METHODS FOR ATTENUATING RELEASE OF INFLAMMATORY MEDIATORS AND PEPTIDES USEFUL THEREIN

Cross Reference to Related Application

[0001] The present application claims priority to U.S. Serial No.: 60/833,239 filed on July 26, 2006, which is incorporated in its entirety by reference.

Field of Invention

[0002] The present invention relates to peptides or peptide compositions and methods of their use to attenuate (or inhibit or reduce) the stimulated release of mediators of inflammation from inflammatory cells during inflammation. The present invention also relates to use of these peptides or peptide compositions to modulate an intracellular signaling mechanism regulating the secretion of inflammatory mediators from inflammatory cells.

Background of the Invention

[0003] Inflammatory leukocytes synthesize a number of inflammatory mediators that are isolated intracellularly and stored in cytoplasmic membrane-bound granules. Examples of such mediators include, but are not limited to, myeloperoxidase [MPO] in neutrophils (see, for example, Borregaard N, Cowland JB. Granules of the human neutrophilic polymorphonuclear leukocyte. *Blood* 1997; 89:3503-3521), eosinophil peroxidase [EPO] and major basic protein [MBP] in eosinophils (see, for example, Gleich G J. Mechanisms of eosinophil-associated inflammation. *J Allergy Clin Immunol* 2000; 105:651-663), lysozyme in monocytes/macrophages (see, for example, Hoff T, Spencker T, Emmendoerffer A., Goppelt-Struebe M. Effects of glucocorticoids on the TPA-induced monocytic differentiation. *J Leukoc Biol* 1992; 52:173-182; and Balboa M A, Saez Y, Balsinde J. Calcium-independent phospholipase A2 is required for lysozyme secretion in U937 promonocytes. *J Immunol* 2003; 170:5276-5280), and granzyme in natural killer (NK) cells and cytotoxic lymphocytes (see, for example, Bochan MR, Goebel WS, Brahmi Z. Stably transfected antisense granzyme B and perforin constructs inhibit human granule-mediated lytic ability. *Cell Immunol* 1995;164:234-239; Gong JH., Maki G, Klingemann HG. Characterization of a human cell line (NK-92) with phenotypical and functional characteristics of activated natural killer cells. *Leukemia* 1994;

8:652-658; Maki G, Klingemann HG, Martinson JA, Tam YK. Factors regulating the cytotoxic activity of the human natural killer cell line, NK-92. *J Hematother Stem Cell Res* 2001; 10:369-383; and Takayama H, Trenn G, Sitkovsky MV. A novel cytotoxic T lymphocyte activation assay. *J Immunol Methods* 1987; 104:183-190). Such mediators are released at sites of injury and contribute to inflammation and tissue repair such as in the lung and elsewhere. It is known that leukocytes release these granules via an exocytotic mechanism (see, for example, Burgoyne RD, Morgan A. Secretory granule exocytosis. *Physiol Rev* 2003; 83:581-632; and Logan MR, Odemuyiwa SO, Moqbel R. Understanding exocytosis in immune and inflammatory cells: the molecular basis of mediator secretion. *J Allergy Clin Immunol* 2003; 111: 923-932), but regulatory molecules and specific pathways involved in the exocytotic process have not been fully described.

[0004] Several exogenous stimuli can provoke degranulation of leukocytes via a pathway that involves activation of protein kinase C and subsequent phosphorylation events (see, for example, Burgoyne RD, Morgan A. Secretory granule exocytosis. *Physiol Rev* 2003; 83:581-632; Logan MR, Odemuyiwa SO, Moqbel R. Understanding exocytosis in immune and inflammatory cells: the molecular basis of mediator secretion. *J Allergy Clin Immunol* 2003; 111: 923-932; Smolen JE, Sandborg RR. Ca2+-induced secretion by electropermeabilized human neutrophils: the roles of Ca2+, nucleotides and protein kinase C. *Biochim Biophys Acta* 1990; 1052:133-142; Niessen HW, Verhoeven AJ. Role of protein phosphorylation in the degranulation of electropermeabilized human neutrophils. *Biochim. Biophys. Acta* 1994; 1223:267-273; and Naucler C, Grinstein S, Sundler R., Tapper H. Signaling to localized degranulation in neutrophils adherent to immune complexes. *J Leukoc Biol* 2002; 71:701-710).

[0005] MARCKS protein (where MARCKS as used herein means "Myristoylated Alanine-Rich C Kinase Substrate"), is a ubiquitous phosphorylation target of protein kinase C (PKC), and is highly expressed in leukocytes (see, for example, Aderem AA, Albert KA, Keum MM, Wang JK, Greengard P, Cohn ZA. Stimulus-dependent myristoylation of a major substrate for protein kinase C. *Nature* 1988; 332:362-364; Thelen M, Rosen A, Nairn AC, Aderem A. Regulation by phosphorylation of reversible association of a myristoylated protein kinase C substrate with the plasma membrane. *Nature* 1991; 351:320-322; and Hartwig JH, Thelen M, Rosen A, Janmey PA, Nairn AC, Aderem A. MARCKS is an actin filament crosslinking protein regulated by

protein kinase C and calcium-calmodulin. *Nature* 1992; 356:618-622. MARCKS protein is mechanistically involved in a process of exocytotic secretion of mucin by goblet cells that line respiratory airways (see, for example, Li et al., *J Biol Chem* 2001; 276:40982-40990; and Singer et al., *Nat Med* 2004; 10:193-196). MARCKS is myristoylated via an amide bond at the N-terminal amino acid in the MARCKS protein's amino acid sequence at the alpha-amine position of the glycine which resides at the N-terminus (i.e., at position 1) of amino acid sequence. In airway epithelial cells, the myristoylated N-terminal region of MARCKS appears to be integral to the secretory process. By the N-terminus of the MARCKS protein is meant the MANS peptide which contains Myristoyl-GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO: 1), which are L-amino acids. Additionally, the peptide fragments of the MANS peptide disclosed herein, also preferably are composed of L-amino acids. The mechanism appears to involve binding of MARCKS, a myristoylated protein, to membranes of intracellular granules.

[0006] An N-terminal myristoylated peptide from the N-terminus of MARCKS has been shown to block both mucin secretion and binding of MARCKS to mucin granule membranes in goblet cells (see, for example, Singer et al., *Nat Med* 2004; 10:193-196). This peptide contains 24 amino acids of the MARCKS protein beginning with the N-terminal glycine of the MARCKS protein which is myristoylated via an amide bond and is known as myristoylated alpha-N-terminal sequence (MANS); i.e., Myristoyl-GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO: 1). Also Vergeres *et al.*, *J. Biochem.* 1998, 330; 5-11, discloses that the N-terminal glycine residue of MARCKS proteins is myristoylated via a reaction catalyzed by myristoyl CoA:protein N-myristoyl transferase (NMT).

[0007] In inflammatory diseases, such as asthma, COPD and chronic bronchitis; in genetic diseases such as cystic fibrosis; in allergic conditions (atopy, allergic inflammation); in bronchiectasis; and in a number of acute, infectious respiratory illnesses such as pneumonia, rhinitis, influenza or the common cold, arthritis or auto-immune diseases, inflammatory cells are usually found in or migrate to areas of injury or infection associated with inflammatory disease states, especially in or to respiratory passages or airways of patients suffering from such diseases. These inflammatory cells can contribute greatly to the pathology of diseases via tissue damage done by inflammatory mediators released from these cells. One example of such tissue damage or destruction via this chronic inflammation occurs in cystic fibrosis patients where mediators

released from neutrophils (e.g., myeloperoxidase [MPO]) induce the desquamation of the airway epithelial tissue.

[0008] MARCKS, a protein of approximately 82 kD, has three evolutionarily-conserved regions (Aderem et al., Nature 1988; 332:362-364; Thelen et al., Nature 1991; 351:320-322; Hartwig et al., Nature 1992; 356:618-622; Seykora et al., J Biol Chem 1996; 271:18797-18802): an N-terminus, a phosphorylation site domain (or PSD), and a multiple homology 2 (MH2) domain. Human MARCKS cDNA and protein is known and reported by Harlan *et al.*, *J.Biol. Chem.* 1991, 266:14399 (GenBank Accession No. M68956) and also by Sakai *et al.*, *Genomics* 1992, 14: 175. These sequences are also provided in a WO 00/50062, which is incoporated in its entirety by reference. The N-terminus, an alpha-amino acid sequence comprising 24 amino acid residues with a myristic acid moiety attached via an amide bond to the N-terminal glycine residue is involved in binding of MARCKS to membranes in cells (Seykora et al., J Biol Chem 1996; 271:18797-18802) and possibly to calmodulin (Matsubara et al., J Biol Chem 2003; 278:48898-48902). This 24 amino acid sequence is known as the MANS peptide.

Summary of the Invention

[0009] Involvement of MARCKS protein in release of inflammatory mediators from the granules of infiltrating leukocytes is relevant to inflammation in diseases in all tissues and organs, including lung diseases characterized by airway inflammation, such as asthma, COPD and cystic fibrosis. However, inflammation and mucus secretion in the airways are two separate and independent processes (Li et al., *J Biol Chem* 2001; 276:40982-40990; Singer et al., *Nat Med* 2004; 10:193-196). While mucus production and secretion can be provoked by a number of factors, including mediators released by inflammatory cells, there is no known direct link whereby excess mucus causes inflammation.

[00010] In one aspect of this invention, the MANS peptide can play a role in the reducing the rate and/or amount of release of inflammatory mediators granules or vesicles in inflammatory leukocytes.

[00011] In another aspect, peptides derived from the MARCKS N-terminus, especially from the 24 amino acid N-terminal sequence, i.e., active contiguous peptide fragments derived from

within the N-terminal 1-to-24 amino acid sequence of MARCKS having a glycine at position 1, as well as N-terminal amides of such fragments, such as N-terminal acetic acid amides of such fragments, and/or as well as C-terminal amides of such fragments, such as C-terminal amides of ammonia, can inhibit or reduce the rate and/or amount of release of inflammatory mediators from inflammatory leukocytes. Such inhibition or reduction in release comprises inhibition of a MARCKS-related release of inflammatory mediators from inflammatory leukocytes.

[00012] In another aspect, peptides derived from the MARCKS N-terminus, especially from the 1-to-24 amino acid N-terminal sequence, i.e., active contiguous peptide fragments derived from within the N-terminal 1 to 24 amino acid sequence of MARCKS having a glycine at position 1, as well as N-terminal amides of such fragments such as N-terminal acetic acid amides of such fragments, and as well as C-terminal amides of such fragments such as C-terminal amides of ammonia, can inhibit the rate of release and/or amount of release of inflammatory mediators such as those identified herein in this invention, by inhibiting the process of degranulation in inflammatory leucocytes.

[00013] In another aspect, the MANS peptide and active fragments thereof, and active amides of such fragments as described herein, can compete for membrane binding in inflammatory cells with native MARCKS protein to attenuate (lessen or reduce) MARCKS-related release of mediators of inflammation from granules or vesicles containing such mediators of inflammation in such inflammatory cells.

[00014] Leukocyte cell types and model cell types that secrete specific granule contents in response to phorbol ester induced activation of PKC are useful for in vitro demonstration of efficacy of peptides of this invention and of substituted peptides (e.g., alpha-N-amides, C-terminal amides and esters) of this invention.

[00015] The attenuation of release of membrane-bound inflammatory mediators by compounds and compositions of this invention can be demonstrated using human leukocyte cell lines. For example, neutrophils isolated from human blood can be used to demonstrate attenuation or inhibition of release of myeloperoxidase (MPO). The human promyelocytic cell line HL-60 clone 15 can be used to demonstrate attenuation of release or inhibition of release or secretion of eosinophil peroxidase (EPO) by compounds and compositions of this invention (see, for

example, Fischkoff SA. Graded increase in probability of eosinophilic differentiation of HL-60 promyelocytic leukemia cells induced by culture under alkaline conditions. Leuk Res 1988; 12:679-686; Rosenberg HF, Ackerman S J, Tenen DG. Human eosinophil cationic protein: molecular cloning of a cytotoxin and helminthotoxin with ribonuclease activity. J Exp Med 1989; 170:163-176; Tiffany HL, Li F, Rosenberg HF. Hyperglycosylation of eosinophil ribonucleases in a promyelocytic leukemia cell line and in differentiated peripheral blood progenitor cells. J Leukoc Biol 1995; 58:49-54; and Badewa AP, Hudson CE, Heiman AS. Regulatory effects of eotaxin, eotaxin-2, and eotaxin-3 on eosinophil degranulation and superoxide anion generation. Exp Biol Med 2002; 227:645-651). The monocytic leukemia cell line U937 can be used to demonstrate attenuation of release or inhibition of release or secretion of lysozyme by compounds and compositions of this invention (see, for example, Hoff T, Spencker T, Emmendoerffer A., Goppelt-Struebe M. Effects of glucocorticoids on the TPA-induced monocytic differentiation. J Leukoc Biol 1992; 52:173-182; Balboa M A, Saez Y, Balsinde J. Calcium-independent phospholipase A2 is required for lysozyme secretion in U937 promonocytes. J Immunol 2003; 170:5276-5280; and Sundstrom C, Nilsson K. Establishment and characterization of a human histiocytic lymphoma cell line (U-937). Int J Cancer 1976; 17:565-577). The lymphocyte natural killer cell line NK-92 can be used to demonstrate attenuation or inhibition of release of granzyme by compounds and compositions of this invention (see, for example, Gong JH., Maki G, Klingemann HG. Characterization of a human cell line (NK-92) with phenotypical and functional characteristics of activated natural killer cells. Leukemia 1994; 8:652-658; Maki G, Klingemann HG, Martinson JA, Tam YK. Factors regulating the cytotoxic activity of the human natural killer cell line, NK-92. J Hematother Stem Cell Res 2001; 10:369-383; and Takayama H, Trenn G, Sitkovsky MV. A novel cytotoxic T lymphocyte activation assay. J Immunol Methods 1987; 104:183-190). In an in vitro method to inhibit or attenuate the release of a mediator of inflammation such as those described herein, each of the cell types is preincubated with a peptide compound or peptide composition of this invention over a range of concentrations followed by incubation of these cells by a stimulator of release of inflammatory mediators, such as phorbol ester. The percent of inhibition of release of a mediator of inflammation is determined as compared to the release of the mediator in the absence of the peptide compound or peptide composition, such as in a specrophotometric readout of a concentration of the mediator released.

[00016] To demonstrate the importance of the relative amino acid sequence positioning in the peptides of the invention, the relative ability to inhibit or reduce the amount of inflammatory mediator released by a peptide which is identical to the 24 amino acid sequence of the MARCKS protein N-terminus region (i.e., the MANS- myristoylated alpha-N-terminal sequence peptide) was compared to the ability to inhibit or reduce the amount of inflammatory mediator released by a peptide containing the same 24 amino acid residues present in MANS but which are sequenced in a random order (i.e., an RNS peptide, otherwise referred to as a "Random N-terminal sequence peptide") with respect to the sequence order in MANS. In each of the cell types examined, the MANS peptide, but not the RNS peptide, attenuated release of inflammatory mediators in a concentration-dependent manner over a time course of 0.5-3.0 hrs. These results suggest that the relative amino acid sequence positioning in the peptides of the invention which are in the order found in the MARCKS protein, specifically its N-terminal region, and more specifically its 24 amino acid residue N-terminal region are involved in at least one intracellular pathway dealing with the inhibition of leukocyte degranulation.

[00017] The invention relates to a new use for the 24 amino acid peptide sequence, and to the alpha-N-terminal acetylated peptide sequence, the myristoylated polypeptide, also known as the MANS peptide, and to active fragments thereof, which active fragments can be selected from the group of peptides having from 4 to 23 contiguous amino acid residues of the MANS peptide amino acid sequence, and which fragments may be N-terminal-myristoylated if they do not begin with the N-terminal glycine at position 1 in SEQ ID NO: 1, or which may be N-terminal-acylated with C2 to C12 acyl groups, including N-terminal-acetylated, and/or C-terminal amidated with an NH2 group.

[00018] The invention also relates to a new method for blocking MARCKS-related cellular secretory processes, especially those that involve the MARCKS-related release of inflammatory mediators from inflammatory cells, whose stimulatory pathways involve the protein kinase C (PKC) substrate MARCKS protein and release of contents from intracellular vesicles or granules.

[00019] The present invention is directed to a method of inhibiting the exocytotic release of at least one inflammatory mediator from at least one inflammatory cell comprising contacting the at

least one inflammatory cell, which cell comprises at least one inflammatory mediator contained within a vesicle inside the cell, with at least one peptide selected from the group consisting of a MANS peptide and an active fragment thereof as described herein in an effective amount to reduce the release of the inflammatory mediator from the inflammatory cell as compared to the release of the inflammatory mediator from the same type of inflammatory cell that would occur in the absence of the at least one peptide.

[00020] The present invention is further directed to a method of inhibiting the release of at least one inflammatory mediator from at least one inflammatory cell in a tissue or fluid of a subject comprising the administration to the subject's tissue and/or fluid, which comprises at least one inflammatory cell comprising at least one inflammatory mediator contained within a vesicle inside the cell, a therapeutically effective amount of a pharmaceutical composition comprising at least one peptide selected from the group consisting of a MANS peptide and an active fragment thereof in a therapeutically effective amount to reduce the release of the inflammatory mediator from at least one inflammatory cell as compared to release of the inflammatory mediator from at least one of the same type of inflammatory cell that would occur in the absence of the at least one peptide. More specifically, inhibiting the release of an inflammatory mediator comprises blocking or reducing the release of an inflammatory mediator from the inflammatory cell.

[00021] More particularly, the present invention includes a method of reducing inflammation in a subject comprising the administration of a therapeutically effective amount of a pharmaceutical composition comprising a MANS peptide (i.e., N-myristoyl-GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO: 1)) or an active fragment thereof. The active fragment is at least four and preferably at least six amino acids in length. As used herein, an "active fragment" of a MARCKS protein is one that affects (inhibits or reduces) MARCKS protein-mediated release, such as MARCKS protein-mediated release of an inflammatory mediator. An active fragment can be selected from the group consisting of GAQFSKTAAKGEAAAERPGEAAV (SEQ ID NO: 2); GAQFSKTAAKGEAAAERPGEAA (SEQ ID NO: 4); GAQFSKTAAKGEAAAERPGEA (SEQ ID NO: 7); GAQFSKTAAKGEAAAERPGE (SEQ ID NO: 11); GAQFSKTAAKGEAAAERPG (SEQ ID NO: 16); GAQFSKTAAKGEAAAERP (SEQ ID NO: 22); GAQFSKTAAKGEAAAER (SEQ ID NO: 29); GAQFSKTAAKGEAAAE (SEQ ID NO: 37); GAQFSKTAAKGEAAA (SEQ ID

NO: 46); GAQFSKTAAKGEAA (SEQ ID NO: 56); GAQFSKTAAKGEA (SEQ ID NO: 67); GAQFSKTAAKGE (SEQ ID NO: 79); GAQFSKTAAKG (SEQ ID NO: 92); GAQFSKTAAK (SEQ ID NO: 106); GAQFSKTAA (SEQ ID NO: 121); GAQFSKTA (SEQ ID NO: 137); GAQFSKT (SEQ ID NO: 154); GAQFSK (SEQ ID NO: 172); GAQFS (SEQ ID NO: 191) and GAQF (SEQ ID NO: 211). These peptides, instead of containing a myristoyl moiety at the N-terminal amino acid, either contain no chemical moiety or a non-myristoyl chemical moiety at the N-terminal amino acid and/or a chemical moiety at the C-terminal amino acid, such as an N-terminal acetyl group and/or a C-terminal amide group as described herein. The presence of the hydrophobic N-terminal myristoyl moiety in the MANS peptides and N-terminal myristoylated fragments thereof can enhance their compatibility with and presumably their permeability to plasma membranes, and potentially enable the peptides to be taken up by cells. The hydrophobic insertion of a myristoyl group into a membrane lipid bilayer can provide a partition coefficient or apparent association constant with lipids of up to 10^4 M^{-1} or a unitary Gibbs free binding energy of about 8 kcal/mol (see, for example, Peitzsch, R.M., and McLaughlin, S. 1993, Binding of acylated peptides and fatty acids to phospholipid vesicles: pertinence to myristoylated proteins. Biochemistry. 32: 10436-10443) which is sufficient, at least in part, to permit a partitioning of the MANS peptide and of myristoylated MANS peptide fragments into the plasma membrane of a cell while additional functional groups and their interactions within the MANS peptide (which is myristoylated) and within myristoylated MANS peptide fragments can potentiate their relative membrane permeabilities. The fragments can each exhibit partition coefficients and membrane affinities that are representative of their respective structure. The fragments can be prepared by methods of peptide synthesis known in the art, such as by solid phase peptide synthesis (see, for example, the methods described in Chan, Weng C. and White, Peter D.Eds., Fmoc Solid Phase Peptide Synthesis: A Practical Approach, Oxford University Press, New York, New York (2000); and Lloyd-Williams, P. et al. Chemical Approaches to the Synthesis of Peptides and Proteins (1997)) and purified by methods known in the art, such as by high pressure liquid chromatography. Molecular weight of each peptide can be confirmed by mass spectroscopy with each showing a peak with an appropriate molecular mass. Efficacy of the individual peptides and of combinations of individual peptides (for example, combinations of 2 of the peptides, combinations of 3 of the peptides, combinations of 4 of the peptides) in the methods of this disclosure can be readily determined without undue experimentation using the procedures

described in the examples disclosed herein. A preferred combination will comprise two of the peptides; a preferred molar ratio of the peptides can be from 50:50 (i.e., 1:1) to 99.99 to 0.01, which ratio can be readily determined using the procedures described in the examples disclosed herein.

[00022] Preferably the MANS peptide or active fragment thereof is contained in a pharmaceutical composition which is useful to block inflammation. The present invention also includes methods for inhibiting a cellular secretory process in a subject comprising the administration of a therapeutically effective amount of a compound comprising a MANS peptide or an active fragment thereof, that inhibits an inflammatory mediator in a subject. The administration is generally selected from the group consisting of topical administration, parenteral administration, rectal administration, pulmonary administration, inhalation and nasal or oral administration, wherein pulmonary administration generally includes either an aerosol, a dry powder inhaler, a metered dose inhaler, or a nebulizer.

[00023] Administration of a composition comprising a degranulation-inhibiting amount of the MANS peptide or a degranulation-inhibiting amount of an active fragment thereof, such as a pharmaceutical composition of the MANS peptide or an active fragment thereof, for human or animal use provides the MANS peptide or active fragment thereof at least to the site in or on a tissue or to a fluid-containing layer in contact with the surface of a tissue where an inflammatory granulocytic cell resides or into which an inflammatory granulocytic cell will invade, thus enabling the MANS peptide or an active fragment thereof to contact the inflammatory granulocytic cell. In one aspect, administration of such a composition can be made at the first onset or first detection of inflammation or first perception of inflammation by the human or animal or at the first perceptible change in the level of inflammation in a human or animal to reduce the amount of inflammation that would otherwise occur in the absence of the MANS peptide or active fragment thereof. In another aspect, administration can be made during an ongoing inflammation of a tissue in the human or animal to reduce the amount of additional inflammation that would otherwise occur in the absence of the MANS peptide or active fragment thereof. While the amount and frequency of dose can be determined by clinical evaluation and be a function of the disease or source of inflammation and the extent of tissue involved and the age and size of the patient, it is anticipated that dosing of a pharmaceutical composition can be

repeated after 3 to 8 hours, preferably after 6 to 8 hours after the first administration of the pharmaceutical composition.

[00024] The present invention also includes methods of reducing inflammation in a subject comprising the administration of a therapeutically effective amount of a compound that inhibits the MARCKS-related release of inflammatory mediators, whereby the release of at least one inflammatory mediator in the subject is reduced compared to that which would occur in the absence of said treatment. As used herein "reducing" generally means a lessening of the effects of inflammation. Preferably, release of inflammatory mediators are inhibited or blocked by the methods disclosed.

[00025] Another embodiment of the present invention includes methods of reducing inflammation in a subject comprising administering a therapeutically effective amount of a compound that inhibits the MARCKS-related release of inflammatory mediators, whereby the inflammation in the subject is reduced compared to that which would occur in the absence of said treatment. The present invention also discloses methods of reducing or inhibiting inflammation in a subject comprising the administration of a therapeutically effective amount of a MANS peptide or an active fragment thereof effective to inhibit an inflammatory mediator at the inflammation site. The term "inhibiting" means a reduction in the amount of inflammatory mediator secretion. The term "completely inhibiting" means a reduction to zero in the amount of inflammatory mediator secretion. Again, as stated above, the active fragment is at least four and preferably at least six amino acids in length. The term "exocytotic process" means exocytosis, i.e., a process of cellular secretion or excretion in which substances contained in a vesicle, which vesicle resides inside a cell, are discharged from the cell by fusion of the vesicular membrane of the vesicle with the outer cell membrane. "Degranulation" means the release of cellular granule contents. The term "degranulation-inhibiting" means a reduction in the release of the inflammatory mediators contained within the granules of the inflammatory cell. Thus, a degranulation-inhibiting amount of the MANS peptide and/or an active fragment thereof is the amount of these peptides that is sufficient to reduce the release of the inflammatory mediators contained in the granules as compared to release in the absence of the same peptide.

[00026] In the reference peptide, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO: 1), at the N-terminal position of the reference peptide, G is at position 1; adjacent to G at position 1 is A at position 2; adjacent to A at position 2 is Q at position 3; adjacent to Q at position 3 is F at position 4; adjacent to F at position 4 is S at position 5; adjacent to S at position 5 is K at position 6; adjacent to K at position 6 is T at position 7; adjacent to T at position 7 is A at position 8; adjacent to A at position 8 is A at position 9; adjacent to A at position 9 is K at position 10; adjacent to K at position 10 is G at position 11; adjacent to G at position 11 is E at position 12; adjacent to E at position 12 is A at position 13; adjacent to A at position 13 is A at position 14; adjacent to A at position 14 is A at position 15; adjacent to A at position 15 is E at position 16; adjacent to E at position 16 is R at position 17; adjacent to R at position 17 is P at position 18; adjacent to P at position 18 is G at position 19; adjacent to G at position 19 is E at position 20; adjacent to E at position 20 is A at position 21; adjacent to A at position 21 is A at position 22; adjacent to A at position 22 is V at position 23; and adjacent to V at position 23 is A at position 24, wherein position 24 is the C-terminal position of the reference peptide.

[00027] A "variant" of a reference peptide or a variant of a 4 to 23 amino acid segment of a reference peptide is a peptide which has an amino acid sequence which differs from the amino acid sequence of the reference peptide or from the amino acid sequence of the segment of the reference peptide, respectively, in at least one amino acid position in the reference peptide or reference peptide segment amino acid sequence, respectively, but which retains mucin- or mucus-inhibiting activity, which activity is typically between 0.1 to 10 times the activity of the reference peptide or segment, respectively, preferably between 0.2 to 6 times the activity of the reference peptide or segment, respectively, more preferably between 0.3 to 5 times the activity of the reference peptide or segment, respectively. A "variant" of a reference amino acid sequence or a variant of a 4 to 23 amino acid segment of a reference amino acid sequence is an amino acid sequence that differs by at least one amino acid from the reference amino acid sequence or from the segment of the reference amino acid sequence, respectively, but has an amino acid sequence of a peptide that retains mucin- or mucus-inhibiting activity of the peptide or segment, respectively, encoded by the reference amino acid sequence, which activity is typically between 0.1 to 10 times the activity of the peptide or segment, respectively, of the reference sequence, preferably between 0.2 to 6 times the activity of the peptide or segment of the reference sequence, respectively, more preferably between 0.3 to 5 times the activity of the peptide or

segment of the reference sequence, respectively. A substitution variant peptide or a substitution variant amino acid sequence may vary (i.e., differ) from a reference peptide or reference amino acid sequence by one or more amino acid substitutions in the reference amino acid sequence; a deletion variant peptide or a deletion variant amino acid sequence may vary (i.e., differ) from a reference peptide or reference amino acid sequence by one or more amino acid deletions in the reference amino acid sequence; and an addition variant peptide or an addition variant amino acid sequence may vary (i.e., differ) from a reference peptide sequence or reference amino acid sequence by one or more amino acid additions in the reference sequence. A variant peptide or variant amino acid sequence can result from a substitution of one or more amino acids (e.g., substitution of at least 1, 2, 3, 4, 5, 6, 7, or 8 amino acids) in a reference sequence, or can result from a deletion of one or more amino acids (e.g., deletion of at least 1, 2, 3, 4, 5, 6, 7, or 8 amino acids) in a reference sequence, or can result from an addition of one or more amino acids (e.g., addition of at least 1, 2, 3, 4, 5, 6, 7, or 8 amino acids) in a reference sequence, or a combination thereof in any order. A substitution variant 4 to 23 amino acid peptide segment or a substitution variant 4 to 23 amino acid segment sequence may vary (i.e., differ) from a reference 4 to 23 amino acid peptide segment or reference 4 to 23 amino acid segment sequence by one or more amino acid substitutions in the reference amino acid segment sequence; a deletion variant 4 to 23 amino acid peptide segment or a 4 to 22 amino acid deletion variant amino acid segment sequence may vary (i.e., differ) from a 5 to 23 reference peptide segment or a 5 to 23 amino acid reference amino acid segment sequence by one or more amino acid deletions in the reference amino acid segment sequence; and an 4 to 23 amino acid addition variant peptide or a 4 to 23 amino acid addition variant amino acid sequence may vary (i.e., differ) from a 4 to 22 amino acid reference peptide sequence or a 4 to 22 amino acid reference amino acid sequence by one or more amino acid additions in the reference sequence. A 4 to 23 amino acid variant peptide or a 4 to 23 amino acid variant amino acid sequence can result from a substitution of one or more amino acids (e.g., substitution of at least 1, 2, 3, 4, 5, 6, 7, 8 amino acids) in a 4 to 23 amino acid segment of a reference amino acid sequence, or can result from a deletion of one or more amino acids (e.g., deletion of at least 1, 2, 3, 4, 5, 6, 7, or 8 amino acids) in a respectively larger reference amino acid sequence, or can result from an addition of one or more amino acids (e.g., addition of at least 1, 2, 3, 4, 5, 6, 7, or 8 amino acids) in a respectively smaller reference amino acid sequence, or from a combination thereof. Preferably, a variant peptide or amino acid

sequence varies from a reference peptide or from a segment of a reference peptide or from a reference amino acid sequence or from a segment of a reference amino acid sequence, respectively, by less than 10 amino acid substitutions, deletions, and/or additions; more preferably less than 8 amino acid substitutions, deletions, and/or additions; even more preferably less than 6 amino acid substitutions, deletions, and/or additions; and even more preferably less than 5 amino acid substitutions, deletions, and/or additions; and yet even more preferably less than 4 amino acid substitutions, deletions, and/or additions. Most preferably the variant amino acid sequence differs from a reference peptide or segment amino acid sequence by one or two or three amino acids.

[00028] "Sequence identity" means, with respect to amino acid sequences of two peptides, the number of positions with identical amino acids divided by the number of amino acids in the shorter of the two sequences.

[00029] "Substantially identical" means, with respect to comparison of the amino acid sequences of two peptides or comparison of the amino acid sequences of two peptide segments (e.g. segments of a reference peptide amino acid sequence), that the amino acid sequence of the peptides or segments of peptides have at least 75% sequence identity, preferably at least 80% sequence identity, more preferably at least 90% sequence identity, and most preferably at least 95% sequence identity.

[00030] The term "peptide" as used herein includes the peptide as well as pharmaceutically acceptable salts of the peptide.

[00031] An "isolated" peptide, as used herein, means a naturally-occurring peptide that has been separated or substantially separated from the cellular components (e.g., nucleic acids and other peptides) that naturally accompany it by purification, recombinant synthesis, or chemical synthesis, and also encompasses non-naturally-occurring recombinantly or chemically synthesized peptides that have been purified or substantially purified from cellular components, biological materials, chemical precursors, or other chemicals.

[00032] The following three-letter and one-letter amino acid abbreviations are used throughout the text: Alanine: (Ala) A; Arginine: (Arg) R; Asparagine: (Asn) N; Aspartic acid: (Asp) D;

Cysteine: (Cys) C; Glutamine: (Gln) Q; Glutamic acid: (Glu) E; Glycine: (Gly) G; Histidine: (His) H; Isoleucine: (Ile) I; Leucine: (Leu) L; Lysine: (Lys) K; Methionine: (Met) M; Phenylalanine: (Phe) F; Proline: (Pro) P; Serine: (Ser) S; Threonine: (Thr) T; Tryptophan: (Trp) W; Tyrosine: (Tyr) Y; Valine: (Val) V. Additional three letter symbols of amino acids useful herein include, in brackets, (Hyp) for hydroxyproline, (Nle) for norleucine, (Orn) for ornithine, (Pyr) for pyroglutamic acid and (Sar) for sarcosine. By convention, the amino (or N-terminal) end of a peptide appears at the left end of a written amino acid sequence of the peptide and the carboxy (or C-terminal) end appears at the right end of a written amino acid sequence. The amino acid sequence of a peptide can be written in single letter symbols to represent the amino acids which are covalently linked by peptide amide bonds in the peptide.

[00033] Active fragments of the MANS peptide can be useful in the prevention or reduction in amount of inflammation in a tissue in an animal caused by inflammatory mediators. Active fragments of the MANS peptide also can be useful in the prevention or reduction in amount of tissue damage in an animal produced or caused by inflammatory mediators. An active fragment of the MANS peptide is composed of at least 4 contiguous amino acids and no more than 23 contiguous amino acids of the MANS peptide (SEQ ID NO: 1). The term "active fragment" within the context of the present invention is intended to encompass those fragments of the MANS peptides that are capable of preventing or reducing the release of inflammatory mediators from an inflammatory cell. The reduction of release of inflammatory mediators by the active fragments can range from at least 5% to at least 99% reduction as compared to a reference peptide, such as MANS peptide.

