thr	Pro	Ile	Asp	Glu	Phe
		115					120					125			
Ser	Pro	Val	Thr	Arg	Thr	Thr	Ser	Val	Asn	Ile	Lys	Leu	Ser	Thr	Asn
	130					135					140				
Val	Glu	Ser	Ser	Met	Leu	Leu	Asn	Leu	Leu	Val	Leu	Gly	Ala	Gly	Pro
145				150						155				160	
Asp	Ile	Phe	Glu	Ser	Cys	Cys	Tyr	Pro	Val	Arg	Lys	Leu	Ile	Asp	Pro
			165					170						175	
Asp	Val	Val	Tyr	Asp	Pro	Ser	Asn	Tyr	Gly	Phe	Gly	Ser	Ile	Asn	Ile
			180					185					190		
Val	Thr	Phe	Ser	Pro	Glu	Tyr	Glu	Tyr	Thr	Phe	Asn	Asp	Ile	Ser	Gly
		195					200					205			

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Gly His Asn Ser Ser Thr Glu Ser Phe Ile Ala Asp Pro Ala Ile Ser
 210 215 220
 Leu Ala His Glu Leu Ile His Ala Leu His Gly Leu Tyr Gly Ala Arg
 225 230 235 240
 Gly Val Thr Tyr Glu Glu Thr Ile Glu Val Lys Gln Ala Pro Leu Met
 245 250 255
 Ile Ala Glu Lys Pro Ile Arg Leu Glu Glu Phe Leu Thr Phe Gly Gly
 260 265 270
 Gln Asp Leu Asn Ile Ile Thr Ser Ala Met Lys Glu Lys Ile Tyr Asn
 275 280 285
 Asn Leu Leu Ala Asn Tyr Glu Lys Ile Ala Thr Arg Leu Ser Glu Val
 290 295 300
 Asn Ser Ala Pro Pro Glu Tyr Asp Ile Asn Glu Tyr Lys Asp Tyr Phe
 305 310 315 320
 Gln Trp Lys Tyr Gly Leu Asp Lys Asn Ala Asp Gly Ser Tyr Thr Val
 325 330 335
 Asn Glu Asn Lys Phe Asn Glu Ile Tyr Lys Lys Leu Tyr Ser Phe Thr
 340 345 350
 Glu Ser Asp Leu Ala Asn Lys Phe Lys Val Lys Cys Arg Asn Thr Tyr
 355 360 365
 Phe Ile Lys Tyr Glu Phe Leu Lys Val Pro Asn Leu Leu Asp Asp Asp
 370 375 380
 Ile Tyr Thr Val Ser Glu Gly Phe Asn Ile Gly Asn Leu Ala Val Asn
 385 390 395 400
 Asn Arg Gly Gln Ser Ile Lys Leu Asn Pro Lys Ile Ile Asp Lys Asn
 405 410 415
 Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile
 420 425 430
 Ile Thr Ser Lys
 435

<210> SEQ ID NO 141
 <211> LENGTH: 483
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(483)
 <223> OTHER INFORMATION: BoNT/A-BoNT/B chimeric LC

