NEUBLASTIN VARIANTS

Cross Reference To Related Applications

This application claims priority from provisional application number 60/602,825, filed August 19, 2004 and provisional application number 60/694,067, filed June 24, 2005. The entire content of each of these prior applications is incorporated herein by reference in its entirety.

Technical Field

The invention relates to protein chemistry, molecular biology, and neurobiology.

Background

Neublastin, also known as Artemin and Enovin, is a 24-kDa homodimeric secreted protein that promotes the survival of neurons of the peripheral and central nervous system such as dopaminergic neurons (Baudet et al., 2000, *Development,* 127:4335; Rosenblad et al., 2000, *Mol. Cell Neurosci.*, 15(2):199; GenBank AF120274). The gene encoding neublastin has been cloned and sequenced (Roseblad et al., 2000, *Mol. Cell Neurosci.*, 15(2):199; Baloh et al., *Neuron,* 21:1291).

Neublastin is a member of the glial cell line-derived neurotrophic factor (GDNF) ligand family. At the cellular level, GDNF members activate the receptor tyrosine kinase, RET. RET associates with a co-receptor, GDNF family receptor alpha (GFRalpha), a glycosylphosphatidyl inositol (GPI) linked membrane protein that provides ligand specificity for RET. Four GFRalphas are known (GFRalpha1-4). Neublastin binds to GFRalpha3 together with RET forming a ternary signaling complex (Baudet et al. 2000, *Development,* 127:4335; Baloh et al., 1998, *Neuron,* 21:1291), which is localized predominantly on nociceptive sensory neurons (Orozco et al., 2001, *Eur. J. Neurosci.,* 13(11):2177). These neurons detect pain and injury. Thus, neublastin has clinical application in the general treatment of neuropathy and more specifically in the treatment of neuropathic pain.

Neublastin and the other GDNF family members are members of the transforming growth factor beta (TGF beta) superfamily and thus, are characterized by the presence of seven conserved cysteine residues with similar spacing which form the structure of a cysteine knot (Saarma, 1999, *Microsc. Res. Tech.*, 45:292). Each monomer contains two disulfide bonds that form a closed loop structure encircling the third disulfide to form a tight knot structure. The seventh cysteine contained within each monomer forms an intermolecular disulfide bond, covalently linking the monomers to form the final dimer product (Rattenholl et al 2000, *J. Mol. Biol.*, 305:523).

TGF beta family members are synthesized as pre pro proteins that eventually are secreted as a mature homodimer after cleavage of the signal peptide and pro-domain (*see e.g.* Rattenholl, et al., 2000, *J. Mol. Biol.*, 305:523; Fairlie et al., 2001, *J. Biol. Chem.*, 276(20):16911). Both the signal peptide and pro-domain mediate proper secretion for TGF beta family members (Rattenholl et al., 2000, *J. Mol. Biol.*, 305:523; Rattenholl et al., 2001, *Eur. J. Biochem.*, 268:3296).

Summary

The invention is based, at least in part, on the discovery that Neublastin binds to heparin sulfate and that particular amino acid residues in the Neublastin polypeptide contribute to this binding event. Substitution of selected amino acid residues was found to decrease heparin binding by variant Neublastin polypeptides and increase bioactivity and bioavailability of the variants.

In one aspect, the invention features a polypeptide containing an amino acid sequence that is at least 80% identical to amino acids 15-113 of SEQ ID NO:1, wherein the amino acid sequence contains at least one amino acid substitution, relative to SEQ ID NO:1, selected from the group consisting of: (i) an amino acid other than arginine at the position corresponding to position 48 of SEQ ID NO:1 (e.g., the arginine is substituted with a non-conservative amino acid residue such as glutamic acid); (ii) an amino acid other than arginine at the position corresponding to position 49 of SEQ ID NO:1 (e.g., the arginine is substituted with a non-conservative amino acid residue such as glutamic acid); and (iii) an amino acid other than arginine at the position corresponding to position 51 of SEQ ID NO:1 (e.g., the arginine is substituted with a non-conservative amino acid

residue such as glutamic acid). The polypeptide, when dimerized, binds to a complex containing GFRalpha3 and RET.

In some embodiments, the amino acid sequence contains amino acids other than arginine at the positions corresponding to position 48 and position 49 of SEQ ID NO:1. For example, the arginine residue at position 48 and the arginine reside at position 49 of SEQ ID NO:1 can be substituted with non-conservative amino acid residues (e.g., glutamic acid).

In some embodiments, the amino acid sequence is at least 90%, at least 95%, or at least 98% identical to amino acids 15-113 of SEQ ID NO:1.

Also disclosed is a polypeptide containing amino acids 15-113 of SEQ ID NO:2, amino acids 15-113 of SEQ ID NO:3, amino acids 15-113 of SEQ ID NO:4, amino acids 15-113 of SEQ ID NO:5, amino acids 15-113 of SEQ ID NO:8, or amino acids 15-113 of SEQ ID NO:9. In some embodiments, the polypeptide contains amino acids 10-113 of SEQ ID NO:2, amino acids 10-113 of SEQ ID NO:3, amino acids 10-113 of SEQ ID NO:4, amino acids 10-113 of SEQ ID NO:5, amino acids 10-113 of SEQ ID NO:8, or amino acids 10-113 of SEQ ID NO:9. In some embodiments, the polypeptide contains the amino acid sequence of SEQ ID NO:2, the amino acid sequence of SEQ ID NO:3, the amino acid sequence of SEQ ID NO:4, the amino acid sequence of SEQ ID NO:5, the amino acid sequence of SEQ ID NO:8, or the amino acid sequence of SEQ ID NO:9.

Also disclosed is a polypeptide containing an amino acid sequence at least 80% identical to amino acids 15-113 of SEQ ID NO:1, wherein the amino acid sequence comprises at least one amino acid substitution, relative to SEQ ID NO:1, selected from the group consisting of: (i) an amino acid other than serine at the position corresponding to position 20 of SEQ ID NO:1 (e.g., the serine is substituted with a non-conservative amino acid residue); (ii) an amino acid other than glutamine at the position corresponding to position 21 of SEQ ID NO:1 (e.g., the glutamine is substituted with a non-conservative amino acid residue); (iii) an amino acid other than histidine at the position corresponding to position 32 of SEQ ID NO:1 (e.g., the histidine is substituted with a non-conservative amino acid residue); (iv) an amino acid other than arginine at the position corresponding to position 33 of SEQ ID NO:1 (e.g., the arginine is substituted with a non-conservative amino acid residue); (v) an amino acid other than arginine at the position corresponding

to position 39 of SEQ ID NO:1 (e.g., the arginine is substituted with a non-conservative amino acid residue); (vi) an amino acid other than serine at the position corresponding to position 46 of SEQ ID NO:1 (e.g., the serine is substituted with a non-conservative amino acid residue); (vii) an amino acid other than arginine at the position corresponding to position 68 of SEQ ID NO:1 (e.g., the arginine is substituted with a non-conservative amino acid residue); (viii) an amino acid other than glycine at the position corresponding to position 72 of SEQ ID NO:1 (e.g., the glycine is substituted with a non-conservative amino acid residue); (ix) an amino acid other than serine at the position corresponding to position 73 of SEQ ID NO:1 (e.g., the serine is substituted with a non-conservative amino acid residue); and (x) an amino acid other than valine at the position corresponding to position 94 of SEQ ID NO:1 (e.g., the valine is substituted with a non-conservative amino acid residue). The polypeptide, when dimerized, binds to a complex containing GFRalpha3 and RET. In some embodiments, the amino acid sequence is at least 90%, at least 95%, or at least 98% identical to amino acids 15-113 of SEQ ID NO:1.

Also disclosed is a polypeptide containing an amino acid sequence at least 80% identical to SEQ ID NO:1, wherein the amino acid sequence comprises at least one amino acid substitution, relative to SEQ ID NO:1, selected from the group consisting of: (i) an amino acid other than arginine at the position corresponding to position 7 of SEQ ID NO:1 (e.g., the arginine is substituted with a non-conservative amino acid residue such as glutamic acid); (ii) an amino acid other than arginine at the position corresponding to position 9 of SEQ ID NO:1 (e.g., the arginine is substituted with a non-conservative amino acid residue such as glutamic acid); and (iii) an amino acid other than arginine at the position corresponding to position 14 of SEQ ID NO:1 (e.g., the arginine is substituted with a non-conservative amino acid residue such as glutamic acid). The polypeptide, when dimerized, binds to a complex containing GFRalpha3 and RET. In some embodiments, the amino acid sequence is at least 90%, at least 95%, or at least 98% identical to SEQ ID NO:1.