[00034] Table 1 contains a list of amino acid sequences in single letter abbreviation format together with a respectively corresponding peptide number and SEQ ID NO. The reference peptide amino acid sequence (MANS peptide) is listed as peptide 1. Amino acid sequences of peptides of the invention having an amino acid sequence of from 4 to 23 contiguous amino acids of the reference amino acid sequence are listed as peptides 2 to 231, together with the amino acid sequence of a random N-terminal sequence (RNS) comprising amino acids of the MANS peptide as peptide 232. Amino acid sequences of representative variants of amino acid sequences of peptides of the invention as described herein and are also listed as peptides 233 to 245 and 247 to 251. This variant peptides listed are not intended to be a limiting group of peptides, but are

presented only to serve as representative examples of variant peptides of the invention. Also presented is a representative reverse amino acid sequence (peptide 246) and a representative random amino acid sequence of peptide (peptide 232) of the invention. The reverse and random amino acid sequences in the table are not intended to be representative of the invention.

[00035] Table 1 contains a listing of peptides of this invention and their respective amino acid sequences and corresponding SEQ ID NOS.

Table 1 Peptides and Amino Acid Sequences

Peptide No.	Sequence	Sequence ID No.
peptide 1	GAQFSKTAAKGEAAAERPGEAAVA	SEQ ID NO. 1
peptide 2	GAQFSKTAAKGEAAAERPGEAAV	SEQ ID NO. 2
peptide 3	AQFSKTAAKGEAAAERPGEAAVA	SEQ ID NO. 3
peptide 4	GAQFSKTAAKGEAAAERPGEAA	SEQ ID NO. 4
peptide 5	AQFSKTAAKGEAAAERPGEAAV	SEQ ID NO. 5
peptide 6	QFSKTAAKGEAAAERPGEAAVA	SEQ ID NO. 6
peptide 7	GAQFSKTAAKGEAAAERPGEA	SEQ ID NO. 7
peptide 8	AQFSKTAAKGEAAAERPGEAA	SEQ ID NO. 8
peptide 9	QFSKTAAKGEAAAERPGEAAV	SEQ ID NO. 9
peptide 10	FSKTAAKGEAAAERPGEAAVA	SEQ ID NO. 10
peptide 11	GAQFSKTAAKGEAAAERPGE	SEQ ID NO. 11
peptide 12	AQFSKTAAKGEAAAERPGEA	SEQ ID NO. 12
peptide 13	QFSKTAAKGEAAAERPGEAA	SEQ ID NO. 13
peptide 14	FSKTAAKGEAAAERPGEAAV	SEQ ID NO. 14
peptide 15	SKTAAKGEAAAERPGEAAVA	SEQ ID NO. 15
peptide 16	GAQFSKTAAKGEAAAERPG	SEQ ID NO. 16
peptide 17	AQFSKTAAKGEAAAERPGE	SEQ ID NO. 17
peptide 18	QFSKTAAKGEAAAERPGEA	SEQ ID NO. 18
peptide 19	FSKTAAKGEAAAERPGEAA	SEQ ID NO. 19
peptide 20	SKTAAKGEAAAERPGEAAV	SEQ ID NO. 20
peptide 21	KTAAKGEAAAERPGEAAVA	SEQ ID NO. 21
peptide 22	GAQFSKTAAKGEAAAERP	SEQ ID NO. 22
peptide 23	AQFSKTAAKGEAAAERPG	SEQ ID NO. 23
peptide 24	QFSKTAAKGEAAAERPGE	SEQ ID NO. 24
peptide 25	FSKTAAKGEAAAERPGEA	SEQ ID NO. 25
peptide 26	SKTAAKGEAAAERPGEAA	SEQ ID NO. 26
peptide 27	KTAAKGEAAAERPGEAAV	SEQ ID NO. 27
peptide 28	TAAKGEAAAERPGEAAVA	SEQ ID NO. 28
peptide 29	GAQFSKTAAKGEAAAER	SEQ ID NO. 29
peptide 30	AQFSKTAAKGEAAAERP	SEQ ID NO. 30
peptide 31	QFSKTAAKGEAAAERPG	SEQ ID NO. 31
peptide 32	FSKTAAKGEAAAERPGE	SEQ ID NO. 32
peptide 33	SKTAAKGEAAAERPGEA	SEQ ID NO. 33
peptide 34	KTAAKGEAAAERPGEAA	SEQ ID NO. 34
peptide 35	TAAKGEAAAERPGEAAV	SEQ ID NO. 35
peptide 36	AAKGEAAAERPGEAAVA	SEQ ID NO. 36
peptide 37	GAQFSKTAAKGEAAAE	SEQ ID NO. 37

peptide 38	AQFSKTAAKGEAAAER	SEQ ID NO. 38
peptide 39	QFSKTAAKGEAAAERP	SEQ ID NO. 39
peptide 40	FSKTAAKGEAAAERPG	SEQ ID NO. 40
peptide 41	SKTAAKGEAAAERPGE	SEQ ID NO. 41
peptide 42	KTAAKGEAAAERPGEA	SEQ ID NO. 42
peptide 43	TAAKGEAAAERPGEAA	SEQ ID NO. 43
peptide 44	AAKGEAAAERPGEAAV	SEQ ID NO. 44
peptide 45	AKGEAAAERPGEAAVA	SEQ ID NO. 45
peptide 46	GAQFSKTAAKGEAAA	SEQ ID NO. 46
peptide 47	AQFSKTAAKGEAAAE	SEQ ID NO. 47
peptide 48	QFSKTAAKGEAAAER	SEQ ID NO. 48
peptide 49	FSKTAAKGEAAAERP	SEQ ID NO. 49
peptide 50	SKTAAKGEAAAERPG	SEQ ID NO. 50
peptide 51	KTAAKGEAAAERPGE	SEQ ID NO. 51
peptide 52	TAAKGEAAAERPGEA	SEQ ID NO. 52
peptide 53	AAKGEAAAERPGEAA	SEQ ID NO. 53
peptide 54	AKGEAAAERPGEAAV	SEQ ID NO. 54
peptide 55	KGEAAAERPGEAAVA	SEQ ID NO. 55
peptide 56	GAQFSKTAAKGEAA	SEQ ID NO. 56
peptide 57	AQFSKTAAKGEAAA	SEQ ID NO. 57
peptide 58	QFSKTAAKGEAAAE	SEQ ID NO. 58
peptide 59	FSKTAAKGEAAAER	SEQ ID NO. 59
peptide 60	SKTAAKGEAAAERP	SEQ ID NO. 60
peptide 61	KTAAKGEAAAERPG	SEQ ID NO. 61
peptide 62	TAAKGEAAAERPGE	SEQ ID NO. 62
peptide 63	AAKGEAAAERPGEA	SEQ ID NO. 63
peptide 64	AKGEAAAERPGEAA	SEQ ID NO. 64
peptide 65	KGEAAAERPGEAAV	SEQ ID NO. 65
peptide 66	GEAAAERPGEAAVA	SEQ ID NO. 66
peptide 67	GAQFSKTAAKGEA	SEQ ID NO. 67
peptide 68	AQFSKTAAKGEAA	SEQ ID NO. 68
peptide 69	QFSKTAAKGEAAA	SEQ ID NO. 69
peptide 70	FSKTAAKGEAAAE	SEQ ID NO. 70
peptide 71	SKTAAKGEAAAER	SEQ ID NO. 71
peptide 72	KTAAKGEAAAERP	SEQ ID NO. 72
peptide 73	TAAKGEAAAERPG	SEQ ID NO. 73
peptide 74	AAKGEAAAERPGE	SEQ ID NO. 74
peptide 75	AKGEAAAERPGEA	SEQ ID NO. 75
peptide 76	KGEAAAERPGEAA	SEQ ID NO. 76
peptide 77	GEAAAERPGEAAV	SEQ ID NO. 77
peptide 78	EAAAERPGEAAVA	SEQ ID NO. 78
peptide 79	GAQFSKTAAKGE	SEQ ID NO. 79
peptide 80	AQFSKTAAKGEA	SEQ ID NO. 80
peptide 81	QFSKTAAKGEAA	SEQ ID NO. 81
peptide 82	FSKTAAKGEAAA	SEQ ID NO. 82
peptide 83	SKTAAKGEAAAE	SEQ ID NO. 83
peptide 84	KTAAKGEAAAER	SEQ ID NO. 84
peptide 85	TAAKGEAAAERP	SEQ ID NO. 85
peptide 86	AAKGEAAAERPG	SEQ ID NO. 86
peptide 87	AKGEAAAERPGE	SEQ ID NO. 87
peptide 88	KGEAAAERPGEA	SEQ ID NO. 88
peptide 89	GEAAAERPGEAA	SEQ ID NO. 89
peptide 90	EAAAERPGEAAV	SEQ ID NO. 90

peptide 91	AAAERPGEAAVA	SEQ ID NO. 91
peptide 92	GAQFSKTAAKG	SEQ ID NO. 92
peptide 93	AQFSKTAAKGE	SEQ ID NO. 93
peptide 94	QFSKTAAKGEA	SEQ ID NO. 94
peptide 95	FSKTAAKGEAA	SEQ ID NO. 95
peptide 96	SKTAAKGEAAA	SEQ ID NO. 96
peptide 97	KTAAKGEAAAE	SEQ ID NO. 97
peptide 98	TAAKGEAAAER	SEQ ID NO. 98
peptide 99	AAKGEAAAERP	SEQ ID NO. 99
peptide 100	AKGEAAAERPG	SEQ ID NO. 100
peptide 101	KGEAAAERPGE	SEQ ID NO. 101
peptide 102	GEAAAERPGEA	SEQ ID NO. 102
peptide 103	EAAAERPGEAA	SEQ ID NO. 103
peptide 104	AAAERPGEAAV	SEQ ID NO. 104
peptide 105	AAERPGEAAVA	SEQ ID NO. 105
peptide 106	GAQFSKTAAK	SEQ ID NO. 106
peptide 107	AQFSKTAAKG	SEQ ID NO. 107
peptide 108	QFSKTAAKGE	SEQ ID NO. 108
peptide 109	FSKTAAKGEA	SEQ ID NO. 109
peptide 110	SKTAAKGEAA	SEQ ID NO. 110
peptide 111	KTAAKGEAAA	SEQ ID NO. 111
peptide 112	TAAKGEAAAE	SEQ ID NO. 112
peptide 113	AAKGEAAAER	SEQ ID NO. 113
peptide 114	AKGEAAAERP	SEQ ID NO. 114
peptide 115	KGEAAAERPG	SEQ ID NO. 115
peptide 116	GEAAAERPGE	SEQ ID NO. 116
peptide 117	EAAAERPGEA	SEQ ID NO. 117
peptide 118	AAAERPGEAA	SEQ ID NO. 118
peptide 119	AAERPGEAAV	SEQ ID NO. 119
peptide 120	AERPGEAAVA	SEQ ID NO. 120
peptide 121	GAQFSKTAA	SEQ ID NO. 121
peptide 122	AQFSKTAAK	SEQ ID NO. 122
peptide 123	QFSKTAAKG	SEQ ID NO. 123
peptide 124	FSKTAAKGE	SEQ ID NO. 124
peptide 125	SKTAAKGEA	SEQ ID NO. 125
peptide 126	KTAAKGEAA	SEQ ID NO. 126
peptide 127	TAAKGEAAA	SEQ ID NO. 127
peptide 128	AAKGEAAAE	SEQ ID NO. 128
peptide 129	AKGEAAAER	SEQ ID NO. 129
peptide 130	KGEAAAERP	SEQ ID NO. 130
peptide 131	GEAAAERPG	SEQ ID NO. 131
peptide 132	EAAAERPGE	SEQ ID NO. 132
peptide 133	AAAERPGEA	SEQ ID NO. 133
peptide 134	AAERPGEAA	SEQ ID NO. 134
peptide 135	AERPGEAAV	SEQ ID NO. 135
peptide 136	ERPGEAAVA	SEQ ID NO. 136
peptide 137	GAQFSKTA	SEQ ID NO. 137
peptide 138	AQFSKTAA	SEQ ID NO. 138
peptide 139	QFSKTAAK	SEQ ID NO. 139
peptide 140	FSKTAAKG	SEQ ID NO. 140
peptide 141	SKTAAKGE	SEQ ID NO. 141
peptide 142	KTAAKGEA	SEQ ID NO. 142
peptide 143	TAAKGEAA	SEQ ID NO. 143

peptide 144	AAKGEAAA	SEQ ID NO. 144
peptide 145	AKGEAAAE	SEQ ID NO. 145
peptide 146	KGEAAAER	SEQ ID NO. 146
peptide 147	GEAAAERP	SEQ ID NO. 147
peptide 148	EAAAERPG	SEQ ID NO. 148
peptide 149	AAAERPGE	SEQ ID NO. 149
peptide 150	AAERPGEA	SEQ ID NO. 150
peptide 151	AERPGEAA	SEQ ID NO. 151
peptide 152	ERPGEAAV	SEQ ID NO. 152
peptide 153	RPGEAAVA	SEQ ID NO. 153
peptide 154	GAQFSKT	SEQ ID NO. 154
peptide 155	AQFSKTA	SEQ ID NO. 155
peptide 156	QFSKTAA	SEQ ID NO. 156
peptide 157	FSKTAAK	SEQ ID NO. 157
peptide 158	SKTAAKG	SEQ ID NO. 158
peptide 159	KTAAKGE	SEQ ID NO. 159
peptide 160	TAAKGEA	SEQ ID NO. 160
peptide 161	AAKGEAA	SEQ ID NO. 161
peptide 162	AKGEAAA	SEQ ID NO. 162
peptide 163	KGEAAAE	SEQ ID NO. 163
peptide 164	GEAAAER	SEQ ID NO. 164
peptide 165	EAAAERP	SEQ ID NO. 165
peptide 166	AAAERPG	SEQ ID NO. 166
peptide 167	AAERPGE	SEQ ID NO. 167
peptide 168	AERPGEA	SEQ ID NO. 168
peptide 169	ERPGEAA	SEQ ID NO. 169
peptide 170	RPGEAAV	SEQ ID NO. 170
peptide 171	PGEAAVA	SEQ ID NO. 171
peptide 172	GAQFSK	SEQ ID NO. 172
peptide 173	AQFSKT	SEQ ID NO. 173
peptide 174	QFSKTA	SEQ ID NO. 174
peptide 175	FSKTAA	SEQ ID NO. 175
peptide 176	SKTAAK	SEQ ID NO. 176
peptide 177	KTAAKG	SEQ ID NO. 177
peptide 178	TAAKGE	SEQ ID NO. 178
peptide 179	AAKGEA	SEQ ID NO. 179
peptide 180	AKGEAA	SEQ ID NO. 180
peptide 181	KGEAAA	SEQ ID NO. 181
peptide 182	GEAAAE	SEQ ID NO. 182
peptide 183	EAAAER	SEQ ID NO. 183
peptide 184	AAAERP	SEQ ID NO. 184
peptide 185	AAERPG	SEQ ID NO. 185
peptide 186	AERPGE	SEQ ID NO. 186
peptide 187	ERPGEA	SEQ ID NO. 187
peptide 188	RPGEAA	SEQ ID NO. 188
peptide 189	PGEAAV	SEQ ID NO. 189
peptide 190	GEAAVA	SEQ ID NO. 190
peptide 191	GAQFS	SEQ ID NO. 191
peptide 192	AQFSK	SEQ ID NO. 192
peptide 193	QFSKT	SEQ ID NO. 193
peptide 194	FSKTA	SEQ ID NO. 194
peptide 195	SKTAA	SEQ ID NO. 195
peptide 196	KTAAK	SEQ ID NO. 196

peptide 197	TAAKG	SEQ ID NO. 197
peptide 198	AAKGE	SEQ ID NO. 198
peptide 199	AKGEA	SEQ ID NO. 199
peptide 200	KGEAA	SEQ ID NO. 200
peptide 201	GEAAA	SEQ ID NO. 201
peptide 202	EAAAE	SEQ ID NO. 202
peptide 203	AAAER	SEQ ID NO. 203
peptide 204	AAERP	SEQ ID NO. 204
peptide 205	AERPG	SEQ ID NO. 205
peptide 206	ERPGE	SEQ ID NO. 206
peptide 207	RPGEA	SEQ ID NO. 207
peptide 208	PGEAA	SEQ ID NO. 208
peptide 209	GEAAV	SEQ ID NO. 209
peptide 210	EAAVA	SEQ ID NO. 210
peptide 211	GAQF	SEQ ID NO. 211
peptide 212	AQFS	SEQ ID NO. 212
peptide 213	QFSK	SEQ ID NO. 213
peptide 214	FSKT	SEQ ID NO. 214
peptide 215	SKTA	SEQ ID NO. 215
peptide 216	KTAA	SEQ ID NO. 216
peptide 217	TAAK	SEQ ID NO. 217
peptide 218	AAKG	SEQ ID NO. 218
peptide 219	AKGE	SEQ ID NO. 219
peptide 220	KGEA	SEQ ID NO. 220
peptide 221	GEAA	SEQ ID NO. 221
peptide 222	EAAA	SEQ ID NO. 222
peptide 223	AAAE	SEQ ID NO. 223
peptide 224	AAER	SEQ ID NO. 224
peptide 225	AERP	SEQ ID NO. 225
peptide 226	ERPG	SEQ ID NO. 226
peptide 227	RPGE	SEQ ID NO. 227
peptide 228	PGEA	SEQ ID NO. 228
peptide 229	GEAA	SEQ ID NO. 229
peptide 230	EAAV	SEQ ID NO. 230
peptide 231	AAVA	SEQ ID NO. 231
peptide 232	GTAPAAEGAGAEVKRASAEAKQAF	SEQ ID NO. 232
peptide 233	GKQFSKTAAKGE	SEQ ID NO. 233
peptide 234	GAQFSKTKAKGE	SEQ ID NO. 234
peptide 235	GKQFSKTKAKGE	SEQ ID NO. 235
peptide 236	GAQASKTAAK	SEQ ID NO. 236
peptide 237	GAQASKTAAKGE	SEQ ID NO. 237
peptide 238	GAEFSKTAAKGE	SEQ ID NO. 238
peptide 239	GAQFSKTAAAGE	SEQ ID NO. 239
peptide 240	GAQFSKTAAKAE	SEQ ID NO. 240
peptide 241	GAQFSKTAAKGA	SEQ ID NO. 241
peptide 242	AAQFSKTAAK	SEQ ID NO. 242
peptide 243	GAAFSKTAAK	SEQ ID NO. 243
peptide 244	GAQFAKTAAK	SEQ ID NO. 244
peptide 245	GAQFSATAAK	SEQ ID NO. 245
peptide 246	KAATKSFQAG	SEQ ID NO. 246
peptide 247	GAQFSKAAAK	SEQ ID NO. 247
peptide 248	GAQFSKTAAA	SEQ ID NO. 248
peptide 249	GAQFSATAAA	SEQ ID NO. 249

peptide 250	GAQASKTA	SEQ ID NO. 250
peptide 251	AAGE	SEQ ID NO. 251
peptide 252	GKASQFAKTA	SEQ ID NO. 252

[00036] An amino acid sequence of a peptide listed in Table 1 can be chemically modified. For example, if an amino acid sequence of a peptide listed in Table 1 is chemically modified at the N-terminal amine to form an amide with a carboxylic acid, the resulting peptide is sometimes referred to herein by a combination of an identifier for the carboxylic acid as a prefix linked by a hyphen to the peptide number. For example, with respect to peptide 79 as an example, an N-terminal myristoylated peptide 79 may sometimes be referred to herein as "myristoylated-peptide 79" or "myr-peptide 79"; an N-terminal acetylated peptide 79 may sometimes be referred to herein as "acetyl-peptide 79" or "Ac-peptide 79". A cyclic version of peptide 79 may be referred to as "cyclic-peptide 79" or "cyc-peptide 79". Also, for example, if an amino acid sequence of a peptide listed in Table 1 is chemically modified at the C-terminal carboxylic group, for example by an amine such as ammonia to form a C-terminal amide, the resulting peptide is sometimes referred to herein by a combination of an identifier for the amine residue as a suffix linked by a hyphen to the peptide number. Thus, for example, a C-terminal amide of peptide 79 can be sometimes referred to as "peptide-NH2". When the N-terminal amine of the peptide (e.g., peptide 79) is chemically modified by, for example, a myristoyl group and the C-terminal carboxylic group is chemically modified by, for example, an ammonia group to form an amide as above, the resulting peptide can be sometimes referred to, using both prefix and suffix notation, as "myr-peptide 79-NH2".

[00037] The invention involves peptides having amino acid sequences comprising less than 24 amino acids with amino acid sequences related to the amino acid sequence of MANS peptide (i.e., the MANS peptide is myristoyl-peptide 1 and the reference 24-amino acid sequence of the MANS peptide is peptide 1). The peptides of the current invention consist of amino acid sequences containing less than 24 amino acids, and may consist of from 8 to 14, from 10 to 12, from 9 to 14, from 9 to 13, from 10 to 13, from 10 to 14, at least 9, at least 10, or the like amino acids. The peptides are typically straight chains, but may be cyclic peptides as well. In addition, the peptides may be isolated peptides.

[00038] With respect to peptide 1 (SEQ ID NO: 1), the reference 24 amino acid sequence, a segment of 23 continuous amino acids of the reference amino acid sequence is sometimes referred to herein as a 23-mer. Analogously, a segment of 22 continuous amino acids of the reference sequence is sometimes referred to herein as a 22-mer; a 21 amino acid sequence as a 21-mer; a 20 amino acid sequence as a 20-mer; a 19 amino acid sequence as a 19-mer; an 18 amino acid sequence as an 18-mer; a 17 amino acid sequence as a 17-mer; a 16 amino acid sequence as a 16-mer; a 15 amino acid sequence as a 15-mer; a 14 amino acid sequence as a 14-mer; a 13 amino acid sequence as a 13-mer; a 12 amino acid sequence as a 12-mer; an 11 amino acid sequence as an 11-mer; a 10 amino acid sequence as a 10-mer; a 9 amino acid sequence as a 9-mer; an 8 amino acid sequence as an 8-mer; a 7 amino acid sequence as a 7-mer; a 6 amino acid sequence as a 6-mer; a 5 amino acid sequence as a 5-mer; and a 4 amino acid sequence as a 4-mer. In one aspect, any of these "4- to 23-mer" amino acid sequences, which are themselves peptides (sometimes herein denoted as H2N-peptide-COOH), can be independently chemically modified, for example, by chemical modification, which chemical modification can be selected from the group consisting of (i) amide formation at the N-terminal amine group (H2N-peptide-) such as with, for example, a C1 or preferably with a C2 (acetic acid) to C22 carboxylic acid; (ii) amide formation at the C-terminal carboxylic group (-peptide-COOH) such as with, for example, ammonia or with a C1 to C22 primary or secondary amine; and (iii) a combination of thereof.

[00039] The peptides have an amino acid sequence selected from the group consisting of (a) an amino acid sequence having from 4 to 23 contiguous amino acids of the reference sequence, peptide 1; (b) a sequence substantially similar to the amino acid sequence defined in (a); and (c) a variant of the amino acid sequence defined in (a), which variant is selected from the group consisting of a substitution variant, a deletion variant, an addition variant, and combinations thereof. In some embodiments, the peptides have an amino acid sequence selected from the group consisting of: (a) an amino acid sequence having from 8 to 14 contiguous amino acids of the reference sequence, peptide 1; (b) an amino acid sequence substantially identical to the sequence defined in (a); and (c) a variant of the amino acid sequence defined in (a), which variant is selected from the group consisting of a substitution variant, a deletion variant, an addition variant, and combinations thereof. In yet other embodiments, the peptides have an amino acid sequence selected from the group consisting of: (a) an amino acid sequence having from 10 to 12 contiguous amino acids of the reference sequence, peptide 1; (b) an amino acid

sequence substantially identical to the sequence defined in (a); and (c) a variant of the amino acid sequence defined in (a), which variant is selected from the group consisting of a substitution variant, a deletion variant, an addition variant, and combinations thereof. In further embodiments, the peptides have an amino acid sequence having at least 9, at least 10, from 9 to 14, from 9 to 13, from 10 to 13, from 10 to 14, or the like contiguous amino acids of the reference sequence, peptide 1; an amino acid sequence substantially identical thereto; or a variant thereof, which variant is selected from the group consisting of a substitution variant, a deletion variant, an addition variant, and combinations thereof. As explained further below, one or more of the amino acids of the peptides (e.g., the N-terminal and/or C-terminal amino acids) may be optionally independently chemically modified; in some embodiments, one or more amino acids of a peptide will be chemically modified while in other embodiments none of the amino acids of the peptide will be chemically modified. In one aspect, preferred modification can occur at the amine ($-NH_2$) group of the N-terminal amino acid of the peptide or peptide seqment (which amine group would form a peptide amide bond if present internally within a peptide sequence rather than at the N-terminal position). In another aspect, preferred modification can occur at the carboxy (-COOH) group of the C-terminal amino acid of the peptide or peptide seqment (which carboxy group would form a peptide amide bond if present internally within a peptide sequence rather than at the C-terminal position). In another aspect, preferred modification can occur at both the N-terminal amine ($-NH_2$) group and at the C-terminal carboxylic (-COOH) group.

[00040] In some embodiments, the amino acid sequence of the peptide begins from the N-terminal amino acid of the reference sequence peptide 1. For example, the peptides may have an amino acid sequence selected from the group consisting of (a) an amino acid sequence having from 4 to 23 contiguous amino acids of the reference sequence peptide 1, wherein the amino acid sequence begins from the N-terminal amino acid of the reference sequence (i.e., peptide 2, peptide 4, peptide 7, peptide 11, peptide 16, peptide 22, peptide 29, peptide 37, peptide 46, peptide 56, peptide 67, peptide 79, peptide 92, peptide 106, peptide 121, peptide 137, peptide 154, peptide 172, peptide 191, or peptide 211); (b) a sequence substantially similar to the amino acid sequence defined in (a); and (c) a variant of the amino acid sequence defined in (a). These peptides contain no chemical moiety or a chemical moiety on the N-terminal glycine other than a myristoyl group. Preferably, the chemical moiety is an acyl group, in the form of an amide bond, such as an acetyl group, or alkyl group.

[00041] In other embodiments, the amino acid sequence of the peptide ends at the C-terminal amino acid of the reference sequence peptide 1. For example, the peptides may have an amino acid sequence selected from the group consisting of (a) an amino acid sequence having from 4 to 23 contiguous amino acids of the reference sequence peptide 1, wherein the amino acid sequence ends at the C-terminal amino acid of the reference sequence (i.e., peptide 3, peptide 6, peptide 10, peptide 15, peptide 21, peptide 28, peptide 36, peptide 45, peptide 55, peptide 66, peptide 78, peptide 91, peptide 105, peptide 120, peptide 136, peptide 153, peptide 171, peptide 190, peptide 210, or peptide 231); (b) a sequence substantially similar to the amino acid sequence defined in (a); and (c) a variant of the amino acid sequence defined in (a).

[00042] In other embodiments, the amino acid sequence of the peptide does not begin at the N-terminal amino acid of the reference sequence, peptide 1, (SEQ ID NO: 1) but rather begins at the amino acid at position 2 through the amino acid at position 21 of the reference sequence peptide 1. For example, the peptides may have an amino acid sequence selected from the group consisting of (a) an amino acid sequence having from 4 to 23 contiguous amino acids of the reference sequence peptide 1, wherein the amino acid sequence begins at any amino acid between position 2 through position 21of the reference sequence. These peptides may be between 4 and 23 contiguous amino acids long and may represent peptides in the middle of the reference sequence, peptide 1; (b) a sequence substantially similar to the amino acid sequence defined in (a); and (c) a variant of the amino acid sequence defined in (a). These peptides are disclosed in Tables 1 or 2. These peptides may contain no covalently bound chemical moiety or a chemical moiety on the N-terminal amino acid which is not the N-terminal glycine from or equivalent to the N-terminal glycine of the amino acid sequence SEQ ID NO: 1. Preferably, the chemical moiety is an acyl group, such as an acetyl group or a myristoyl group, in the form of an amide bond, or an alkyl group.

[00043] Peptide amino acid sequences which are useful in the current invention to inhibit mucin hypersecretion in a mammal, and which are useful to reduce the amount of mucin hypersecretion in a mammal, and which are useful in the methods of inhibition of mucin hypersecretion and in the methods of reduction of mucin hypersecretion include amino acid sequences of isolated peptides and amino acid sequences of peptides which optionally contain N-terminal- and/or C-terminal-chemically modified groups of the current invention, which peptide amino acid

sequences are selected from the group consisting of the 23-mers (i.e., peptides having a 23 amino acid sequence): peptide 2; and peptide 3; the 22-mers (i.e., peptides having a 22 amino acid sequence): peptide 4; peptide 5; and peptide 6; the 21-mers (i.e., peptides having a 21 amino acid sequence): peptide 7; peptide 8; peptide 9; and peptide 10; the 20-mers (i.e., peptides having a 20 amino acid sequence): peptide 11; peptide 12; peptide 13; peptide 14; and peptide 15; the 19-mers (i.e., peptides having a 19 amino acid sequence): peptide 16; peptide 17; peptide 18; peptide 19; peptide 20; and peptide 21; the 18-mers (i.e., peptides having a 18 amino acid sequence): peptide 22; peptide 23; peptide 25; peptide 26; peptide 27; and peptide 28; the 17-mers (i.e., peptides having a 17 amino acid sequence): peptide 29; peptide 30; peptide 31; peptide 32; peptide 33; peptide 34; peptide 35; and peptide 36; the 16-mers (i.e., peptides having a 16 amino acid sequence): peptide 37; peptide 38; peptide 39; peptide 40; peptide 41; peptide 42; peptide 43; peptide 44; and peptide 45; the 15-mers (i.e., peptides having a 15 amino acid sequence): peptide 46; peptide 47; peptide 48; peptide 49; peptide 50; peptide 51; peptide 52; peptide 53; peptide 54; and peptide 55; the 14-mers (i.e., peptides having a 14 amino acid sequence): peptide 56; peptide 57; peptide 58; peptide 59; peptide 60; peptide 61; peptide 62; peptide 63; peptide 64; peptide 65; and peptide 66; the 13-mers (i.e., peptides having a 13 amino acid sequence): peptide 67; peptide 68; peptide 69; peptide 70; peptide 71; peptide 72; peptide 73; peptide 74; peptide 75; peptide 76; peptide 77; and peptide 78; the 12-mers (i.e., peptides having a 12 amino acid sequence): peptide 79; peptide 80; peptide 81; peptide 82; peptide 83; peptide 84; peptide 85; peptide 86; peptide 87; peptide 88; peptide 89; peptide 90; and peptide 91; the 11-mers (i.e., peptides having a 11 amino acid sequence): peptide 92; peptide 93; peptide 94; peptide 95; peptide 96; peptide 97; peptide 98; peptide 99; peptide 100; peptide 101; peptide 102; peptide 103; peptide 104; and peptide 105; the 10-mers (i.e., peptides having a 10 amino acid sequence): peptide 106; peptide 107; peptide 108; peptide 109; peptide 110; peptide 111; peptide 112; peptide 113; peptide 114; peptide 115; peptide 116; peptide 117; peptide 118; peptide 119; and peptide 120; the 9-mers (i.e., peptides having a 9 amino acid sequence): peptide 121; peptide 122; peptide 123; peptide 124; peptide 125; peptide 126; peptide 127; peptide 128; peptide 129; peptide 130; peptide 131; peptide 132; peptide 133; peptide 134; peptide 135; and peptide 136; the 8-mers (i.e., peptides having a 8 amino acid sequence): peptide 137; peptide 138; peptide 139; peptide 140; peptide 141; peptide 142; peptide 143; peptide 144; peptide 145; peptide 146; peptide 147; peptide 148; peptide 149; peptide 150; peptide 151; peptide 152; and

peptide 153; the 7-mers (i.e., peptides having a 7 amino acid sequence): peptide 154; peptide 155; peptide 156; peptide 157; peptide 158; peptide 159; peptide 160; peptide 161; peptide 162; peptide 163; peptide 164; peptide 165; peptide 166; peptide 167; peptide 168; peptide 169; peptide 170; and peptide 171; the 6-mers (i.e., peptides having a 6 amino acid sequence): peptide 172; peptide 173; peptide 174; peptide 175; peptide 176; peptide 177; peptide 178; peptide 179; peptide 180; peptide 181; peptide 182; peptide 183; peptide 184; peptide 185; peptide 186; peptide 187; peptide 188; peptide 189; and peptide 190; the 5-mers (i.e., peptides having a 5 amino acid sequence): peptide 191; peptide 192; peptide 193; peptide 194; peptide 195; peptide 196; peptide 197; peptide 198; peptide 199; peptide 200; peptide 201; peptide 202; peptide 203; peptide 204; peptide 205; peptide 206; peptide 207; peptide 208; peptide 209; and peptide 210; and the 4-mers (i.e., peptides having a 4 amino acid sequence): peptide 211; peptide 212; peptide 213; peptide 214; peptide 215; peptide 216; peptide 217; peptide 218; peptide 219; peptide 220; peptide 221; peptide 222; peptide 223; peptide 224; peptide 225; peptide 226; peptide 227; peptide 228; peptide 229; peptide 230; and peptide 231.