<400> SEQUENCE: 141

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

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Lys	Pro	Glu	Asp	Phe	Asn	Lys	Ser	Ser	Gly	Ile	Phe	Asn	Arg	Asp	Val
			100					105					110		
Cys	Glu	Tyr	Tyr	Asp	Pro	Asp	Tyr	Leu	Asn	Thr	Asn	Asp	Lys	Lys	Asn
		115					120					125			
Ile	Phe	Phe	Gln	Thr	Leu	Ile	Lys	Leu	Phe	Asn	Arg	Ile	Lys	Ser	Lys
		130				135					140				
Pro	Leu	Gly	Glu	Lys	Leu	Leu	Glu	Met	Ile	Ile	Asn	Gly	Ile	Pro	Tyr
145					150					155					160
Leu	Gly	Asp	Arg	Arg	Val	Pro	Leu	Glu	Glu	Phe	Asn	Thr	Asn	Ile	Ala
				165					170						175
Ser	Val	Thr	Val	Asn	Lys	Leu	Ile	Ser	Asn	Pro	Gly	Glu	Val	Glu	Arg
		180						185					190		
Lys	Lys	Gly	Ile	Phe	Ala	Asn	Leu	Ile	Ile	Phe	Gly	Pro	Gly	Pro	Val
		195					200					205			
Leu	Asn	Glu	Asn	Glu	Thr	Ile	Asp	Ile	Gly	Ile	Gln	Asn	His	Phe	Ala
	210					215					220				
Ser	Arg	Glu	Gly	Phe	Gly	Gly	Ile	Met	Gln	Met	Lys	Phe	Cys	Pro	Glu
225					230					235					240
Tyr	Val	Ser	Val	Phe	Asn	Asn	Val	Gln	Glu	Asn	Lys	Gly	Ala	Ser	Ile
				245				250						255	
Phe	Asn	Arg	Arg	Gly	Tyr	Phe	Ser	Asp	Pro	Ala	Leu	Ile	Leu	Met	His
		260					265						270		
Glu	Leu	Ile	His	Val	Leu	His	Gly	Leu	Tyr	Gly	Ile	Lys	Val	Asp	Asp
		275				280						285			
Leu	Pro	Ile	Val	Pro	Asn	Glu	Lys	Lys	Phe	Phe	Met	Gln	Ser	Thr	Asp
	290					295					300				
Thr	Ile	Gln	Ala	Glu	Glu	Leu	Tyr	Thr	Phe	Gly	Gly	Gln	Asp	Pro	Ser
305					310					315					320
Ile	Ile	Ser	Pro	Ser	Thr	Asp	Lys	Ser	Ile	Tyr	Asp	Lys	Val	Leu	Gln
			325					330						335	
Asn	Phe	Arg	Gly	Ile	Val	Asp	Arg	Leu	Asn	Lys	Val	Leu	Val	Cys	Ile
		340					345						350		
Ser	Asp	Pro	Asn	Ile	Asn	Ile	Asn	Ile	Tyr	Lys	Asn	Lys	Phe	Lys	Asp
		355				360						365			
Lys	Tyr	Lys	Phe	Val	Glu	Asp	Ser	Glu	Gly	Lys	Tyr	Ser	Ile	Asp	Val
	370					375					380				
Glu	Ser	Phe	Asn	Lys	Leu	Tyr	Lys	Ser	Leu	Met	Leu	Gly	Phe	Thr	Glu
385					390					395					400
Ile	Asn	Ile	Ala	Glu	Asn	Tyr	Lys	Ile	Lys	Thr	Arg	Ala	Ser	Tyr	Phe
			405					410						415	
Ser	Asp	Ser	Leu	Pro	Pro	Val	Lys	Ile	Lys	Asn	Leu	Leu	Asp	Asn	Glu
			420				425						430		
Ile	Tyr	Thr	Ile	Glu	Glu	Gly	Phe	Asn	Ile	Ser	Asp	Lys	Asn	Met	Gly
		435				440						445			
Lys	Glu	Tyr	Arg	Gly	Gln	Asn	Lys	Ala	Ile	Asn	Lys	Gln	Ala	Tyr	Glu
	450					455					460				
Glu	Ile	Ser	Lys	Glu	His	Leu	Ala	Val	Tyr	Lys	Ile	Gln	Met	Cys	Lys
465					470					475					480
Ser	Val	Lys													

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<211> LENGTH: 458
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (1)...(458)
<223> OTHER INFORMATION: BoNT/A-BoNT/E chimeric LC

<400> SEQUENCE: 142

Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp Arg
 1             5             10            15

Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe Tyr Lys Ser
 20            25            30

Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile
 35            40            45

Gly Thr Thr Pro Gln Asp Phe His Pro Pro Thr Ser Leu Lys Asn Gly
 50            55            60

Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Glu Glu Lys
 65            70            75            80

Asp Arg Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asn
 85            90            95

Asn Leu Ser Gly Gly Ile Leu Leu Glu Glu Leu Ser Lys Ala Asn Pro
100           105           110

Tyr Leu Gly Asn Asp Asn Thr Pro Asp Asn Gln Phe His Ile Gly Asp
115           120           125

Ala Ser Ala Val Glu Ile Lys Phe Ser Asn Gly Ser Gln Asp Ile Leu
130           135           140

Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr
145           150           155           160

Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His
165           170           175

Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe
180           185           190

Arg Phe Asn Asp Asn Ser Met Asn Glu Phe Ile Gln Asp Pro Ala Leu
195           200           205

Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala
210           215           220

Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys Gln Asn Pro Leu
225           230           235           240

Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe Leu Thr Phe Gly
245           250           255

Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser Asn Asp Ile Tyr
260           265           270

Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser Lys Leu Ser Lys
275           280           285

Val Gln Val Ser Asn Pro Leu Leu Asn Pro Tyr Lys Asp Val Phe Glu
290           295           300

Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn
305           310           315           320

Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr Ser Phe Thr Glu
325           330           335

Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg Gln Thr Tyr Ile
340           345           350

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Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu Asn Asp Ser Ile
 355 360 365

Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe
 370 375 380

Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile Ile Thr Pro Gly Phe
 385 390 395 400

Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln Asn Thr
 405 410 415

Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr Gly Leu
 420 425 430

Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr Ser Lys
 435 440 445

Asn Ile Val Ser Val Lys Gly Ile Arg Lys
 450 455

<210> SEQ ID NO 143

<211> LENGTH: 443

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<221> NAME/KEY: DOMAIN

<222> LOCATION: (1)...(443)

<223> OTHER INFORMATION: BoNT/A-BoNT/E chimeric LC

<400> SEQUENCE: 143

Met Pro Lys Ile Asn Ser Phe Asn Tyr Met Pro Phe Val Asn Lys Gln
 1 5 10 15

Phe Asn Tyr Lys Asp Pro Val Asn Gly Val Asp Ile Ala Tyr Ile Lys
 20 25 30

Ile Pro Asn Ala Gly Gln Met Tyr Ile Lys Pro Gly Gly Cys Gln Glu
 35 40 45

Phe Tyr Lys Ser Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu
 50 55 60

Arg Asn Val Ile Gly Thr Thr Pro Gln Asp Phe His Pro Pro Thr Ser
 65 70 75 80

Leu Lys Asn Gly Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser
 85 90 95

Asp Glu Glu Lys Asp Arg Phe Leu Lys Ile Val Thr Lys Ile Phe Asn
 100 105 110

Arg Ile Asn Asn Asn Leu Ser Gly Gly Ile Leu Leu Glu Glu Leu Ser
 115 120 125

Lys Ala Asn Pro Tyr Leu Gly Asn Asp Asn Thr Pro Asp Asn Gln Phe
 130 135 140

His Ile Gly Asp Ala Ser Ala Val Glu Ile Lys Phe Ser Asn Gly Ser
 145 150 155 160

Gln Asp Ile Leu Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp
 165 170 175

Leu Phe Glu Thr Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met
 180 185 190

Pro Ser Asn His Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro
 195 200 205

Glu Tyr Ser Phe Arg Phe Asn Asp Asn Ser Met Asn Glu Phe Ile Gln
 210 215 220

Asp Pro Ala Leu Thr Leu Met His Glu Leu Ile His Ser Leu His Gly

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225	230	235	240
Leu Tyr Gly Ala Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys	245	250	255
Gln Asn Pro Leu Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe	260	265	270
Leu Thr Phe Gly Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser	275	280	285
Asn Asp Ile Tyr Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser	290	295	300
Lys Leu Ser Lys Val Gln Val Ser Asn Pro Leu Leu Asn Pro Tyr Lys	305	310	315
Asp Val Phe Glu Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile	325	330	335
Tyr Ser Val Asn Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr	340	345	350
Ser Phe Thr Glu Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg	355	360	365
Gln Thr Tyr Ile Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu	370	375	380
Asn Asp Ser Ile Tyr Asn Ile Ser Glu Gly Phe Asn Leu Arg Asn Thr	385	390	395
Asn Leu Ala Ala Asn Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met	405	410	415
Asn Phe Thr Lys Leu Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys	420	425	430
Leu Leu Cys Val Arg Gly Ile Ile Thr Ser Lys	435	440	

<210> SEQ ID NO 144
 <211> LENGTH: 461
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(461)
 <223> OTHER INFORMATION: BoNT/A-BoNT/B chimeric LC

<400> SEQUENCE: 144

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

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Leu Glu Met Ile Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val
 130                135                140

Pro Leu Glu Glu Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys
145                150                155                160

Leu Ile Ser Asn Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala
                165                170                175

Asn Leu Ile Ile Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr
                180                185                190

Ile Asp Ile Gly Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly
195                200                205

Gly Ile Met Gln Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn
210                215                220

Asn Val Gln Glu Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr
225                230                235                240

Phe Ser Asp Pro Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu
                245                250                255