The invention also features conjugates containing a polypeptide described herein conjugated to a non-naturally occurring polymer. An exemplary polymer is a water-soluble synthetic polymer such as a polyalkylene glycol (e.g., polyethylene glycol).

The invention also features a fusion protein containing a polypeptide described herein and a heterologous amino acid sequence.

The invention also features a dimer containing two of the polypeptides, conjugates, or fusion proteins described herein.

The invention also features a pharmaceutical composition containing a polypeptide, dimer, conjugate, or fusion protein described herein and a pharmaceutically acceptable carrier or excipient.

Also disclosed is a nucleic acid containing a sequence that encodes a polypeptide described herein, an expression vector containing the nucleic acid, and a cell containing the expression vector.

Also disclosed is a method of making a polypeptide, the method including the following steps: (i) providing a cell containing an expression vector containing a nucleic acid encoding a polypeptide described herein, and (ii) culturing the cell under conditions that permit expression of the nucleic acid.

The invention also features a method of treating or preventing a nervous system disorder in a mammal by administering to the mammal a therapeutically effective amount of a polypeptide, dimer, conjugate, fusion protein, or pharmaceutical composition described herein.

The invention also features a method of treating neuropathic pain in a mammal by administering to the mammal a therapeutically effective amount of a polypeptide, dimer, conjugate, fusion protein, or pharmaceutical composition described herein.

The invention also features a method of activating the RET receptor in a mammal by administering to the mammal an effective amount of a polypeptide, dimer, conjugate, fusion protein, or pharmaceutical composition described herein.

An advantage of selected variant Neublastin polypeptides described herein is that they have decreased heparin binding ability as compared to wild type Neublastin. Decreased heparin binding results in a decreased clearance of the variant polypeptide *in vivo*.

A variant Neublastin polypeptide having substitutions at amino acid positions 48 and 49 was unexpectedly found to have greatly deceased heparin binding ability and greatly increased potency and bioavailabilty as compared to single amino acid mutants

and/or wild type Neublastin. For example, the double mutant was found to exhibit an approximately 185-fold increase in serum exposure as compared to wild type Neublastin. In addition, this double mutant was found to exhibit an over five fold increase in expression *in vitro* as compared to wild type Neublastin, thereby facilitating large scale production of the protein.

The advantages and unexpected properties of the variant Neublastin polypeptides allow for treatment of subjects using lower doses of protein and/or allow for lengthened intervals between administrations (as compared to treatments with the wild type protein).

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the exemplary methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present application, including definitions, will control. The materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

Brief Description of the Drawings

Fig. 1 is an alignment of wild type human (SEQ ID NO:10), mouse (SEQ ID NO:11), and rat (SEQ ID NO:12) pre pro Neublastin polypeptides. The left and right vertical lines indicate, respectively, the start of the mature 113 amino and 104 amino acid forms. The RRXR heparin binding motif is boxed.

Fig. 2A depicts a cationic elution profile of wild-type Neublastin (Peak D) and three single Arg-to-Glu substitution mutants (Peaks A, B, and C) (sloping line represents the theoretical sodium chloride concentration for any given volume eluted from the column). Data are a representation of the OD280 values of the eluted sample.

Fig. 2B depicts a Heparin Sepharose elution profile of wild-type Neublastin (Peak H) and three single Arg-to-Glu substitution mutants (Peaks E, F, and G) (sloping

line represents the theoretical sodium chloride concentration for any given volume eluted from the column). Data are a representation of the OD280 values of the eluted sample.

Figs. 3A-3B are photographs depicting SDS/PAGE of wild-type Neublastin following anionic chromatography in the presence (2A) or absence (2 B) of heparin.

Fig. 4 is a graph depicting the results of a Neublastin CHO cell binding assay. Following SDS/PAGE and desitometry, OD values of Neublastin wild type and Arg48E mutant bands were plotted against the heparin concentration in each sample.

Fig. 5 is a graph depicting the results of a heparin binding ELISA using wild type human NBN113, wild type human NBN104, Arg48E, Arg49E, Arg51E, and Arg48, 49E.

Fig. 6 is a graph depicting the results of KIRA analysis of wild type rat NBN113, Arg51E, Arg48E, Arg49E, and rat NBN113.

Fig. 7A is a graph depicting the results of KIRA analysis of wild type human Neublastin and Arg48,49E mutant human Neublastin (113 amino acid form).

Fig. 7B is a graph depicting the results of KIRA analysis of wild type human Neublastin, Arg48,49E mutant human Neublastin (104 amino acid form), Arg48,51E human Neublastin (113 amino acid form), and Arg49,51E human Neublastin (113 amino acid form).

Fig. 8 is a graph depicting the results of ternary complex analysis of wild type human Neublastin, Arg48E, Arg49E, Arg51E, Arg48,49E, and Arg48,49,51E Neublastin forms.

Fig. 9 is a graph depicting the results of ternary complex analysis of wild type Neublastin, Arg48E, Arg49E, Arg51E, Arg48,49E, and Arg48,49,51E Neublastin forms.

Fig. 10 is a graph depicting the results of pharmacokinetics analysis of wild type Neublastin and Arg48,49E following a single bolus 7 mg/kg subcutaneous injection (Neublastin plasma concentrations were determined using the Neublastin detection ELISA).

Fig. 11 is a graph depicting the results of pharmacokinetics analysis of wild type Neublastin and Arg48,49E following a single bolus 1 mg/kg intravenous injection (Neublastin plasma concentrations were determined using the Neublastin detection ELISA).

Fig. 12 is a graph depicting the results of pharmacokinetics analysis of 2X10K PEGylated Arg48,49E Neublastin following a single bolus subcutaneous 7mg/kg (data presented are extrapolated down to 1 mg/kg) injection and 2X10K PEGylated Arg48,49E Neublastin administered intravenously at 1 mg/kg (Neublastin plasma concentrations were determined using the Neublastin detection ELISA).

Fig. 13 is a graph depicting relative Neublastin expression levels in CHO cells transfected with plasmids encoding wild type Neublastin or Arg48,49E.

Fig. 14 is a graph depicting relative Neublastin expression levels in the leading Arg48,49E double mutant transfected CHO cell lines and a leading wild type Neublastin transfected CHO cell line.

Detailed Description

The present invention provides variant Neublastin polypeptides having substitutions at selected amino acid residues. As disclosed in the accompanying Examples, specific residues in the wild type Neublastin polypeptide have been found to be important for heparin binding. Because heparin binding is believed to contribute to clearance of Neublastin *in vivo*, substitutions at one or more of these specific residues are expected to decrease heparin binding and thereby increase serum exposure of the variant polypeptide.

Variant Neublastin Polypeptides

Mature wild type human Neublastin is 113 amino acids in length and has the following amino acid sequence: AGGPGSRARAAGARGCRLRSQLVPVRALGLGHR SDELVRFRFCSGSCRRARSPHDLSLASLLGAGALRPPPGSRPVSQPCCRPTRYEAV SFMDVNSTWRTVDRLSATACGCLG (SEQ ID NO:1).

Disclosed herein are polypeptides that have substitutions at one or more selected amino acid residues of the Neublastin polypeptide. Mutations at one or more of these residues are expected to result in a variant Neublastin polypeptide having reduced or absent heparin binding ability as compared to wild type Neublastin. A variant Neublastin polypeptide contains an amino acid substitution, relative to SEQ ID NO:1, at (i) an arginine residue at one or more of positions 48, 49, or 51, and/or (ii) one or more of

Ser 46, Ser 73, Gly 72, Arg 39, Gln 21, Ser 20, Arg 68, Arg 33, His 32, Val 94, Arg 7, Arg 9, or Arg 14. Unless otherwise stated, any reference herein to a Neublastin amino acid reside by position number refers to the numbering of residues relative to SEQ ID NO:1.

A Neublastin amino acid residue designated for substitution (e.g., an arginine residue at position 48, 49, and/or 51) can be substituted with a non-conservative amino acid residue (e.g., glutamic acid) or a conservative or amino acid residue. As detailed in the accompanying Examples, substitution of Arg48, Arg 49, and/or Arg 51 with a non-conservative amino acid can result in a variant Neublastin polypeptide that has reduced heparin binding activity but retained (or even enhanced) Neublastin biological activity. Exemplary amino acids that can be substituted an amino acid residue identified herein (e.g., an arginine residue at position 48, 49, and/or 51) include glutamic acid, aspartic acid, and alanine.

A biologically active variant Neublastin polypeptide, when dimerized, binds to a ternary complex containing GFRalpha3 and RET. Any method for detecting binding to this complex can be used to evaluate the biological activity a variant Neublastin polypeptide. Exemplary assays for detecting the ternary complex-binding ability of a variant Neublastin polypeptide are described in WO00/01815 and in Example 7.