[00044] Preferred amino acid sequences of isolated peptides and of N-terminal- and/or C-terminal-chemically modified peptides of the current invention are selected from the group consisting of the 23-mers: peptide 2; and peptide 3; the 22-mers: peptide 4; peptide 5; and peptide 6; the 21-mers: peptide 7; peptide 8; peptide 9; and peptide 10; the 20-mers: peptide 11; peptide 12; peptide 13; peptide 14; and peptide 15; the 19-mers: peptide 16; peptide 17; peptide 18; peptide 19; peptide 20; and peptide 21; the 18-mers: peptide 22; peptide 23; peptide 24; peptide 25; peptide 26; peptide 27; and peptide 28; the 17-mers: peptide 29; peptide 30; peptide 31; peptide 32; peptide 33; peptide 34; peptide 35; and peptide 36; the 16-mers: peptide 37; peptide 38; peptide 39; peptide 40; peptide 41; peptide 42; peptide 43; peptide 44; and peptide 45; the 15-mers: peptide 46; peptide 47; peptide 48; peptide 49; peptide 50; peptide 51; peptide 52; peptide 53; and peptide 54; the 14-mers: peptide 56; peptide 57; peptide 58; peptide 59; peptide 60; peptide 61; peptide 62; peptide 63; and peptide 64; the 13-mers: peptide 67; peptide 68; peptide 69; peptide 70; peptide 71; peptide 72; peptide 73; peptide 74; and peptide 75; the 12-mers: peptide 79; peptide 80; peptide 81; peptide 82; peptide 83; peptide 84; peptide 85; peptide 86; and peptide 87; the 11-mers: peptide 92; peptide 93; peptide 94; peptide 95; peptide 96; peptide 97; peptide 98; peptide 99; and peptide 100; the 10-mers: peptide 106; peptide 107; peptide 108; peptide 109; peptide 110; peptide 111; peptide 112; peptide 113; and peptide 114;

the 9-mers: peptide 122; peptide 123; peptide 124; peptide 125; peptide 126; peptide 127; peptide 128; and peptide 129; the 8-mers: peptide 139; peptide 140; peptide 141; peptide 142; peptide 143; peptide 144; and peptide 145; the 7-mers: peptide 157; peptide 158; peptide 159; peptide 160; peptide 161; and peptide 162; the 6-mers: peptide 176; peptide 177; peptide 178; peptide 179; and peptide 180; the 5-mers: peptide 196; peptide 197; peptide 198; and peptide 199; and the 4-mers: peptide 217; and peptide 219.

[00045] More preferred amino acid sequences of isolated peptides and of N-terminal- and/or C-terminal-chemically modified peptides of the current invention are selected from the group consisting of the 23-mers: peptide 2; and peptide 3; the 22-mers: peptide 4; peptide 5; and peptide 6; the 21-mers: peptide 7; peptide 8; peptide 9; and peptide 10; the 20-mers: peptide 11; peptide 12; peptide 13; peptide 14; and peptide 15; the 19-mers: peptide 16; peptide 17; peptide 18; peptide 19; peptide 20; and peptide 21; the 18-mers: peptide 22; peptide 23; peptide 24; peptide 25; peptide 26; peptide 27; and peptide 28; the 17-mers: peptide 29; peptide 30; peptide 31; peptide 32; peptide 33; peptide 34; peptide 35; and peptide 36; the 16-mers: peptide 37; peptide 38; peptide 39; peptide 40; peptide 41; peptide 42; peptide 43; peptide 44; and peptide 45; the 15-mers: peptide 46; peptide 47; peptide 48; peptide 49; peptide 50; peptide 51; peptide 52; peptide 53; and peptide 54; the 14-mers: peptide 56; peptide 57; peptide 58; peptide 59; peptide 60; peptide 61; peptide 62; peptide 63; and peptide 64; the 13-mers: peptide 67; peptide 68; peptide 69; peptide 70; peptide 71; peptide 72; peptide 73; peptide 74; peptide 80; peptide 81; peptide 82; peptide 83; peptide 84; peptide 85; peptide 86; and peptide 87; the 11-mers: peptide 92; peptide 93; peptide 94; peptide 95; peptide 96; peptide 97; peptide 98; peptide 99; and peptide 100; the 10-mers: peptide 106; peptide 108; peptide 109; peptide 110; peptide 111; peptide 112; peptide 113; and peptide 114; the 9-mers: peptide 124; peptide 125; peptide 126; peptide 127; peptide 128; and peptide 129; the 8-mers: peptide 141; peptide 142; peptide 143; peptide 144; and peptide 145; the 7-mers: peptide 159; peptide 160; peptide 161; and peptide 162; the 6-mers: peptide 178; peptide 179; and peptide 180; the 5-mers: peptide 198; and peptide 199; and the 4-mer: peptide 219.

[00046] In yet other embodiments, the amino acid sequence of the peptide includes the contiguous residues A,K,G, and E as in peptide 219 of the reference sequence peptide 1. For example, the peptides may have an amino acid sequence selected from the group consisting of

(a) an amino acid sequence having from 4 to 23 contiguous amino acids of the reference sequence peptide 1, wherein the amino acid sequence of the peptide includes the contiguous residues A,K,G, and E as in peptide 219 of the reference peptide 1 (e.g., peptide 219, peptide 45, peptide 79, peptide 67, peptide 80, etc.); (b) a sequence substantially similar to the amino acid sequence defined in (a); and (c) a variant of the amino acid sequence defined in (a).

[00047] Examples of peptide segments which contain the amino acid sequence AKGE of the reference peptide amino acid sequence, peptide 1, include (a) the 23-mers: peptide 2; and peptide 3; the 22-mers: peptide 4; peptide 5; and peptide 6; the 11-mers: peptide 7; peptide 8; peptide 9; and peptide 10; the 20-mers: peptide 11; peptide 12; peptide 13; peptide 14; and peptide 15; the 19-mers: peptide 16; peptide 17; peptide 18; peptide 19; peptide 20; and peptide 21; the 18-mers: peptide 22; peptide 23; peptide 24; peptide 25; peptide 26; peptide 27; and peptide 28; the 17-mers: peptide 29; peptide 30; peptide 31; peptide 32; peptide 33; peptide 34; peptide 35; and peptide 36; the 16-mers: peptide 37; peptide 38; peptide 39; peptide 40; peptide 41; peptide 42; peptide 43; peptide 44; and peptide 45; the 15-mers: peptide 46; peptide 47; peptide 48; peptide 49; peptide 50; peptide 51; peptide 52; peptide 53; and peptide 54; the 14-mers: peptide 56; peptide 57; peptide 58; peptide 59; peptide 60; peptide 61; peptide 62; peptide 63; and peptide 64; the 13-mers: peptide 67; peptide 68; peptide 69; peptide 70; peptide 71; peptide 72; peptide 73; peptide 74; and peptide 75; the 12-mers: peptide 79; peptide 80; peptide 81; peptide 82; peptide 83; peptide 84; peptide 85; peptide 86; and peptide 87; the 11-mers: peptide 93; peptide 94; peptide 95; peptide 96; peptide 97; peptide 98; peptide 99; and peptide 100; the 10-mers: peptide 108; peptide 109; peptide 110; peptide 111; peptide 112; peptide 113; and peptide 114; the 9-mers: peptide 124; peptide 125; peptide 126; peptide 127; peptide 128; and peptide 129; the 8-mers: peptide 141; peptide 142; peptide 143; peptide 144; and peptide 145; the 7-mers: peptide 159; peptide 160; peptide 161; and peptide 162; the 6-mers: peptide 178; peptide 179; and peptide 180; the 5-mers: peptide 198; and peptide 199; and the 4-mer: peptide 219, (b) a sequence substantially similar to the amino acid sequence defined in (a); and (c) a variant of the amino acid sequence defined in (a), which variant is selected from the group consisting of a substitution variant, a deletion variant, an addition variant, and combinations thereof, wherein the segment comprises or consists of from 4 to 23 contiguous amino acids.

[00048] In another embodiment, preferred peptide sequences have an amino acid sequence selected from the group consisting of (a) an amino acid sequence having from 10 to 23 contiguous amino acids of the reference sequence, peptide 1; (b) a sequence substantially similar to the amino acid sequence defined in (a); and (c) a variant of the amino acid sequence defined in (a), which variant is selected from the group consisting of a substitution variant, a deletion variant, an addition variant, and combinations thereof, wherein the preferred amino acid sequences comprise the 23-mer: peptide 2; the 22-mer: peptide 4; the 21-mer: peptide 7; the 20-mer: peptide 11; the 19-mer: peptide 16; the 18-mer: peptide 22; the 17-mer: peptide 29; the 16-mer: peptide 37; the 15-mer: peptide 46; the 14-mer: peptide 56; the 13-mer: peptide 67; the 12-mer: peptide 79; the 11-mer: peptide 92; and the 10-mer: peptide 106.

[00049] In further embodiments, the amino acid sequence of the peptide begins from the N-terminal amino acid of the reference sequence peptide 1 and includes the contiguous residues A,K,G, and E as in peptide 219 of the reference sequence peptide 1, while in other embodiments the amino acid sequence of the peptide ends at the C-terminal amino acid of the reference sequence peptide 1 and includes the contiguous residues A,K,G, and E as in peptide 219 of the reference sequence peptide 1.

[00050] The peptides may include one or more amino acid deletions, substitutions, and/or additions with respect to the reference amino acid sequence. Preferably, the substitutions may be conservative amino acid substitutions, or the substitutions may be non-conservative amino acid substitutions. In some embodiments, the peptides, including the peptides with amino acid sequences that are substantially identical to or variants of the reference amino acid sequence, will not have deletions or additions as compared to the corresponding contiguous amino acids of the reference amino acid sequence, but may have conservative or non-conservative substitutions. Amino acid substitutions that may be made to the reference amino acid sequence in the peptides of the invention include, but are not limited to, the following: alanine (A) may be substituted with lysine (K), valine (V), leucine (L), or isoleucine (I); glutamic acid (E) may be substituted with aspartic acid (D); glycine (G) may be substituted with proline (P); lysine (K) may be substituted with arginine (R), glutamine (Q), or asparagine (N); phenylalanine (F) may be substituted with leucine (L), valine (V), isoleucine (I), or alanine (A); proline (P) may be substituted with glycine (G); glutamine (Q) may be substituted with glutamic acid (E) or

asparagine (N); arginine (R) may be substituted with lysine (K), glutamine (Q), or asparagine (N); serine (S) may be substituted with threonine; threonine (T) may be substituted with serine (S); and valine (V) may be substituted with leucine (L), isoleucine (I), methionine (M), phenylalanine (F), alanine (A), or norleucine (Nle). For example, substitutions that could be made to the reference amino acid sequence in the peptides of the invention include substituting alanine (A) for phenylalanine (F) (e.g., at amino acid position 4 of the reference amino acid sequence), glutamic acid (E) for glutamine (Q) (e.g., at amino acid position 3 of the reference amino acid sequence), lysine (K) for alanine (A) (e.g., at amino acid positions 2 and/or 8 of the reference amino acid sequence), and/or serine (S) for threonine (T) (e.g., at amino acid position 7 of the reference amino acid sequence).

[00051] When substitutions are included in the amino acid sequences of the peptides of the invention (which peptides comprise unmodified as well as peptides which are chemically modified for example by N-terminal and/or C-terminal modification such as by amide formation) with respect to the reference amino acid sequence, there is preferably at least 80% sequence identity between the amino acid sequence of the peptide and the reference amino acid sequence. Peptides having 5 to 23 amino acids and including one amino acid substitution with respect to the reference amino acid sequence will have between about 80% to about 96% (i.e., ~95.7%) sequence identity to the reference amino acid sequence. Peptides having 10 to 23 amino acids and including one amino acid substitution with respect to the reference amino acid sequence will have between about 90% to about 96% (i.e., ~95.7%) sequence identity to the reference amino acid sequence. Peptides having 20 to 23 amino acids and including one amino acid substitution with respect to the reference amino acid sequence will have between about 95% to about 96% (i.e., ~95.7%) sequence identity to the reference amino acid sequence. Peptides having 10 to 23 amino acids and including two amino acid substitutions with respect to the reference amino acid sequence will have between about 80% to about 92% (i.e., ~91.3%) sequence identity to the reference amino acid sequence. Peptides having 16 to 23 amino acids and including two amino acid substitutions with respect to the reference amino acid sequence will have between about 87.5% to about 92% (i.e., ~91.3%) sequence identity to the reference amino acid sequence. Peptides having 20 to 23 amino acids and including two amino acid substitutions with respect to the reference amino acid sequence will have between about 90% to about 92% (i.e., ~91.3%) sequence identity to the reference amino acid sequence. Peptides having 15 to 23 amino acids

and including three amino acid substitutions with respect to the reference amino acid sequence will have between about 80% to about 87% sequence identity to the reference amino acid sequence. Peptides having 20 to 23 amino acids and including three amino acid substitutions with respect to the reference amino acid sequence will have between about 85% to about 87% sequence identity to the reference amino acid sequence. Peptides having 20 to 23 amino acids and including four amino acid substitutions with respect to the reference amino acid sequence will have between about 80% to about 83% (i.e., ~82.6%) sequence identity to the reference amino acid sequence.

[00052] In peptides of the current invention, with respect to the contiguous amino acid sequence of the reference peptide (which is a 24-mer) substitution of one amino acid in a contiguous 23 amino acid sequence (a 23-mer) selected from the reference 24 amino acid sequence provides a peptide with an amino acid sequence which has a 95.65% (or ~96%) sequence identity to the amino acid segment in the reference peptide with which the 23-mer has identity. Analogously, substitution of two, three, four, and five amino acids in said 23-mer provides a peptide with an amino acid sequence which has a 91.30% (or ~91%), 86.96% (or ~87%), 82.61% (or ~83%), and 78.27% (or ~78%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one, two, three, four, and five amino acids in a 22-mer provides a peptide with an amino acid sequence which has a 95.45% (or ~95%), 90.91% (or ~91%), 86.36% (or ~86%), 81.82% (or ~82%), and 77.27% (or ~77%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one, two, three, four, and five amino acids in a 21-mer provides a peptide with an amino acid sequence which has a 95.24% (~95%), 90.48 (~91%), 85.71% (~86%), 80.95 (~81%), and 76.19% (~76%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one, two, three, four, and five amino acids in a 20-mer provides a peptide with an amino acid sequence which has a 95.00% (95%), 90.00% (90%), 85.00% (85%), 80.00% (80%), and 75.00% (75%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one, two, three, and four amino acids in a 19-mer provides a peptide with an amino acid sequence which has a 94.74% (~95%), 89.47% (~89%), 84.21% (~84%), and 78.95% (~79%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one, two, three, and four amino acids in an 18-mer provides a peptide with an amino acid sequence which has a 94.44% (~94%), 88.89% (~89%), 83.33%

(~83%), and 77.78% (~78%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one, two, three, and four amino acids in an 17-mer provides a peptide with an amino acid sequence which has a 94.12% (~94%), 88.23% (~88%), 82.35% (~82%), and 76.47% (~76%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one, two, three, and four amino acids in a 16-mer provides a peptide with an amino acid sequence which has a 93.75% (~94%), 87.50% (~88%), 81.25% (~81%), and 75.00% (75%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one, two, and three amino acids in a 15-mer provides a peptide with an amino acid sequence which has a 93.33% (~93%), 86.67% (~87%), and 80.00% (80%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one, two, and three amino acids in a 14-mer provides a peptide with an amino acid sequence which has a 92.86% (~93%), 85.71% (~86%), and 78.57% (79%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one, two, and three amino acids in a 13-mer provides a peptide with an amino acid sequence which has a 92.31% (~92%), 84.62% (~85%), and 76.92% (~77%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one, two, and three amino acids in a 12-mer provides a peptide with an amino acid sequence which has a 91.67% (~92%), 83.33% (~83%), and 75.00% (75%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one and two amino acids in an 11-mer provides a peptide with an amino acid sequence which has a 90.91% (~91%) and 81.82% (~82%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one and two amino acids in a 10-mer provides a peptide with an amino acid sequence which has a 90.00% (90%) and 80.00% (80%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one and two amino acids in a 9-mer provides a peptide with an amino acid sequence which has a 88.89% (~89%) and 77.78% (~78%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one and two amino acids in an 8-mer provides a peptide with an amino acid sequence which has a 87.50% (~88%) and 75.00% (75%) sequence identity, respectively, to the reference peptide amino acid sequence. Analogously, substitution of one amino acid in a 7-mer, 6-mer, 5-mer, and 4-mer provides a peptide with an amino acid sequence which has a 85.71% (~86%), 83.33% (~83.3%), 80.00% (80%), and 75.00% (75%)

sequence identity, respectively, to the reference peptide. Preferred amino acid sequences of this invention have greater than 80% sequence identity to the amino acid sequence in the reference sequence, more preferably between 81% and 96% sequence identity to the amino acid sequence in the reference sequence, and more preferably between 80% and 96% sequence identity to the amino acid sequence in the reference sequence. The preferred amino acid sequences can be optionally N-terminally chemically bonded at the terminal peptide amino group to a C2 to C22 linear aliphatic carboxylic acid moiety, more preferably to a C2 to C16 linear aliphatic carboxylic acid moiety, most preferably to a C2 or C16 linear aliphatic carboxylic acid moiety, by an amide bond, and optionally C-terminally chemically bonded at the terminal peptide carboxylic group to an amine such as ammonia or a primary or secondary amine such as a C1 to C16 linear aliphatic primary amine, by an amide bond.

[00053] Examples of substitution variants of peptide 79, a 12-mer, include, for example, peptide 238, where Q at position 3 in peptide 79 has been substituted by E in sequence 238; peptide 233, where A at position 2 in peptide 79 has been substituted by K in peptide 233; peptide 234, where A at position 8 in peptide 79 has been substituted by K in peptide 234; peptide 235, where A at positions 2 and 8 in peptide 79 have been substituted by K in peptide 235; peptide 237, where F at position 4 in peptide 79 has been substituted by A in peptide 237; peptide 239, where K at position 10 in peptide 79 has been substituted by A in peptide 239; peptide 240, where G at position 11 in peptide 79 has been substituted by A in peptide 240; and peptide 241, where E at position 12 in peptide 79 has been substituted by A in peptide 241.

[00054] Examples of substitution variants of peptide 106, a 10-mer, include, for example, peptide 236, where F at position 4 in peptide 106 has been substituted by A in peptide 236; peptide 242, where G at position 1 in peptide 106 has been substituted by A in peptide 242; peptide 243, where Q at position 3 in peptide 106 has been substituted by A in peptide 243; peptide 244, where S at position 5 in peptide 106 has been substituted by A in peptide 244; peptide 245, where K at position 6 in peptide 106 has been substituted by A in peptide 245; peptide 247, where T at position 7 in peptide 106 has been substituted by A in peptide 247; peptide 248, where K at position 10 in peptide 106 has been substituted by A in peptide 248; peptide 249, where K at positions 6 and 10 in peptide 106 have both been substituted, each by A, in peptide 249.

[00055] Examples of a substitution variant of peptide 137, an 8-mer, include for example, peptide 250, where F at position 4 in peptide 137 has been substituted by A in peptide 250.

[00056] Examples of a substitution variant of peptide 219, a 4-mer, include for example, peptide 251, where K at position 2 in peptide 219 has been substituted by A in peptide 251.

[00057] A substitution variant peptide such as described herein can be in the form of an isolated peptide or in the form of a chemically modified peptide such as, for example, an N-terminal amide such as a myristoyl amide, an acetyl amide, and the like as described herein, and such as, for example, a C-terminal amide such as an amide formed with ammonia, and such as both an N-terminal amide and a C-terminal amide.

[00058] When deletions are included in the amino acid sequences of the peptides of the invention with respect to the reference amino acid sequence, there is preferably at least 80% sequence identity between the amino acid sequence of the peptide to the reference amino acid sequence. Peptides having 5 to 23 amino acids and including one amino acid deletion with respect to the reference peptide will have between 80% to about 96% (i.e., ~95.7%) sequence identity to the reference amino acid sequence. Peptides having 10 to 23 amino acids and including one amino acid deletion with respect to the reference peptide will have between about 90% to about 96% (i.e., ~95.7%) sequence identity to the reference amino acid sequence. Peptides having 20 to 23 amino acids and including one amino acid deletion with respect to the reference peptide will have between 95% to about 96% (i.e., ~95.7%) sequence identity to the reference amino acid sequence. Peptides having 10 to 23 amino acids and including two amino acid deletions with respect to the reference peptide will have between about 80% to about 92% (i.e., ~91.3%) sequence identity to the reference amino acid sequence. Peptides having 16 to 23 amino acids and including two amino acid deletions with respect to the reference peptide will have between about 87.5% to about 92% (i.e., ~91.3%) sequence identity to the reference amino acid sequence. Peptides having 20 to 23 amino acids and including two amino acid deletions with respect to the reference peptide will have between about 90% to about 92% (i.e., ~91.3%) sequence identity to the reference amino acid sequence. Peptides having 15 to 23 amino acids and including three amino acid deletions with respect to the reference peptide will have between about 80% to about 87% sequence identity to the reference amino acid sequence. Peptides

having 20 to 23 amino acids and including three amino acid deletions with respect to the reference peptide will have between about 85% to about 87% sequence identity to the reference amino acid sequence. Peptides having 20 to 23 amino and including four amino acid deletions with respect to the reference peptide will have between about 80% to about 83% (i.e., ~82.6%) sequence identity to the reference amino acid sequence.

[00059] As stated above, one or more of the amino acids of the peptides may also be chemically modified. Any amino acid modifications known in the art may be made to the amino acids of the peptides using any method known in the art.

[00060] In some embodiments, the N-terminal and/or C-terminal amino acid may be modified. For example, the alpha-N-terminal amino acid of the peptides may be alkylated, amidated, or acylated at the alpha-N-terminal (N-terminal) amino (alpha-H2N-) group, and, for example, the C-terminal amino acid of the peptides may be amidated or esterified at the C-terminal carboxyl (-COOH) group. For example, the N-terminal amino group may be modified by acylation to include any acyl or fatty acyl group to form an amide, including an acetyl group (i.e., CH3–C(=O)- or a myristoyl group, both of which are currently preferred groups). In some embodiments, the N-terminal amino group may be modified to include an acyl group having formula –C(O)R, wherein R is a linear or branched alkyl group having from 1 to 15 carbon atoms, or may be modified to include an acyl group having formula –C(O)R1, wherein R1 is a linear alkyl group having from 1 to 15 carbon atoms. The N-amide can also be a formamide (R=H). The C-terminal amino acid of the peptides may also be chemically modified. For example, the C-terminal carboxyl group of the C-terminal amino acid may be chemically modified by conversion to a carboxamide group in place of the carboxyl group. (i.e., amidated). In some embodiments, the N-terminal and/or C-terminal amino acids are not chemically modified. In some embodiments, the N-terminal group is modified and the C-terminal group is not modified. In some embodiments, both the N-terminal and the C-terminal groups are modified.

[00061] The peptide may be acylated at the amino group of the N-terminal amino acid to form an N-terminal amide with an acid selected from the group consisting of:

(i-a) a C2 (acetyl) to C13 aliphatic (saturated or optionally unsaturated) carboxylic acid (for example, an N-terminal amide with acetic acid (which is a preferred group), with propanoic acid, with butanoic acid, with hexanoic acid, with octanoic acid, with decanoic acid, with dodecanoic acid) which may be linear, branched (greater than C3), or comprise a ring (greater than C3);

(i-b) a saturated C14 aliphatic carboxylic acid, which may be linear, branched or comprise a ring;

(i-c) an unsaturated C14 aliphatic carboxylic acid, which may be linear, branched or comprise a ring;

(i-d) C15 to C24 aliphatic (saturated or optionally unsaturated) carboxylic acid, which may be linear, branched or comprise a ring (for example, with tetradecanoic acid (myristic acid which is a preferred group), with hexadecanoic acid, with 9-hexadecenoic acid, with octadecanoic acid, with 9-octadecenoic acid, with 11-octadecenoic acid, with 9,12-octadecadienoic acid, with 9,12,15-octadecatrienoic acid, with 6,9,12-octadecatrienoic acid, with eicosanoic acid, with 9-eicosenoic acid, with 5,8,11,14-eicosatetraenoic acid, with 5,8,11,14,17-eicosapentaenoic acid, with docosanoic acid, with 13-docosenoic acid, with 4,7,10,13,16,19-docosahexaenoic acid, with tetracosanoic acid, and the like);

(ii) trifluoroacetic acid;

(iii) benzoic acid; and

(iv-a) a C1 to C12 aliphatic alkyl sulfonic acid which forms an aliphatic alkyl sulfonamide, wherein the C1 to C12 aliphatic alkyl carbon chain structure of the sulfonic acid is analogous to that of the aliphatic alkyl carboxylic acid chains in the aliphatic alkyl carboxylic acids described above. For example, a peptide may be acylated using a carboxylic acid group represented as (C1-C11)-alkyl–C(O)OH through dehydrative coupling by way of activation of the carboxylic acid group to form an amide represented as (C1-C11-alkyl–C(O)-NH-peptide. Analogously, a sulfonamide may be formed by reacting a sulfonic acid species (represented as (C1-C12)-alkyl–S(O2)-X, e.g., where X is halogen or OCH3 or other compatible leaving group)

with an N-terminal amino group to form a sulfonamide represented as (C1-C12)-alkyl–S(O2)-NH-peptide.

(iv-b) a C14 to C24 aliphatic alkyl sulfonic acid which forms an aliphatic alkyl sulfonamide, wherein the C14 to C24 aliphatic alkyl carbon chain structure of the sulfonic acid is analogous to that of the aliphatic alkyl carboxylic acid chains in the aliphatic alkyl carboxylic acids described above... For example, a peptide may be acylated using a carboxylic acid group represented as (C13-C23)-alkyl–C(O)OH through dehydrative coupling by way of activation of the carboxylic acid group to form an amide represented as (C13-C23)-alkyl–C(O)-NH-peptide. Analogously, a sulfonamide may be formed by reacting a sulfonic acid species (represented as (C14-C24)-alkyl–S(O2)-X, e.g., where X is halogen or OCH3 or other compatible leaving group) with an N-terminal amino group to form a sulfonamide represented as (C14-C24)-alkyl–S(O2)-NH-peptide.

[00062] As another example, the N-terminal amino group of the N-terminal amino acid may be alkylated with a C1 to C12 aliphatic alkyl group, the structure of which aliphatic alkyl group is as described above. Alkylation may be effected, for example, using an aliphatic alkyl halide or an aliphatic alkyl sulfonic acid ester (mesylate, tosylate, etc.), preferably using a primary alkyl halide or a primary alkyl sulfonic acid ester. The N-terminal amino acid may be also modified at the terminal amino to include any acyl or aliphatic acyl fatty acyl group as an amide, including an acetyl group (i.e., –C(O)CH3, which is a preferred group), a myristoyl group (which is a preferred group), a butanoyl group, a hexanoyl group, a octanoyl group, a decanoyl group, a dodecanoyl group, a tetradecanoyl group, a hexadecanoyl group, a 9-hexadecenoyl group, a octadecanoyl group, a 9-octadecenoyl group, a 11-octadecenoyl group, a 9,12-octadecadienoyl group, a 9,12,15-octadecatrienoyl group, a 6,9,12-octadecatrienoyl group, a eicosanoyl group, a 9-eicosenoyl group, a 5,8,11,14-eicosatetraenoyl group, a 5,8,11,14,17-eicosapentaenoyl group, a docosanoyl group, a 13-docosenoyl group, a 4,7,10,13,16,19-docosahexaenoyl group, a tetracosanoyl group, which groups are covalently attached to the terminal amino group of the peptide by an amide bond.

[00063] The C-terminal carboxylic acid group of the C-terminal amino acid of the peptides of the invention may also be chemically modified. For example, the C-terminal amino acid may be

chemically modified by reaction of the C-terminal carboxylic acid group of the peptide with an amine to form an amide group such as an amide of ammonia which is a preferred group; an amide of a C1 to C12 aliphatic alkyl amine, preferably a linear aliphatic alkyl amine; an amide of a hydroxyl-substituted C2 to C12 aliphatic alkyl amine; an amide of a linear 2-(C1 to C12 aliphatic alkyl)oxyethylamine group; and an amide of an omega-methoxy-poly(ethyleneoxy)n-ethylamine group (also referred to as an omega-methoxy-PEG-alpha-amine group or an omega-methoxy-(polyethylene glycol)amine group), where n is from 0 to 10. The C-terminal carboxylic acid group of the C-terminal amino acid of the peptide may also be in the form of an ester selected from the group consisting of an ester of a C1 to C12 aliphatic alkyl alcohol and an ester of a 2-(omega-methoxy-poly(ethyleneoxy)n)-ethanol (MPEG) group, where n is from 0 to 10. In one aspect, a polyethylene glycol component such as in a PEG ester, an MPEG ester, a PEG amide, an MPEG amide and the like preferably has a molecular weight of from about 500 to 40,000 Daltons, more preferably from 1000 to 25,000 Daltons, and most preferably from about 1000 to about 10,000 Daltons.

[00064] The C-terminal carboxylic acid group on the peptide, which may be represented by the formula peptide-C(O)OH, may also be amidated by conversion to an activated form such as a carboxylic acid halide, carboxylic acid anhydride, N-hydroxysuccinimide ester, pentafluorophenyl (OPfp) ester, 3-hydroxy-2,3-dihydro-4-oxo-benzo-triazone (ODhbt) ester, and the like to facilitate reaction with ammonia or a primary or secondary amine, preferably ammonia or a primary amine, and preferably while any other reactive groups in the peptide are protected by synthetic chemically compatible protecting groups well known in the art of peptide synthesis, especially of peptide solid phase synthesis, such as a benzyl ester, a t-butyl ester, a phenyl ester, etc. A resulting peptide amide could be represented by the formula peptide-C(O)-NR3R4 (the amide being at the C-terminal end of the peptide) wherein R3 and R4 are independently selected from the group consisting of hydrogen; C1 to C12 alkyl such as methyl, ethyl, butyl, isobutyl, cyclopropylmethyl, hexyl, dodecyl, and optionally higher e.g., from C14 to C24 such as tetradecyl, and the like as described above.

[00065] The C-terminal carboxylic acid of the C-terminal amino acid may also be converted to an amide of a hydroxyl-substituted C2 to C12 aliphatic alkyl amine (the hydroxyl group being

attached to a carbon atom rather than a nitrogen atom of the amine) such as 2-hydroxyethylamine, 4-hydroxybutylamine, and 12-hydroxydodecylamine, and the like.

[00066] The C-terminal carboxylic acid may also be converted to an amide of a hydroxyl-substituted C2 to C12 aliphatic alkyl amine, wherein the hydroxyl group can be acylated to form an ester with a C2 to C12 aliphatic carboxylic acid as described above. Preferably, in the peptide amide at the C-terminal end of the peptide represented by the formula peptide-C(O)NR5R6, R5 is hydrogen and R6 is selected from the group consisting of hydrogen, C1 to C12 alkyl, and hydroxyl-substituted C2 to C12 alkyl.

[00067] The C-terminal carboxylic acid of the C-terminal amino acid may be converted to an amide of a linear 2-(C1 to C12 aliphatic alkyl)oxyethylamine. Such an amide may be prepared, for example, by reaction of a linear C1 to C12 aliphatic alcohol with potassium hydride in diglyme with 2-chloroethanol to provide a linear C1 to C12 aliphatic alkyl ethanol, which can be converted to an amine by oxidation to an aldehyde, followed by reductive amination to an amine (for example using ammonia), or by conversion to an alkyl halide (e.g. using thionyl chloride) followed by treatment with an amine such as ammonia.

[00068] The C-terminal carboxylic acid of the C-terminal amino acid may be converted to an amide of a linear PEG-amine (e.g., omega-hydroxy-PEG-alpha-amine; omega-(C1-to-C12)-PEG-alpha-amine such as omega-methoxy- PEG-alpha-amine, i.e., MPEG-amine). In one aspect, the polyethylene glycol or PEG component preferably has a molecular weight of from about 500 to 40,000 Daltons, more preferably from 1000 to 25,000 Daltons, and most preferably from about 1000 to about 10,000 Daltons.

[00069] The C-terminal carboxylic acid of the C-terminal amino acid may also be converted to an amide of an omega-methoxy-poly(ethyleneoxy)n-ethylamine, where n is from 0 to 10, which can be prepared from the corresponding omega-methoxy-poly(ethyleneoxy)n-ethanol, for example, by conversion of the alcohol to an amine as described above.

[00070] In another embodiment, the C-terminal carboxyl may be converted to an amide represented by the formula peptide-C(O)-NR7R8, wherein R7 is hydrogen and R8 is a linear 2-(C1 to C12 aliphatic alkyl)oxyethyl group wherein the C1 to C12 aliphatic alkyl portion is as

described above and includes groups such as methoxyethyl (i.e., CH3O-CH2CH2-), 2-dodecyloxyethyl, and the like; or R7 is hydrogen and R8 is an omega-methoxy-poly(ethyleneoxy)n-ethyl group where the n of the poly(ethyleneoxy) portion is from 0 to 10, such as 2-methoxyethyl (i.e., CH3O-CH2CH2-), omega-methoxyethoxyethyl (i.e., CH3O-CH2CH2O-CH2CH2-) up to CH3O-(CH2CH2O)10-CH2CH2-.

[00071] The C-terminal carboxylic acid group of the C-terminal amino acid of the peptide may also be in the form of an ester of a C1 to C12 aliphatic alkyl alcohol, the aliphatic alkyl portion of the alcohol as described above. The C-terminal carboxylic acid group of the C-terminal amino acid of the peptide may also be in the form of an ester of a 2-(omega-methoxy-poly(ethyleneoxy)n)-ethanol group where n is from 0 to 10, which can be prepared from reaction of 2-methoxyethanol as a sodium 2-methoxyethanolate with stoichiometric amounts of ethylene oxide, the stoichiometric amount dependent on the size of n.