His Gly Leu Tyr Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn
                260                265                270

Glu Lys Lys Phe Phe Met Gln Ser Thr Asp Thr Ile Gln Ala Glu Glu
275                280                285

Leu Tyr Thr Phe Gly Gly Gln Asp Pro Ser Ile Ile Ser Pro Ser Thr
290                295                300

Asp Lys Ser Ile Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val
305                310                315                320

Asp Arg Leu Asn Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn
                325                330                335

Ile Asn Ile Tyr Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu
                340                345                350

Asp Ser Glu Gly Lys Tyr Ser Ile Asp Val Glu Ser Phe Asn Lys Leu
355                360                365

Tyr Lys Ser Leu Met Leu Gly Phe Thr Glu Ile Asn Ile Ala Glu Asn
370                375                380

Tyr Lys Ile Lys Thr Arg Ala Ser Tyr Phe Ser Asp Ser Leu Pro Pro
385                390                395                400

Val Lys Ile Lys Asn Leu Leu Asp Asn Glu Ile Gly Phe Asn Leu Arg
                405                410                415

Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln Asn Thr Glu Ile Asn
                420                425                430

Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr Gly Leu Phe Glu Phe
435                440                445

Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr Ser Lys
450                455                460

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<210> SEQ ID NO 145

<211> LENGTH: 456

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<221> NAME/KEY: DOMAIN

<222> LOCATION: (1)...(456)

<223> OTHER INFORMATION: BoNT/A-BoNT/F chimeric LC

<400> SEQUENCE: 145

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Met	Pro	Val	Ala	Ile	Asn	Ser	Phe	Asn	Met	Pro	Phe	Val	Asn	Lys	Gln
1				5					10					15	
Phe	Asn	Tyr	Lys	Asp	Pro	Val	Asn	Gly	Val	Asp	Ile	Ala	Tyr	Ile	Lys
			20					25					30		
Ile	Pro	Asn	Ala	Gly	Gln	Met	Leu	Tyr	Met	Gln	Ile	Pro	Tyr	Glu	Glu
		35					40					45			
Lys	Ser	Lys	Lys	Tyr	Tyr	Lys	Ala	Phe	Glu	Ile	Met	Arg	Asn	Val	Trp
	50					55					60				
Ile	Ile	Pro	Glu	Arg	Asn	Thr	Ile	Gly	Thr	Asn	Pro	Ser	Asp	Phe	Asp
65					70					75				80	
Pro	Pro	Ala	Ser	Leu	Lys	Asn	Gly	Ser	Ser	Ala	Tyr	Tyr	Asp	Pro	Asn
				85					90					95	
Tyr	Leu	Thr	Thr	Asp	Ala	Glu	Lys	Asp	Arg	Tyr	Leu	Lys	Thr	Thr	Ile
			100					105					110		
Lys	Leu	Phe	Lys	Arg	Ile	Asn	Ser	Asn	Pro	Ala	Gly	Lys	Val	Leu	Leu
		115				120						125			
Gln	Glu	Ile	Ser	Tyr	Ala	Lys	Pro	Tyr	Leu	Gly	Asn	Asp	His	Thr	Pro
	130					135					140				
Ile	Asp	Glu	Phe	Ser	Pro	Val	Thr	Arg	Thr	Thr	Ser	Val	Asn	Ile	Lys
145					150					155				160	
Leu	Ser	Thr	Asn	Val	Glu	Ser	Ser	Met	Leu	Leu	Asn	Leu	Leu	Val	Leu
				165					170					175	
Gly	Ala	Gly	Pro	Asp	Ile	Phe	Glu	Ser	Cys	Cys	Tyr	Pro	Val	Arg	Lys
			180					185					190		
Leu	Ile	Asp	Pro	Asp	Val	Val	Tyr	Asp	Pro	Ser	Asn	Tyr	Gly	Phe	Gly
		195					200					205			
Ser	Ile	Asn	Ile	Val	Thr	Phe	Ser	Pro	Glu	Tyr	Glu	Tyr	Thr	Phe	Asn
	210					215					220				
Asp	Ile	Ser	Gly	Gly	His	Asn	Ser	Ser	Thr	Glu	Ser	Phe	Ile	Ala	Asp
225					230					235				240	
Pro	Ala	Ile	Ser	Leu	Ala	His	Glu	Leu	Ile	His	Ala	Leu	His	Gly	Leu
				245					250					255	
Tyr	Gly	Ala	Arg	Gly	Val	Thr	Tyr	Glu	Glu	Thr	Ile	Glu	Val	Lys	Gln
			260					265					270		
Ala	Pro	Leu	Met	Ile	Ala	Glu	Lys	Pro	Ile	Arg	Leu	Glu	Glu	Phe	Leu
		275					280					285			
Thr	Phe	Gly	Gly	Gln	Asp	Leu	Asn	Ile	Ile	Thr	Ser	Ala	Met	Lys	Glu
	290					295					300				
Lys	Ile	Tyr	Asn	Asn	Leu	Leu	Ala	Asn	Tyr	Glu	Lys	Ile	Ala	Thr	Arg
305				310						315				320	
Leu	Ser	Glu	Val	Asn	Ser	Ala	Pro	Pro	Glu	Tyr	Asp	Ile	Asn	Glu	Tyr
			325						330					335	
Lys	Asp	Tyr	Phe	Gln	Trp	Lys	Tyr	Gly	Leu	Asp	Lys	Asn	Ala	Asp	Gly
			340					345					350		
Ser	Tyr	Thr	Val	Asn	Glu	Asn	Lys	Phe	Asn	Glu	Ile	Tyr	Lys	Lys	Leu
		355					360					365			
Tyr	Ser	Phe	Thr	Glu	Ser	Asp	Leu	Ala	Asn	Lys	Phe	Lys	Val	Lys	Cys
	370					375					380				
Arg	Asn	Thr	Tyr	Phe	Ile	Lys	Tyr	Glu	Phe	Leu	Lys	Val	Pro	Asn	Leu
385					390					395				400	
Leu	Asp	Asp	Asp	Ile	Tyr	Gly	Phe	Asn	Leu	Arg	Asn	Thr	Asn	Leu	Ala