A variant Neublastin polypeptide can also be assessed to evaluate its ability to trigger the Neublastin signaling cascade. For example, the Kinase Receptor Activation (KIRA) assay described in Example 6 can be used to assess the ability of a variant Neublastin polypeptide to induce RET autophosphorylation (*See also,* Sadick et al., 1996, *Anal. Biochem.*, 235(2):207).

In addition to the specific amino acid substitutions identified herein, a variant Neublastin polypeptide can also contain one or more additions, substitutions, and/or deletions at other amino acid positions, as detailed in the following sections.

A variant Neublastin polypeptide can, in addition to having one or more of the amino acid substitutions described herein, also vary in length. Although the mature human Neublastin polypeptide (SEQ ID NO:1) consists of the carboxy terminal 113 amino acids of pre pro Neublastin, not all of the 113 amino acids are required to achieve useful Neublastin biological activity. Amino terminal truncation is permissible. Thus, a

variant Neublastin polypeptide can contain one or more of the amino acid substitutions described herein in the context of the carboxy terminal 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, or 113 amino acids of SEQ ID NO:1 (i.e., its length can be 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, or 113 amino acids).

A variant Neublastin polypeptide can, in addition to having one or more of the amino acid substitutions described herein (and optionally having a truncation described herein), also vary in sequence. In particular, certain amino acid substitutions can be introduced into the Neublastin sequence without appreciable loss of a Neublastin biological activity. In exemplary embodiments, a polypeptide (i) contains one or more of the amino acid substitutions described herein, and (ii) is at least 70%, 80%, 85%, 90%, 95%, 98% or 99% identical to SEQ ID NO:1 (or 70%, 80%, 85%, 90%, 95%, 98% or 99% identical to amino acids 15-113 of SEQ ID NO:1). A variant Neublastin polypeptide differing in sequence from SEQ ID NO:1 (or differing in sequence from amino acids 15-113 of SEQ ID NO:1) may include one or more conservative amino acid substitutions, one or more non-conservative amino acid substitutions, and/or one or more deletions or insertions.

Fig. 1 is an alignment of the wild type human, mouse, and rat pre pro Neublastin polypeptides. The vertical lines in Fig.1 indicate the start of the mature 113 amino acid form (left vertical line) and 104 amino acid form (right vertical line) of Neublastin. The RRXR heparin binding motif is boxed. This alignment of naturally occurring, bioactive forms of Neublastin indicates specific exemplary residues (i.e., those that are not conserved among the human, mouse, and rat forms) that can be substituted without eliminating bioactivity.

Percent identity between amino acid sequences can be determined using the BLAST 2.0 program. Sequence comparison can be performed using an ungapped alignment and using the default parameters (Blossom 62 matrix, gap existence cost of 11, per residue gap cost of 1, and a lambda ratio of 0.85). The mathematical algorithm used in BLAST programs is described in Altschul et al., 1997, *Nucleic Acids Research* 25:3389-3402.

A conservative substitution is the substitution of one amino acid for another with similar characteristics. Conservative substitutions include substitutions within the following groups: valine, alanine and glycine; leucine, valine, and isoleucine; aspartic acid and glutamic acid; asparagine and glutamine; serine, cysteine, and threonine; lysine and arginine; and phenylalanine and tyrosine. The non-polar hydrophobic amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Any substitution of one member of the above-mentioned polar, basic or acidic groups by another member of the same group can be deemed a conservative substitution.

Non-conservative substitutions include those in which (i) a residue having an electropositive side chain (e.g., Arg, His or Lys) is substituted for, or by, an electronegative residue (e.g., Glu or Asp), (ii) a hydrophilic residue (e.g., Ser or Thr) is substituted for, or by, a hydrophobic residue (e.g., Ala, Leu, Ile, Phe or Val), (iii) a cysteine or proline is substituted for, or by, any other residue, or (iv) a residue having a bulky hydrophobic or aromatic side chain (e.g., Val, Ile, Phe or Trp) is substituted for, or by, one having a smaller side chain (e.g., Ala, Ser) or no side chain (e.g., Gly).

Exemplary variant Neublastin polypeptides are disclosed in Table 1. Amino acid residues of the variant Neublastin polypeptides that are mutated as compared to the corresponding wild type position are bolded and underlined. In addition, the Neublastin polypeptide (113, 99, or 104 amino acids in length) used as the background for the substitution is depicted in Table 1.

Table 1: Variant Neublastin Polypeptides

SEQ ID NO	Position Substituted	Length of Polypeptide	Amino Acid Sequence
2	Arg 48	113	AGGPGSRARAAGARGCRLRSQLVPVRA LGLGHRSDELVRFRFCSGSCERARSPHD LSLASLLGAGALRPPPGSRPVSQPCCRPT RYEAVSFMDVNSTWRTVDRLSATACGC LG
3	Arg 49	113	AGGPGSRARAAGARGCRLRSQLVPVRA LGLGHRSDELVRFRFCSGSCREARSPHD LSLASLLGAGALRPPPGSRPVSQPCCRPT RYEAVSFMDVNSTWRTVDRLSATACGC LG
4	Arg 51	113	AGGPGSRARAAGARGCRLRSQLVPVRA LGLGHRSDELVRFRFCSGSCRRAESPHD LSLASLLGAGALRPPPGSRPVSQPCCRPT RYEAVSFMDVNSTWRTVDRLSATACGC LG
5	Arg 48 and Arg 49	113	AGGPGSRARAAGARGCRLRSQLVPVRA LGLGHRSDELVRFRFCSGSCEEARSPHD LSLASLLGAGALRPPPGSRPVSQPCCRPT RYEAVSFMDVNSTWRTVDRLSATACGC LG
6	Arg 48 and Arg 49	99	GCRLRSQLVPVRALGLGHRSDELVRFRF CSGSCEEARSPHDLSLASLLGAGALRPPP GSRPVSQPCCRPTRYEAVSFMDVNSTW RTVDRLSATACGCLG
7	Arg 48 and Arg 49	104	AAGARGCRLRSQLVPVRALGLGHRSDE LVRFRFCSGSCEEARSPHDLSLASLLGA GALRPPPGSRPVSQPCCRPTRYEAVSFM DVNSTWRTVDRLSATACGCLG
8	Arg 49 and Arg 51	113	AGGPGSRARAAGARGCRLRSQLVPVRA LGLGHRSDELVRFRFCSGSCREAESPHD LSLASLLGAGALRPPPGSRPVSQPCCRPT RYEAVSFMDVNSTWRTVDRLSATACGC LG
9	Arg 48 and Arg 51	113	AGGPGSRARAAGARGCRLRSQLVPVRA LGLGHRSDELVRFRFCSGSCERAESPHD LSLASLLGAGALRPPPGSRPVSQPCCRPT RYEAVSFMDVNSTWRTVDRLSATACGC LG

A variant Neublastin polypeptide can be optionally coupled to a polymer (e.g., a polyalkylene glycol moiety such as a polyethylene glycol moiety). In some embodiments, the polymer is coupled to the polypeptide at a site on the Neublastin polypeptide that is an N terminus. In some embodiments, the variant Neublastin polypeptide includes at least one amino acid substitution with respect to SEQ ID NO:1 (or with respect to amino acids 15-113 of SEQ ID NO:1), which provides an internal polymer conjugation site to which a polymer can be conjugated. In some embodiments, the polymer is coupled to the variant Neublastin polypeptide at a residue (numbered in accordance with the sequence of SEQ ID NO:1) selected from the group consisting of position 14, position 39, position 68, and position 95. Exemplary Neublastin variants that provide internal polymer conjugation sites are described in WO 02/060929 and WO 04/069176 (the contents of which are incorporated herein by reference).

A polypeptide can optionally contain heterologous amino acid sequences in addition to a variant Neublastin polypeptide. "Heterologous," as used when referring to an amino acid sequence, refers to a sequence that originates from a source foreign to the particular host cell, or, if from the same host cell, is modified from its original form. Exemplary heterologous sequences include a heterologous signal sequence (e.g., native rat albumin signal sequence, a modified rat signal sequence, or a human growth hormone signal sequence) or a sequence used for purification of a variant Neublastin polypeptide (e.g., a histidine tag).

Neublastin polypeptides can be isolated using methods known in the art. Naturally occurring Neublastin polypeptides can be isolated from cells or tissue sources using standard protein purification techniques. Alternatively, mutated Neublastin polypeptides can be synthesized chemically using standard peptide synthesis techniques. The synthesis of short amino acid sequences is well established in the peptide art. *See, e.g.*, Stewart, *et al.*, Solid Phase Peptide Synthesis (2d ed., 1984).