[00072] A side chain in an amino acid of the peptides may also be chemically modified. For example, a phenyl group in phenylalanine or tyrosine may be substituted with a substituent selected from the group consisting of:

a C1 to C24 aliphatic alkyl group (i.e., linear or branched, and/or saturated or unsaturated, and/or containing a cyclic group) such as methyl (preferred), ethyl, propyl, isopropyl, butyl, isobutyl, cyclopropyl, 2-methylcyclopropyl, cyclohexyl, octyl, decyl, dodecyl, hexadecyl, octadecyl, eicosanyl, docosanyl, tetracosanyl, 9-hexadecenyl, 9-octadecenyl, 11-octadecenyl, 9,12-octadecadienyl, 9,12,15-octadecatrienyl, 6,9,12-octadecatrienyl, 9-eicosenyl, 5,8,11,14-eicosatetraenyl, 5,8,11,14,17-eicosapentaenyl, 13-docosenyl, and 4,7,10,13,16,19-docosahexaenyl;

a C1 to C12 aliphatic alkyl group substituted with a hydroxyl group at least one carbon atom away from a site of unsaturation, examples of which hydroxyalkyl group include hydroxymethyl, hydroxyethyl, hydroxydodecyl, and the like;

a C1 to C12 alkyl group substituted with a hydroxyl group that is esterified with a C2 to C25 aliphatic carboxyl group of an acid such as acetic acid, butanoic acid, hexanoic acid, octanoic acid, decanoic acid, dodecanoic acid, tetradecanoic acid, hexadecanoic acid, 9-

hexadecenoic acid, octadecanoic acid, 9-octadecenoic acid, 11-octadecenoic acid, 9,12-octadecadienoic acid, 9,12,15-octadecatrienoic acid, 6,9,12-octadecatrienoic acid, eicosanoic acid, 9-eicosenoic acid, 5,8,11,14-eicosatetraenoic acid, 5,8,11,14,17-eicosapentaenoic acid, docosanoic acid, 13-docosenoic acid, 4,7,10,13,16,19-docosahexaenoic acid, tetracosanoic acid, and the like, a dicarboxylic acid such as succinic acid, or a hydroxyacid such as lactic acid, wherein the total number of carbon atoms of the ester substituent is between 3 and 25;

halogen such as fluoro-, chloro-, bromo-, and iodo-; nitro-;

amino- such as NH2, methyl amino, dimethylamino; trifluoromethyl-;

carboxyl (-COOH);

a C1 to C24 alkoxy (such as can be formed by alkylation of tyrosine) such as methoxy, ethoxy, propyloxy, isopropyloxy, butyloxy, isobutyloxy, cyclopropyloxy, 2-methoxycyclopropyloxy, cyclohexyloxy, octyloxy, decyloxy, dodecyloxy, hexadecyloxy, octadecyloxy, eicosanyloxy, docosanyloxy, tetracosanyloxy, 9-hexadecenyloxy, 9-octadecenyloxy, 11-octadecenyloxy, 9,12-octadecadienyloxy, 9,12,15-octadecatrienyloxy, 6,9,12-octadecatrienyloxy, 9-eicosenyloxy, 5,8,11,14-eicosatetraenyloxy, 5,8,11,14,17-eicosapentaenyloxy, 13-docosenyloxy, and 4,7,10,13,16,19-docosahexaenyloxy; and

a C2 to C12 hydroxyalkyloxy such as 2-hydroxyethyloxy and esters thereof with carboxylic acids as described above or with trifluoroacetic acid.

[00073] A serine hydroxyl group may be esterified with a substituent selected from the group consisting of:

a C2 to C12 aliphatic carboxylic acid group such as described above;

a trifluoroacetic acid group; and

a benzoic acid group.

[00074] The epsilon amino group in lysine may be chemically modified, for example, by amide formation with: a C2 to C12 aliphatic carboxylic acid group (for example, by reaction of the

amine with a chemically activated form of a carboxylic acid such as an acid chloride, an anhydride, an N-hydroxysuccinimide ester, a pentafluorophenyl (OPfp) ester, a 3-hydroxy-2,3-dihydro-4-oxo-benzo-triazone (ODhbt) ester, and the like) such as described above, or a benzoic acid group, or an amino acid group. Additionally, the epsilon amino group in lysine may be chemically modified by alkylation with one or two C1 to C4 aliphatic alkyl groups.

[00075] The carboxylic acid group in glutamic acid may be modified by formation of an amide with an amine such as: ammonia; a C1 to C12 primary aliphatic alkyl amine (the alkyl portion of which is as described above) including with methylamine; or an amino group of an amino acid.

[00076] The carboxylic acid group in glutamic acid may be modified by formation of an ester with a C1 to C12 aliphatic hydroxyalkyl group as described above, preferably an ester with a primary alcohol of a C1 to C12 aliphatic alkyl such as methanol, ethanol, propan-1-ol, n-dodecanol, and the like as described above.

[00077] In a preferred embodiment, the present invention comprises a method of inhibiting the release of at least one inflammatory mediator from a granule in at least one inflammatory cell in a tissue and/or fluid of a subject comprising administration to said tissue and/or fluid a therapeutically effective amount of a pharmaceutical composition comprising at least one peptide having an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence having from 4 to 23 contiguous amino acids of a reference sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1);

(b) an amino acid sequence having the sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1); and

(c) an amino acid sequence substantially identical to the sequence defined in (a), wherein the C-terminal amino acid of the peptide is optionally independently chemically modified, and the N-terminal amino acid of the peptide is independently chemically modified by acylation with a carboxylic acid selected from the group consisting of a C2 to C13 saturated or unsaturated aliphatic carboxylic acid, a C14 saturated (myristic acid) or unsaturated aliphatic carboxylic acid, a C15 to C24 saturated or unsaturated aliphatic carboxylic acid, and trifluoroacetic acid, or is not chemically modified, with the proviso that said peptide can be modified by acylation when its amino acid sequence begins with the sequence GAQF of the

reference sequence by acylation only with a carboxylic acid selected from the group consisting of a C2 to C13 saturated or unsaturated aliphatic carboxylic acid, a C14 unsaturated aliphatic carboxylic acid, a C15 to C24 saturated or unsaturated aliphatic carboxylic acid, and trifluoroacetic acid, or is not chemically modified, wherein said peptide, optionally combined with a pharmaceutically acceptable carrier, and in a therapeutically effective inflammatory mediator release-reducing amount to reduce the release of said inflammatory mediator from at least one inflammatory cell as compared to release of said inflammatory mediator from at least one of the same type of inflammatory cell that would occur in the absence of said at least one peptide.

[00078] The method preferably employs a peptide that can be acetylated at the alpha N-terminal amino acid. This peptide can consist of at least ten contiguous amino acid residues and is preferably embodied by acetyl - peptide 106 (SEQ ID NO: 106).

[00079] The method also employs a peptide consisting of at least four contiguous amino acid residues and more preferably at least six contiguous amino acid residues. Further, the peptide can be myristoylated at the alpha N-terminal amino acid when the peptide. The method also can utilized peptide that can be amidated with ammonia at the alpha C-terminal amino acid.

[00080] The method in a further embodiment utilizes a peptide comprises an amino acid sequence of (a) an amino acid sequence having from 4 to 23 contiguous amino acids of a reference sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1), wherein the N-terminal amino acid of the amino acid sequence of (a) is selected from amino acid position 2 to 21 of the reference sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1). Further, these peptides can be myristoylated at the alpha N-terminal amino acid and also can be amidated with ammonia at the alpha C-terminal amino acid.

[00081] The method of administration according to the present invention defines the reduction of the release of an inflammatory mediator as blocking or inhibiting the mechanism that releases an inflammatory mediator from the inflammatory cell in said subject.

[00082] The method of aministration includes incorporating or mixing the disclosed peptides with a pharmaceutically acceptable carrier to form a pharmaceutical composition.

[00083] The method of administration of the present invention release of at least one inflammatory mediator release-reducing amount to reduce the release of said inflammatory mediator from at least one inflammatory cell as compared to release of said inflammatory mediator from at least one of the same type of inflammatory cell that would occur in the absence of said at least one peptide. The inflammatory cell in said subject can be a leukocyte, a granulocyte, a basophil, an eosinophil, monocyte, macrophage or a combination thereof.

[00084] The inflammatory mediator released from at least one granule of at least one inflammatory cell is selected from the group consisting of myeloperoxidase (MPO), eosinophil peroxidase (EPO), major basic protein [MBP], lysozyme, granzyme, histamine, proteoglycan, protease, a chemotactic factor, cytokine, a metabolite of arachidonic acid, defensin, bactericidal permeability-increasing protein (BPI), elastase, cathepsin G, cathepsin B, cathepsin D, beta-D-glucuronidase, alpha-mannosidase, phospholipase A_2, chondroitin-4-sulphate, proteinase 3, lactoferrin, collagenase, complement activator, complement receptor, N-formylmethionyl-leucyl-phenylalanine (FMLP) receptor, laminin receptor, cytochrome b_{558}, monocyte-chemotactic factor, histaminase, vitamin B12 binding protein, gelatinase, plasminogen activator, beta-D-glucuronidase, and a combination thereof. Preferably the inflammatory mediator is selected from the group consisting of myeloperoxidase (MPO), eosinophil peroxidase (EPO), major basic protein (MBP), lysozyme, granzyme and a combination thereof.

[00085] The method according to claim 13, wherein said effective inflammatory mediator release-reducing amount of said peptide comprises a degranulation-inhibiting amount of peptide that reduces the amount of an inflammatory mediator released from at least one inflammatory cell from about 1% to about 99% or preferably about 5-50% to about 99%, as compared to the amount released from at least one inflammatory cell in the absence of the peptide.

[00086] The method of the present invention is useful for the treatment of a subject afflicted by or suffering from a respiratory disease. This respiratory disease may be asthma, chronic bronchitis, chronic obstructive pulmonary disease (COPD) and cystic fibrosis. The subjects that can be treated by the present invention are preferably mammals, such as humans, canines, equines and felines.

[00087] The method of administration of the peptides of the present invention are by topical administration, parenteral administration, rectal administration, pulmonary administration, nasal administration, and oral administration. More preferably, the pulmonary administration comprises an aerosol, which can be generated from a dry powder inhaler, a metered dose inhaler or nebulizer. Additionally, the administration to the subject can further include the administration of a second molecule selected from the group consisting of an antibiotic, an antiviral compound, an antiparasitic compound, an anti-inflammatory compound, and an immunomodulator.

[00088] The method is also useful for the treatment of a subject who is afflicted by or suffering from a disease selected from the group consisting of a bowel disease, a skin disease, an autoimmune disease, a pain syndrome, and combinations thereof. More specifically, the bowel disease is selected from the group consisting of ulcerative colitis, Crohn's disease and irritable bowel syndrome. Skin diseases also treatable by the present method includes rosacea, eczema, psoriasis and severe acne. Additiona a subject suffering from arthritis may also be treated by the present invention.

[00089] The present invention in one embodiment encompasses the administration of peptides comprising an amino acid sequence substantially identical to the amino acid sequence of (a) having from 4 to 23 contiguous amino acids of a reference sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1). These peptides preferably are selected from the group consisting of SEQ ID NOS: 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 247, 248, 249, 250, 251 and 252. These peptides can be further acetylated at the alpha N-terminal amino acid or myristoylated at the alpha N-terminal amino acid and optionally amidated with ammonia at the alpha C-terminal amino acid.

[00090] The method of the present invention also is useful for reducing mucus hypersecretion in a subject by the administration of the peptides of the present invention as described herein for also reducing MARCKS-related mucus hypersecretion from at least one mucus secreting cell or tissue in the subject, whereby mucus hypersecretion in the subject is reduced compared to that which would occur in the absence of said administration of said peptide.

[00091] The present invention is directed to an isolated peptide having an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence having from 4 to 23 contiguous amino acids of a reference sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1);

(b) an amino acid sequence having the sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1); and

(c) an amino acid sequence substantially identical to the sequence defined in (a),

wherein the C-terminal amino acid of the peptide is optionally independently chemically modified, and the N-terminal amino acid of the peptide is independently chemically modified by acylation with a carboxylic acid selected from the group consisting of a C2 to C13 saturated or unsaturated aliphatic carboxylic acid, a C14 saturated or unsaturated aliphatic carboxylic acid, a C15 to C24 saturated or unsaturated aliphatic carboxylic acid, and trifluoroacetic acid, or is not chemically modified, with the proviso that said peptide is modified by acylation when its amino acid sequence begins with the sequence GAQF of the reference sequence by acylation only with a carboxylic acid selected from the group consisting of a C2 to C13 saturated or unsaturated aliphatic carboxylic acid, a C14 unsaturated aliphatic carboxylic acid, a C15 to C24 saturated or unsaturated aliphatic carboxylic acid, and trifluoroacetic acid, or is not chemically modified, wherein said peptide, optionally combined with a pharmaceutically acceptable carrier, and in a therapeutically effective inflammatory mediator release-reducing amount to reduce the release of said inflammatory mediator from at least one inflammatory cell as compared to release of said inflammatory mediator from at least one of the same type of inflammatory cell that would occur in the absence of said at least one peptide.

[00092] The isolated peptide can be acetylated at the alpha N-terminal amino acid. The isolated peptide consists of at least ten contiguous amino acid residues and preferably is an isolated peptide consists of acetyl - peptide 106 (SEQ ID NO: 106).

[00093] In a further embodiment, the peptide consists of at least four contiguous amino acid residues or peptide consists of at least six contiguous amino acid residues.

[00094] The peptide can also be myristoylated at the alpha N-terminal amino acid and/or peptide can be amidated with ammonia at the alpha C-terminal amino acid.

[00095] The isolated peptide can further comprise an amino acid sequence of (a) described above, (a) an amino acid sequence having from 4 to 23 contiguous amino acids of a reference sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1); wherein the N-terminal amino acid of the amino acid sequence of (a) is selected from amino acid position 2 to 21 of the reference sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1). This peptide can be further myristoylated or acetylated at the alpha N-terminal amino acid or optionally amidated with ammonia at the alpha C-terminal amino acid.

[00096] The isolated peptide in a further embodiment, wherein the amino acid sequence is substantially identical to the amino acid sequence of (a) having from 4 to 23 contiguous amino acids of a reference sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1). These peptides preferably are selected from the group consisting of SEQ ID NOS: 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 247, 248, 249, 250, 251 and 252. These peptides can be further acetylated at the alpha N-terminal amino acid or myristoylated at the alpha N-terminal amino acid and optionally amidated with ammonia at the alpha C-terminal amino acid. amino acid sequence of (c) substantially identical to the amino acid sequence of (a) is selected from the group consisting of SEQ ID NOS: 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 247, 248, 249, 250, 251 and 252.

[00097] The invention also emcompasses a composition comprising an isolated peptide as described in the paragraphs above and described herein and an excipient. The invention also encompasses a pharmaceutical composition comprising an isolated peptide an isolated peptide as described in the paragraphs above and described herein and a pharmaceutically acceptable carrier. The pharmaceutical composition can further preferably be sterile, sterilizable or sterilized. These peptides can be contained in a kit with reagents useful for administration.

Brief Description of the Drawings

[00098] FIGS. 1A-1B illustrate that PKC-dependent phosphorylation releases MARCKS from the plasma membrane to the cytoplasm.

[00099] FIGS.2A-2C show that PKG induces dephosphorylation of MARCKS by activating PP2A.

[000100] FIG. 3 depicts bar graphs that demonstrate that PP2A is an essential component of the mucin secretory pathway.

[000101] FIG. 4 is a gel that illustrates that MARCKS associates with actin and myosin in the cytoplasm.

[000102] FIG. 5 depicts a signaling mechanism controlling MPO secretion in neutrophils.

[000103] FIG. 6 is a bar graph depicting the ability of MANS peptide to block secretion of myloperoxidase from isolated canine neutrophils.

[000104] FIG. 7 is a bar graph depicting the ability of MANS peptide to block secretion of myloperoxidase from isolated human neutrophils.

[000105] FIG. 8 is a bar graph showing that PMA stimulates a small increase in MPO secretion from LPS-stimulated human neutrophils which is enhanced in a concentration-dependent manner by co-stimulation with 8-Br-cGMP.

[000106] FIG. 9 is a bar graph showing that 8-Br-cGMP simulation has little effect on MPO secretion from LPS-stimulated human neutrophils until a co-stimulation with PMA occurs in a concentration-dependent manner.

[000107] FIG. 10 is a bar graph showing that PMA stimulates a small increase in MPO secretion from LPS-stimulated canine neutrophils which is enhanced in a concentration-dependent manner by co-stimulation with 8-Br-cGMP.

[000108] FIG. 11 is a bar graph showing that 8-Br-cGMP simulation has little effect on MPO secretion from LPS-stimulated canine neutrophils until a co-stimulation with PMA occurs in a concentration-dependent manner.

[000109] FIG. 12 is a bar graph showing that co-stimulation with PMA+8-Br-cGMP is required for maximal MPO secretion from LPS-stimulated canine neutrophils.

Detailed Description of the Invention

[000110] The present invention will now be described more fully hereinafter with reference to the accompanying figures, in which preferred embodiments of the invention are illustrated. This invention may, however, be embodied in different forms and should not be construed as limited to the embodiments set forth herein. Rather, these embodiments are provided so that this disclosure will be thorough and complete, and will fully convey the scope of the invention to those skilled in the art.

[000111] 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. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. The use of the words "a" or "an" herein to describe any aspect of the present invention is to be interpreted as indicating one or more.

[000112] The present invention is directed to a method of inhibiting the exocytotic release of at least one inflammatory mediator from at least one inflammatory cell comprising contacting the at least one inflammatory cell, which cell comprises at least one inflammatory mediator contained within a vesicle inside the cell, with at least one peptide selected from the group consisting of a MANS peptide and an active fragment thereof in an effective amount to reduce the release of the inflammatory mediator from the inflammatory cell as compared to the release of the inflammatory mediator from the same type of inflammatory cell that would occur in the absence of the at least one peptide.

[000113] The present invention is further directed to a method of inhibiting the release of at least one inflammatory mediator from at least one inflammatory cell in a tissue or fluid of a subject comprising the administration to the subject's tissue and/or fluid, which comprises at least one inflammatory cell comprising at least one inflammatory mediator contained within a vesicle inside the cell, a therapeutically effective amount of a pharmaceutical composition comprising at least one peptide selected from the group consisting of a MANS peptide and an active fragment thereof in a therapeutically effective amount to reduce the release of the inflammatory mediator from at least one inflammatory cell as compared to release of the inflammatory mediator from at least one of the same type of inflammatory cell that would occur in the absence of the at least one peptide. More specifically, reducing the release of an inflammatory mediator comprises

blocking or inhibiting the mechanism that releases an inflammatory mediator from the inflammatory cell.

[000114] The present invention is directed to the contact and/or administration of the peptide described above and throughout the specification with any known inflammatory cell that may be contained in the tissue or fluid of a subject which contains at least one inflammatory mediator contained within a vesicle inside the cell. The inflammatory cell is preferably a leukocyte, more preferably a granulocyte, which can be further classified as a neutrophil, a basophil, an eosinophil or a combination thereof. The inflammatory cells contacted in the present method may also be a monocyte/macrophage.

[000115] The present invention is directed to reducing the release of inflammatory mediators contained within the vesicles of inflammatory cells and these inflammatory mediators are selected from the group consisting of myeloperoxidase (MPO), eosinophil peroxidase (EPO), major basic protein (MBP), lysozyme, granzyme, histamine, proteoglycan, protease, a chemotactic factor, cytokine, a metabolite of arachidonic acid, defensin, bactericidal permeability-increasing protein (BPI), elastase, cathepsin G, cathepsin B, cathepsin D, beta-D-glucuronidase, alpha-mannosidase, phospholipase A_2, chondroitin-4-sulphate, proteinase 3, lactoferrin, collagenase, complement activator, complement receptor, N-formylmethionyl-leucyl-phenylalanine (FMLP) receptor, laminin receptor, cytochrome b_{558}, monocyte-chemotactic factor, histaminase, vitamin B12 binding protein, gelatinase, plasminogen activator, beta-D-glucuronidase, and a combination thereof. Preferably, these inflammatory mediators are selected from the group consisting of myeloperoxidase (MPO), eosinophil peroxidase (EPO), major basic protein (MBP), lysozyme, granzyme and a combination thereof.

[000116] The present invention contacts an effective amount of the peptide with an inflammatory cell, wherein the effective amount is defined as a degranulation-inhibiting amount of MANS peptide or an active fragment thereof that reduces the amount of an inflammatory mediator released from at least one inflammatory cell from about 1% to about 99% as compared to the amount released from at least one inflammatory cell in the absence of MANS peptide or an active fragment thereof. This amount is also known as an effective inflammatory mediator release-reducing amount. More preferably, this effective amount of the contacted peptide

comprises a degranulation-inhibiting amount of MANS peptide or an active fragment thereof that reduces the amount of an inflammatory mediator released from at least one inflammatory cell from between about 5-50% to about 99% as compared to the amount released from at least one inflammatory cell in the absence of MANS peptide or an active fragment thereof.

[000117] The present invention in one embodiment is directed to the administration of at least one peptide comprising a MANS peptide and an active fragment thereof in a therapeutically effective amount into tissue or fluid of a subject where the subject is afflicted by a respiratory disease, which is preferably asthma, chronic bronchitis or COPD. In a further embodiment, the subject may be afflicted by a bowel disease, a skin disease, an autoimmune disease, a pain syndrome, and combinations thereof. The bowel disease may be ulcerative colitis, Crohn's disease or irritable bowel syndrome. The subject may be afflicted with a skin disease, such as rosacea, eczema, psoriasis or severe acne. The subject may also be afflicted with arthritis, such as rheumatoid arthritis, psoriatic arthritis, systemic lupus erythematosus. Subjects afflicted by cystic fibrosis may also be treated by the present method and peptides. The present method is preferably useful for the treatment of subjects, such as mammals, and preferably humans, canines, equines and felines.

[000118] The present method of treatment of subjects is by the administration of one or more peptides including the MANS peptide or an active fragment described herein to include topical administration, parenteral administration, rectal administration, pulmonary administration, nasal administration, or oral administration. More specifically, pulmonary administration is selected from the group of aerosol, dry powder inhaler, metered dose inhaler, and nebulizer. Additionally, the disclosed method may further comprise the administration to the subject of a second molecule selected from the group consisting of an antibiotic, an antiviral compound, an antiparasitic compound, an anti-inflammatory compound, and an immunomodulator.

[000119] In one aspect, the invention relates to a method of administering a pharmaceutical composition. The pharmaceutical composition comprises a therapeutically effective amount of a known compound and a pharmaceutically acceptable carrier. A "therapeutically effective" amount as used herein is an amount of a compound that is sufficient to ameliorate symptoms exhibited by a subject. The therapeutically effective amount will vary with the age and physical

condition of the patient, the severity of the condition of the patient being treated, the duration of the treatment, the nature of any concurrent treatment, the pharmaceutically acceptable carrier used and like factors within the knowledge and expertise of those skilled in the art. Pharmaceutically acceptable carriers are preferably solid dosage forms such as tablets or capsules. Liquid preparations for oral administration also may be used and may be prepared in the form of syrups or suspensions, e.g., solutions containing an active ingredient, sugar, and a mixture of ethanol, water, glycerol, and propylene glycol. If desired, such liquid preparations may include one or more of following: coloring agents, flavoring agents, and saccharin. Additionally, thickening agents such as carboxymethylcellulose also may be used as well as other acceptable carriers, the selection of which are known in the art.

[000120] As stated above, the present invention relates to methods for regulating cellular secretory processes, especially those releasing inflammatory mediators from inflammatory cells. As used herein, the term "regulating" means blocking, inhibiting, decreasing, reducing, increasing, enhancing or stimulating. A number of cellular secretory processes involve the release of contents from membrane-bound vesicles or granules within cells A membrane-bound vesicle or granule is defined as an intracellular particle, which is primarily vesicular (or a vesicle inside a cell) and which contains stored material that can be secreted. Some of the contents of these vesicles, such as those contained in inflammatory cells, have been found to be responsible for a variety of pathologies in numerous mammalian tissues. Some of the effects of these secretions appear to include damage of previously healthy tissue during inflammation. This invention provides a means of blocking secretion from any membrane-bound vesicle, including those found in inflammatory cells, by targeting a specific molecule important in the intracellular secretory pathway with a synthetic peptide. This approach may be of therapeutic importance for the treatment of a wide variety of hypersecretory and inflammatory conditions in humans and animals.

[000121] More specifically, the present invention targets inflammatory cells that contain the inflammatory mediators in one or more granules or vesicles within the cells' cytoplasm. The cells are contacted with one or more peptides that are selected from the MANS peptide or an active fragment thereof, all of which are described in detail herein. Preferably the contact of the peptide with the inflammatory cell is via administration to a subject afflicted by or suffering

from a disease in which these inflammatory cells are present in specific tissue or fluid within the tissue. Upon administration or contact of the peptide with the cell, the peptide competitively competes for and competitively inhibits the binding of the native MARCKS protein to the membrane of the intracellular granules or vesicles which contain the inflammatory mediators. As a result of blocking the binding of the MARCKS protein to the vesicles in the inflammatory cells, these vesicles in these cells do not move to the plasma membrane of the cells as they would normally do when stimulated to exocytotically release their contents of inflammatory mediators out of the cells. Thus, the method of the present invention inhibits the movement of the vesicles to the cells' plasma membrane, which in turn, reduces the release of the inflammatory mediators from the inflammatory cells. The amount of inflammatory mediators released from the cells over time is reduced because both the rate of release and the amount of release of the mediators from the inflammatory cells is dependent upon the concentration of the peptide administered and contacted with the inflammatory cells.

[000122] One benefit of the present invention is that it may combine a therapy that includes the direct blocking of mucus secretion with a unique anti-inflammatory therapy. A benefit of the present invention over current anti-inflammation therapies that affect a general suppression of the immune system is that the peptide is thought to block secretion of only intracellular components secreted from inflammatory cells. Thus, many aspects of the immune system should still function even with the inhibition of the inflammatory mediators.

[000123] The compounds of the invention may regulate, i.e. block, inflammatory mediator release from cells. This inhibition of release of inflammatory mediators is an attractive means for preventing and treating a variety of disorders, e.g., diseases and pathological conditions involving inflammation. Thus, the compounds of the invention may be useful for the treatment of such conditions. These encompass airway diseases and chronic inflammatory diseases including, but not limited to, osteoarthritis, multiple sclerosis, Guillain-Barre syndrome, Crohn's disease, ulcerative colitis, psoriasis, graft versus host disease and systemic lupus erythematosus. The compounds of the invention can also be used to treat other disorders associated with the activity of elevated levels of proinflammatory mediators and enzymes such as responses to various infectious agents and a number of diseases of autoimmunity such as rheumatoid arthritis, toxic shock syndrome, diabetes and inflammatory bowel diseases.

[000124] Uses of the peptide and methods of the invention include therapies to combat inflammation along with therapies that will combine the anti-inflammatory activity of the peptide with its ability to block mucus secretion. Diseases that may be treated by the peptide's ability to block both inflammation and mucus secretion include but are not limited to inflammatory bowel diseases, digestive disorders (i.e., inflamed gall bladder, Menetier's disease) and inflammatory airway diseases.

[000125] Other proinflammatory mediators have been correlated with a variety of disease states that correlate with influx of neutrophils into sites of inflammation or injury. Blocking antibodies have been demonstrated as useful therapies against the neutrophil-associated tissue injury in acute inflammation (Harada *et al.*, 1996, *Molecular Medicine Today* 2, 482). Cells other than neutrophils that may release inflammatory mediators include other leukocytes, such as basophils, eosinophils, monocytes and lymphocytes, and therapies may be directed against secretion from these cells. Neutrophils, eosinophils, and basophils are each a type of granulocyte, i.e., a leukocyte that has granules in its cytoplasm. Leukocytes synthesize a number of inflammatory mediators that are packaged and stored in cytoplasmic granules. Among these mediators are, for example, myeloperoxidase [MPO] in neutrophils (Borregaard N, Cowland JB. Granules of the human neutrophilic polymorphonuclear leukocyte. Blood 1997; 89:3503-3521), eosinophil peroxidase [EPO] and major basic protein [MBP] in eosinophils (Gleich G J. Mechanisms of eosinophil-associated inflammation. J Allergy Clin Immunol 2000; 105:651-663), lysozyme in monocytes/macrophages (Hoff T, Spencker T, Emmendoerffer A., Goppelt-Struebe M. Effects of glucocorticoids on the TPA-induced monocytic differentiation. J Leukoc Biol 1992; 52:173-182; Balboa M A, Saez Y, Balsinde J. Calcium-independent phospholipase A2 is required for lysozyme secretion in U937 promonocytes. J Immunol 2003; 170:5276-5280), and granzyme in natural killer (NK) cells and cytotoxic lymphocytes (Bochan MR, Goebel WS, Brahmi Z. Stably transfected antisense granzyme B and perforin constructs inhibit human granule-mediated lytic ability. Cell Immunol 1995; 164:234-239; Gong J H., Maki G, Klingemann HG. Characterization of a human cell line (NK-92) with phenotypical and functional characteristics of activated natural killer cells. Leukemia 1994; 8:652-658; Maki G, Klingemann HG, Martinson JA, Tam YK. Factors regulating the cytotoxic activity of the human natural killer cell line, NK-92. J Hematother Stem Cell Res 2001; 10:369-383; and Takayama H, Trenn G, Sitkovsky MV. A novel cytotoxic T lymphocyte activation assay. J Immunol Methods 1987; 104:183-1907-10).

These mediators can be released at sites of injury and can contribute to inflammation and repair, such as in the lung and elsewhere, as a result of the infiltration of these cells to the tissue site of injury or disease. Leukocytes release these granules via an exocytotic mechanism (Burgoyne RD, Morgan A. Secretory granule exocytosis. Physiol Rev 2003; 83:581-632; Logan MR, Odemuyiwa SO, Moqbel R. Understanding exocytosis in immune and inflammatory cells: the molecular basis of mediator secretion. J Allergy Clin Immunol 2003; 111: 923-932),

[000126] Mast cells, which usually do not circulate in the blood stream, and basophils contain secretory cytoplasmic granules which store and can release, upon cell activation, preformed inflammatory (anaphylactic) mediators, such as histamine; proteoglycans, such as heparin and chondroitin sulphate; proteases such as tyrptase, chymase, carboxypeptidase, and cathepsin G-like protease; chemotactic factors, cytokines and metabolites of arachidonic acid that act on the vasculature, smooth muscle, connective tissue, mucous glands and inflammatory cells.

[000127] Neutrophils, also known as polymorphonuclear leukocytes (PMN), comprise 50 to 60% of the total circulating leukocytes. Neutrophils act against infectious agents, such as bacteria, fungi, protozoa, viruses, virally infected cells, as well as tumor cells, that penetrate the body's physical barriers at sites of infection or injury. Neutrophils mature through six morphological stages: myeloblast, promyeloblast, myelocyte, metamyelocyte, non-segmented (band) neutrophil, and segmented (functionally active) neutrophil.

[000128] In neutrophils, inflammatory mediators are stored in primary (azurophil), secondary (specific), and tertiary (gelatinase) granules, as well as in secretory vesicles. Among numerous mediators of inflammation, primary (azurophil) granules contain myeloperoxidase (MPO), lysozyme, defensins, bactericidal permeability-increasing protein (BPI), elastase, cathepsin G, cathepsin B, cathepsin D, beta-D-glucuronidase, alpha-mannosidase, phospholipase A_2, chondroitin-4-sulphate, and proteinase 3 (see, for example, Hartwig JH, Thelen M, Rosen A, Janmey PA, Nairn AC, Aderem A. MARCKS is an actin filament crosslinking protein regulated by protein kinase C and calcium-calmodulin. Nature 1992; 356:618-622); secondary (specific) granules contain lysozyme, lactoferrin, collagenase, complement activator, phospholipase A_2, complement receptors, e.g., CR3, CR4, N-formylmethionyl-leucyl-phenylalanine (FMLP) receptors, laminin receptors, cytochrome b_{558}, monocyte-chemotactic factor, histaminase, and

vitamin B12 binding protein; and small storage granules contain gelatinase, plasminogen activator, cathepsin B, cathepsin D, beta-D-glucuronidase, alpha-mannosidase, and cytochrome b_{558}.

[000129] Neutrophil granules contain antimicrobial or cytotoxic substances, neutral proteinases, acid hydrolases and a pool of cytoplasmic membrane receptors. Among azurophil granule constituents myeloperoxidase (MPO) is a critical enzyme in the conversion of hydrogen peroxide to hypochlorous acid. Together with hydrogen peroxide and a halide cofactor it forms an effective microbicidal and cytotoxic mechanism of leukocytes - the myeloperoxidase system.

[000130] Defensins, which constitute 30 to 50% of azurophilic granule protein, are small (molecule weight < 4000) potent antimicrobial peptides that are cytotoxic to a broad range of bacteria, fungi and some viruses. Their toxicity may be due to membrane permeabilization of the target cell which is similar to other channel-forming proteins (perforins).

[000131] Bacterial permeability-increasing (BPI) protein is a member of perforins. It is highly toxic to gram-negative bacteria but not to gram-positive bacteria or fungi and can also neutralize endotoxin, the toxic lipopolysaccharide component of gram-negative bacterial cell envelope.