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405	410	415
Ala Asn Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr		
420	425	430
Lys Leu Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys		
435	440	445
Val Arg Gly Ile Ile Thr Ser Lys		
450	455	

<210> SEQ ID NO 146
 <211> LENGTH: 449
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(449)
 <223> OTHER INFORMATION: BoNT/A-BoNT/E chimeric LC

<400> SEQUENCE: 146

Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Thr Ile Asn		
1	5	10
Asn Phe Asn Tyr Asp Arg Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys		
20	25	30
Gln Glu Phe Tyr Lys Ser Phe Asn Ile Met Lys Asn Ile Trp Ile Ile		
35	40	45
Pro Glu Arg Asn Val Ile Gly Thr Thr Pro Gln Asp Phe His Pro Pro		
50	55	60
Thr Ser Leu Lys Asn Gly Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu		
65	70	75
Gln Ser Asp Glu Glu Lys Asp Arg Phe Leu Lys Ile Val Thr Lys Ile		
85	90	95
Phe Asn Arg Ile Asn Asn Asn Leu Ser Gly Gly Ile Leu Leu Glu Glu		
100	105	110
Leu Ser Lys Ala Asn Pro Tyr Leu Gly Asn Asp Asn Thr Pro Asp Asn		
115	120	125
Gln Phe His Ile Gly Asp Ala Ser Ala Val Glu Ile Lys Phe Ser Asn		
130	135	140
Gly Ser Gln Asp Ile Leu Leu Pro Asn Val Ile Ile Met Gly Ala Glu		
145	150	155
Pro Asp Leu Phe Glu Thr Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn		
165	170	175
Tyr Met Pro Ser Asn His Gly Phe Gly Ser Ile Ala Ile Val Thr Phe		
180	185	190
Ser Pro Glu Tyr Ser Phe Arg Phe Asn Asp Asn Ser Met Asn Glu Phe		
195	200	205
Ile Gln Asp Pro Ala Leu Thr Leu Met His Glu Leu Ile His Ser Leu		
210	215	220
His Gly Leu Tyr Gly Ala Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr		
225	230	235
Gln Lys Gln Asn Pro Leu Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu		
245	250	255
Glu Phe Leu Thr Phe Gly Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala		
260	265	270
Gln Ser Asn Asp Ile Tyr Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile		
275	280	285

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Ala Ser Lys Leu Ser Lys Val Gln Val Ser Asn Pro Leu Leu Asn Pro
 290 295 300

Tyr Lys Asp Val Phe Glu Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser
 305 310 315 320