In some embodiments, variant Neublastin polypeptides are produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding a variant Neublastin polypeptide can be inserted into a vector, *e.g.*, an expression vector, and the nucleic acid can be introduced into a cell. Suitable cells include, *e.g.*, mammalian cells (such as human cells or CHO cells), fungal cells, yeast cells, insect cells, and bacterial

cells. When expressed in a recombinant cell, the cell is preferably cultured under conditions allowing for expression of a variant Neublastin polypeptide. The variant Neublastin polypeptide can be recovered from a cell suspension if desired. As used herein, "recovered" means that the mutated polypeptide is removed from those components of a cell or culture medium in which it is present prior to the recovery process. The recovery process may include one or more refolding or purification steps.

Variant Neublastin polypeptides can be constructed using any of several methods known in the art. One such method is site-directed mutagenesis, in which a specific nucleotide (or, if desired a small number of specific nucleotides) is changed in order to change a single amino acid (or, if desired, a small number of predetermined amino acid residues) in the encoded variant Neublastin polypeptide. Many site-directed mutagenesis kits are commercially available. One such kit is the "Transformer Site Directed Mutagenesis Kit" sold by Clontech Laboratories (Palo Alto, CA).

Pharmaceutical Compositions

A variant Neublastin polypeptide can be incorporated into a pharmaceutical composition containing a therapeutically effective amount of the polypeptide and one or more adjuvants, excipients, carriers, and/or diluents. Acceptable diluents, carriers and excipients typically do not adversely affect a recipient's homeostasis (e.g., electrolyte balance). Acceptable carriers include biocompatible, inert or bioabsorbable salts, buffering agents, oligo- or polysaccharides, polymers, viscosity-improving agents, preservatives and the like. One exemplary carrier is physiologic saline (0.15 M NaCl, pH 7.0 to 7.4). Another exemplary carrier is 50 mM sodium phosphate, 100 mM sodium chloride. Further details on techniques for formulation and administration of pharmaceutical compositions can be found in, e.g., REMINGTON'S PHARMACEUTICAL SCIENCES (Maack Publishing Co., Easton, Pa.).

Administration of a pharmaceutical composition containing a variant Neublastin polypeptide can be systemic or local. Pharmaceutical compositions can be formulated such that they are suitable for parenteral and/or non-parenteral administration. Specific administration modalities include subcutaneous, intravenous, intramuscular, intraperitoneal transdermal, intrathecal, oral, rectal, buccal, topical, nasal, ophthalmic,

intra-articular, intra-arterial, sub-arachnoid, bronchial, lymphatic, vaginal, and intra-uterine administration.

Formulations suitable for parenteral administration conveniently contain a sterile aqueous preparation of the variant Neublastin polypeptide, which preferably is isotonic with the blood of the recipient (*e.g.*, physiological saline solution). Formulations may be presented in unit-dose or multi-dose form.

An exemplary formulation contains a variant Neublastin polypeptide described herein and the following buffer components: sodium succinate (e.g., 10 mM); NaCl (e.g., 75 mM); and L-arginine (e.g., 100 mM).

Formulations suitable for oral administration may be presented as discrete units such as capsules, cachets, tablets, or lozenges, each containing a predetermined amount of the variant Neublastin polypeptide; or a suspension in an aqueous liquor or a non-aqueous liquid, such as a syrup, an elixir, an emulsion, or a draught.

Therapeutically effective amounts of a pharmaceutical composition may be administered to a subject in need thereof in a dosage regimen ascertainable by one of skill in the art. For example, a composition can be administered to the subject, e.g., systemically at a dosage from 0.01μg/kg to 1000 μg/kg body weight of the subject, per dose. In another example, the dosage is from 1 μg/kg to 100 μg/kg body weight of the subject, per dose. In another example, the dosage is from 1 μg/kg to 30 μg/kg body weight of the subject, per dose, e.g., from 3 μg/kg to 10 μg/kg body weight of the subject, per dose.

In order to optimize therapeutic efficacy, a variant Neublastin polypeptide is first administered at different dosing regimens. The unit dose and regimen depend on factors that include, *e.g.*, the species of mammal, its immune status, the body weight of the mammal. Typically, protein levels in tissue are monitored using appropriate screening assays as part of a clinical testing procedure, *e.g.*, to determine the efficacy of a given treatment regimen.

The frequency of dosing for a variant Neublastin polypeptide is within the skills and clinical judgement of physicians. Typically, the administration regime is established by clinical trials which may establish optimal administration parameters. However, the practitioner may vary such administration regimes according to the subject's age, health,

weight, sex and medical status. The frequency of dosing may also vary between acute and chronic treatments for neuropathy. In addition, the frequency of dosing may be varied depending on whether the treatment is prophylactic or therapeutic.

Methods of Treatment

Variant Neublastin polypeptides are useful for modulating metabolism, growth, differentiation, or survival of a nerve or neuronal cell. In particular, variant Neublastin polypeptides can be used to treat or alleviate a disorder or disease of a living animal, *e.g.*, a human, which disorder or disease is responsive to the activity of a neurotrophic agent.

The variant Neublastin polypeptides disclosed herein (and pharmaceutical compositions comprising same) can be used in methods for treating a disorder characterized by damage to sensory neurons or retinal ganglion cells, including neurons in the dorsal root ganglia or in any of the following tissues: the geniculate, petrosal and nodose ganglia; the vestibuloacoustic complex of the eighth cranial nerve; the ventrolateral pole of the maxillomandibular lobe of the trigeminal ganglion; and the mesencephalic trigeminal nucleus.

In some embodiments, sensory and/or autonomic system neurons can be treated. In particular, nociceptive and mechanoreceptive neurons can be treated, more particularly A-delta fiber, C-fiber and A-beta fiber neurons. In addition, sympathetic and parasympathetic neurons of the autonomic system can be treated.

In some embodiments, motor neuron diseases such as amyotrophic lateral sclerosis ("ALS") and spinal muscular atrophy can be treated. In other embodiments, the variant Neublastin polypeptides can be used to enhance nerve recovery following traumatic injury. Alternatively, or in addition, a nerve guidance channel with a matrix containing polymer-conjugated Neublastin polypeptides, or fusion or conjugates of mutated Neublastin polypeptides can be used. Such nerve guidance channels are disclosed, *e.g.*, United States Patent No. 5,834,029.

In some embodiments, the variant Neublastin polypeptides (and pharmaceutical compositions comprising same) are used in the treatment of various disorders in the eye, including photoreceptor loss in the retina in patients afflicted with macular degeneration, retinitis pigmentosa, glaucoma, and similar diseases.

In some embodiments, the variant Neublastin polypeptides (and pharmaceutical compositions comprising same) are used for treating neuropathic pain, for treating tactile allodynia, for reducing loss of pain sensitivity associated with neuropathy, for treating viral infections and viral-associated neuropathies, for treating painful diabetic neuropathy, and for treating nervous system disorders. The methods are discussed in detail in the following subsections.

1. Treatment of Neuropathic Pain

The variant Neublastin polypeptides disclosed herein (and pharmaceutical compositions comprising same) can be used in methods for treating neuropathic pain in a subject comprising administering to the subject an effective amount of a variant Neublastin polypeptide either alone, or by also administering to the subject an effective amount of an analgesia-inducing compound selected from the group consisting of opioids, anti-arrhythmics, topical analgesics, local anaesthetics, anticonvulsants, antidepressants, corticosteroids and non-steroidal anti-inflammatory drugs (NSAIDS). In one embodiment, the analgesia-inducing compound is an anticonvulsant. In another embodiment, the analgesia-inducing compound is gabapentin ((1-aminomethyl)cyclohexane acetic acid) or pregabalin (S-(+)-4-amino-3-(2-methylpropyl) butanoic acid).

The variant Neublastin polypeptides disclosed herein (and pharmaceutical compositions comprising same) can be used in the treatment of pain associated with peripheral neuropathies. Among the peripheral neuropathies which can be treated are trauma-induced neuropathies, *e.g.*, those caused by physical injury or disease state, physical damage to the brain, physical damage to the spinal cord, stroke associated with brain damage, and neurological disorders related to neurodegeneration.