[000132] Lactoferrin sequesters free iron, thereby preventing the growth of ingested microorganisms that survive the killing process and increases bacterial permeability to lysozyme.

[000133] Serine proteases such as elastase and cathepsin G hydrolyze proteins in bacterial cell envelopes. Substrates of granulocyte elastase include collagen cross-linkages and proteoglycans, as well as elastin components of blood vessels, ligaments, and cartilage. Cathepsin D cleaves cartilage proteoglycans, whereas granulocyte collagenases are active in cleaving type I and, to a lesser degree, type III collagen from bone, cartilage, and tendon. Collagen breakdown products have chemotactic activity for neutrophils, monocytes, and fibroblasts.

[000134] Regulation of tissue destructive potential of lysosomal proteases is mediated by protease inhibitors such as alpha2-macroglobulin and alpha1-antiprotease. These antiproteases are present in serum and synovial fluids. They may function by binding to and covering the active sites of proteases. Protease-antiprotease imbalance can be important in the pathogenesis of emphysema.

[000135] Azurophil granules function predominantly in the intracellular milieu (in the phagolysosomal vacuole), where they are involved in the killing and degradation of microorganisms. Neutrophil specific granules are susceptible to release their contents extracellularly and have an important role in initiating inflammation. Specific granules represent an intracellular reservoir of various plasma membrane components including cytochrome b (component of NADPH oxidase, an enzyme responsible for the production of superoxide), receptors for complement fragment iC3b (CR3, CR4), for laminin, and formylmethionyl-peptide chemoattractants. In addition to others, there is histaminase which is relevant for the degradation of histamine, vitamin binding protein, and plasminogen activator which is responsible for plasmin formation and cleavage of C5a from C5.

[000136] The importance of neutrophil granules in inflammation is apparent from studies of several patients with congenital abnormalities of the granules. Patients with Chédiak-Higashi syndrome have a profound abnormality in the rate of establishment of an inflammatory response and have abnormally large lysosomal granules. The congenital syndrome of specific granule deficiency is an exceedingly rare disorder characterized by diminished inflammatory responses and severe bacterial infections of skin and deep tissues.

[000137] Although mechanisms regulating exocytotic secretion of these granules are only partially understood, several key molecules in the process have been identified, including intracellular Ca2+ transients (Richter et al. Proc Natl Acad Sci USA 1990; 87:9472–9476; Blackwood et al., Biochem J 1990; 266:195-200), G proteins, tyrosine and protein kinases (PK, especially PKC) (Smolen et al., Biochim Biophys Acta 1990; 1052:133-142; Niessen et al., Biochim. Biophys. Acta 1994; 1223:267-273; Naucler et al., Pettersen et al., Chest 2002; 121; 142-150), Rac2 (Abdel-Latif et al., Blood 2004; 104:832-839; Lacy et al., J Immunol 2003; 170:2670-2679) and various SNARE's, SNAP's and VAMP's (Sollner et al., Nature 1993; 362: 318-324; Lacy, Pharmacol Ther 2005; 107:358-376).

[000138] SNARE (Soluble N-ethylmaleimide attachment protein receptor) proteins are a family of membrane-associated proteins characterized by an alpha-helical coiled-coil domain called the SNARE motif (Li et al., Cell. Mol. Life Sci. 60: 942-960 (2003)). These proteins are classified as v-SNAREs and t-SNAREs based on their localization on vesicle or target membrane; another

classification scheme defines R-SNAREs and Q-SNAREs, as based on the conserved arginine or glutamine residue in the centre of the SNARE motif. SNAREs are localized to distinct membrane compartments of the secretory and endocytic trafficking pathways, and contribute to the specificity of intracellular membrane fusion processes. The t-SNARE domain consists of a 4-helical bundle with a coiled-coil twist. The SNARE motif contributes to the fusion of two membranes. SNARE motifs fall into four classes: homologues of syntaxin 1a (t-SNARE), VAMP-2 (v-SNARE), and the N- and C-terminal SNARE motifs of SNAP-25. One member from each class may interact to form a SNARE complex. The SNARE motif is found in the N-terminal domains of certain syntaxin family members such as syntaxin 1a, which is required for neurotransmitter release (Lerman et al., Biochemistry 39: 8470-8479 (2000)), and syntaxin 6, which is found in endosomal transport vesicles (Misura et al., Proc. Natl. Acad. Sci. U.S.A. 99: 9184-9189 (2002)).

[000139] SNAP-25 (synaptosome-associated protein 25 kDa) proteins are components of SNARE complexes, which may account for the specificity of membrane fusion and to directly execute fusion by forming a tight complex (the SNARE or core complex) that brings the synaptic vesicle and plasma membranes together. The SNAREs constitute a large family of proteins that are characterized by 60-residue sequences known as SNARE motifs, which have a high propensity to form coiled coils and often precede carboxy-terminal transmembrane regions. The synaptic core complex is formed by four SNARE motifs (two from SNAP-25 and one each from synaptobrevin and syntaxin 1) that are unstructured in isolation but form a parallel four-helix bundle on assembly. The crystal structure of the core complex has revealed that the helix bundle is highly twisted and contains several salt bridges on the surface, as well as layers of interior hydrophobic residues. A polar layer in the centre of the complex is formed by three glutamines (two from SNAP-25 and one from syntaxin 1) and one arginine (from synaptobrevin) (Rizo et al., Nat Rev Neurosci 3: 641-653 (2002)). Members of the SNAP-25 family contain a cluster of cysteine residues that can be palmitoylated for membrane attachment (Risinger et al., J. Biol. Chem. 268: 24408-24414 (1993)).

[000140] The major role of neutrophils is to phagocytose and destroy infectious agents. They also limit the growth of some microbes, prior to onset of adaptive (specific) immunological responses. Although neutrophils are essential to host defense, they have also been implicated in

the pathology of many chronic inflammatory conditions and in ischemia-reperfusion injury. Hydrolytic enzymes of neutrophil origin and oxidatively inactivated protease inhibitors can be detected in fluid isolated from inflammatory sites. Under normal conditions, neutrophils can migrate to sites of infection without damage to host tissues. However, undesirable damage to a host tissue can sometimes occur. This damage may occur through several independent mechanisms. These include premature activation during migration, extracellular release of toxic products during the killing of some microbes, removal of infected or damage host cells and debris as a first step in tissue remodeling, or failure to terminate acute inflammatory responses. Ischemia-reperfusion injury is associated with an influx of neutrophils into the affected tissue and subsequent activation. This may be triggered by substances released from damaged host cells or as a consequence of superoxide generation through xantine oxidase.

[000141] Under normal conditions, blood may contain a mixture of normal, primed, activated and spent neutrophils. In an inflammatory site, mainly activated and spent neutrophils are present. Activated neutrophils have enhanced production of reactive oxygen intermediates (ROI). A subpopulation of neutrophils with the enhanced respiratory burst has been detected in the blood of people with an acute bacterial infection and patients with the adult respiratory distress syndrome (ARDS). This is an example of a neutrophil paradox. Neutrophils have been implicated in the pathology of this condition because of the large influx of these cells into the lung and the associated tissue damage caused by oxidants and hydrolytic enzymes released from activated neutrophils. The impairment of neutrophil microbicidal activity that occurs as the ARDS worsens may be a protective response on the part of the host, which is induced locally by inflammatory products.

[000142] The acute phase of thermal injury is also associated with neutrophil activation, and this is followed by a general impairment in various neutrophil functions. Activation of neutrophils by immune complexes in synovial fluid contributes to the pathology of rheumatoid arthritis. Chronic activation of neutrophils may also initiate tumor development because some ROI generated by neutrophils damage DNA and proteases promote tumor cell migration. In patients suffering from severe burns, a correlation has been established between the onset of bacterial infection and reduction in the proportion and absolute numbers of neutrophils positive for antibody and complement receptors. Oxidants of neutrophil origin have also been shown to

oxidize low-density lipoproteins (LDL), which are then more effectively bound to the plasma membrane of macrophages through specific scavenger receptors. Uptake of these oxidized LDL by macrophages may initiate atherosclerosis. In addition, primed neutrophils have been found in people with essential hypertension, Hodgkin's disease, inflammatory bowel disease, psoriasis, sarcoidosis, and septicemia, where priming correlates with high concentrations of circulating TNF-alpha (cachectin).

[000143] Hydrolytic damage to host tissue and therefore chronic inflammatory conditions may occur when antioxidant and antiprotease screens are overwhelmed. Antiprotease deficiency is thought to be responsible for the pathology of emphysema. Many antiproteases are members of the serine protease inhibitor (SERPIN) family. Although the circulation is rich in antiproteases, these large proteins may be selectively excluded at sites of inflammation because neutrophils adhere to their targets. Oxidative stress may initiate tissue damage by reducing the concentration of extracellular antiproteases to below the level required to inhibit released proteases. Chlorinated oxidants and hydrogen peroxide can inactivate antiproteases such as alpha1-protease inhibitor and alpha2-macroglobulin, which are endogenous inhibitors of elastase, but simultaneously activate latent metalloproteases such as collagenases and gelatinase, which contribute to the further inactivation of antiproteases.

[000144] Cytoplasmic constituents of neutrophils may also be a cause of formation of specific anti-neutrophil cytoplasmic antibodies (ANCA), which are closely related to the development of systemic vasculitis and glomerulonephritis. ANCA are antibodies directed against enzymes that are found mainly within the azurophil or primary granules of neutrophils. There are three types of ANCA that can be distinguished by the patterns they produce by indirect immunofluorescence on normal ethanol-fixed neutrophils. Diffuse fine granular cytoplasmic fluorescence (cANCA) is typically found in Wegener's granulomatosis, in some cases of microscopic polyarteritis and Churg Strauss syndrome, and in some cases of crescentic and segmental necrotizing glomerulonephritis. The target antigen is usually proteinase 3. Perinuclear fluorescence (pANCA) is found in many cases of microscopic polyarteritis and glomerulonephritis. These antibodies are often directed against myeloperoxidase but other targets include elastase, cathepsin G, lactoferrin, lysozyme and beta-D-glucuronidase. The third group designated "atypical" ANCA includes neutrophil nuclear fluorescence and some unusual cytoplasmic

patterns and while a few of the target antigens are shared with pANCA, the others have not been identified yet. pANCA are also found in a third of patients with Crohn's disease. The reported incidence of ANCA in rheumatoid arthritis and SLE varies considerably but the patterns are predominantly pANCA and atypical ANCA.

[000145] The eosinophil is a terminally differentiated, end-stage leukocyte that resides predominantly in submucosal tissue and is recruited to sites of specific immune reactions, including allergic diseases. The eosinophil cytoplasm contains large ellipsoid granules with an electron-dense crystalline nucleus and partially permeable matrix. In addition to these large primary crystalloid granules, there is another granule type that is smaller (small granule) and lacks the crystalline nucleus. The large specific granules of eosinophils contain at least four distinct cationic proteins, which exert a range of biological effects on host cells and microbial targets: major basic protein (MBP), eosinophil cationic protein (ECP), eosinophil derived neurotoxin (EDN), and eosinophil peroxidase (EPO). Basophils contain about one fourth as much major basic protein as eosinophils together with detectable amounts of EDN, ECP and EPO. Small amounts of EDN and ECP are also found in neutrophils (Gleich G J. Mechanisms of eosinophil-associated inflammation. J Allergy Clin Immunol 2000; 105:651-663). MBP appears to lack enzymatic activity but is a highly cationic polypeptide which may exert its toxic activities by interactions with lipid membranes leading to their derangement. Both MBP and EPO can act as selective allosteric inhibitors of agonist binding to M2 muscarinic receptors. These proteins may contribute to M2 receptor dysfunction and enhance vagally mediated bronchoconstriction in asthma. EDN can specifically damage the myelin coat of neurons. Histaminase and a variety of hydrolytic lysosomal enzymes are also present in the large specific granules of eosinophils. Among the enzymes in small granules of eosinophils are aryl sulphatase, acid phosphatase, and a 92 kDa metalloproteinase, a gelatinase. Eosinophils can elaborate cytokines which include those with potential autocrine growth-factor activities for eosinophils and those with potential roles in acute and chronic inflammatory responses. Three cytokines have growth-factor activities for eosinophils: granulocyte-macrophage colony-stimulating factor (GM-CSF), IL-3 and IL-5. Other cytokines produced by human eosinophils that may have activities in acute and chronic inflammatory responses include IL-1-alpha, IL-6, IL-8, TNF-alpha and both transforming growth factors, TGF-alpha and TGF-beta.

[000146] Eosinophils contain crystalloid granules that contain MBP, eosinophil cationic protein, EPO, and eosinophil-derived neurotoxin (Gleich, J Allergy Clin Immunol 2000; 105:651-663). The human promyelocytic cell line HL-60 clone 15 can be used to examine secretion of EPO. This cell line was established from a clone of HL-60 that had been grown at an elevated pH for two months (Fischkoff, Leuk Res 1988; 12:679-686) and then treated with butyric acid to allow the cells to differentiate so as to exhibit many of the characteristics of peripheral blood eosinophils, including expression of eosinophil-specific granule proteins (Rosenberg et al., J Exp Med 1989; 170:163-176; Tiffany et al., J Leukoc Biol 1995; 58:49-54; Badewa et al., Exp Biol Med 2002; 227:645-651).

[000147] Eosinophils can participate in hypersensitivity reactions, especially through two lipid inflammatory mediators, leukotriene C^4 (LTC^4) and platelet activating factor (PAF). Both mediators contract airway smooth muscle, promote the secretion of mucus, alter vascular permeability and elicit eosinophil and neutrophil infiltration. In addition to the direct activities of these eosinophil-derived mediators, MBP can stimulate the release of histamine from basophils and mast cells, and MBP can stimulate the release of EPO from mast cells. Eosinophils can serve as a local source of specific lipid mediators as well as induce the release of mediators from mast cells and basophils. Eosinophil granule content is released following similar stimuli to neutrophil granules, e.g. during phagocytosis of opsonized particles and by chemotactic factors. Neutrophil lysosomal enzymes act primarily on material engulfed in phagolysosomes, while the eosinophil granule contents act mainly on extracellular target structure such as parasites and inflammatory mediators.

[000148] Monocyte and macrophage development takes place in the bone marrow and passes through the following steps: stem cell; committed stem cell; monoblast; promonocyte; monocyte in bone marrow; monocyte in peripheral blood; and macrophage in tissues. Monocyte differentiation in the bone marrow proceeds rapidly (1.5 to 3 days). During differentiation, granules are formed in monocyte cytoplasm and these can be divided as in neutrophils into at least two types. However, they are fewer and smaller than their neutrophil counterparts (azurophil and specific granules). Their enzyme content is similar.

[000149] Granule-bound enzymes of monocytes/macrophages include lysozyme, acid phosphatase, and beta-glucuronidase. As a model for in vivo studies, lysozyme secretion from U937 cells was used. This cell line is derived from a human histiocytic lymphoma and has been used as a monocytic cell line that can be activated by a variety of agonists, such as PMA (Hoff et al., J Leukoc Biol 1992; 52:173-182; Balboa et al., J Immunol 2003; 170:5276-5280; Sundstrom et al., Int J Cancer 1976; 17:565-577).

[000150] Natural killer (NK) cells and cytotoxic lymphocytes contain potent cytotoxic granules including perforin, a pore-forming protein, and granzymes, lymphocyte-specific serine proteases. For example, the NK-92 cell line is an IL-2-dependent human line established from a patient with rapidly progressive non-Hodgkin's lymphoma (Gong JH., Maki G, Klingemann HG. Characterization of a human cell line (NK-92) with phenotypical and functional characteristics of activated natural killer cells. Leukemia 1994; 8:652-658). NK-92 cells express high levels of molecules involved in the perforin-granzyme cytolytic pathway that targets a wide range of malignant cells (Gong et al, vide infra, and Maki G, Klingemann HG, Martinson JA, Tam YK. Factors regulating the cytotoxic activity of the human natural killer cell line, NK-92. J Hematother Stem Cell Res 2001; 10:369-383).

[000151] Granzymes are exogenous serine proteases that are released by cytoplasmic granules within cytotoxic T cells and natural killer cells. Granzymes can induce apoptosis within virus-infected cells, thus destroying them.

[000152] Extracellular release of a mediator of inflammation (inflammatory mediator) from a granulocyte (or leukocyte), and extracellular release of more than one mediator of inflammation (inflammatory mediator) from a granulocyte (or leukocyte) is sometimes referred to herein as degranulation. In a preferred embodiment, the release of a mediator of inflammation comprises release of said mediator from a granule located in the interior of a granulocyte or leukocyte. The release of inflammatory mediator is preferably the release of an inflammatory mediator from these granules.

[000153] Neutrophils and macrophages, upon priming by pro-inflammatory agents (inflammatory stimulants) such as TNFα, dramatically increase their synthesis of MARCKS protein: as much as 90% of the new protein formed by neutrophils in response to either TNFα or

lipopolysaccharide (LPS) is MARCKS (Thelen M, Rosen A, Nairn AC, Aderem A. Tumor necrosis factor alpha modifies agonist-dependent responses in human neutrophils by inducing the synthesis and myristoylation of a specific protein kinase C substrate. Proc Natl Acad Sci USA 1990; 87:5603-5607). MARCKS can thus have an important role in subsequent release of inflammatory mediators when granule-containing cells, such as neutrophils and macrophages, are stimulated by agonists, especially those that work by activating PKC (Burgoyne et al., Physiol Rev 2003; 83:581-632; Logan et al. J Allergy Clin Immunol 2003; 111: 923-932; Smolen et al., Biochim Biophys Acta 1990; 1052:133-142; Niessen et al., Biochim. Biophys. Acta 1994; 1223:267-273 ; Naucler et al., J Leukoc Biol 2002; 71:701-710).

[000154] In one aspect of this invention, administration of a degranulation-inhibiting amount of MANS peptide or an active fragment thereof as described herein to a site of inflammation in a subject, which site of inflammation has resulted from the onset of entry of a disease, a condition, a trauma, a foreign body, or a combination thereof at the site of inflammation in the subject, can reduce the amount of a mediator of inflammation released from infiltrating leukocytes at the site of inflammation, where the leukocytes are preferably granulocytes. The administration of the MANS peptide and/or at least one active fragment thereof can reduce the amount of a mediator of inflammation released from leukocytes such as granulocytes infiltrating into the site of inflammation. The degranulation-inhibiting amount of MANS peptide, or the degranulation-inhibiting amount of an active fragment thereof, is sufficient to reduce or inhibit the exocytotic release of inflammatory mediators from granules contained within the inflammatory cells infiltrating into the site. Degranulation-inhibiting efficacy is measured at a time after administration of the MANS peptide or the active fragment thereof by comparison of the percent of inhibition (i.e., percent of reduction) of the release of mediators of inflammation from said cells (leukocytes or granulocytes or other inflammatory cells) relative to the level or amount or concentration of said mediators of inflammation released or produced at approximately the same time in the absence of MANS peptide and/or in the absence of the active fragment thereof. Additionally, a skilled clinician can determine whether inflammation at the tissue site has been reduced by measuring symptoms and parameters of inflammation known as indicators of the disease to determine whether a sufficient or therapeutically effective amount MANS peptide and/or an active fragment thereof has been administered. A sufficient degranulation-inhibiting amount is the amount which produces a percentage of reduction of a mediator of inflammation

released from a granulocyte, at the site of inflammation, which percentage is from about 1% to about 99%, preferably from 5% to about 99%, more preferably from about 10% to about 99%, even more preferably from about 25% to 99%, and even more preferably from about 50% to about 99% of the amount of said mediator of inflammation released from said granulocyte in the absence of MANS peptide or an active fragment thereof tested under the same conditions.

[000155] In one aspect of this invention, administration of a degranulation-inhibiting amount of MANS peptide to a site of inflammatory stimulation in an animal, which site of inflammatory stimulation has been created by administration of an inflammation-stimulating amount of an inflammatory stimulant to said site, can reduce the amount of a mediator of inflammation released from a granulocyte, which granulocyte is stimulated by said inflammatory stimulant at said site of inflammatory stimulation, from about 1% to about 99%, preferably from 5% to about 99%, more preferably from about 10% to about 99%, even more preferably from about 25% to 99%, and even more preferably from about 50% to about 99% of the amount of said mediator of inflammation released from said granulocyte in the absence of MANS peptide in the presence of the identical inflammation-stimulating amount of said inflammatory stimulant.

[000156] In another aspect of this invention, administration of a degranulation-inhibiting amount of MANS peptide to a site of inflammatory stimulation in an animal, which site of inflammatory stimulation has been created by administration of an inflammation-stimulating amount of an inflammatory stimulant to said site, can reduce the amount of a mediator of inflammation released from a granulocyte, which granulocyte is stimulated by said inflammatory stimulant at said site of inflammatory stimulation, by 100% of the amount of said mediator of inflammation released from said granulocyte in the absence of MANS peptide in the presence of the identical inflammation-stimulating amount of said inflammatory stimulant.

[000157] An example of an inflammatory stimulant used in *in vitro* examples herein is phorbol 12-myristate 13-acetate (PMA). Monocyte chemoattractant protein (MCP-1) is nearly as effective as C5a, and much more potent than IL-8, in the degranulation of basophils, resulting in histamine release. Histamine release can occur after stimulation with chemokines (i.e., chemoattractant cytokines), RANTES and MIP-1.

[000158] In a preferred embodiment, relative to the basal concentration of MARCKS peptide present at the site of inflammatory stimulation, the degranulation-inhibiting amount of MANS peptide administered to a site of inflammatory stimulation in an animal comprises from about 1 time to about 1,000,000 times the concentration of the MARCKS peptide at said site of inflammatory stimulation, preferably from about 1 time to about 100,000 times the concentration of the MARCKS peptide at said site of inflammatory stimulation, more preferably from about 1 time to about 10,000 times the concentration of the MARCKS peptide at said site of inflammatory stimulation, even more preferably from about 1 time to about 1,000 times the concentration of the MARCKS peptide at said site of inflammatory stimulation, even more preferably from about 1 time to about 100 times the concentration of the MARCKS peptide at said site of inflammatory stimulation, and even more preferably from about 1 time to about 10 times the concentration of the MARCKS peptide at said site of inflammatory stimulation.

[000159] In a preferred embodiment, the granulocyte resides on or in the airway of an animal, preferably a human, and the MANS peptide is administered by inhalation, such as by inhalation of a pharmaceutical composition comprising the MANS peptide, for example a pharmaceutical composition comprising the MANS peptide and an aqueous solution, which composition is administered in the form of an aerosol, or a pharmaceutical composition comprising the MANS peptide in the form of a dry powder, which composition is administered using a dry powder inhaler. Other methods and devices known in the art for administration of a solution or powder by inhalation such as, for example, droplets, sprays, and nebulizers, can be useful.

[000160] In some embodiments, it is possible that the peptide of the present invention may block secretory processes that are physiologically important, including basal secretory functions. Although inventors do not wish to be bound to any particular theory of the invention, it is thought that the mechanisms regulating such basal secretion are different than those regulating stimulated secretion. Alternatively, basal secretory mechanisms may require less MARCKS protein than stimulated secretion. Basal secretion may be preserved since all therapies to block MARCKS-mediated secretion may not eliminate all MARCKS function.

[000161] As used herein, the term "MARCKS nucleotide sequence" refers to any nucleotide sequence derived from a gene encoding a MARCKS protein, including, for example, DNA or

RNA sequence, DNA sequence of the gene, any transcribed RNA sequence, RNA sequence of the pre-mRNA or mRNA transcript, and DNA or RNA bound to protein.

[000162] Precise delivery of the MARCKS-blocking peptide may also overcome any potential limitations of blocking important secretory processes. Delivering such agents to the respiratory tract should be readily accomplished with inhaled formulations. Since these agents may be useful in treating inflammatory bowel disease, one can envision delivery of the blocking agents into the rectum/colon/intestinal tract via enema or suppositories. Intraarticular injections or transdermal delivery into inflamed joints may yield relief to patients with arthritic or autoimmune diseases by limiting the secretion from localized inflammatory cells. Injection into areas surrounding nerve endings may inhibit secretion of some types of neurotransmitters, blocking transmission of severe pain or uncontrolled muscle spasms. Delivery of the peptide for the treatment of inflammatory skin diseases should be readily accomplished using various topical formulations known in the art.

[000163] It is believed that MARCKS interacts with actin and myosin in the cytoplasm and thus may be able to tether the granules to the cellular contractile apparatus, thus, mediating subsequent granule movement and exocytosis. Secretion of the inflammatory mediatory MPO from neutrophils may also be maximized by activation of both PKC and PKG. It is possible that MARCKS serves as the point of convergence for coordinating actions of these two protein kinases that control secretion from membrane-bound compartments in inflammatory cells (i.e. secretion of MPO from neutrophils).

[000164] The present invention demonstrates secretion of the inflammatory mediator MPO from canine or human neutrophils was enhanced by concurrent activation of both PKC and PKG, while activation of either kinase alone was insufficient to induce a maximal secretory response. An enhanced secretory response to PMA alone has been documented in NHBE cells and in neutrophils as demonstrated herein, although the magnitude of the response was much less than that observed by others in a rat goblet-like cell line. See, Abdullah et al, supra. In addition, although it was reported previously that a cGMP analogue could induce significant mucin secretion from cultured guinea pig tracheal epithelial cells (Fischer *et al., supra*), it should be noted that this response did not reach significant levels until 8 h of exposure. A secretory

response with such a long lag period is unlikely to be a direct effect and probably involves de novo protein synthesis as opposed to release of preformed and stored cytoplasmic granules.

[000165] As stated above, the present invention may be used in a pharmaceutical formulation. In certain embodiments, the drug product is present in a solid pharmaceutical composition that may be suitable for oral administration. A solid composition of matter according to the present invention may be formed and may be mixed with and/or diluted by an excipient. The solid composition of matter also may be enclosed within a carrier, which may be, for example, in the form of a capsule, sachet, tablet, paper, or other container. When the excipient serves as a diluent, it may be a solid, semi-solid, or liquid material that acts as a vehicle, carrier, or medium for the composition of matter.

[000166] Various suitable excipients will be understood by those skilled in the art and may be found in the *National Formulary*, 19: 2404-2406 (2000), the disclosure of pages 2404 to 2406 being incorporated herein in their entirety. Examples of suitable excipients include, but are not limited to, starches, gum arabic, calcium silicate, microcrystalline cellulose, methacrylates, shellac, polyvinylpyrrolidone, cellulose, water, syrup, and methylcellulose. The drug product formulations additionally can include lubricating agents such as, for example, talc, magnesium stearate and mineral oil; wetting agents; emulsifying and suspending agents; preserving agents such as methyl- and propyl hydroxybenzoates; sweetening agents; or flavoring agents. Polyols, buffers, and inert fillers also may be used. Examples of polyols include, but are not limited to, mannitol, sorbitol, xylitol, sucrose, maltose, glucose, lactose, dextrose, and the like. Suitable buffers include, but are not limited to, phosphate, citrate, tartrate, succinate, and the like. Other inert fillers that may be used include those that are known in the art and are useful in the manufacture of various dosage forms. If desired, the solid formulations may include other components such as bulking agents and/or granulating agents, and the like. The drug products of the invention may be formulated so as to provide quick, sustained, or delayed release of the active ingredient after administration to the patient by employing procedures well known in the art.

[000167] To form tablets for oral administration, the composition of matter of the present invention may be made by a direct compression process. In this process, the active drug

ingredients may be mixed with a solid, pulverant carrier such as, for example, lactose, saccharose, sorbitol, mannitol, starch, amylopectin, cellulose derivatives or gelatin, and mixtures thereof, as well as with an antifriction agent such as, for example, magnesium stearate, calcium stearate, and polyethylene glycol waxes. The mixture may then be pressed into tablets using a machine with the appropriate punches and dies to obtain the desired tablet size. The operating parameters of the machine may be selected by the skilled artisan. Alternatively, tablets for oral administration may be formed by a wet granulation process. Active drug ingredients may be mixed with excipients and/or diluents. The solid substances may be ground or sieved to a desired particle size. A binding agent may be added to the drug. The binding agent may be suspended and homogenized in a suitable solvent. The active ingredient and auxiliary agents also may be mixed with the binding agent solution. The resulting dry mixture is moistened with the solution uniformly. The moistening typically causes the particles to aggregate slightly, and the resulting mass is pressed through a stainless steel sieve having a desired size. The mixture is then dried in controlled drying units for the determined length of time necessary to achieve a desired particle size and consistency. The granules of the dried mixture are sieved to remove any powder. To this mixture, disintegrating, antifriction, and/or anti-adhesive agents may be added. Finally, the mixture is pressed into tablets using a machine with the appropriate punches and dies to obtain the desired tablet size. The operating parameters of the machine may be selected by the skilled artisan.

[000168] If coated tablets are desired, the above prepared core may be coated with a concentrated solution of sugar or cellulosic polymers, which may contain gum arabic, gelatin, talc, titanium dioxide, or with a lacquer dissolved in a volatile organic solvent or a mixture of solvents. To this coating various dyes may be added in order to distinguish among tablets with different active compounds or with different amounts of the active compound present. In a particular embodiment, the active ingredient may be present in a core surrounded by one or more layers including enteric coating layers.

[000169] Soft gelatin capsules may be prepared in which capsules contain a mixture of the active ingredient and vegetable oil. Hard gelatin capsules may contain granules of the active ingredient in combination with a solid, pulverulent carrier, such as, for example, lactose, saccharose, sorbitol, mannitol, potato starch, corn starch, amylopectin, cellulose derivatives, and/or gelatin.

[000170] Liquid preparations for oral administration may be prepared in the form of syrups or suspensions, e.g., solutions containing an active ingredient, sugar, and a mixture of ethanol, water, glycerol, and propylene glycol. If desired, such liquid preparations may comprise one or more of following: coloring agents, flavoring agents, and saccharin. Thickening agents such as carboxymethylcellulose also may be used.

[000171] In the event that the above pharmaceuticals are to be used for parenteral administration, such a formulation may comprise sterile aqueous injection solutions, non-aqueous injection solutions, or both, comprising the composition of matter of the present invention. When aqueous injection solutions are prepared, the composition of matter may be present as a water soluble pharmaceutically acceptable salt. Parenteral preparations may contain anti-oxidants, buffers, bacteriostats, and solutes which render the formulation isotonic with the blood of the intended recipient. Aqueous and non-aqueous sterile suspensions may comprise suspending agents and thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example sealed ampules and vials. Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets of the kind previously described.

[000172] The composition of matter also may be formulated such that it may be suitable for topical administration (e.g., skin cream). These formulations may contain various excipients known to those skilled in the art. Suitable excipients may include, but are not limited to, cetyl esters wax, cetyl alcohol, white wax, glyceryl monostearate, propylene glycol, monostearate, methyl stearate, benzyl alcohol, sodium lauryl sulfate, glycerin, mineral oil, water, carbomer, ethyl alcohol, acrylate adhesives, polyisobutylene adhesives, and silicone adhesives.

[000173] In a preferred embodiment, peptide fragments are disclosed in Table 2 and are of a length of at least 4 to 23 amino acid residues in length and having amino acid sequences identical to an amino acid sequence of the MANS peptide, wherein the N-terminal amino acid of the peptides are selected from position 2 to 21 of the MANS peptide sequence (SEQ ID NO: 1). The more preferred peptide fragment length is from at least 6 amino acids to 23 amino acids. Preferably these peptides are acylated at the alpha N-terminal amino acid, and more preferably these peptides are myristoylated at the alpha-N-terminal amino acid position.

Table 2.