Gly Ile Tyr Ser Val Asn Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys
 325 330 335

Leu Tyr Ser Phe Thr Glu Phe Asp Leu Ala Thr Lys Phe Gln Val Lys
 340 345 350

Cys Arg Gln Thr Tyr Ile Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn
 355 360 365

Leu Leu Asn Asp Ser Ile Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn
 370 375 380

Asn Leu Lys Val Asn Phe Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg
 385 390 395 400

Ile Ile Thr Pro Ile Thr Gly Arg Gly Leu Val Lys Lys Ile Ile Arg
 405 410 415

Phe Cys Lys Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr Gly
 420 425 430

Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr Ser
 435 440 445

Lys

<210> SEQ ID NO 147
 <211> LENGTH: 459
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: DOMAIN
 <222> LOCATION: (1)...(459)
 <223> OTHER INFORMATION: BoNT/A-BoNT/B-BoNT/F chimeric LC

<400> SEQUENCE: 147

Met Pro Val Ala Ile Asn Ser Phe Asn Tyr Asn Asp Val Thr Ile Asn
 1 5 10 15

Asn Phe Asn Tyr Thr Ile Leu Tyr Met Gln Ile Pro Tyr Glu Glu Lys
 20 25 30

Ser Lys Lys Tyr Tyr Lys Ala Phe Glu Ile Met Arg Asn Val Trp Ile
 35 40 45

Ile Pro Glu Arg Asn Thr Ile Gly Thr Asn Pro Ser Asp Phe Asp Pro
 50 55 60

Pro Ala Ser Leu Lys Asn Gly Ser Ser Ala Tyr Tyr Asp Pro Asn Tyr
 65 70 75 80

Leu Thr Thr Asp Ala Glu Lys Asp Arg Tyr Leu Lys Thr Thr Ile Lys
 85 90 95

Leu Phe Lys Arg Ile Asn Ser Asn Pro Ala Gly Lys Val Leu Leu Gln
 100 105 110

Glu Ile Ser Tyr Ala Lys Pro Tyr Leu Gly Asn Asp His Thr Pro Ile
 115 120 125

Asp Glu Phe Ser Pro Val Thr Arg Thr Thr Ser Val Asn Ile Lys Leu
 130 135 140

Ser Thr Asn Val Glu Ser Ser Met Leu Leu Asn Leu Leu Val Leu Gly
 145 150 155 160

Ala Gly Pro Asp Ile Phe Glu Ser Cys Cys Tyr Pro Val Arg Lys Leu

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165										170										175																																			
Ile	Asp	Pro	Asp	Val	Val	Tyr	Asp	Pro	Ser	Asn	Tyr	Gly	Phe	Gly	Ser																																								
			180						185					190																																									
Ile	Asn	Ile	Val	Thr	Phe	Ser	Pro	Glu	Tyr	Glu	Tyr	Thr	Phe	Asn	Asp																																								
			195				200						205																																										
Ile	Ser	Gly	Gly	His	Asn	Ser	Ser	Thr	Glu	Ser	Phe	Ile	Ala	Asp	Pro																																								
			210				215					220																																											
Ala	Ile	Ser	Leu	Ala	His	Glu	Leu	Ile	His	Ala	Leu	His	Gly	Leu	Tyr																																								
			225				230				235				240																																								
Gly	Ala	Arg	Gly	Val	Thr	Tyr	Glu	Glu	Thr	Ile	Glu	Val	Lys	Gln	Ala																																								
				245					250					255																																									
Pro	Leu	Met	Ile	Ala	Glu	Lys	Pro	Ile	Arg	Leu	Glu	Glu	Phe	Leu	Thr																																								
				260					265					270																																									
Phe	Gly	Gly	Gln	Asp	Leu	Asn	Ile	Ile	Thr	Ser	Ala	Met	Lys	Glu	Lys																																								
				275					280					285																																									
Ile	Tyr	Asn	Asn	Leu	Leu	Ala	Asn	Tyr	Glu	Lys	Ile	Ala	Thr	Arg	Leu																																								
							295					300																																											
Ser	Glu	Val	Asn	Ser	Ala	Pro	Pro	Glu	Tyr	Asp	Ile	Asn	Glu	Tyr	Lys																																								
							310				315				320																																								
Asp	Tyr	Phe	Gln	Trp	Lys	Tyr	Gly	Leu	Asp	Lys	Asn	Ala	Asp	Gly	Ser																																								
				325					330					335																																									
Tyr	Thr	Val	Asn	Glu	Asn	Lys	Phe	Asn	Glu	Ile	Tyr	Lys	Lys	Leu	Tyr																																								
				340					345					350																																									
Ser	Phe	Thr	Glu	Ser	Asp	Leu	Ala	Asn	Lys	Phe	Lys	Val	Lys	Cys	Arg																																								
				355					360					365																																									
Asn	Thr	Tyr	Phe	Ile	Lys	Tyr	Glu	Phe	Leu	Lys	Val	Pro	Asn	Leu	Leu																																								
							375					380																																											
Asp	Asp	Asp	Ile	Tyr	Thr	Val	Ser	Glu	Gly	Phe	Asn	Ile	Gly	Asn	Leu																																								
							390				395				400																																								
Ala	Val	Asn	Asn	Arg	Gly	Gln	Ser	Ile	Lys	Leu	Asn	Pro	Lys	Ile	Ile																																								
							405				410				415																																								
Asp	Ser	Ile	Pro	Asp	Lys	Gly	Leu	Val	Glu	Lys	Asn	Asn	Met	Asn	Phe																																								
				420					425					430																																									
Thr	Lys	Leu	Lys	Asn	Phe	Thr	Gly	Leu	Phe	Glu	Phe	Tyr	Lys	Leu	Leu																																								
				435					440					445																																									
Cys	Val	Arg	Gly	Ile	Ile	Thr	Ser	Lys	Arg	Lys																																													
				450					455																																														