The variant Neublastin polypeptides disclosed herein (and pharmaceutical compositions comprising same) can be used in the treatment of a number of peripheral neuropathies, including: (a) trauma-induced neuropathies, (b) chemotherapy-induced neuropathies, (c) toxin-induced neuropathies (including but not limited to neuropathies induced by alcoholism, vitamin B6 intoxication, hexacarbon intoxication, amiodarone, chloramphenicol, disulfiram, isoniazide, gold, lithium, metronidazole, misonidazole, nitrofurantoin), (d) drug-induced neuropathies, including therapeutic drug-induced

neuropathic pain (such as caused by anti-cancer agents, particularly anti-cancer agents selected from the group consisting of taxol, taxotere, cisplatin, nocodazole, vincristine, vindesine and vinblastine; and such as caused by anti-viral agents, particularly anti-viral agents selected from the group consisting of ddI, DDC, d4T, foscarnet, dapsone, metronidazole, and isoniazid), (e) vitamin-deficiency-induced neuropathies (including but not limited to vitamin B12 deficiency, vitamin B6 deficiency, and vitamin E deficiency), (f) idiopathic neuropathies, (g) diabetic neuropathies, (h) pathogen-induced nerve damage, (i) inflammation-induced nerve damage, (j) neurodegeneration, (k) hereditary neuropathy (including but not limited to Friedreich ataxia, familial amyloid polyneuropathy, Tangier disease, Fabry disease), (l) metabolic disorders (including but not limited to renal insufficiency and hypothyroidism), (m) infectious and viral neuropathies (including but not limited to neuropathic pain associated with leprosy, Lyme disease, neuropathic pain associated with infection by a virus, particularly a virus selected from the group consisting of a herpes virus (*e.g.* herpes zoster which may lead to post-herpetic neuralgia), a human immunodeficiency virus (HIV), and a papilloma virus), (n) auto-immune neuropathies (including but not limited to Guillain-Barre syndrome, chronic inflammatory de-myelinating polyneuropathy, monoclonal gammopathy of undetermined significance and polyneuropathy), (o) trigeminal neuralgia and entrapment syndromes (including but not limited to Carpel tunnel), and (p) other neuropathic pain syndromes including post-traumatic neuralgia, phantom limb pain, multiple sclerosis pain, complex regional pain syndromes (including but not limited to reflex sympathetic dystrophy, causalgia), neoplasia- associated pain, vasculitic/angiopathic neuropathy, and sciatica. Neuropathic pain may be manifested as allodynia, hyperalgesia, spontaneous pain or phantom pain.

2. Treatment of Tactile Allodynia

The variant Neublastin polypeptides disclosed herein (and pharmaceutical compositions comprising same) can be used in the treatment of tactile allodynia in a subject. The term "tactile allodynia" typically refers to the condition in a subject where pain is evoked by stimulation of the skin (*e.g.* touch) that is normally innocuous.

In some embodiments, tactile allodynia is treated by administering to the subject a pharmaceutically effective amount of a variant Neublastin polypeptide. In a related

embodiment, tactile allodynia may be treated by administering to a subject an effective amount of a variant Neublastin polypeptide either alone, or by administering to the subject an effective amount of a variant Neublastin polypeptide with an effective amount of an analgesia-inducing compound selected from the group consisting of opioids, anti-arrhythmics, topical analgesics, local anaesthetics, anticonvulsants, antidepressants, corticosteroids and NSAIDS. In one embodiment, the analgesia-inducing compound is an anticonvulsant. In another preferred embodiment, the analgesia-inducing compound is gabapentin ((1-aminomethyl)cyclohexane acetic acid) or pregabalin (S-(+)-4-amino-3-(2-methylpropyl)butanoic acid).

In some embodiments, a variant Neublastin polypeptide is administered in association with a therapeutic agent, including but not limited to an anti-cancer agent or an anti-viral agent. Anti-cancer agents include, but are not limited to, taxol, taxotere, cisplatin, nocodazole, vincristine, vindesine and vinblastine. Anti-viral agents include, but are not limited to, ddI, DDC, d4T, foscarnet, dapsone, metronidazole, and isoniazid.

3. Treatment for Reduction of Loss of Pain Sensitivity

In another embodiment, variant Neublastin polypeptides disclosed herein (and pharmaceutical compositions comprising same) can be used in a method for reducing the loss of pain sensitivity in a subject afflicted with a neuropathy. In one embodiment, the neuropathy is diabetic neuropathy. In some embodiments, the loss of pain sensitivity is a loss in thermal pain sensitivity. This methods include both prophylactic and therapeutic treatment.

In prophylactic treatment, a variant Neublastin polypeptide is administered to a subject at risk of developing loss of pain sensitivity (such a subject would be expected to be a subject with an early stage neuropathy). The treatment with a variant Neublastin polypeptide under such circumstances would serve to treat at-risk patients preventively.

In therapeutic treatment, a variant Neublastin polypeptide is administered to a subject who has experienced loss of pain sensitivity as a result of affliction with a neuropathy (such a subject would be expected to be a subject with a late stage neuropathy). The treatment with a variant Neublastin polypeptide under such circumstances would serve to rescue appropriate pain sensitivity in the subject.

4. Treatment of Viral Infections and Viral-Associated Neuropathies

Prophylactic treatment of infectious and viral neuropathies is contemplated. Prophylactic treatment is indicated after determination of viral infection and before onset of neuropathic pain. During treatment, a variant Neublastin polypeptide is administered to prevent appearance of neuropathic pain including but not limited to neuropathic pain associated with leprosy, Lyme disease, neuropathic pain associated with infection by a virus, particularly a virus selected from the group consisting of a herpes virus (and more particularly by a herpes zoster virus, which may lead to post-herpetic neuralgia), a human immunodeficiency virus (HIV), and a papilloma virus). In an alternative embodiment, a variant Neublastin polypeptide is administered to reduce the severity of neuropathic pain, should it appear.

Symptoms of acute viral infection often include the appearance of a rash. Other symptoms include, for example, the development of persistent pain in the affected area of the body, which is a common complication of a herpes zoster infection (shingles). Post-herpetic neuralgia can last for a month or more, and may appear several months after any rash-like symptoms have disappeared.

5. Treatment of Painful Diabetic Neuropathy

Prophylactic treatment of painful diabetic neuropathy is contemplated. Prophylactic treatment of diabetic neuropathies would commence after determination of the initial diagnosis of diabetes or diabetes-associated symptoms and before onset of neuropathic pain. Prophylactic treatment of painful diabetic neuropathy may also commence upon determining that a subject is at risk for developing diabetes or diabetes-associated symptoms. During treatment, a variant Neublastin polypeptide is administered to prevent appearance of neuropathic pain. In an alternative embodiment, a variant Neublastin polypeptide is administered to reduce the severity of neuropathic pain that has already appeared.

6. Treatment of Nervous System Disorders

The variant Neublastin polypeptides disclosed herein (and pharmaceutical compositions comprising same) can be used in the treatment or prevention of a nervous system disorder in a subject (such as a human), by administering to a subject in need thereof a therapeutically effective amount of a variant Neublastin polypeptide, a

composition containing a variant Neublastin polypeptide, or a complex that includes a stable, aqueous soluble conjugated variant Neublastin polypeptide coupled to a polyalkylene moiety such as, e.g., PEG.

The nervous system disorder can be a peripheral nervous system disorder, such as a peripheral neuropathy or a neuropathic pain syndrome. Humans are preferred subjects for treatment.

A variant Neublastin polypeptide is useful for treating a defect in a neuron, including without limitation lesioned neurons and traumatized neurons. Peripheral nerves that experience trauma include, but are not limited to, nerves of the medulla or of the spinal cord. Variant Neublastin polypeptides are useful in the treatment of neurodegenerative disease, e.g., cerebral ischemic neuronal damage; neuropathy, e.g., peripheral neuropathy, Alzheimer's disease, Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS). Such variant Neublastin polypeptides can be used in the treatment of impaired memory, e.g., memory impairment associated with dementia.

The following are examples of the practice of the invention. They are not to be construed as limiting the scope of the invention in any way.

Examples

Example 1: Design and Synthesis of Variant Neublastin Polypeptides

Human Neublastin was crystallized and its structure revealed a triad of sulfate ions interacting with the following four Neublastin residues in close proximity to each other: Arg14, Arg48, Arg49, and Arg51. Based upon the presence of this triad and their relative spacing to one another, it was postulated that this region of Neublastin could be a potential heparin sulfate-binding domain. Subsequently, a previously solved heparin sulfate structure was docked (in-silico) to Neublastin at the site of the sulfate triad. Heparin sulfate fit precisely in this position, suggesting that this region within Neublastin has potential for heparin sulfate binding.

The Neublastin crystallization data also revealed that the following amino acid residues provide supplementary interactions with either the triad of sulfate ions or with

one or more of three other sulfate ions that interact with Neublastin: Ser 46, Ser 73, Gly 72, Arg 39, Gln 21, Ser 20, Arg 68, Arg 33, His 32, and Val 94. In addition to the sulfate binding sites revealed by the crystal structure, Neublastin contains a heparin sulfate binding site consensus sequence (GPGS**R**A**R**) at residues 3-9 at its N-terminus. This region was unstructured in the crystal structure but may become ordered upon binding glycosaminoglycans. The region is likely to be close in space to the three sulfate cluster observed in the crystal structure (Arg14 contributes to the heparin-binding site that is mainly centered in the hinge region of the protein).