Peptide No.	Sequence	Sequence ID No.
peptide 3	AQFSKTAAKGEAAAERPGEAAVA	SEQ ID NO. 3
peptide 5	AQFSKTAAKGEAAAERPGEAAV	SEQ ID NO. 5
peptide 8	AQFSKTAAKGEAAAERPGEAA	SEQ ID NO. 8
peptide 12	AQFSKTAAKGEAAAERPGEA	SEQ ID NO. 12
peptide 17	AQFSKTAAKGEAAAERPGE	SEQ ID NO. 17
peptide 23	AQFSKTAAKGEAAAERPG	SEQ ID NO. 23
peptide 30	AQFSKTAAKGEAAAERP	SEQ ID NO. 30
peptide 38	AQFSKTAAKGEAAAER	SEQ ID NO. 38
peptide 47	AQFSKTAAKGEAAAE	SEQ ID NO. 47
peptide 57	AQFSKTAAKGEAAA	SEQ ID NO. 57
peptide 68	AQFSKTAAKGEAA	SEQ ID NO. 68
peptide 80	AQFSKTAAKGEA	SEQ ID NO. 80
peptide 93	AQFSKTAAKGE	SEQ ID NO. 93
peptide 107	AQFSKTAAKG	SEQ ID NO. 107
peptide 122	AQFSKTAAK	SEQ ID NO. 122
peptide 138	AQFSKTAA	SEQ ID NO. 138
peptide 155	AQFSKTA	SEQ ID NO. 155
peptide 173	AQFSKT	SEQ ID NO. 173
peptide 192	AQFSK	SEQ ID NO. 192
peptide 212	AQFS	SEQ ID NO. 212
peptide 6	QFSKTAAKGEAAAERPGEAAVA	SEQ ID NO. 6
peptide 9	QFSKTAAKGEAAAERPGEAAV	SEQ ID NO. 9
peptide 13	QFSKTAAKGEAAAERPGEAA	SEQ ID NO. 13
peptide 18	QFSKTAAKGEAAAERPGEA	SEQ ID NO. 18
peptide 24	QFSKTAAKGEAAAERPGE	SEQ ID NO. 24
peptide 31	QFSKTAAKGEAAAERPG	SEQ ID NO. 31
peptide 39	QFSKTAAKGEAAAERP	SEQ ID NO. 39
peptide 48	QFSKTAAKGEAAAER	SEQ ID NO. 48
peptide 58	QFSKTAAKGEAAAE	SEQ ID NO. 58
peptide 69	QFSKTAAKGEAAA	SEQ ID NO. 69
peptide 81	QFSKTAAKGEAA	SEQ ID NO. 81
peptide 94	QFSKTAAKGEA	SEQ ID NO. 94
peptide 108	QFSKTAAKGE	SEQ ID NO. 108
peptide 123	QFSKTAAKG	SEQ ID NO. 123
peptide 139	QFSKTAAK	SEQ ID NO. 139
peptide 156	QFSKTAA	SEQ ID NO. 156
peptide 174	QFSKTA	SEQ ID NO. 174
peptide 193	QFSKT	SEQ ID NO. 193
peptide 213	QFSK	SEQ ID NO. 213

peptide 10	FSKTAAKGEAAAERPGEAAVA	SEQ ID NO. 10
peptide 14	FSKTAAKGEAAAERPGEAAV	SEQ ID NO. 14
peptide 19	FSKTAAKGEAAAERPGEAA	SEQ ID NO. 19
peptide 25	FSKTAAKGEAAAERPGEA	SEQ ID NO. 25
peptide 32	FSKTAAKGEAAAERPGE	SEQ ID NO. 32
peptide 40	FSKTAAKGEAAAERPG	SEQ ID NO. 40
peptide 49	FSKTAAKGEAAAERP	SEQ ID NO. 49
peptide 59	FSKTAAKGEAAAER	SEQ ID NO. 59
peptide 70	FSKTAAKGEAAAE	SEQ ID NO. 70
peptide 82	FSKTAAKGEAAA	SEQ ID NO. 82
peptide 95	FSKTAAKGEAA	SEQ ID NO. 95
peptide 109	FSKTAAKGEA	SEQ ID NO. 109
peptide 124	FSKTAAKGE	SEQ ID NO. 124
peptide 140	FSKTAAKG	SEQ ID NO. 140
peptide 157	FSKTAAK	SEQ ID NO. 157
peptide 175	FSKTAA	SEQ ID NO. 175
peptide 194	FSKTA	SEQ ID NO. 194
peptide 214	FSKT	SEQ ID NO. 214
peptide 15	SKTAAKGEAAAERPGEAAVA	SEQ ID NO. 15
peptide 20	SKTAAKGEAAAERPGEAAV	SEQ ID NO. 20
peptide 26	SKTAAKGEAAAERPGEAA	SEQ ID NO. 26
peptide 33	SKTAAKGEAAAERPGEA	SEQ ID NO. 33
peptide 41	SKTAAKGEAAAERPGE	SEQ ID NO. 41
peptide 50	SKTAAKGEAAAERPG	SEQ ID NO. 50
peptide 60	SKTAAKGEAAAERP	SEQ ID NO. 60
peptide 71	SKTAAKGEAAAER	SEQ ID NO. 71
peptide 83	SKTAAKGEAAAE	SEQ ID NO. 83
peptide 96	SKTAAKGEAAA	SEQ ID NO. 96
peptide 110	SKTAAKGEAA	SEQ ID NO. 110
peptide 125	SKTAAKGEA	SEQ ID NO. 125
peptide 141	SKTAAKGE	SEQ ID NO. 141
peptide 158	SKTAAKG	SEQ ID NO. 158
peptide 176	SKTAAK	SEQ ID NO. 176
peptide 195	SKTAA	SEQ ID NO. 195
peptide 215	SKTA	SEQ ID NO. 215
peptide 21	KTAAKGEAAAERPGEAAVA	SEQ ID NO. 21
peptide 27	KTAAKGEAAAERPGEAAV	SEQ ID NO. 27
peptide 34	KTAAKGEAAAERPGEAA	SEQ ID NO. 34
peptide 42	KTAAKGEAAAERPGEA	SEQ ID NO. 42
peptide 51	KTAAKGEAAAERPGE	SEQ ID NO. 51
peptide 61	KTAAKGEAAAERPG	SEQ ID NO. 61
peptide 72	KTAAKGEAAAERP	SEQ ID NO. 72

peptide 84	KTAAKGEAAAER	SEQ ID NO. 84
peptide 97	KTAAKGEAAAE	SEQ ID NO. 97
peptide 111	KTAAKGEAAA	SEQ ID NO. 111
peptide 126	KTAAKGEAA	SEQ ID NO. 126
peptide 142	KTAAKGEA	SEQ ID NO. 142
peptide 159	KTAAKGE	SEQ ID NO. 159
peptide 177	KTAAKG	SEQ ID NO. 177
peptide 196	KTAAK	SEQ ID NO. 196
peptide 216	KTAA	SEQ ID NO. 216
peptide 28	TAAKGEAAAERPGEAAVA	SEQ ID NO. 28
peptide 35	TAAKGEAAAERPGEAAV	SEQ ID NO. 35
peptide 43	TAAKGEAAAERPGEAA	SEQ ID NO. 43
peptide 52	TAAKGEAAAERPGEA	SEQ ID NO. 52
peptide 62	TAAKGEAAAERPGE	SEQ ID NO. 62
peptide 73	TAAKGEAAAERPG	SEQ ID NO. 73
peptide 85	TAAKGEAAAERP	SEQ ID NO. 85
peptide 98	TAAKGEAAAER	SEQ ID NO. 98
peptide 112	TAAKGEAAAE	SEQ ID NO. 112
peptide 127	TAAKGEAAA	SEQ ID NO. 127
peptide 143	TAAKGEAA	SEQ ID NO. 143
peptide 160	TAAKGEA	SEQ ID NO. 160
peptide 178	TAAKGE	SEQ ID NO. 178
peptide 197	TAAKG	SEQ ID NO. 197
peptide 217	TAAK	SEQ ID NO. 217
peptide 36	AAKGEAAAERPGEAAVA	SEQ ID NO. 36
peptide 44	AAKGEAAAERPGEAAV	SEQ ID NO. 44
peptide 53	AAKGEAAAERPGEAA	SEQ ID NO. 53
peptide 63	AAKGEAAAERPGEA	SEQ ID NO. 63
peptide 74	AAKGEAAAERPGE	SEQ ID NO. 74
peptide 86	AAKGEAAAERPG	SEQ ID NO. 86
peptide 99	AAKGEAAAERP	SEQ ID NO. 99
peptide 113	AAKGEAAAER	SEQ ID NO. 113
peptide 128	AAKGEAAAE	SEQ ID NO. 128
peptide 144	AAKGEAAA	SEQ ID NO. 144
peptide 161	AAKGEAA	SEQ ID NO. 161
peptide 179	AAKGEA	SEQ ID NO. 179
peptide 198	AAKGE	SEQ ID NO. 198
peptide 218	AAKG	SEQ ID NO. 218
peptide 45	AKGEAAAERPGEAAVA	SEQ ID NO. 45
peptide 54	AKGEAAAERPGEAAV	SEQ ID NO. 54
peptide 64	AKGEAAAERPGEAA	SEQ ID NO. 64
peptide 75	AKGEAAAERPGEA	SEQ ID NO. 75

peptide 87	AKGEAAAERPGE SEQ ID NO. 87
peptide 100	AKGEAAAERPG SEQ ID NO. 100
peptide 114	AKGEAAAERP SEQ ID NO. 114
peptide 129	AKGEAAAER SEQ ID NO. 129
peptide 145	AKGEAAAE SEQ ID NO. 145
peptide 162	AKGEAAA SEQ ID NO. 162
peptide 180	AKGEAA SEQ ID NO. 180
peptide 199	AKGEA SEQ ID NO. 199
peptide 219	AKGE SEQ ID NO. 219
peptide 55	KGEAAAERPGEAAVA SEQ ID NO. 55
peptide 65	KGEAAAERPGEAAV SEQ ID NO. 65
peptide 76	KGEAAAERPGEAA SEQ ID NO. 76
peptide 88	KGEAAAERPGEA SEQ ID NO. 88
peptide 101	KGEAAAERPGE SEQ ID NO. 101
peptide 115	KGEAAAERPG SEQ ID NO. 115
peptide 130	KGEAAAERP SEQ ID NO. 130
peptide 146	KGEAAAER SEQ ID NO. 146
peptide 163	KGEAAAE SEQ ID NO. 163
peptide 181	KGEAAA SEQ ID NO. 181
peptide 200	KGEAA SEQ ID NO. 200
peptide 220	KGEA SEQ ID NO. 220
peptide 66	GEAAAERPGEAAVA SEQ ID NO. 66
peptide 77	GEAAAERPGEAAV SEQ ID NO. 77
peptide 89	GEAAAERPGEAA SEQ ID NO. 89
peptide 102	GEAAAERPGEA SEQ ID NO. 102
peptide 116	GEAAAERPGE SEQ ID NO. 116
peptide 131	GEAAAERPG SEQ ID NO. 131
peptide 147	GEAAAERP SEQ ID NO. 147
peptide 164	GEAAAER SEQ ID NO. 164
peptide 182	GEAAAE SEQ ID NO. 182
peptide 201	GEAAA SEQ ID NO. 201
peptide 221	GEAA SEQ ID NO. 221
peptide 78	EAAAERPGEAAVA SEQ ID NO. 78
peptide 90	EAAAERPGEAAV SEQ ID NO. 90
peptide 103	EAAAERPGEAA SEQ ID NO. 103
peptide 117	EAAAERPGEA SEQ ID NO. 117
peptide 132	EAAAERPGE SEQ ID NO. 132
peptide 148	EAAAERPG SEQ ID NO. 148
peptide 165	EAAAERP SEQ ID NO. 165
peptide 183	EAAAER SEQ ID NO. 183
peptide 202	EAAAE SEQ ID NO. 202
peptide 222	EAAA SEQ ID NO. 222

peptide 91	AAAERPGEAAVA SEQ ID NO. 91
peptide 104	AAAERPGEAAV SEQ ID NO. 104
peptide 118	AAAERPGEAA SEQ ID NO. 118
peptide 133	AAAERPGEA SEQ ID NO. 133
peptide 149	AAAERPGE SEQ ID NO. 149
peptide 166	AAAERPG SEQ ID NO. 166
peptide 184	AAAERP SEQ ID NO. 184
peptide 203	AAAER SEQ ID NO. 203
peptide 223	AAAE SEQ ID NO. 223
peptide 105	AAERPGEAAVA SEQ ID NO. 105
peptide 119	AAERPGEAAV SEQ ID NO. 119
peptide 134	AAERPGEAA SEQ ID NO. 134
peptide 150	AAERPGEA SEQ ID NO. 150
peptide 167	AAERPGE SEQ ID NO. 167
peptide 185	AAERPG SEQ ID NO. 185
peptide 204	AAERP SEQ ID NO. 204
peptide 224	AAER SEQ ID NO. 224
peptide 120	AERPGEAAVA SEQ ID NO. 120
peptide 135	AERPGEAAV SEQ ID NO. 135
peptide 151	AERPGEAA SEQ ID NO. 151
peptide 168	AERPGEA SEQ ID NO. 168
peptide 186	AERPGE SEQ ID NO. 186
peptide 205	AERPG SEQ ID NO. 205
peptide 225	AERP SEQ ID NO. 225
peptide 136	ERPGEAAVA SEQ ID NO. 136
peptide 152	ERPGEAAV SEQ ID NO. 152
peptide 169	ERPGEAA SEQ ID NO. 169
peptide 187	ERPGEA SEQ ID NO. 187
peptide 206	ERPGE SEQ ID NO. 206
peptide 226	ERPG SEQ ID NO. 226
peptide 153	RPGEAAVA SEQ ID NO. 153
peptide 170	RPGEAAV SEQ ID NO. 170
peptide 188	RPGEAA SEQ ID NO. 188
peptide 207	RPGEA SEQ ID NO. 207
peptide 227	RPGE SEQ ID NO. 227
peptide 171	PGEAAVA SEQ ID NO. 171
peptide 189	PGEAAV SEQ ID NO. 189
peptide 208	PGEAA SEQ ID NO. 208
peptide 228	PGEA SEQ ID NO. 228
peptide 190	GEAAVA SEQ ID NO. 190
peptide 209	GEAAV SEQ ID NO. 209
peptide 229	GEAA SEQ ID NO. 229

peptide 210	EAAVA SEQ ID NO. 210
peptide 230	EAAV SEQ ID NO. 230
peptide 231	AAVA SEQ ID NO. 231

[000174] As illustrated in FIG. 5, MARCKS was phosphorylated by PKC and consequently translocated from the membrane to the cytoplasm. Here, PKG appeared to induce dephosphorylation of MARCKS (FIG. 2A, lane 4, and FIG. 2B). This dephosphorylation was reversed by the PKG inhibitor R_p-8-Br-PET-cGMP (FIG. 2A, lane 5), indicating the dephosphorylation was specifically PKG-dependent. In FIG. 2, the NHBE cells were labeled with [^{32}P]orthophosphate and then exposed to the indicated reagents. MARCKS phosphorylation in response to the treatments was evaluated by immunoprecipitation assay. In FIG 2A, 8-Br-cGMP reversed MARCKS phosphorylation induced by PMA, and this effect of 8-Br-cGMP could be blocked by R_p-8-Br-PET-cGMP (PKG inhibitor) or okadaic acid (PP1/2A inhibitor). For FIG. 2B, PMA-induced phosphorylation of MARCKS was reversed by subsequent exposure of cells to 8-Br-cGMP. Lane 1, medium alone for 8 min; lane 2, 100 nM PMA for 3 min; lane 3, 100 nM PMA for 3 min and then with 1 μM 8-Br-cGMP for 5 min; lane 4, 100 nM PMA for 8 min; lane 5, medium alone for 3 min and then 100 nM PMA+1 μM 8-Br-cGMP for 5 min. In FIG 2C, 8-Br-cGMP-induced MARCKS dephosphorylation was attenuated by fostriecin in a concentration-dependent manner.

[000175] It is believed that PKG acts to dephosphorylate MARCKS via activation of a protein phosphatase. As illustrated in FIG. 2A (lane 6), okadaic acid at 500 nM, a concentration that could inhibit both PP1 and PP2A, blocked PKG-induced dephosphorylation of MARCKS, suggesting that PKG caused dephosphorylation by activating PP1 and/or PP2A. Further studies with fostriecin and direct assay of phosphatase activities indicated that only PP2A was activated by PKG and was responsible for removal of the phosphate groups from MARCKS (FIG. 2C). It is likely that either okadaic acid or fostriecin, at concentrations that inhibited PKG-induced dephosphorylation of MARCKS, attenuated mucin secretion induced by PMA+8-Br-cGMP or UTP as exhibited in FIG. 3. FIG. 3 helps to demonstrate that PP2A is an essential component of the mucin secretory pathway. NHBE cells were preincubated with the indicated concentration of fostriecin, okadaic acid (500 nM), or medium alone for 15 min and then stimulated with PMA (100 nM)+8-Br-cGMP (1 μM) for 15 min or with UTP (100 μM) for 2 h. Secreted mucin was

measured by ELISA. Data are presented as mean.+-.S.E. (n=6 at each point) wherein * stands for significantly different from medium control ($p<0.05$); † stands for significantly different from PMA+8-Br-cGMP stimulation ($p<0.05$); and ‡ stands for significantly different from UTP stimulation $p<0.05$). Thus, dephosphorylation of MARCKS by a PKG-activated PP2A appears to be an essential component of the signaling pathway leading to mucin granule exocytosis.

[000176] To reveal molecular events by which MARCKS links kinase activation to mucin secretion, phosphorylation of MARCKS in response to PKC/PKG activation was investigated in depth. As illustrated in FIG. 1A, PMA (100 nM) likely induced a significant increase (3-4-fold) in MARCKS phosphorylation in NHBE cells, and this phosphorylation was attenuated by the PKC inhibitor calphostin C (500 nM). Once phosphorylated, MARCKS was translocated from the plasma membrane to the cytoplasm (FIG. 1B). More specifically, FIG. 1A shows the activation of PKC results in MARCKS phosphorylation in NHBE cells. Cells were labeled with [^{32}P]orthophosphate for 2 h and then exposed to the stimulatory and/or inhibitory reagents. MARCKS phosphorylation in response to the treatments was evaluated by immunoprecipitation as described. Lane 1, medium control; lane 2 the vehicle, 0.1% Me.sub.2SO; lane 3, 100 nM 4α-PMA; lane 4, 100 nM PMA; lane 5, 100 nM PMA+500 nM calphostin C; lane 6, 500 nM calphostin C. FIG. 1B demonstrates phosphorylated MARCKS is translocated from the plasma membrane to the cytoplasm. ^{32}P-Labeled cells were exposed to PMA (100 nM) or medium alone for 5 min, and then the membrane and the cytosol fractions were isolated. Activation of PKG by 8-Br-cGMP (1 μM, another kinase activation event necessary for provoking mucin secretion, did not lead to MARCKS phosphorylation, but, in fact, the opposite effect was observed: MARCKS phosphorylation induced by PMA was reversed by 8-Br-cGMP (FIG. 2A). This effect of 8-Br-cGMP was not due to suppression of PKC activity, as the PMA-induced phosphorylation could be reversed by subsequent addition of 8-Br-cGMP to the cells (FIG. 2B). Therefore, PKG activation likely results in dephosphorylation of MARCKS.

[000177] Further investigation demonstrated that PKG-induced MARCKS dephosphorylation was blocked by 500 nM okadaic acid, a protein phosphatase (type 1 and/or 2A (PP1/2A)) inhibitor (FIG. 2A, lane 6). Thus, it appeared that the dephosphorylation was mediated by PP1 and/or PP2A. To define the subtype of protein phosphatase involved, a novel and more specific inhibitor of PP2A, fostriecin (IC_{50}=3.2 nM), was utilized in additional phosphorylation studies.

As illustrated in FIG. 2C, fostriecin inhibited PKG-induced MARCKS dephosphorylation in a concentration-dependent manner (1-500 nM), suggesting that PKG induced the dephosphorylation via activation of PP2A. To confirm further activation of PP2A by PKG in NHBE cells, cytosolic PP1 and PP2A activities were determined after exposure of the cells to 8-Br-cGMP. PP2A activity was increased approximately 3-fold (from 0.1 to 0.3 nmol/min/mg proteins, $p<0.01$) at concentrations of 8-Br-cGMP as low as 0.1 .mu.M, whereas PP1 activity remained unchanged. This data indicates that PP2A may be activated by PKG and is responsible for the dephosphorylation of MARCKS. Accordingly, this PP2A activity appeared critical for mucin secretion to occur; when PKG-induced MARCKS dephosphorylation was blocked by okadaic acid or fostriecin, the secretory response to PKC/PKG activation or UTP stimulation was ameliorated (FIG. 3).

MARCKS associates with Actin and Myosin in the Cytoplasm

[000178] FIG. 4 depicts a radiolabeled immunoprecipitation assay which reveals that MARCKS may associate with two other proteins (about 200 and about 40 kDa) in the cytoplasm. In FIG. 4 NHBE cells were labeled with [^{3}H]leucine and [^{3}H]proline overnight, and the membrane and the cytosol fractions were prepared as described under "Experimental Procedures." Isolated fractions were precleared with the nonimmune control antibody (6F6). The cytosol was then divided equally into two fractions and used for immunoprecipitation carried out in the presence of 10 μM cytochalasin D (Biomol, Plymouth Meeting, Pa.) with the anti-MARCKS antibody 2F12 (lane 2) and the nonimmune control antibody 6F6 (lane 3), respectively. MARCKS protein in the membrane fraction was also assessed by immunoprecipitation using the antibody 2F12 (lane 1). The precipitated protein complex was resolved by 8% SDS-polyacrylamide gel electrophoresis and visualized by enhanced autoradiography. MARCKS appeared to associate with two cytoplasmic proteins with molecular masses of about 200 and about 40 kDa, respectively. These two MARCKS-associated proteins were excised from the gel and analyzed by matrix-assisted laser desorption ionization/time of flight mass spectrometry/internal sequencing (the Protein/DNA Technology Center of Rockefeller University, N.Y.). The obtained peptide mass and sequence data were used to search protein databases via Internet programs ProFound and MS-Fit. Results indicate that they are myosin (heavy chain, non-muscle type A) and actin, respectively. Matrix-assisted laser desorption ionization/time of flight mass spectrometry/internal

sequence analysis indicates that these two MARCKS-associated proteins were myosin (heavy chain, non-muscle type A) and actin, respectively.

[000179] These studies suggest a new paradigm for the signaling mechanism controlling exocytotic secretion of airway mucin granules as well as providing what is believed to be the first direct evidence demonstrating a specific biological function of MARCKS in a physiological process. MARCKS serves as a key mediator molecule regulating mucin granule release in human airway epithelial cells. It is believed that elicitation of airway mucin secretion requires dual activation and synergistic actions of PKC and PKG. Activated PKC phosphorylates MARCKS, resulting in translocation of MARCKS from the inner face of the plasma membrane into the cytoplasm. Activation of PKG in turn activates PP2A, which dephosphorylates MARCKS in the cytoplasm. Because the membrane association ability of MARCKS is dependent on its phosphorylation state this dephosphorylation may allow MARCKS to regain its membrane-binding capability and may enable MARCKS to attach to membranes of cytoplasmic mucin granules. By also interacting with actin and myosin in the cytoplasm (FIG. 4), MARCKS may then be able to tether granules to the cellular contractile apparatus, mediating granule movement to the cell periphery and subsequent exocytotic release. The wide distribution of MARCKS suggests the possibility that this or a similar mechanism may regulate secretion of membrane-bound granules in various cell types under normal or pathological conditions.

[000180] As indicated in FIG. 5, MARCKS may function as a molecular linker by interacting with granule membranes at its N-terminal domain and binding to actin filaments at its PSD site, thereby tethering granules to the contractile cytoskeleton for movement and exocytosis. FIG. 5 shows a possible mechanism depicting that mucin secretagogue interacts with airway epithelial (goblet) cells and activates two separate protein kinases, PKC and PKG. Activated PKC phosphorylates MARCKS, causing MARCKS translocation from the plasma membrane to the cytoplasm, whereas PKG, activated via the nitric oxide (NO) → GC-S → cGMP → PKG pathway, in turn activates a cytoplasmic PP2A, which dephosphorylates MARCKS. This dephosphorylation stabilizes MARCKS attachment to the granule membranes. In addition, MARCKS also interacts with actin and myosin, thereby linking granules to the cellular contractile machinery for subsequent movement and exocytotic release of inflammatory mediators, such as MPO. The attachment of MARCKS to the granules after it is released into the

cytoplasm may also be guided by specific targeting proteins or some other forms of protein-protein interactions in which the N-terminal domain of MARCKS is involved. In either case, the MANS peptide, or an active fragment thereof, comprising at least 4 amino acids, would act to inhibit competitively targeting of MARCKS to the membranes of mucin granules, thereby blocking secretion.

[000181] The invention also relates to a new method for blocking any cellular exocytotic secretory process, especially those releasing inflammatory mediators from granules contained within inflammatory cells, whose stimulatory pathways involve the protein kinase C (PKC) substrate MARCKS protein and release of contents from membrane-bound vesicles. Specifically, the inventors have shown that stimulated release of the inflammatory mediator myloperoxidase from human (FIG.6) or canine (FIG. 7) neutrophils can be blocked in a concentration-dependent manner by the MANS peptide. Specifically, FIG. 6 shows isolated neutrophils that were stimulated to secrete myloperoxidase (MPO) with 100 nM PMA and 10 .mu.M 8-Br-cGMP. 100 μM MANS peptide decreased secretion of MPO to control levels (*=$p<0.05$). 10 μM MANS causes a slight decrease in MPO secretion. 10 or 100 μM of a control peptide (RNS) has no effect on MPO secretion. In FIG. 7, isolated neutrophils were stimulated to secrete myloperoxidase (MPO) with 100 nM PMA and 10 μM 8-Br-cGMP. 100 μM MANS peptide decreased secretion of MPO to control levels (*=$p<0.05$). 10 μM MANS causes a slight decrease in MPO secretion. 10 or 100 μM of a control peptide (RNS) has no effect on MPO secretion. Thus, the peptide may be used therapeutically to block the release of mediators of inflammation secreted from infiltrating inflammatory cells in any tissues. Many of these released mediators are responsible for the extensive tissue damage observed in a variety of chronic inflammatory diseases (i.e., respiratory diseases such as asthma, chronic bronchitis and COPD, inflammatory bowel diseases including ulcerative colitis and Crohn's disease, autoimmune diseases, skin diseases such as rosacea, eczema; and severe acne, arthritic and pain syndromes such as rheumatoid arthritis and fibromyalgia). This invention may be useful for treating diseases such as arthritis, chronic bronchitis, COPD and cystic fibrosis. This invention is accordingly useful for the treatment in both human and animal diseases, especially those affecting equines, canines, felines, and other household pets.

[000182] FIGS. 8-12 show MPO secretion for both humans and canines. In all of these experiments, isolated neutrophils were stimulated with LPS at a concentration of 1 x 10^{-6} M for 10 minutes at 37 °C. prior to adding the stimuli as indicated in the figures. The LPS primes the cells so they can respond to a secretagogue.

[000183] In one embodiment, this invention discloses a method of regulating an inflammation in a subject comprising administering a therapeutically effective amount of a pharmaceutical composition comprising a MANS peptide or an active fragment thereof. In one aspect of this embodiment, said active fragment of the MANS protein comprises at least four and preferably six amino acids. In another aspect, said inflammation is caused by respiratory diseases, bowel diseases, skin diseases, autoimmune diseases and pain syndromes. In another aspect, said respiratory diseases are selected from the group consisting of asthma, chronic bronchitis, and COPD. In another aspect, said bowel diseases are selected from the group consisting of ulcerative colitis, Crohn's disease and irritable bowel syndrome. In another aspect, said skin diseases are selected from the group consisting of rosacea, eczema, psoriasis and severe acne. In another aspect, said inflammation is caused by arthritis or cystic fibrosis. In another aspect, said subject is a mammal. Additionally, in another aspect, said mammal is selected from the group consisting of humans, canines, equines and felines. In another aspect, said administering step is selected from the group consisting of topical administration, parenteral administration, rectal administration, pulmonary administration, nasal administration, inhalation and oral administration. In another aspect, said pulmonary administration is selected from the group of aerosol, dry powder inhaler, metered dose inhaler, and nebulizer.

[000184] In another embodiment, this invention discloses a method for regulating a cellular secretory process in a subject comprising administering a therapeutically effective amount of a pharmaceutical composition comprising at least one compound comprising a MANS peptide or an active fragment thereof, that regulates an inflammatory mediator in a subject. In one aspect of this embodiment, said active fragment of the MANS protein comprises at least four, and preferably six amino acids. In another aspect, said regulating a cellular secretory process is blocking or reducing a cellular secretory process. In another aspect, said inflammatory mediator is caused by respiratory diseases, bowel diseases, skin diseases, autoimmune diseases and pain syndromes. In another aspect, said respiratory diseases are selected from the group consisting of

asthma, chronic bronchitis, and COPD. In another aspect, said bowel diseases are selected from the group consisting of ulcerative colitis, Crohn's disease and irritable bowel syndrome. In another aspect, said skin diseases are selected from the group consisting of rosacea, eczema, psoriasis and severe acne. In another aspect, said inflammatory mediator is caused by arthritis or cystic fibrosis. In another aspect, said subject is a mammal. In another aspect, said mammal is selected from the group consisting of humans, canines, equines and felines. In another aspect, said administering step is selected from the group consisting of topical administration, parenteral administration, rectal administration, pulmonary administration, nasal administration, inhalation and oral administration. In another aspect, said pulmonary administration is selected from the group of aerosol, dry powder inhaler, metered dose inhaler, and nebulizer.

[000185] In another embodiment, this invention discloses a method of reducing inflammation in a subject comprising administering a therapeutically effective amount of a compound that inhibits the MARCKS-related release of inflammatory mediators, whereby the release of inflammatory mediators in the subject is reduced compared to that which would occur in the absence of said treatment. In one aspect of this embodiment, said compound is at least one active fragment of a MARCKS protein. In another aspect, said active fragment is at least four and preferably six amino acids in length. In another aspect, said compound is a MANS peptide or an active fragment thereof. In another aspect, said compound is an antisense oligonucleotide directed against the coding sequence of a MARCKS protein or an active fragment thereof. In another aspect, said active fragment is at least four and preferably six amino acids in length.

[000186] In another embodiment, this invention discloses a method of reducing inflammation in a subject comprising administering a therapeutically effective amount of a pharmaceutically active composition comprising a compound that inhibits the MARCKS-related release of inflammatory mediators, whereby the inflammation in the subject is reduced compared to that which would occur in the absence of said treatment. In one aspect of this embodiment, said compound is an active fragment of a MARCKS protein. In another aspect, said active fragment is at least four and preferably six amino acids in length. In another aspect, said compound is a MANS peptide or an active fragment thereof. In another aspect, said compound is an antisense oligonucleotide directed against the coding sequence of a MARCKS protein or an active fragment thereof. In another aspect, said active fragment is at least four and preferably six amino

acids in length. The present invention is intended to encompass a composition that contains one or more of the MANS peptide or its active fragments and use thereof in the treatment of inhibiting the release of inflammatory mediators from granules or vesicles of inflammatory cells.

[000187] In another embodiment, this invention discloses a method of reducing or inhibiting inflammation in a subject comprising administering a therapeutically effective amount of at least one peptide comprising MANS peptide or an active fragment thereof effective to inhibit or suppress release of an inflammatory mediator at the inflammation site. In one aspect of this embodiment, said active fragment is at least four and preferably at least six amino acids in length. In another aspect, said inflammatory mediators are produced by cells selected from the group consisting of neutrophils, basophils, eosinophils, monocytes and leukocytes. Preferably the cells are leukocytes, more preferably granulocytes, and even more preferably neutrophils, basophils, eosinophils or a combination thereof. In another aspect, the agent is administered orally, parenterally, cavitarily, rectally or through an air passage. In another aspect, said composition further comprises a second molecule selected from the group consisting of an antibiotic, an antiviral compound, an antiparasitic compound, an anti-inflammatory compound, and an immunosuppressant.

[000188] An active fragment of a MANS peptide can be selected from the group consisting of the peptides of disclosed in Table 1. As disclosed herein, these peptides may be contain optional chemical moieties at the N-terminal and/or C-terminal amino acid.

[000189] In another aspect of this invention, the methods disclosed in this invention can be accomplished by use of or administering of combinations of the peptides disclosed in the invention in Table 1, i.e., by use of or administering of one or more of these peptides. Preferably a single peptide is used or administered in the methods disclosed herein.

[000190] In response to protein kinase C (PKC) activation by an inflammatory stimulant, degranulation in a cell selected from the group consisting of neutrophils, eosinophils, monocytes/macrophages and lymphocytes can be attenuated by pre-incubation and by co-incubation with a peptide identical to the N-terminal region of MARCKS protein, wherein the peptide is selected from the group of MANS peptide fragments as disclosed in Table 1.

Although time courses and concentrations can vary among cell types, in all cases the MANS peptide attenuates PKC-induced degranulation.

[000191] Having now described the invention, the same will be illustrated with reference to certain examples, which are included herein for illustration purposes only, and which are not intended to be limiting of the invention.

EXAMPLES

Methods and Materials

[000192] *Radiolabeled Immunoprecipitation Assay*--When labeling with [^{32}P]phosphate, cells were preincubated for 2 h in phosphate-free Dulbecco's modified Eagle's medium containing 0.2% bovine serum albumin and then labeled with 0.1 mCi/ml [^{32}P]orthophosphate (9000 Ci/mmol, PerkinElmer Life Sciences) for 2 h. For labeling with [^{3}H]myristic acid or ^{3}H -amino acids, cells were incubated overnight in medium containing 50 μCi/ml [^{3}H]myristic acid (49 Ci/mmol, PerkinElmer Life Sciences) or 0.2 mCi/ml [^{3}H]leucine (159 Ci/mmol, PerkinElmer Life Sciences) plus 0.4 mCi/ml [^{3}H]proline (100 Ci/mmol, PerkinElmer Life Sciences). Following labeling, cells were exposed to stimulatory reagents for 5 min. When an inhibitor was used, cells were preincubated with the inhibitor for 15 min prior to stimulation. At the end of the treatments, cells were lysed in a buffer containing 50 mM Tris-HCl (pH 7.5), 150 mM NaCl, 1 mM EDTA, 10% glycerol, 1% Nonidet P-40, 1 mM phenylmethylsulfonyl fluoride, 1 mM benzamidine, 10 μg/ml pepstatin A, and 10 μg/ml leupeptin. Trichloroacetic acid precipitation and scintillation counting may determine the radiolabeling efficiency in each culture. Immunoprecipitation of MARCKS protein was carried out according to the method of Spizz and Blackshear using cell lysates containing equal counts/min. Spizz *et al.*, *J. Biol. Chem.* 271, 553-562 (1996). Precipitated proteins were resolved by 8% SDS-polyacrylamide gel electrophoresis and visualized by autoradiography. Anti-human MARCKS antibody (2F12) and nonimmune control antibody (6F6) were used in this assay.

[000193] To assess MARCKS or MARCKS-associated protein complexes in different subcellular fractions, radiolabeled and treated cells were scraped into a homogenization buffer (50 mM Tris-HCl (pH 7.5), 10 mM NaCl, 1 mM EDTA, 1 mM phenylmethylsulfonyl fluoride, 1 mM

benzamidine, 10 μg/ml pepstatin A, 10 μg/ml leupeptin) and then disrupted by nitrogen cavitation (800 pounds/square inch for 20 min at 4 °C.). Cell lysates were centrifuged at 600 x g for 10 min at 4 °C. to remove nuclei and unbroken cells. Post-nuclear supernatants were separated into membrane and cytosol fractions by ultracentrifugation at 400,000 x g for 30 min at 4 °C. The membrane pellet was solubilized in the lysis buffer by sonication. Immunoprecipitation was then carried out as described above.