<210> SEQ ID NO 148
 <211> LENGTH: 59
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)...(59)
 <223> OTHER INFORMATION: Peptide comprising a 6x His tag and S-tag

<400> SEQUENCE: 148

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

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Ser	Pro	Asp	Leu	Gly	Thr	Asp	Asp	Asp	Asp	Lys	Ala	Met	Gly	Ser	Phe
		35					40					45			

Val	Asn	Lys	Gln	Phe	Asn	Tyr	Lys	Asp	Pro	Val
	50					55				

What is claimed is:

1. A modified botulinum neurotoxin type A, wherein the modification is one or more additional amino acid sequences comprising SEQ ID NO: 27 within the N-terminal 30 amino acids of a wild-type botulinum toxin type A light chain and one or more additional leucine-based motifs within the C-terminal 50 amino acids of the wild-type botulinum toxin type A light chain,

wherein the one or more additional leucine-based motifs is SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, or any combination thereof,

wherein the additional amino acid sequence comprising SEQ ID NO: 27 increases biological half-life of the modified botulinum neurotoxin type A relative to an identical botulinum neurotoxin type A without the additional amino acid sequence comprising SEQ ID NO: 27, and

wherein the additional leucine-based motif increases biological half-life of the modified botulinum neurotoxin type A relative to an identical botulinum neurotoxin type A without the additional leucine-based motif.

2. The modified botulinum neurotoxin type A of claim 2, wherein the additional leucine-based motif is SEQ ID NO: 2 or SEQ ID NO: 3.

3. The modified botulinum neurotoxin type A of claim 2, wherein the additional leucine-based motif is SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 10, or SEQ ID NO: 12.

4. The modified botulinum neurotoxin type A of claim 2, wherein the additional leucine-based motif is SEQ ID NO: 8.

5. The modified botulinum neurotoxin type A of claim 2, wherein the additional leucine-based motif is SEQ ID NO: 9.

6. A modified botulinum neurotoxin type A, wherein the modification is one or more additional amino acid sequences comprising SEQ ID NO: 27 within the N-terminal 30 amino acids of a wild-type botulinum toxin type A light chain and one or more additional leucine-based motifs of SEQ ID NO: 11 within the C-terminal 50 amino acids of the wild-type botulinum toxin type A light chain,

wherein the additional amino acid sequence comprising SEQ ID NO: 27 increases biological half-life of the modified botulinum neurotoxin type A relative to an identical botulinum neurotoxin type A without the additional amino acid sequence comprising SEQ ID NO: 27, and

wherein the additional leucine-based motif of SEQ ID NO: 11 increases biological half-life of the modified botulinum neurotoxin type A relative to an identical botulinum neurotoxin type A without the additional leucine-based motif.

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