To investigate the biological relevance of the potential heparin sulfate-binding domain, three individual single amino acid residue substitutions were made within the mature 113 amino acid human Neublastin (SEQ ID NO:1). The arginine residues at each of position 48 (variant named "Arg48E"; SEQ ID NO:2), position 49 (variant named "Arg49E"; SEQ ID NO:3), and position 51 (variant named "Arg51E"; SEQ ID NO:4) were replaced by glutamate (i.e., three different single amino acid variant constructs were prepared) with the intention of changing the residue charge from one that would attract sulfate to one that would repel, and to potentially stabilize surrounding arginine residues. Proteins were refolded and purified from *E. coli* inclusion bodies (see WO 04/069176). Each Neublastin variant was subjected to analysis to verify structural integrity and confirm the correct residue substitution. All three mutants were structurally comparable to the wild-type human Neublastin.

Example 2: Cationic and Heparin Sepharose Chromatography

The variant Neublastin polypeptides were subjected to further biochemical analysis to determine the effect each mutation had on heparin binding. Heparin Sepharose and cationic chromatography were both employed. Since wild-type human Neublastin is a basic protein with an apparent pI of 11.31, Neublastin binds efficiently to cationic-based resins. A single conversion of arginine to glutamate decreases the apparent pI to 10.88. However, this lower pI was not expected to dramatically alter cationic resin-binding nor was it expected to alter the elution profile of the mutants compared to that of the wild-type control.

Each of the mutants (along with the wild-type Neublastin control) was subjected to cationic chromatography. The samples were loaded onto resin in buffer containing 5 mM phosphate pH 6.5 and 150 mM sodium chloride followed by elution with a linear salt gradient starting at 150 mM and ending with 1M sodium chloride. Wild-type Neublastin eluted at ~800 mM sodium chloride (Fig. 2A; Peak D), whereas each of the three mutants eluted within a salt range of approximately 500 mM, thus reflecting their lower pI. Arg49E and Arg51E (Fig. 2A; Peaks B and C) eluted with slightly higher salt than was required to elute Arg48E (Fig. 2A; Peak A) (520 mM vs 490 mM, respectively). This difference suggested that Arg48 is more surface accessible and contributes more to cationic binding than that of the other two mutations.

To determine whether the Arg-to-Glu substitutions had an effect on heparin binding, each of the three mutants (along with wild-type human Neublastin) was subjected to Heparin Sepharose chromatography (Fig. 2B). Binding and elution conditions were similar to those used for cationic chromatography. However, the observed elution profile was significantly different from the cationic resin elution profile. Wild-type Neublastin eluted at approximately 720 mM sodium chloride (Fig. 2B; Peak H) whereas Arg51E, Arg49E, and Arg48E eluted at 570 mM (Fig. 2B; Peak G), 510 mM (Fig. 2B; Peak F), and 450 mM (Fig. 2B; Peak E) sodium chloride, respectively. Arg48E appeared to have a particularly dramatic effect on heparin binding. Taken together, these chromatography profiles suggested that each mutation decreases Neublastin's apparent affinity for heparin.

Example 3: Anionic Chromatography

At standard pH conditions of 6.5 and a sodium chloride concentration of 150 mM, Neublastin does not bind to anionic resins. In contrast, heparin sulfate does bind to anionic resins under these same conditions.

When Neublastin was pre-mixed in a 1:1 molar ratio with 16-kDa-heparin sulfate and applied to an anionic matrix using the above conditions, Neublastin bound and eluted with 600 mM sodium chloride (Fig. 3B, lanes marked "FT"), suggesting that Neublastin was binding the anionic matrix through its interaction with heparin sulfate. In the absence of heparin, Neublastin did not bind to the anionic resin (Fig. 3A, lanes marked

"FT") and no Neublastin eluted with 600 mM sodium chloride (Fig. 3A, lanes marked "Elution"). These data provide further evidence of Neublastin's ability to bind to heparin.

Example 4: Chinese Hamster Ovary Cell Binding Studies

Neublastin has been shown previously to bind non-specifically to the surface of Chinese Hamster Ovary (CHO) cells. A Neublastin CHO cell-binding assay was established to determine whether this interaction is mediated, at least in part, through Neublastin's binding to cell surface heparin sulfate molecules.

Wild-type human Neublastin (40 ug) or the Arg48E mutant was pre-mixed with CHO cells (10^6 cells) at a cell density which completely binds both Neublastin forms along with increasing amounts of 16 kDa heparin sulfate and incubated at 37°C for 4 hours. Following incubation, the cells were pelleted by centrifugation and remaining non-bound Neublastin in the supernatant was subjected to SDS/PAGE analysis. After quantification of each protein band by densitometry, the resulting optical density value was plotted against the heparin concentration in each sample (Fig. 4).

At the two lower heparin concentrations, both the wild type and the mutant Neublastin forms had equal amounts of protein identified in the supernatant. However, as the heparin concentration increased to 0.5 ug/ml and higher, more wild-type Neublastin was identified in the supernatant than that of the Arg48E mutant. This observation suggested that heparin can compete with cell surface-bound heparin for wild-type Neublastin binding (i.e., binding of heparin to wild-type Neublastin results in its removal from the cell surface), whereas heparin cannot as readily compete off the Arg48E mutant. At the highest heparin concentration (50 ug/ml), the Arg48E mutant began to elute off the cell surface, suggesting an ionic interaction between heparin and the Arg48E mutant might be responsible for this observation.

Example 5: Heparin Binding of Wild Type Neublastin and Variant Neublastin Polypeptides

To further investigate the role of the identified arginine triad as a heparin-binding site of Neublastin, a heparin binding ELISA was established. In brief, an anti-Neublastin

monoclonal antibody was coated onto a 96-well plate, followed by washing and the addition of one of the Neublastin forms. Biotinylated heparin was then added to the plate. Following an additional wash step, the Neublastin/Heparin complex was identified using a Strepavidin-HRP conjugate with a chemiluminescent substrate. This heparin-binding ELISA was used to compare wild type human Neublastin 113 amino acid (SEQ ID NO:1) and 104 amino acid (amino acids 10-113 of SEQ ID NO:1) forms to variant Neublastin polypeptides containing a single amino acid substitution (Arg48E, Arg49E, and Arg51E; SEQ ID NOS:2-4) as well as a double substitution (Arg48, 49E; SEQ ID NO:5).

Both wild-type forms of Neublastin bound heparin with an EC50 of ~1 ng/ml heparin (Fig. 5). Arg49E and Arg51E bound less efficiently, with an apparent EC50 of ~10ng/ml, but maximum binding remained the same (Fig. 5). Of the three single point mutations, Arg48E had the most dramatic effect on heparin binding, with an apparent EC50 of ~100 ng/ml, but still achieved the same maximum heparin binding value when compared to the unmodified Neublastin forms (Fig. 5). The Arg48E mutant was thus one hundred fold less efficient in binding heparin as compared to the unmodified Neublastin forms and ten fold less efficient as compared to the other single substitution mutants. When both Arg48 and Arg49 were substituted with glutamate, heparin binding was almost eliminated, resulting in a seven-fold decrease in maximum heparin binding, but the EC50 remained within range of the single point mutants. These results suggest that Arg48 plays an important role in heparin binding due to its central location in the putative heparin-binding site.

Example 6: Kinase Receptor Activation Analysis of Wild-Type Neublastin and Heparin Binding Mutants

To determine whether heparin-binding site mutations have an effect on Neublastin receptor signaling in a cell-based bioassay, mutant Neublastin forms along with the wild-type Neublastin were subjected to Kinase Receptor Activation (KIRA) analysis.

Each of the single Arg-to-Glu substitution mutants appeared identical to the unmodified control with respect to KIRA activity, suggesting that these mutants are structurally similar to the wild-type and are capable of activating the Neublastin receptor

and signaling cascade (Fig. 6). Furthermore, these data suggest that heparin binding to Neublastin may not be required for receptor activation.

When the Arg48,49E double mutant (SEQ ID NO:5; 113 amino acid form) was subjected to KIRA analysis, its apparent EC50 was shifted to the left by approximately one order of magnitude with an increase in its maximum receptor activation when compared with the wild-type human Neublastin control (Fig. 7A). Similarly, the Arg48,49E double mutant (SEQ ID NO:7; 104 amino acid form) also exhibited increased potency as compared to wild-type Neublastin (Fig. 7B). Each of the Arg48,51E and Arg49,51E double mutants (SEQ ID NO:9 and SEQ ID NO:8, respectively; 113 amino acid forms) appeared similar to the unmodified Neublastin control with respect to KIRA activity (Fig. 7B).