[000194] *MARCKS-related Peptides*--Both the myristoylated N-terminal sequence (MANS) and the random N-terminal sequence (RNS) peptides were synthesized at Genemed Synthesis, Inc. (San Francisco, Calif.), then purified by high pressure liquid chromatography (>95% pure), and confirmed by mass spectroscopy with each showing one single peak with an appropriate molecular mass. The MANS peptide consisted of sequence identical to the first 24 amino acids of MARCKS, i.e. the myristoylated N-terminal region that mediates MARCKS insertion into membranes, MA-GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO: 1 (where MA is N-terminal myristoyl chain). The corresponding control peptide (RNS) contained the same amino acid composition as the MANS but arranged in random order, MA-GTAPAAEGAGAEVKRASAEAKQAF (SEQ ID NO: 232). The presence of the hydrophobic myristate moiety in these synthetic peptides enhances their permeability to the plasma membranes, enabling the peptides to be taken up readily by cells. To determine the effects of these peptides on mucin secretion, cells were preincubated with the peptides for 15 min prior to addition of secretagogues, and mucin secretion was then measured by ELISA.

[000195] *Antisense Oligonucleotides*--MARCKS antisense oligonucleotide and its corresponding control oligonucleotide were synthesized at Biognostik GmbH (Gottingen, Germany). NHBE cells were treated with 5 μM antisense or control oligonucleotide apically for 3 days (in the presence of 2 μg/ml lipofectin for the first 24 h). Cells were then incubated with secretagogues, and mucin secretion was measured by ELISA. Total RNA and protein were isolated from treated cells. MARCKS mRNA was assessed by Northern hybridization according to conventional procedures using human MARCKS cDNA as a probe. MARCKS protein level was determined by Western blot using purified anti-MARCKS IgG1 (clone 2F12) as the primary detection antibody.

[000196] *Transient Transfection*--The phosphorylation site domain (PSD) of MARCKS contains the PKC-dependent phosphorylation sites and the actin filament-binding site. To construct a PSD-deleted MARCKS cDNA, two fragments flanking the PSD sequence (coding for 25 amino acids) were generated by polymerase chain reaction and then ligated through the XhoI site that was attached to the 5'-ends of oligonucleotide primers designed for the polymerase chain reaction. The resultant mutant cDNA and the wild-type MARCKS cDNA were each inserted into a mammalian expression vector pcDNA4/TO (Invitrogen, Carlsbad, Calif.). Isolated recombinant constructs were confirmed by restriction digests and DNA sequencing.

[000197] HBE1 is a papilloma virus-transformed human bronchial epithelial cell line capable of mucin secretion when cultured in air/liquid interface. Transfection of HBE1 cells was carried out using the Effectene transfection reagent (Qiagen, Valencia, Calif.) according to the manufacturer's instructions. Briefly, differentiated HBE1 cells grown in air/liquid interface were dissociated by trypsin/EDTA and re-seeded in 12-well culture plates at 1 x 10^5 cells/cm^2. After overnight incubation, cells were transfected with the wild-type MARCKS cDNA, the PSD-truncated MARCKS cDNA, or vector DNA. Cells were cultured for 48 h to allow gene expression and then exposed to secretagogues and mucin secretion measured by ELISA. All transfections were carried out in the presence of pcDNA4/TO/lacZ plasmid (Invitrogen) (DNA ratio 6:1, total 1 μg DNA, ratio of DNA to Effectene reagent=1:25) to monitor variations in transfection efficiency. Results showed no significant difference in .beta.-galactosidase activities in cell lysates isolated from the transfected cells, indicating similar transfection efficiency among different DNA constructs (data not shown).

[000198] *Protein Phosphatase Activity Assay*--PP1 and PP2A activities were measured using a protein phosphatase assay system (Life Technologies, Inc.) as known in the art with slight modification. Huang et al., Adv. Exp. Med Biol. 396, 209-215 (1996). Briefly, NHBE cells were treated with 8-Br-cGMP or medium alone for 5 min. Cells were then scraped into a lysis buffer (50 mM Tris-HCl (pH 7.4), 0.1% .beta.-mecaptoethanol, 0.1 mM EDTA, 1 mM benaamidine, 10 μg/ml pepstatin A, 10 μg/ml leupeptin) and disrupted by sonication for 20 s at 4 °C. Cell lysates were centrifuged and the supernatants saved for phosphatase activity assay. The assay was performed using ^{32}P-labeled phosphorylase A as a substrate. Released $^{32}P_i$ was counted by scintillation. The protein concentration of each sample was determined by the Bradford assay.

PP2A activity was expressed as the sample total phosphatase activity minus the activity remaining in the presence of 1 nM okadaic acid. PP1 activity was expressed as the difference between the activities remaining in the presence of 1 nM and 1 μM okadaic acid, respectively. Protein phosphatase activities were reported as nmol of P_i released per min/mg total protein.

[000199] *Cytotoxicity Assay*--All reagents used in treating NHBE cells were examined for cytotoxicity by measuring the total release of lactate dehydrogenase from the cells. The assay was carried out using the Promega Cytotox 96 Kit according to the manufacturer's instructions. All experiments were performed with reagents at non-cytotoxic concentrations.

[000200] *Statistical Analysis*--Data were analyzed for significance using one-way analysis of variance with Bonferroni post-test corrections. Differences between treatments were considered significant at $p<0.05$.

[000201] *Isolation of PMNs from canine blood*--The steps involved in isolating PMN include collecting 10 ml ACD anticoagulated blood. Then layering 5 ml on 3.5 ml PMN isolation media while ensuring that the PMN isolation media (IM) was at room temperature (RI). Next, the blood was centrifuged at room temperature for 30', 550 X g at 1700 RPMs. The low lower white band was transferred into 15 ml conical centrifuge tube (CCFT). Next, 2V HESS with 10% fetal bovine serum (PBS) was added and centrifuged at room temperature for 10', 400 X g at 1400 RPMs. The pellet was then resuspended in 5 ml 1-1ESS with PBS. The cell suspension was added to 50 ml CCFT containing 20 ml of ice cold 0.88% NH_4Cl and inverted two to three times. The resulting product was centrifuged for 10', 800 X g at 2000 RPMs, then aspirated and resuspended in 5 ml HBSS with FBS. The prep was examined by counting and cytospin and preferably for whole blood, the cell number should be between 10^9-10^{11} cells and for PMNs, cell number should be between 2-4 x 10^7 cells. *See generally,* Wang *et al., J. Immunol.*, "Neutrophil-induced changes in the biomechanical properties of endothelial cells: roles of ICAM-1 and reactive oxygen species," 6487-94 (2000).

[000202] *MPO Colorimetric Enzyme Assay*--Samples were assayed for MPO activity in 96 well round bottom microtiter plates using a sandwich ELISA kit (R & D Systems, Minneapolis, Minn.). Briefly, 20 microliters of sample is mixed with 180 microliters of substrate mixture containing 33 mM potassium phosphate, pH 6.0, 0.56% Triton X-100, 0.11 mM hydrogen

peroxide, and 0.36 mM O-Diannisidine Dihydrochloride in an individual microtiter well. The final concentrations in the assay mixture are: 30 mM potassium phosphate, pH 6.0, 0.05% Triton X-100, 0.1 mM hydrogen peroxide, and 0.32 mM O-Diannisidine Dihydrochloride. After mixing, the assay mixture was incubated at room temperature for 5 minutes, and MPO enzyme activity determined spectrophotometrically at 550 nanometers. Samples were assayed in duplicate.

Example 1.

Inflammatory mediator secretion studies

[000203] Four different leukocyte types or models that secrete specific granule contents in response to phorbol ester induced activation of PKC were used. Neutrophils were isolated from human blood and in vitro release of MPO by these cells was assessed. Release of membrane-bound inflammatory mediators from commercially-available human leukocyte cell lines was also evaluated. The human promyelocytic cell line HL-60 clone 15 was used to assess secretion of EPO (Fischkoff SA. Graded increase in probability of eosinophilic differentiation of HL-60 promyelocytic leukemia cells induced by culture under alkaline conditions. Leuk Res 1988; 12:679-686; Rosenberg HF, Ackerman S J, Tenen DG. Human eosinophil cationic protein: molecular cloning of a cytotoxin and helminthotoxin with ribonuclease activity. J Exp Med 1989; 170:163-176; Tiffany HL, Li F, Rosenberg HF. Hyperglycosylation of eosinophil ribonucleases in a promyelocytic leukemia cell line and in differentiated peripheral blood progenitor cells. J Leukoc Biol 1995; 58:49-54; Badewa AP, Hudson CE, Heiman AS. Regulatory effects of eotaxin, eotaxin-2, and eotaxin-3 on eosinophil degranulation and superoxide anion generation. Exp Biol Med 2002; 227:645-651). The monocytic leukemia cell line U937 was used to assess secretion of lysozyme (Hoff T, Spencker T, Emmendoerffer A., Goppelt-Struebe M. Effects of glucocorticoids on the TPA-induced monocytic differentiation. J Leukoc Biol 1992; 52:173-182; Balboa M A, Saez Y, Balsinde J. Calcium-independent phospholipase A2 is required for lysozyme secretion in U937 promonocytes. J Immunol 2003; 170:5276-5280; Sundstrom C, Nilsson K. Establishment and characterization of a human histiocytic lymphoma cell line (U-937). Int J Cancer 1976; 17:565-577). The lymphocyte natural killer cell line NK-92 used to assess release of granzyme (Gong JH., Maki G, Klingemann HG.

Characterization of a human cell line (NK-92) with phenotypical and functional characteristics of activated natural killer cells. Leukemia 1994; 8:652-658; Maki G, Klingemann HG, Martinson JA, Tam YK. Factors regulating the cytotoxic activity of the human natural killer cell line, NK-92. J Hematother Stem Cell Res 2001; 10:369-383; Takayama H, Trenn G, Sitkovsky MV. A novel cytotoxic T lymphocyte activation assay. J Immunol Methods 1987; 104:183-190). In all cases, the cells were preincubated with a range of concentrations of a synthetic peptide identical to the 24 amino acid MARCKS N-terminus (MANS- myristoylated N-terminal sequence peptide; MA-GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO:1) wherein MA is myristoyl attached to the N-terminal amine of the peptide by an amide bond), or a missense control peptide (RNS: Random N-terminal sequence peptide; MA-GTAPAAEGAGAEVKRASAEAKQAF, SEQ ID NO: 232) which consists of the same 24 amino acids but arranged in random order sequence which possesses less than 13% sequence identity to the MANS peptide sequence. Alternatively, the cells were pretreated with one of the synthetic truncated peptides listed in Table 3 below.

[000204] In each of the cell types, MANS, but not RNS, attenuates release of inflammatory mediators in a concentration-dependent manner. A useful time course of observation is 0.5-3.0 hrs. The results are consistent with the N-terminal region of the MARCKS protein being involved in intracellular pathways leading to leukocyte degranulation.

[000205] *Human neutrophil isolation* - These studies were approved by the human studies Institutional Review Board (IRB). Human neutrophils were isolated as previously described (see Takashi S, OkuboY, Horie S. Contribution of CD54 to human eosinophil and neutrophil superoxide production. J Appl Physiol 2001; 91:613-622) with slight modifications. Briefly, heparinized venous blood was obtained from normal healthy volunteers, diluted with RPMI-1640 (Cellgro; Mediatech, Inc., Herndon, VA) at a ratio of 1:1, layered onto a Histopaque (density, 1.077g/ml; Sigma-Aldrich Co., St. Louis, MO) and centrifuged at 400 g for 20 min at 4°C. The supernatant and mononuclear cells at the interface were carefully removed, and erythrocytes in the sediment were lysed in chilled distilled water. Isolated granulocytes were washed twice with Hanks' balanced salts solution (HBSS) and resuspended in HBSS on ice. The neutrophils used for the experiments were of >98% purity with <2% contamination by eosinophils, and the viability was >99% as determined by Trypan blue dye exclusion.

[000206] *Measurement of released neutrophil MPO activity* - For measurement of MPO release, purified human neutrophils suspended in HBSS were aliquoted at 4×10^6 cells/ml in 15 ml tubes and preincubated with either 50 or 100 μM of MANS, RNS, or one of the peptides of invention for 10 min at 37°C. The cells then were stimulated with 100 nM phorbol 12-myristate 13-acetate (PMA) for up to 3 hrs. A control reference (PMA control reference) was established using purified human neutrophils suspended in HBSS aliquoted at 4×10^6 cells/ml in 15 mL tubes and stimulated with 100 nM phorbol 12-myristate 13-acetate (PMA) in the absence of a test peptide for the same time periods. The reaction was terminated by placing the tubes on ice and centrifugation at 400g for 5 min at 4°C.

[000207] MPO activity in the cell supernatant was assayed using tetramethylbenzidine (TMB) based on a previously established technique (Abdel-Latif D, Steward M, Macdonald DL, Francis GA., Dinauer MC, Lacy P. Rac2 is critical for neutrophil primary granule exocytosis. Blood 2004; 104:832-839). Briefly, 100 μL of TMB substrate solution was added to 50 μL of cell supernatants or standard human MPO (EMD Biosciences, Inc., San Diego, CA) in a 96-well microplate followed by incubation at room temperature for 15 min. The reaction was terminated by addition of 50 μL of 1M H_2SO_4 and absorbance was read at 450 nm in a spectrophotometric microplate reader (VERSA max, Molecular Devices, Sunnyvale, CA).

Leukocyte culture studies.

[000208] Three types of human leukocyte cell lines, specifically the promyelocytic cell line HL-60 clone 15, the monocytic cell line U937, and the lymphocyte natural killer cell line NK-92 were purchased from American Type Culture Collection (ATCC; Rockville, MD). HL-60 clone 15 cells (ATCC CRL-1964) were maintained in medium consisting of RPMI 1640 with L-glutamine supplemented with 10% heat-inactivated fetal bovine serum (Gibco; Invitrogen Co., Carlsbad, CA), 50 IU/ml penicillin, 50 μg/mL streptomycin, and 25 mM HEPES buffer, pH 7.8, at 37°C in an atmosphere containing 5% CO2. Final differentiation to an eosinophil-like phenotype was initiated by culturing cells at 5×10^5 cells/ml in the above medium containing 0.5 mM butyric acid (Sigma-Aldrich Co.) for 5 days as previously described (Tiffany HL, Li F, Rosenberg HF. Hyperglycosylation of eosinophil ribonucleases in a promyelocytic leukemia cell line and in differentiated peripheral blood progenitor cells. J Leukoc Biol 1995; 58:49-54;

Tiffany HL, Alkhatib G, Combadiere C, Berger EA, Murphy PM. CC chemokine receptors 1 and 3 are differentially regulated by IL-5 during maturation of eosinophilic HL-60 cells. J Immunol 1998; 160:1385-1392). U937 cells (ATCC CRL-1593.2) were grown at 37°C in an atmosphere of 5% CO_2 in complete medium consisting of RPMI 1640 with L-glutamine supplemented with 10% FBS, 50 IU/ml penicillin, and 50 μg/mL streptomycin. NK-92 cells (ATCC CRL-2407) were maintained in alpha-MEM medium (Sigma-Aldrich Co.) supplemented with 20% FBS, 100 U/ml of interleukin-2 (IL-2) (Chemicon International, Inc., Temecula, CA), 5 x 10^{-5} M of 2-mercaptoethanol, 50 IU/mL penicillin, and 50 μg/ml streptomycin at 37°C in an atmosphere containing 5% CO_2. Cell morphology was judged by assessment of Wright-Giemsa-stained cells. Viability of cells harvested for experiments was assessed by trypan blue exclusion and populations of cells with viability >95% were used.

Incubation of cells for degranulation assays.

[000209] HL-60 clone 15, U937, and NK-92 cells were washed and resuspended at 2.5 × 10^6 cells/ml in phenol red-free RPMI-1640 (Cellgro; Mediatech, Inc.) for all degranulation assays. Aliquots of cells in 15 ml tubes were preincubated with indicated concentrations of MANS, RNS, or a test peptide for 10 min at 37°C. The cells then were stimulated with PMA for up to 2 hr. A control reference (PMA control reference) was established for each cell type using HL-60 clone 15, U937, and NK-92 cells, respectively, which were washed and resuspended at 2.5 × 10^6 cells/ml in phenol red-free RPMI-1640 and stimulated with PMA but in the absence of MANS, RNS, or a test peptide for the same time periods. The reaction was terminated by placing tubes on ice and centrifuging cells at 400g for 5 min at 4°C.

[000210] For measurements of released MPO from neutrophils and released lysozyme from U937 cells, we were able to quantify secretion by using as standards human MPO and egg white ovalbumin, respectively. For released EPO from HL-60 clone 15 cells and for released granzyme from NK-92 cells, no standards were available to use for quantification. Hence, both released and intracellular (from lysed cells) levels of EPO and granzyme were measured, and the released EPO and granzyme were expressed as a percentage of total (intracellular and released) for each. To measure intracellular EPO in HL-60 clone 15 cells and intracellular granzyme in NK-92 cells, appropriate aliquots of 0.1% triton X-100-lysed cells were taken for quantification of

intracellular granule proteins as described below. All treatments were expressed as percentage of control to minimize variability between cultures.

Measurement of HL-60 EPO release.

[000211] EPO activity released by HL-60 clone 15 cells was assayed using TMB according to a previously established technique (Lacy P, Mahmudi-Azer S, Bablitz B, Hagen SC, Velazquez JR, Man SF, Moqbel R. Rapid mobilization of intracellularly stored RANTES in response to interferon-gamma in human eosinophils. Blood 1999; 94:23-32). Thus, 100 μL of TMB substrate solution was added to 50 μL (μL = microliters) of sample in a 96-well microplate and incubated at room temperature for 15 min (min = minutes). The reaction was terminated by addition of 50 μL of 1.0M H_2SO_4 and absorbance was read at 450 nm (nm = nanometers) in a spectrophotometric microplate reader. The amount of secreted EPO was expressed as percentage of total content, using the amount obtained in the same number of triton X-100-lysed cells.

Measurement of monocyte lysozyme secretion.

[000212] Lysozyme secreted by U937 cells was measured using a spectrophotometric assay as described previously (Balboa M A, Saez Y, Balsinde J. Calcium-independent phospholipase A2 is required for lysozyme secretion in U937 promonocytes. J Immunol 2003; 170:5276-5280) with slight modification. Thus, 100 μL of sample was mixed with 100 μL of a Micrococcus lysodeikticus (Sigma-Aldrich Co.) suspension (0.3 mg/ml in 0.1 M sodium phosphate buffer, pH 7.0) in a 96-well microplate. The decrease in absorbance at 450 nm was measured at room temperature. A calibration curve was constructed using chicken egg white lysozyme (EMD Biosciences, Inc.) as a standard.

Measurement of NK cell granzyme secretion.

[000213] Granzyme secreted from NK-92 cells was assayed by measuring hydrolysis of Nα-benzyloxycarbonyl-L-lysine thiobenzyl ester (BLT) essentially as described previously (Takayama H, Trenn G, Sitkovsky MV. A novel cytotoxic T lymphocyte activation assay. J Immunol Methods 1987; 104:183-190). Briefly, 50 μL of supernatant was transferred to a 96-well plate, and 150 μL of BLT solution (0.2 mM BLT; EMD Biosciences, Inc., and 0.22 mM DTNB; Sigma-Aldrich Co.) (mM = millimolar) in phosphate-buffered saline (PBS, pH 7.2) was

added to the supernatant. Absorbance at 410 nm was read after incubation for 30 min at room temperature. Results were expressed as percentage of total cellular enzyme content, using the amount obtained in the same number of triton X-100-lysed cells.

Statistical analysis.

[000214] Statistical significance of the differences between various treatment groups was assessed with one-way ANOVA. P values of <0.05 were taken as significant.

Inhibition of MPO release from human neutrophils

[000215] It was found that 100 nM PMA (as a stimulator of inflammatory mediator release) increased human neutrophil MPO release by approximately threefold versus control level at 30 min in the PMA control reference, the release of MPO increasing to approximately 5-6 fold after 3 hrs. At 30 minutes, relative to the control MPO activity as 100% absent PMA and absent PMA plus MANS, RNS,or test peptide, MPO activity of the PMA control reference was about 275%, PMA plus 50 μM MANS was about 275%, and 100 μM MANS was about 305%. Thus, the MANS peptide had no detected effect at 30 min. However, by 1 hr the higher concentration of MANS (100 μM) had a significant inhibitory effect (measured at about 260% of control) or about 25% reduction in MPO release versus the PMA control reference level (which was measured at about 340% of control). The 50 μM MANS sample measured about 290% of control or about 15% reduction relative to the PMA control reference. By 2 hrs and persisting at 3 hrs, the MANS peptide significantly attenuated MPO activity in a concentration-dependent manner. At 2 hours, the PMA control reference MPO activity was about 540% of control, the 50 μM MANS (measuring about 375% of control) caused an approximately 30% reduction of MPO release versus the PMA control reference; and 100 μM MANS (measuring about 295% of control) caused an approximately 45% reduction of MPO release versus the PMA control reference. At 3 hours, the PMA control reference MPO activity was about 560% of control, 50 μM MANS (measuring about 375% of control) caused an approximately 33% reduction of MPO release versus the PMA control reference; 100 μM MANS (measuring about 320% of control) caused an approximately 40% reduction of MPO release versus the PMA control reference. The RNS peptide did not affect PMA-induced MPO release at any of the time points or

concentrations tested. The data presented in the table below represents 100 μM concentration of test peptides and a two hour incubation with 100 nM PMA.

Inhibition of EPO release from HL-60 Cells

[000216] EPO activity in the supernatant of HL-60 clone 15 cells was significantly enhanced at 1 and 2 hrs after PMA stimulation. At 1 hour, relative to EPO activity of the control as 100%, the PMA control reference measured at about 110%; the sample containing 10 μM MANS measured at about 95% to give about 15% reduction in EPO activity relative to the PMA control reference; the sample containing 50 μM MANS measured at about 78% to give about 30% reduction in EPO activity relative to the PMA control reference; and the sample containing 100 μM MANS measured at about 65% to give about 40% reduction in EPO activity relative to the PMA control reference. At 2 hour, relative to EPO activity of the control as 100%, the PMA control reference measured at about 145%; the sample containing 10 μM MANS measured at about 130% to give about 10% reduction in EPO activity relative to the PMA control reference; the sample containing 50 μM MANS measured at about 70% to give about 50% reduction in EPO activity relative to the PMA control reference; and the sample containing 100 μM MANS measured at about 72% to give about 50% reduction in EPO activity relative to the PMA control reference. Thus, at both 1 and 2 hrs, MANS at 50 or 100 μM significantly attenuated EPO release. The RNS peptide did not affect PMA-enhanced EPO release at any of the time points or concentrations tested. The data presented in the table below represents 50 μM concentration of test peptides and a two hour incubation with 100 nM PMA.

Inhibition of lysozyme release from U937 Cells

[000217] Lysozyme secretion by U937 cells was increased by PMA stimulation by 1 hr after incubation, and increased even more at 2 hrs. At 1 hour, relative to lysozyme secretion by U937 cells of the control as 100%, the PMA control reference measured at about 210%; the sample containing 10 μM MANS measured at about 170% to give about 20% reduction in lysozyme secretion by U937 cells relative to the PMA control reference; the sample containing 50 μM MANS measured at about 170% to give about 20% reduction in lysozyme secretion by U937 cells relative to the PMA control reference; and the sample containing 100 μM MANS measured at about 115% to give about 45% reduction in lysozyme secretion by U937 cells relative to the

PMA control reference. At 2 hour, relative to lysozyme secretion by U937 cells of the control as 100%, the PMA control reference measured at about 240%; the sample containing 10 μM MANS measured at about 195% to give about 20% reduction in lysozyme secretion by U937 cells relative to the PMA control reference; the sample containing 50 μM MANS measured at about 185% to give about 25% reduction in lysozyme secretion by U937 cells relative to the PMA control reference; and the sample containing 100 μM MANS measured at about 140% to give about 40% reduction in lysozyme secretion by U937 cells relative to the PMA control reference. Thus, lysozyme secretion was significantly attenuated at both 1 and 2 hours post-stimulation by 100 μM of MANS but not as much by 50 or 10 μM of MANS. The RNS peptide did not affect PMA-enhanced lysozyme secretion at any of the time points or concentrations tested. The data presented in the table below represents 50 μM concentration of test peptides and a two hour incubation with 100 nM PMA.

Inhibition of Granzyme release from NK-92 cells

[000218] The lymphocyte natural killer cell line NK-92 was used to assess release of granzyme (Gong JH, Maki G, Klingemann HG. Characterization of a human cell line (NK-92) with phenotypical and functional characteristics of activated natural killer cells. Leukemia 8:652-658, 1994; Maki G, Klingemann HG, Martinson JA, Tam YK. Factors regulating the cytotoxic activity of the human natural killer cell line, NK-92. J. Hematother. Stem Cell Res., 10:369-383, 2001; Takayama H, Trenn G, Sitkovsky MV. A novel cytotoxic T lymphocyte activation assay. J. Immunol. Methods 104:183-190, 1987).

[000219] Measurement of NK cell granzyme secretion: Granzyme secreted from NK-92 cells was assayed by measuring hydrolysis of Nα-benzyloxycarbonyl-L-lysine thiobenzyl ester (BLT, EMD Bioscience, Inc.) essentially as described previously (Takayama H, Trenn G, Sitkovsky MV. A novel cytotoxic T lymphocyte activation assay. J. Immunol. Methods 104:183-190, 1987). An aliquot of 50 μL of supernatant was transferred to a 96-well plate, and 150 μL of 0.2 mM solution of BLT and 0.22 mM DTNB (Sigma-Aldrich Co.) in phosphate-buffered saline (PBS, pH 7.2) was added to the supernatant. Absorbance at 410 nm was measured after incubation for 30 min at room temperature. Results were expressed as

percentage of total cellular enzyme content, using the amount obtained in the same number of triton X-100-lysed cells.

[000220] Because standard granzyme from NK-92 cells was not available to use for quantification, we measured both released and intracellular (from lysed cells) levels of granzyme, and expressed the released granzyme as a percentage of total (intracellular and released) for each. To measure intracellular granzyme from NK-92 cells, appropriate aliquots of 0.1% triton X-100-lysed cells were taken for quantification of the enzyme as described above. All data are expressed as percentage of control to minimize variability between cultures. The data presented in the table below represents 50 μM concentration of test peptides and a two hour incubation with 100 nM PMA.

Cytotoxicity

[000221] Because standard None of the treatments generated a toxic response in the cells, as assessed by LDH retention/release (data not shown) (see also Park J-A, He F, Martin LD, Li Y, Adler KB. Human neutrophil elastase induces hypersecretion of mucin from human bronchial epithelial cells in vitro via a PKCδ – mediated mechanism. Am J Pathol 2005; 167:651-661).

[000222] In preliminary experiments, the following peptides which are presented in the table below demonstrate respective percent inhibition of release of MPO from human neutrophils, of EPO from HL-60 clone 15 cells, of lysozyme from U937 cells, and of granzyme from NK-92 cells, wherein MA- signifies the presence of a myristoyl substituent group at the alpha-N-terminal position of the peptide; Ac- signifies the presence of an acetyl substituent group at the alpha-N-terminal position of the peptide; H signifies no group attached to the peptide; and NH2 signifies the presence of an amide at the C-terminal position. Inhibition data are averaged from multiple experiments. Qualitative solubility of the peptides in 0.5 N saline at pH 6.5 is given in mg/mL in Table 3 below. Changing the N-terminal chemical moiety from a myristoyl group can lead to changes in solubility of the peptides disclosed herein in aqueous media. For example, changing the myristoyl group to an acetyl group results in the increased aqueous solublility shown in Table 3.

Table 3. Results of Enzyme inhibition assays solubilities for representative peptides and substituted peptides

				% Inhibition				mg/mL
SEQ ID NO.:	N-[1]	Amino Acid Sequence	C-[2]	EPO	Lysozyme	MPO	Granzyme	Solubility[3]
219	Ac	AKGE		87.6	7.2			>200
45	Ac	AKGEAAAERPGEAAVA		72.3	34.3			
37	Ac	GAQFSKTAAKGEAAAE		56.6	8.4			
239	Ac	GAQFSKTAAAGE		55.8	37.2			>50
248	Ac	GAQFSKTAAA		55.2	28.3			>100
91	Ac	AAAERPGEAAVA		51.2	29.5			
11	Ac	GAQFSKTAAKGEAAAERPGE		48.8	0.0			
79	Ac	GAQFSKTAAKGE		46.7	43.3			>100
153	Ac	RPGEAAVA		45.8	0.0			
219	Ac	AKGE	NH2	45.6	26.8			>200
93	Ac	AQFSKTAAKGE	NH2	42.8	51.8			>90
141	Ac	SKTAAKGE	NH2	42.2	0			>200
241	Ac	GAQFSKTAAKGA		40.9	24.1			>50
143	Ac	TAAKGEAA		40.4	0.5			>230
251	Ac	AAGE		39.1	36.9			>200
106	Ac	GAQFSKTAAK		35.7	41.2	25.3		>100
249	Ac	GAQFSATAAA		35.7	3.2			<10
1	Ac	GAQFSKTAAKGEAAAERPGEAAVA		33.7	39.8			> 250
121	Ac	GAQFSKTAA		33.3	28.9			>20
106	Ac	GAQFSKTAAK (all d)		26.9	8.9	40.0		>100
124	Ac	FSKTAAKGE	NH2	25.3	56.7			>100
79	Ac	GAQFSKTAAKGE	NH2	24.7	38.6	26.5		>60
108	Ac	QFSKTAAKGE	NH2	15.7	60.7			>150
179	Ac	AAKGEA		10.6	9.2			>150
159	Ac	KTAAKGE	NH2	0	24.3			>200
137	Ac	GAQFSKTA		0	0			>200
79	H	GAQFSKTAAKGE				27.9		>60
1	MA	GAQFSKTAAKGEAAAERPGEAAVA		46.1	40.8	31.2	76.0	<5.0
106	MA	GAQFSKTAAK		37.4	56.6			>10
11	MA	GAQFSKTAAKGEAAAERPGE		33.6	99			
179	MA	AAKGEA		31.4	28.6			<1.0
37	MA	GAQFSKTAAKGEAAAE		30.3	99			>2.0
79	MA	GAQFSKTAAKGE		25.2	85.2	43.2		>2.0
91	MA	AAAERPGEAAVA		21.6	98			<20
45	MA	AKGEAAAERPGEAAVA		18.1	98			>80
153	MA	RPGEAAVA		0	99			
15	MA	SKTAAKGEAAAERPGEAAVA		0	99			>80
143	MA	TAAKGEAA		0	80.2			<1.0
219	MA	AKGE		0	28.6			<1.0
232	MA	GTAPAAEGAGAEVKRASAEAKQAF		0	0	0	29.5	>15

[1] N- = N-terminal group
[2] C- = C-terminal group
[3] 0.5 N Saline, pH 6.5

234	MA	GAQFSKTKAKGE				65.2		>3.0

Example 2.

In vivo inhibition of Lipopolysaccharide (LPS)-induced lung inflammation by MANS and related peptides

[000223] This example was performed essentially according to methods described by Cox, G, Crossley, J., and Xing, Z.; Macrophage engulfment of apoptotic neutrophils contributes to the resolution of acute pulmonary inflammation in vivo; Am. J. Respir. Cell Mol. Biol. 12:232-237, 1995; Hirano S., Quantitative time-course profiles of bronchoalveolar lavage cells following intratracheal instillation of lipopolysaccharide in mice, Ind. Health 35:353-358, 1997; and Ulich TR, Watson LR, Yin SM, Guo KZ, Wang P, Thang H, and del Castillo, J. Am. J. Pathol. 138:1485-1496, 1991.

[000224] Thus, six to seven week old CD1 female mice weighing 15-20 grams were obtained from Charles River laboratories and housed in groups of 5 mice per cage. The animals received standard rodent diet and filtered water ad libitum. The animals were housed under NIH prescribed guidelines at standard temperature (64° to 79° F) and relative humidity of 30 to 70%.

[000225] Five treatment groups of mice, with 5 animals in each group, were treated either with PBS followed by PBS, with PBS followed by LPS, with (myristoylated) MANS peptide followed by LPS, with acetylated peptide of SEQ ID NO: 1, followed by LPS, or with acetylated peptide of SEQ ID NO: 106, followed by LPS.

[000226] Intranasal peptide instillation pre-treatment: A peptide of the invention to be evaluated in vivo for its ability to inhibit or reduce LPS-induced lung inflammation was dissolved in PBS at a concentration of 1 mM. Animals, anesthetized with 0.8% isofluorane by inhalation, were pretreated with 2x 10 μL intranasal bolus of the peptide solution into one nostril 30 minutes prior to subsequent instillation with LPS.

[000227] Intranasal LPS instillation: Lipopolysaccharide (LPS) Endotoxin (Escherichia coli Serotype 011:B4 derived endotoxin; Sigma, St Louis, MO; see Sigma product information sheet L4130 titled Lipopolysaccharides from Escherichia coli 011:B4) was dissolved into phosphate

buffered saline (PBS) at 2,500 μg/mL. To expose animals to endotoxin, a 10 μL intranasal bolus of 2,500 μg/ml endotoxin solution was administered to animals which had been anesthetized with 0.8% isofluorane by inhalation. The 10 μL bolus was applied into one nostril. Animals were monitored for labored breathing, lethargy, and decreased water/food intake following the endotoxin instillations.