Example 7: Ternary Complex Analysis

Wild-type human Neublastin and each of the heparin mutants were subjected to ternary complex analysis using two slightly different protocols. The first protocol combined Neublastin's receptor components (GFRalpha3 and RET) along with Neublastin in a pool before addition to an ELISA plate coated with capture antibody (Fig. 8). The second protocol added these components sequentially to an ELISA plate with GFRalpha3 added first, followed by Neublastin, and then RET (Fig. 9).

When the components were added together as a pool, maximum binding was achieved with both Arg48E and Arg48,49E, suggesting that these Neublastin forms have the highest affinity for their receptor. Wild-type Neublastin appeared to bind with a similar affinity to that of the Arg49E mutant, whereas the Arg51E and a triple mutant (Arg48, 49 and 51 all substituted to glutamate) demonstrated the weakest receptor binding.

When the receptor components were added sequentially, Arg48E showed the best receptor binding. However under these conditions, the double mutant weakly bound to its receptor with an affinity that appeared similar to the Arg51E mutant. Arg49E and wild-type Neublastin had an affinity for the receptor that was midway between the observed maximum and minimum binding. The triple mutant did not bind under these conditions.

Overall, these data suggest that Arg48 plays a pivotal role in affecting Neublastin's affinity for its receptor.

Example 8: Near and Far UV CD Analysis

To further investigate the effects of the double mutations on Neublastin's secondary and tertiary structure, the Arg48,49E double mutant was subjected to both Near and Far UV CD analysis. Although subtle differences were detected in the secondary and tertiary structures, the conformation of the double mutant was very close to that of the wild-type Neublastin.

Example 9: Pharmacokinetic Analysis of the Neublastin Arg48, 49E Double Mutant

Human Neublastin exhibits poor pharmacokinetics (PK) when administered to rats intravenously (IV) or subcutaneously (SC), with an overall bioavailability of less than 1%. Heparin-based clearance may be one of the reasons for this low bioavailability. To determine whether heparin-based clearance participates in human Neublastin's rapid clearance from the rat, the Arg48,49E double mutant (along with the wild-type control) was subjected to PK analysis.

Both forms were administered separately in rats at 7 mg/kg SC. Serum samples were collected starting at 1 hour, completed at 96 hours, and analyzed for Neublastin (Fig. 10). The observed area under the curve (AUC) for wild-type Neublastin was ~109 whereas the observed AUC for the double mutant was 20,145. This represented a 185-fold increase in AUC for the double mutant (compared to wild-type Neublastin) and a significant increase in serum exposure.

Both the wild type and double mutant Neublastin were also subjected to PK analysis following IV administration (1 mg/kg). The initial plasma concentration of the double mutant was approximately six-fold higher (diamonds) than that of the wild-type control (squares) at five minutes following injection but quickly approached wild type levels within one hour (Fig. 11). These data suggest that the double mutation in Neublastin aids in increasing serum exposure but does not affect the overall clearance rate.

Taken together with the SC observation, heparin-binding appears to be especially relevant following SC administration, perhaps resulting in a depot-like effect. Once Neublastin enters circulation, the rate at which the double mutant and wild type molecules are cleared is approximately the same.

To address the rate at which Neublastin is cleared from circulation in the rat, both the wild type and double mutant forms of Neublastin were PEGylated with 10 kDa PEG using SPA-based coupling chemistry. Since Neublastin is a homo-dimer with no native lysine residues, the 10-kDa moieties specifically labeled the amino terminus of each monomer. 2X10K PEGylated human double mutant neublastin was purified to homogeneity, and subjected to structural and biological analysis prior to PK analysis.

2X10K PEG Arg48, 49E double mutant was injected either IV (1 mg/kg) or SC (7 mg/kg) into rats and serum collected at various time points for analysis. Following IV administration, 2X10K PEG double mutant achieved the theoretical Cmax of 10 ug/ml (diamonds) with typical alpha and beta phases (Fig. 12). SC administration of the PEGylated double mutant demonstrated a Cmax of 40 ng/ml at 24 hours injection (Fig. 12). Once the drug reached circulation, the apparent rate of clearance paralleled that of IV dose. Bioavailability of this construct was approximately 10% compared to less than 1% for the non-PEGylated or PEGylated wild type human Neublastin.

Example 10: Expression of a Neublastin Heparin-Binding Mutant in Chinese Hamster Ovary Cells

Plasmid constructs encoding wild type and mutant Neublastin were expressed in CHO cells and the amount of secreted soluble protein was measured by ELISA. The plasmid constructs used in these experiments encoded a fusion protein containing the human growth hormone signal peptide (SigPep) (with or without an intron included in the plasmid) fused to (i) the carboxy terminal 104 amino acids of wild type human Neublastin, or (ii) the Arg48,49E double mutant (104 amino acid form).

The following are the amino acid sequences of the Neublastin fusion proteins used in these experiments. The Neublastin sequences are in upper case type. The human growth hormone signal peptide sequences are in lower case type. The junction of the

signal peptide and Neublastin sequences is indicated with a carat (^). The amino acids at positions 48 and 49 are underlined.

SigPep-NBN (wild type): matgsrtslllafgllclswlqegsa^AAGARGCRLRSQLVPV RALGLGHRSDELVRFRFCSGSC**RR**ARSPHDLSLASLLGAGALRPPPGSRPVSQPC CRPTRYEAVSFMDVNSTWRTVDRLSATACGCLG (SEQ ID NO:13).

SigPep-NBN (Arg48,49E): matgsrtslllafgllclswlqegsa^AAGARGCRLRSQLVP VRALGLGHRSDELVRFRFCSGSC**EE**ARSPHDLSLASLLGAGALRPPPGSRPVSQP CCRPTRYEAVSFMDVNSTWRTVDRLSATACGCLG (SEQ ID NO:14).

CHO cells were transfected with plasmids encoding each of the foregoing forms of Neublastin and cultured in 384-well plates. After several weeks, wells that contained growing cells were transferred to fresh 96-well culture plates. Conditioned medium was analyzed by ELISA to measure the titer of soluble Neublastin. The cumulative absorbance data for each plasmid tested (mean value with one standard deviation as error bars) was detected.

Transfection of CHO cells with plasmids encoding the Arg48,49E double mutant resulted in a significantly increased number of cell lines exhibiting high expression levels of recombinant protein, as compared to cells transfected with plasmids encoding wild type Neublastin (Fig. 13).

The leading cell lines from each transfection were further expanded. Fixed numbers of cells were cultured for three days and total cell count, viability, and titer were determined. The titers of Neublastin expressed from the leading Arg48,49E double mutant cell lines were roughly five-fold greater than those of a leading wild type Neublastin cell line (Fig. 14).

Other Embodiments

While the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

What is claimed is:

1. A polypeptide comprising an amino acid sequence at least 80% identical to amino acids 15-113 of SEQ ID NO:1, wherein the amino acid sequence comprises at least one amino acid substitution, relative to SEQ ID NO:1, selected from the group consisting of:

an amino acid other than arginine at the position corresponding to position 48 of SEQ ID NO:1;

an amino acid other than arginine at the position corresponding to position 49 of SEQ ID NO:1; and

an amino acid other than arginine at the position corresponding to position 51 of SEQ ID NO:1,

wherein the polypeptide, when dimerized, binds to a complex containing GFRalpha3 and RET.

2. The polypeptide of claim 1, wherein the amino acid sequence comprises an amino acid other than arginine at the position corresponding to position 48 of SEQ ID NO:1.

3. The polypeptide of claim 2, wherein the arginine residue at position 48 of SEQ ID NO:1 is substituted with a non-conservative amino acid residue.

4. The polypeptide of claim 2, wherein the arginine residue at position 48 of SEQ ID NO:1 is substituted with glutamic acid.

5. The polypeptide of claim 1, wherein the amino acid sequence comprises an amino acid other than arginine at the position corresponding to position 49 of SEQ ID NO:1.

6. The polypeptide of claim 5, wherein the arginine residue at position 49 of SEQ ID NO:1 is substituted with a non-conservative amino acid residue.

7. The polypeptide of claim 5, wherein the arginine residue at position 49 of SEQ ID NO:1 is substituted with glutamic acid.

8. The polypeptide of claim 1, wherein the amino acid sequence comprises an amino acid other than arginine at the position corresponding to position 51 of SEQ ID NO:1.

9. The polypeptide of claim 8, wherein the arginine residue at position 51 of SEQ ID NO:1 is substituted with a non-conservative amino acid residue.

10. The polypeptide of claim 8, wherein the arginine residue at position 51 of SEQ ID NO:1 is substituted with glutamic acid.

11. The polypeptide of claim 1, wherein the amino acid sequence comprises amino acids other than arginine at the positions corresponding to position 48 and position 49 of SEQ ID NO:1.

12. The polypeptide of claim 11, wherein the arginine residue at position 48 and the arginine reside at position 49 of SEQ ID NO:1 are substituted with non-conservative amino acid residues.

13. The polypeptide of claim 11, wherein the arginine residue at position 48 and the arginine reside at position 49 of SEQ ID NO:1 are each substituted with glutamic acid.

14. The polypeptide of any of claims 1-13, wherein the amino acid sequence is at least 90% identical to amino acids 15-113 of SEQ ID NO:1.

15. The polypeptide of any of claims 1-13, wherein the amino acid sequence is at least 95% identical to amino acids 15-113 of SEQ ID NO:1.

16. The polypeptide of any of claims 1-13, wherein the amino acid sequence is at least 98% identical to amino acids 15-113 of SEQ ID NO:1.

17. A polypeptide comprising amino acids 15-113 of SEQ ID NO:2, amino acids 15-113 of SEQ ID NO:3, amino acids 15-113 of SEQ ID NO:4, amino acids 15-113 of SEQ ID NO:5, amino acids 15-113 of SEQ ID NO:8, or amino acids 15-113 of SEQ ID NO:9.

18. The polypeptide of claim 17, wherein the polypeptide comprises amino acids 10-113 of SEQ ID NO:2, amino acids 10-113 of SEQ ID NO:3, amino acids 10-113 of SEQ ID NO:4, amino acids 10-113 of SEQ ID NO:5, amino acids 10-113 of SEQ ID NO:8, or amino acids 10-113 of SEQ ID NO:9.

19. The polypeptide of claim 17, wherein the polypeptide comprises the amino acid sequence of SEQ ID NO:2, the amino acid sequence of SEQ ID NO:3, the amino acid sequence of SEQ ID NO:4, the amino acid sequence of SEQ ID NO:5, the amino acid sequence of SEQ ID NO:8, or the amino acid sequence of SEQ ID NO:9.

20. A dimer comprising two polypeptides according to any one of claims 1 to 19.

21. A conjugate comprising the polypeptide of any of claims 1 to 19 conjugated to a non-naturally occurring polymer.

22. A fusion protein comprising the polypeptide of any of claims 1 to 19 and a heterologous amino acid sequence.

23. A pharmaceutical composition comprising the polypeptide of any of claims 1 to 19, the dimer of claim 20, the conjugate of claim 21, or the fusion protein of claim 22 and a pharmaceutically acceptable carrier or excipient.

24. A nucleic acid comprising a sequence that encodes the polypeptide of any of claims 1 to 19.

25. An expression vector comprising the nucleic acid of claim 24.

26. A cell comprising the expression vector of claim 25.

27. A method of making a polypeptide, the method comprising:
providing the cell of claim 26, and
culturing the cell under conditions that permit expression of the nucleic acid.

28. A method of treating or preventing a nervous system disorder in a mammal, the method comprising administering to the mammal a therapeutically effective amount of the pharmaceutical composition of claim 23.

29. A method of treating neuropathic pain in a mammal, the method comprising administering to the mammal a therapeutically effective amount of the pharmaceutical composition of claim 23.

30. A method of activating the RET receptor in a mammal, the method comprising administering to the mammal an effective amount of the polypeptide of any of claims 1 to 19, the dimer of claim 20, the conjugate of claim 21, the fusion protein of claim 22, or the pharmaceutical composition of claim 23.

31. A polypeptide comprising an amino acid sequence at least 80% identical to amino acids 15-113 of SEQ ID NO:1, wherein the amino acid sequence comprises at least one amino acid substitution, relative to SEQ ID NO:1, selected from the group consisting of:

an amino acid other than serine at the position corresponding to position 20 of SEQ ID NO:1;

an amino acid other than glutamine at the position corresponding to position 21 of SEQ ID NO:1;

an amino acid other than histidine at the position corresponding to position 32 of SEQ ID NO:1;

an amino acid other than arginine at the position corresponding to position 33 of SEQ ID NO:1;

an amino acid other than arginine at the position corresponding to position 39 of SEQ ID NO:1;

an amino acid other than serine at the position corresponding to position 46 of SEQ ID NO:1;

an amino acid other than arginine at the position corresponding to position 68 of SEQ ID NO:1;

an amino acid other than glycine at the position corresponding to position 72 of SEQ ID NO:1;

an amino acid other than serine at the position corresponding to position 73 of SEQ ID NO:1; and

an amino acid other than valine at the position corresponding to position 94 of SEQ ID NO:1,

wherein the polypeptide, when dimerized, binds to a complex containing GFRalpha3 and RET.

32. The polypeptide of claim 31, wherein the amino acid sequence is at least 90% identical to amino acids 15-113 of SEQ ID NO:1.

33. The polypeptide of claim 31, wherein the amino acid sequence is at least 95% identical to amino acids 15-113 of SEQ ID NO:1.

34. The polypeptide of claim 31, wherein the amino acid sequence is at least 98% identical to amino acids 15-113 of SEQ ID NO:1.

35. A polypeptide comprising an amino acid sequence at least 80% identical to SEQ ID NO:1, wherein the amino acid sequence comprises at least one amino acid substitution, relative to SEQ ID NO:1, selected from the group consisting of:

an amino acid other than arginine at the position corresponding to position 7 of SEQ ID NO:1;

an amino acid other than arginine at the position corresponding to position 9 of SEQ ID NO:1; and

an amino acid other than arginine at the position corresponding to position 14 of SEQ ID NO:1,

wherein the polypeptide, when dimerized, binds to a complex containing GFRalpha3 and RET.

36. The polypeptide of claim 35, wherein the amino acid sequence comprises an amino acid other than arginine at the position corresponding to position 7 of SEQ ID NO:1.

37. The polypeptide of claim 36, wherein the arginine residue at position 7 of SEQ ID NO:1 is substituted with a non-conservative amino acid residue.

38. The polypeptide of claim 36, wherein the arginine residue at position 7 of SEQ ID NO:1 is substituted with glutamic acid.

39. The polypeptide of claim 35, wherein the amino acid sequence comprises an amino acid other than arginine at the position corresponding to position 9 of SEQ ID NO:1.

40. The polypeptide of claim 39, wherein the arginine residue at position 9 of SEQ ID NO:1 is substituted with a non-conservative amino acid residue.

41. The polypeptide of claim 39, wherein the arginine residue at position 9 of SEQ ID NO:1 is substituted with glutamic acid.

42. The polypeptide of claim 35, wherein the amino acid sequence comprises an amino acid other than arginine at the position corresponding to position 14 of SEQ ID NO:1.

43. The polypeptide of claim 42, wherein the arginine residue at position 14 of SEQ ID NO:1 is substituted with a non-conservative amino acid residue.

44. The polypeptide of claim 42, wherein the arginine residue at position 14 of SEQ ID NO:1 is substituted with glutamic acid.

45. The polypeptide of any of claims 35-44, wherein the amino acid sequence is at least 90% identical to SEQ ID NO:1.

46. The polypeptide of any of claims 35-44, wherein the amino acid sequence is at least 95% identical to SEQ ID NO:1.

47. The polypeptide of any of claims 35-44, wherein the amino acid sequence is at least 98% identical to amino acids 15-113 of SEQ ID NO:1.

48. A dimer comprising two polypeptides according to any one of claims 31 to 47.

49. A conjugate comprising the polypeptide of any of claims 31 to 47 conjugated to a non-naturally occurring polymer.

50. A fusion protein comprising the polypeptide of any of claims 31 to 47 and a heterologous amino acid sequence.

51. A pharmaceutical composition comprising the polypeptide of any of claims 31 to 47, the dimer of claim 48, the conjugate of claim 49, or the fusion protein of claim 50 and a pharmaceutically acceptable carrier or excipient.

52. A nucleic acid comprising a sequence that encodes the polypeptide of any of claims 31 to 47.

53. An expression vector comprising the nucleic acid of claim 52.

54. A cell comprising the expression vector of claim 53.

55. A method of making a polypeptide, the method comprising:
providing the cell of claim 54, and

culturing the cell under conditions that permit expression of the nucleic acid.

56. A method of treating or preventing a nervous system disorder in a mammal, the method comprising administering to the mammal a therapeutically effective amount of the pharmaceutical composition of claim 51.

57. A method of treating neuropathic pain in a mammal, the method comprising administering to the mammal a therapeutically effective amount of the pharmaceutical composition of claim 51.

58. A method of activating the RET receptor in a mammal, the method comprising administering to the mammal an effective amount of the polypeptide of any of claims 31 to 47, the dimer of claim 48, the conjugate of claim 49, the fusion protein of claim 50, or the pharmaceutical composition of claim 51.