[000228] Bronchoalveolar Lavage (BAL): Six hours after the last instillation, the animals were anesthetized (90 mg/kg Nembutal) and sacrificed by exsanguination. The lung was serially lavaged 2 times with 1.0 mL aliquots of PBS. The collected BAL fluid was centrifuged to remove the cells for subsequent counting and differential analysis. Recovered lavage fluid was used for analysis of total protein, myeloperoxidase (MPO), LDH, and hemoglobin.

[000229] Analysis: Aliquots of the BAL fluid were used immediately to assay for the levels of LDH, total protein, or hemoglobin using the COBAS Fara analyzer (COBAS FARA II automated analyzer; Roche Diagnostic Systems Inc., Montclair, NJ). An aliquot of BAL fluid was frozen at -80° C for subsequent quantitation of myeloperoxidase (MPO) with a mouse-specific ELISA assay (Cell Sciences, Inc., Canton, Mass). BAL data were analyzed by standard techniques to examine differences between the control and treatment groups. Results demonstrating inhibition or reduction of inflammation by Test peptide are provided in the following tables.

[000230] Table 4. Average values of markers of inflammation in the presense of MANS peptide, MA-GAQFSKTAAKGEAAAERPGEAAVA, SEQ ID NO.:1

Treatment Regime	Total cells counted	Total neutrophils counted	% Neutrophils of total cells	MPO (ng/mL)	Total Protein (ug/ml)	LDH (units/L)	Hb (g/dl)
PBS / PBS n=5	157,020	29317	18.7	3.28	125.60	68.20	0.00
PBS / LPS n=5	264,200	110,061	41.7	28.98	272.40	60.40	0.19
MANS / LPS n=7	208,457	64,481	30.9	9.49	175.00	68.57	0.05

[000231] Table 5. Average values of markers of inflammation in the presence of an N-terminal acetylated analog of MANS peptide, Ac-GAQFSKTAAKGEAAAERPGEAAVA, SEQ ID NO: 1

Treatment Regime	Total Cell Counts	Total Neutrophil counts	% Neutrophils of total counts	MPO (ng/mL)	Total Protein (μg/mL)	LDH (units/L)	Hb (g/dL)
PBS / PBS n=5	89,440	19,770	22.1	5.45	230.6	84.0	0.00
PBS / LPS n=5	251,360	164,578	65.5	37.90	153.4	89.9	0.01
Ac-SEQ ID NO.:1/ LPS n=5	254,400	105,499	41.47	30.79	182.75	74.5	0.01

[000232] Table 6. Average values of markers of inflammation in the presence of acetylated peptide Ac-GAQFSKTAAK, SEQ ID NO.:106

Treatment Regime	Total Cell Counts	Total Neutrophil counts	% Neutrophils of total counts	MPO (ng/mL)	Total Protein (μg/mL)	LDH (units/L)	Hb (g/dL)
PBS / PBS n=5	312,620	66,521	21.3	4.88	113.8	61.80	0.00
PBS / LPS n=5	327,680	80,077	24.4	7.19	116.4	78.20	0.00
Ac-SEQ ID NO.:106/ LPS n=5	305,688	9,170	3.0	1.50	131.0	106.86	0.00

[000233] Table 7. Inhibition of markers of inflammation by MANS peptide (Myr-SEQ ID NO:1), test peptides (Ac-GAQFSKTAAKGEAAAERPGEAAVA), SEQ ID NO: 1, and Ac-GAQFSKTAAK, SEQ ID NO: 106, relative to PBS/LPS treatment:

Treatment Regime	Inhibition of neutrophil migration	Inhibition of MPO
MANS / LPS	41.4 %	67.2%
SEQ ID NO:1 / LPS	35.9 %	18.75%
Ac-SEQ ID NO. 106 / LPS	88.5%	79.1%

[000234] PBS/PBS indicates only PBS control was administered, and no LPS endotoxin was added to stimulate chemotactic neutrophil migration; PBS/LPS indicates LPS (endotoxin) was added to stimulate chemotactic neutrophil migration; MANS/LPS indicates pretreatment with MANS peptide in PBS followed by LPS stimulation to induce neutrophil migration. The percent of neutrophils in the total cell count in the LPS treatment groups was reduced from 41.7 % to 30.9% by treatment with MANS peptide; from 65.5% to 41.47% by treatment with the peptide Ac-GAQFSKTAAKGEAAAERPGEAAVA, SEQ ID NO. 1; from 24.4% to 3.0% by treatment with the peptide Ac-GAQFSKTAAK, SEQ ID NO. 106. The measured MPO levels in the LPS treatment groups was reduced from 28.98 ng/mL to 9.49 ng/mL by treatment with MANS

peptide; from 37.9 ng/mL to 30.79 ng/mL by treatment with the peptide with acetylated SEQ ID NO:1 and from 7.19 ng/mL to 1.50 ng/mL by treatment with the peptide with acetylated SEQ ID NO:106.

Example 3.

Mouse Model of Ozone-induced COPD

[000235] Oxidative stress by chemical irritants such as ozone is a widely recognized feature of chronic obstructive respiratory disease (COPD). See: Repine JE, Bast A, Lankhorst I, and the Oxidative Stress Study Group, Am. J. Respir. Crit. Care Med. 156:341-357, 1997; and also Harkema JR and Hotchkiss JA, Toxicology Letters, 68:251-263, 1993.

[000236] Ten-week-old Balb/C female mice were obtained from Charles River laboratories and housed under NIH guidelines in groups of 5 per cage. The animals received standard rodent diet and filtered water ad libitum. Three treatment groups of mice, 5 animals in each group, were each anesthetized by intraperitoneal injection of Ketamine (100 mg/kg) and Xylazine (20 mg/kg) and then pretreated by intratracheal administration with 25 μL of either PBS alone, or a solution of 1.0 mM MANS peptide in PBS, or a solution of a 1.0 mM of an acetylated MANS-fragment-peptide Ac-GAQFSKTAAK designated as acetylated SEQ ID NO: 106 in PBS. After 30 minutes, the animals were then placed in the appropriate custom-made chamber for ozone or forced air exposures. The animals were exposed to ozone for 2 hours (at ozone concentrations of 1-10 ppm by a slightly modified method described by Haddad et al, 1995. (Haddad E-B, Salmon M, Sun J, Liu S, Das A, Adcock I, Barnes PJ, and Chung KF, FEBS Letters, 363:285-288, 1995). The ozone was generated using an ozone generator apparatus model OL80F/B from OzoneLab, Burton, British Columbia, Canada. Ozone concentration was continuously monitored using a Teledyne Photometric O3 Analyzer (model 400E, Teledyne Instruments, City of Industry, CA). Two additional groups of mice, each without any pretreatment, were either exposed to ozone under the same conditions or exposed to forced air under conditions similar to the ozone treatment group but absent ozone. After exposure, the animals were sacrificed by exsanguination and the lungs were serially lavaged 2 times with 1.0 mL aliquots of PBS. The collected bronchoalveolar lavage (BAL) fluid was centrifuged to remove the cells for subsequent counting and differential analysis. Recovered lavage fluid was used for protein and additional

analysis of IL-6, IFNγ, and KC (murine IL-8 analog) by ELISA assay (assay kits obtained from R&D Systems, Minneapolis, MN).

[000237] The percent inhibition of neutrophil migration into the BAL fluid as a function of treatment groups and relative to a control group treated with PBS alone are provided in the table.

[000238] Table 8: Inhibition of ozone-induced neutrophil migration by MANS peptide and by peptide acetylated SEQ ID NO: 106, Ac-GAQFSKTAAK.

Treatment Group	% Inhibition of neutrophil migration into BAL fluid
MANS + Ozone	93.0
Ac-SEQ ID NO:106 +Ozone	81.2
PBS + Ozone	Not applicable
Forced air alone	Not applicable

[000239] Concentrations of IL-6 in pg/mL in BAL fluid, as a function of intratracheal injection pretreatment and subsequent treatment with ozone, were obtained as follows. IL-6 levels were found to be: approximately 364.5 pg/mL in a group of mice pretreated with MANS peptide and then exposed to ozone; approximately 130.4 pg/mL in a group of mice pretreated with acetylated MANS-fragment-peptide, Ac-GAQFSKTAAK (SEQ ID NO: 106), and then exposed to ozone; approximately 1041.3 pg/mL in a group of mice pretreated with PBS and exposed to ozone; approximately 43.2 pg/mL in a group of mice exposed directly to forced air without any pretreatment.

[000240] Concentrations of KC in pg/mL in BAL fluid, as a function of intratracheal injection pretreatment and subsequent treatment with ozone, were obtained as follows. KC levels were found to be: approximately 183.6 pg/mL in a group of mice pretreated with MANS peptide and then exposed to ozone; approximately 159.7 pg/mL in a group of mice pretreated with acetylated MANS-fragment-peptide, Ac-GAQFSKTAAK (SEQ ID NO:106), and then exposed to ozone; approximately 466.6 pg/mL in a group of mice pretreated with PBS and exposed to ozone; approximately 36.3 pg/ml in a group of mice exposed to forced air without pretreatment.

[000241] Concentrations of IFNγ in pg/mL in BAL fluid as a function of intratracheal injection pretreatment and subsequent treatment with ozone were obtained as follows. IFNγ levels were found to be: approximately 7.4 pg/mL in a group of mice pretreated with MANS peptide and then exposed to ozone; approximately 3.6 pg/ml in a group of mice pretreated with acetylated MANS-fragment-peptide, Ac-GAQFSKTAAK (SEQ ID NO:106), and then exposed to ozone; approximately 8.6 pg/mL in a group of mice pretreated with PBS and exposed to ozone; and approximately 5.0 pg/mL in a group of mice exposed to forced air.

[000242] Administration of ozone to mice significantly increased infiltrated neutrophil cell numbers, as well as IL-6 and KC levels in the BAL. In comparison to the control group in which the mice were pretreated with PBS, the group pretreated with MANS peptide and the group pretreated with acetylated peptide, Ac-GAQFSKTAAK, acetylated SEQ ID NO:106. each exhibited reduced neutrophil cell infiltration in the BAL fluid after ozone exposure (e.g., 93% ± 10% and 81% ± 10%, respectively vs. PBS control). In parallel, MANS peptide and acetylated peptide acetylated SEQ ID NO:106 also markedly diminished KC concentrations (e.g., 65.8% ± 10% and 71.3% ± 10%, respectively, vs. PBS control) and IL-6 levels (e.g., 67.8% ± 15%, MANS and 91.3% ± 15% acetylated SEQ ID NO:106 vs. PBS control) after ozone exposure but had little effect on interferon-γ levels. Collectively, these data evidence that MANS peptide and acetylated SEQ ID NO:106 peptides markedly diminish or inhibit ozone-induced neutrophil migration into the airways as well as decrease selective chemokine and cytokine. The IL-6 levels in the BAL fluids from animals pretreated with MANS peptide or acetylated peptide SEQ ID NO:106 showed approximately 68% and 91% inhibition, respectively, compared to those pretreated with PBS. Also the KC levels in the BAL fluids from animals pretreated with MANS peptide or acetylated peptide SEQ ID NO:106 showed approximately 65% and 71% inhibition compared to those pretreated with PBS.

Example 4.

Chronic bronchitis model

[000243] The procedure is described by Voynow JA, Fischer BM, Malarkey DE, Burch LH, Wong T, Longphre M, Ho SB, Foster WM, Neutrophil Elastase induces mucus cell metaplasia in mouse lung, Am. J. Physiol. Lung Cell Mol. Physiol. 287:L1293-L1302, 2004 and is followed to

develop a model of chronic bronchitis in the mouse. Specifically, goblet cell hyperplasia, a signature pathological feature of chronic bronchitis, is induced by chronic exposure of mice to human Neutrophil Elastase (NE) instilled into the airways.

[000244] Human NE are aspirated intratracheally by male Balb/c mice. A total of 30 mice (about 25-30 g in weight) are obtained commercially from a supplier such as Jackson Laboratories, Bar Harbor, ME. The mice are maintained on a 12 hr diurnal cycle, with food and water provided ad libitum. The animals receive NE by oropharyngeal aspiration on days 1, 4, and 7. Immediately after inhalational anesthesia with isofluorane (IsoFlo from Abbott Laboratories and Open-Circuit Gas Anesthesia System from Stoelting), animals are suspended by their upper incisors on a 60° incline board, and a liquid volume of human NE [50 ug (43.75 units)/40 μL PBS (Elastin Products, Owensville, MO) is delivered with the animal's tongue extended to the distal part of the oropharynx. With the tongue extended, the animal is unable to swallow, and the liquid volume is aspirated in the respiratory tract.

[000245] At 7 days after the last NE exposure, when the goblet cell hyperplasia modeling the airways in chronic bronchitis is at its maximum (see Voynow et al, 2004), mice (5 animals per group) are instilled intra-tracheally with 50 μL of either PBS (as control), or 100 uM of a solution of MANS peptide, a solution of RNS peptide, or a solution of a peptide such as acetylated peptide SEQ ID NO:106 dissolved in PBS. Fifteen minutes later, mucus secretion is triggered by administration of methacholine, using a Buxco system Nebulizer to provide a fine aerosol delivering methacholine at approximately 60mM for 3 min. Fifteen minutes after methacholine administration, mice are sacrificed by inhalational exposure to 100% CO2 gas.

[000246] Histochemistry. After exposures described above, lungs from animals are flushed to remove blood, then are inflated with OCT (Optimum Cutting Temperature medium (Sakura Finetck, Torrance, CA), half diluted in saline. The lungs are immersed in 10% formaldehyde in PBS overnight at 4°C, and processed to paraffin wax. Five μm sections are treated with Periodic acid Schiff/haematoxylin to stain mucins in the airways, for example as described by Singer M, Vargaftig BB, Martin LD, Park JJ, Gruber AD, Li Y, Adler KB, A MARCKS-related peptide blocks mucus hypersecretion in a murine model of asthma., Nature Medicine 10:193-196, 2004.

[000247] Histological mucus index. A histological mucus index (Whittaker L, Niu N, Temann U-A, Stoddard A, Flavell RA, Ray A, Homer RJ, and Cohn L, Interleukin-13 mediates a fundamental pathway for airway epithelial mucus induced by CD4 T cells and interleukin-9, Am. J. Respir. Cell Mol. Biol. 27:593–602, 2002) is performed on AB/PAS-stained sections that include both central and peripheral airways. The slides are examined with a 10X objective, and images captured with a digital camera. A minimum of four representative cross- or sagittally sectioned airways is imaged per animal. Only airways where the complete circumference of the airway can be visualized and included in the image are analyzed. Airways that open directly in an alveolar space are not included. The extent of PAS-positive staining in each airway imaged will be semi-quantitatively determined by an examiner who does not know the treatment conditions for each section, using the following five-tier grading system: grade 0, no PAS staining; grade 1, 25% or less of the airway epithelium has PAS staining; grade 2, 26–50% of the airway epithelium has PAS staining; grade 3, 51–75% of the airway epithelium has PAS staining; and grade 4, >75% of the airway epithelium has PAS staining. This grading system is used to calculate a mucus index score for each group, and results are presented as means ± SE.

[000248] All results are presented as means ± standard error (n=5 animals, 10-20 sections for each). Significance levels will be calculated using one way ANOVA followed by Scheffe's test, using SPSS 6.1 software (* = significance between data with a threshold of $p < 0.05$).

Example 5.

In vivo assays

[000249] The objective of the following set of experiments is to establish the effects of the peptides of this invention after in vivo delivery, either by local instillation at the site of inflammation or i.v. injection, on inflammation compared to the control peptides such as RNS. Two models are useful for this determination: (i) the murine air pouch inflammation model and (ii) the murine thioglycollate induced peritonitis model. Both are well-characterized models of inflammation in which neutrophils have an essential role. The air pouch model enables determination of the effects of the peptides on a short time course of inflammation (approximately 4 hrs) and the peritonitis model is useful with respect to a longer time course of inflammation (approximately 24 hrs).

Overall experimental design:

[000250] Four studies, two for each model, one testing i.v. delivery of the peptides and one testing local delivery of the peptides are useful for studying the effect of the peptides disclosed in this application. Each study consists of 2 experimental groups, a non-inflamed control (treated with vehicle) and an inflamed group (i.e., treated with an inflammatory stimulus). Each group is divided into 5 and optionally 6 treatment subgroups, n = 6 for each subgroup. Treatments subgroups are, for example: vehicle, MANS, RNS, test peptide, optionally a peptide having a scrambled sequence of the test peptide which scrambled sequence are dubbed "peptide-SCR", and dexamethasone. Dexamethasone serves as a reference anti-inflammatory agent. The selection of appropriate doses for i.v. injection or local instillation are determined from preliminary dose response experiments. Tentative doses based on the inhibitory activity of MANS in human neutrophils are: 1 mg/kg for i.v. delivery administered once or a final concentration of 50 μM delivered locally (into the air pouch or i.p.). The dose for i.v. delivery are chosen assuming a volume of distribution of 2 L/kg.

Air pouch inflammation model:

[000251] Assays for neutrophil infiltration and inflammation in the mouse air pouch are performed as described in Clish CB, O'Brien JA, Gronert K, Stahl GL, Petasis NA, Serhan CN. Local and systemic delivery of a stable aspirin-triggered lipoxin prevents neutrophil recruitment in vivo. Proc Natl Acad Sci U S A. 1999 Jul 6;96(14):8247-52. Thus, white male BALB/c mice (6–8 wk) are anesthetized with isoflurane, and dorsal air pouches are raised by injecting 3 ml of sterile air subcutaneously on days 0 and 3. On day 6 and while the mice are anesthetized with isoflurane, vehicle, MANS, RNS, test peptide, or optionally peptide-SCR are delivered as a bolus injection either i.v. into the tail vein in 100 μL of sterile 0.9% saline or locally into the air pouch in 900 μL of PBS −/− (Dulbecco's Phosphate Buffered Saline without magnesium or calcium ions, BioWhittaker). Dexamethasone (Sigma) delivered i.v. as 0.1 mg/kg in 100 μl sterile 0.9% saline or locally as 10 μg in 900 μL of PBS −/−, serves as a reference anti-inflammatory agent. Inflammation in the air pouch is induced by local injection of recombinant murine tumor necrosis factor α (TNF-α, 20 ng) (Boehringer Mannheim) dissolved in 100 μL of sterile PBS. While the mice are anesthetized with isoflurane, the air pouches are lavaged twice with 3 mL of

sterile PBS 4 hr after the initial TNF-α injection. Aspirates are centrifuged at 2,000 rpm for 15 min at 23°C. The supernatants are removed, and the cells suspended in 500 μL of PBS. Aliquots of the supernatant are assayed for inflammatory mediator concentrations (optionally except for TNFα), MPO activity, and lipid peroxidation.

[000252] Total leukocytes are enumerated in the cell suspension by light microscopy using a hemocytometer. Resuspended aspirate cells (50 μL) are added to 150 μL of 30% BSA and centrifuged onto microscope slides at 2,200 rpm for 4 min by using a cytofuge. Differential leukocyte counts are determined in cytospins stained with Wright Giemsa stain and used to calculate the absolute number of each leukocyte per air pouch exudate. For microscopic analysis, tissues are obtained with a 6-mm tissue biopsy punch (Acu-Punch, Acuderm) and fixed in 10% buffered formaldehyde. Samples are then embedded in paraffin, sliced and stained with hematoxylin-eosin. Neutrophils are enumerated in histological sections by counting number of cells/hpf. Distant dermis serve as a control for the inflamed air pouch dermis.

[000253] Data are presented as total number of neutrophils, monocytes, eosinophils, basophils, and lymphocytes per exudate or the number neutrophils per tissue high power field. Values are reported as the mean ± SEM (n = 6). The significance of any treatment on migration are determined by ANOVA. $P < 0.05$ is to be considered significant.

Example 6.

Inflamed Peritoneum model:

[000254] Male BALB/c mice (6–8 wk) are used and the thioglycollate-induced peritonitis models performed as described in Tedder TF, Steeber DA, Pizcueta P. L-selectin-deficient mice have impaired leukocyte recruitment into inflammatory sites.J Exp Med. 1995 Jun 1;181(6):2259-64. Vehicle, MANS, RNS, test peptide, and optionally peptide-SCR are delivered as a bolus injection either into the tail vein in 100 μL of sterile 0.9% saline or locally into the peritoneum 900 μl of PBS -/- immediately prior to i.p. injection of thioglycollate. Dexamethasone delivered i.v. as 0.1 mg/kg in 100 μL sterile 0.9% saline or locally as 10 μg in 900 μl of PBS −/−, serves as a reference anti-inflammatory agent. Inflammation is induced by injection of 1 mL of thioglycollate solution (3% wt/vol; Sigma Immunochemicals) intraperitoneally into the mice.

Mice are humanely euthanized 24 hrs following induction of inflammation and 5 mL of warm (37°C ~ medium (RPMI 1640, 2% FCS, and 2 mM EDTA) injected into the peritoneum followed by gentle massage of the abdomen. Aspirates of the abdominal lavage fluid are centrifuged at 2,000 rpm for 15 min at 23°C. The supernatants are removed, and the cells suspended in 500 μL of PBS. Aliquots of the supernatant are assayed for MPO activity, inflammatory mediator concentrations, and lipid peroxidation.

[000255] Total leukocytes are enumerated in the cell suspension by light microscopy using a hemocytometer. Resuspended aspirate cells (50 μL) are added to 150 μL of 30% BSA and centrifuged onto microscope slides at 2,200 rpm for 4 min by using a cytofuge. Differential leukocyte counts are determined in cytospins stained with Wright Giemsa stain and used to calculate the absolute number of each leukocyte per air pouch aspirate.

[000256] Data are presented as total number of neutrophils, monocytes, eosinophils, basophils, and lymphocytes per exudate. Values are reported as the mean ± SEM (n = 6). The significance of any treatment on migration is determined by ANOVA. $P < 0.05$ is to be considered significant.

Degranulation:

[000257] Myeloperoxidase is used as a marker of degranulation. Myeloperoxidase activity in the cell supernatant obtained from the air pouch or peritoneal lavage fluid is assayed and analyzed as described above using the TMB method.

Inflammatory mediator concentrations:

[000258] Concentrations of the key pro-inflammatory mediators TNFα, IL-1β, IL-10, IL-6, KC, and PGE2 in air pouch and peritoneal lavage fluid are determined using commercial ELISA kits (R&D Systems) according to the manufactures instructions.

Lipid peroxidation:

[000259] The concentration of F2-isoprostanes is a sensitive and specific measure of oxidative injury resulting from release of reactive oxygen intermediates from neutrophils and other cells {Milne GL, Musiek ES, Morrow JD. F2-isoprostanes as markers of oxidative stress in vivo: an

overview.Biomarkers. 2005 Nov;10 Suppl 1:S10-23}. F2-isoprostane concentration is determined in air pouch and peritoneal exudate supernatants using a commercially available ELISA (8-Isoprostane EIA, Cayman Chemical) according to the manufactures instructions.

End point:

[000260] The experiment is considered to be successful if either local or systemic delivery of the test peptide reduces inflammation by one or more of the above measures of inhibition of release of inflammatory mediator.

[000261] The active fragment peptides of this invention inhibit neutrophil influx into and degranulation in inflamed air pouch or peritoneum, resulting in reduced MPO activity, reduced lipid peroxidation, and reduced inflammatory mediator production.

[000262] The foregoing examples are illustrative of the present invention and are not to be construed as limiting thereof. The invention is defined by the following claims, with equivalents of the claims to be included therein.

I CLAIM:

1. A method of inhibiting the release of at least one inflammatory mediator from a granule in at least one inflammatory cell in a tissue and/or fluid of a subject comprising:

administration to said tissue and/or fluid a therapeutically effective amount of a pharmaceutical composition comprising at least one peptide having an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence having from 4 to 23 contiguous amino acids of a reference sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1);

(b) an amino acid sequence having the sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1); and

(c) an amino acid sequence substantially identical to the sequence defined in (a),

wherein the C-terminal amino acid of the peptide is optionally independently chemically modified, and the N-terminal amino acid of the peptide is independently chemically modified by acylation with a carboxylic acid selected from the group consisting of a C2 to C13 saturated or unsaturated aliphatic carboxylic acid, a C14 saturated or unsaturated aliphatic carboxylic acid, a C15 to C24 saturated or unsaturated aliphatic carboxylic acid, and trifluoroacetic acid, or is not chemically modified, with the proviso that said peptide is modified by acylation when its amino acid sequence begins with the sequence GAQF of the reference sequence by acylation only with a carboxylic acid selected from the group consisting of a C2 to C13 saturated or unsaturated aliphatic carboxylic acid, a C14 unsaturated aliphatic carboxylic acid, a C15 to C24 saturated or unsaturated aliphatic carboxylic acid, and trifluoroacetic acid, or is not chemically modified, wherein said peptide, optionally combined with a pharmaceutically acceptable carrier, and in a therapeutically effective inflammatory mediator release-reducing amount to reduce the release of said inflammatory mediator from at least one inflammatory cell as compared to release of said inflammatory mediator from at least one of the same type of inflammatory cell that would occur in the absence of said at least one peptide.

2. The method according to claim 1, wherein said peptide is acetylated at the alpha N-terminal amino acid.

3. The method according to claim 2, wherein said peptide consists of at least ten contiguous amino acid residues.

4. The method according to claim 3, wherein said peptide consists of acetyl - peptide 106 (SEQ ID NO: 106).

5. The method according to claim 1, wherein said peptide consists of at least four contiguous amino acid residues.

6. The method according to claim 1, wherein said peptide consists of at least six contiguous amino acid residues.

7. The method according to claim 1, wherein said peptide is myristoylated at the alpha N-terminal amino acid.

8. The method according to claim 1, wherein said peptide is amidated with ammonia at the alpha C-terminal amino acid.

9. The method according to claim 1, wherein the peptide comprises an amino acid sequence of (a) wherein the N-terminal amino acid of the amino acid sequence of (a) is selected from amino acid position 2 to 21 of the reference sequence,
GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1).

10. The method according to claim 9, wherein said peptide is myristoylated or acetylated at the alpha N-terminal amino acid.

11. The method according to claim 9, wherein said peptide is amidated with ammonia at the alpha C-terminal amino acid.

12. The method according to claim 1, wherein said reducing the release of an inflammatory mediator comprises blocking or inhibiting the mechanism that releases an inflammatory mediator from said inflammatory cell in said subject.

13. The method according to any one of claims 1-12, wherein said peptide further comprises a pharmaceutically acceptable carrier to form a pharmaceutical composition.

14. The method according to claim 12, wherein said inflammatory cell is a leukocyte.

15. The method according to claim 12, wherein said inflammatory cell is a granulocyte.

16. The method according to claim 12, wherein said inflammatory cell is selected from the group consisting of a neutrophil, a basophil, an eosinophil and a combination thereof.

17. The method according to claim 12, wherein said inflammatory cell is a monocyte or macrophage.

18. The method according to claim 12, wherein said inflammatory mediator is selected from the group consisting of myeloperoxidase (MPO), eosinophil peroxidase (EPO), major basic

protein [MBP], lysozyme, granzyme, histamine, proteoglycan, protease, a chemotactic factor, cytokine, a metabolite of arachidonic acid, defensin, bactericidal permeability-increasing protein (BPI), elastase, cathepsin G, cathepsin B, cathepsin D, beta-D-glucuronidase, alpha-mannosidase, phospholipase A_2, chondroitin-4-sulphate, proteinase 3, lactoferrin, collagenase, complement activator, complement receptor, N-formylmethionyl-leucyl-phenylalanine (FMLP) receptor, laminin receptor, cytochrome b_{558}, monocyte-chemotactic factor, histaminase, vitamin B12 binding protein, gelatinase, plasminogen activator, beta-D-glucuronidase, and a combination thereof.

19. The method according to claim 12, wherein said inflammatory mediator is selected from the group consisting of myeloperoxidase (MPO), eosinophil peroxidase (EPO), major basic protein (MBP), lysozyme, granzyme and a combination thereof.

20. The method according to claim 1, wherein said effective inflammatory mediator release-reducing amount of said peptide comprises a degranulation-inhibiting amount of peptide that reduces the amount of an inflammatory mediator released from at least one inflammatory cell from about 1% to about 99% as compared to the amount released from at least one inflammatory cell in the absence of the peptide.

21. The method according to claim 1, wherein said effective inflammatory mediator release-reducing amount of said peptide comprises a degranulation-inhibiting amount of peptide that reduces the amount of an inflammatory mediator released from at least one inflammatory cell from between about 5-50% to about 99% as compared to the amount released from at least one inflammatory cell in the absence of the peptide.

22. The method according to claim 1, wherein said subject is afflicted by a respiratory disease.

23. The method according to claim 22, wherein said respiratory disease is selected from the group consisting of asthma, chronic bronchitis, COPD and cystic fibrosis.

24. The method according to claim 1, wherein said subject is a mammal.

25. The method according to claim 24, wherein said mammal is selected from the group consisting of humans, canines, equines and felines.

26. The method according to claim 1, wherein said administration is selected from the group consisting of topical administration, parenteral administration, rectal administration, pulmonary administration, nasal administration, and oral administration.

27. The method according to claim 26, wherein said pulmonary administration comprises an aerosol.

28. The method according to claim 27, wherein said aerosol is generated from a dry powder inhaler, a metered dose inhaler or nebulizer.

29. The method according to claim 1, further comprising administration to said subject of a second molecule selected from the group consisting of an antibiotic, an antiviral compound, an antiparasitic compound, an anti-inflammatory compound, and an immunomodulator.

30. The method according to claim 1, wherein said subject is suffering from a disease selected from the group consisting of a bowel disease, a skin disease, an autoimmune disease, a pain syndrome, and combinations thereof.

31. The method according to claim 30, wherein said bowel disease is selected from the group consisting of ulcerative colitis, Crohn's disease and irritable bowel syndrome.

32. The method according to claim 30, wherein said skin disease is selected from the group consisting of rosacea, eczema, psoriasis and severe acne.

33. The method according to claim 1, wherein said subject is suffering from arthritis.

34. The method according to claim 1, wherein the amino acid sequence of (c) substantially identical to the amino acid sequence of (a) is selected from the group consisting of SEQ ID NOS: 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 247, 248, 249, 250, 251 and 252.

35. The method according to claim 34, wherein said peptide is acetylated at the alpha N-terminal amino acid.

36. The method according to claim 34, wherein said peptide is myristoylated at the alpha N-terminal amino acid.

37. The method according to claim 34, wherein said peptide is amidated with ammonia at the alpha C-terminal amino acid.

38. An isolated peptide having an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence having from 4 to 23 contiguous amino acids of a reference sequence, GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1);

(b) an amino acid sequence having the sequence,
GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1); and

(c) an amino acid sequence substantially identical to the sequence defined in (a),

wherein the C-terminal amino acid of the peptide is optionally independently chemically modified, and the N-terminal amino acid of the peptide is independently chemically modified by acylation with a carboxylic acid selected from the group consisting of a C2 to C13 saturated or unsaturated aliphatic carboxylic acid, a C14 saturated or unsaturated aliphatic carboxylic acid, a C15 to C24 saturated or unsaturated aliphatic carboxylic acid, and trifluoroacetic acid, or is not chemically modified, with the proviso that said peptide is modified by acylation when its amino acid sequence begins with the sequence GAQF of the reference sequence by acylation only with a carboxylic acid selected from the group consisting of a C2 to C13 saturated or unsaturated aliphatic carboxylic acid, a C14 unsaturated aliphatic carboxylic acid, a C15 to C24 saturated or unsaturated aliphatic carboxylic acid, and trifluoroacetic acid, or is not chemically modified, wherein said peptide, optionally combined with a pharmaceutically acceptable carrier, and in a therapeutically effective inflammatory mediator release-reducing amount to reduce the release of said inflammatory mediator from at least one inflammatory cell as compared to release of said inflammatory mediator from at least one of the same type of inflammatory cell that would occur in the absence of said at least one peptide.

39. The peptide according to claim 38, wherein said peptide is acetylated at the alpha N-terminal amino acid.

40 The peptide according to claim 39, wherein said peptide consists of at least ten contiguous amino acid residues.

41. The peptide according to claim 40, wherein said peptide consists of acetyl - peptide 106 (SEQ ID NO: 106).

42. The method according to claim 38, wherein said peptide consists of at least four contiguous amino acid residues.

43. The peptide according to claim 38, wherein said peptide consists of at least six contiguous amino acid residues.

44. The peptide according to claim 38, wherein said peptide is myristoylated at the alpha N-terminal amino acid.

45. The peptide according to claim 38, wherein said peptide is amidated with ammonia at the alpha C-terminal amino acid.

46. The peptide according to claim 38, wherein the peptide comprises an amino acid sequence of (a) wherein the N-terminal amino acid of the amino acid sequence of (a) is selected from amino acid position 2 to 21 of the reference sequence,
GAQFSKTAAKGEAAAERPGEAAVA (SEQ ID NO. 1).

47. The peptide according to claim 46, wherein said peptide is myristoylated at the alpha N-terminal amino acid.

48. The peptide according to claim 46, wherein said peptide is amidated with ammonia at the alpha C-terminal amino acid.

49. The peptide according to claim 38, wherein the amino acid sequence of (c) substantially identical to the amino acid sequence of (a) is selected from the group consisting of SEQ ID NOS: 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 247, 248, 249, 250, 251 and 252.

50. The peptide according to claim 49, wherein said peptide is acetylated at the alpha N-terminal amino acid.

51. The peptide according to claim 49, wherein said peptide is myristoylated at the alpha N-terminal amino acid.

52. The peptide according to claim 49, wherein said peptide is amidated with ammonia at the alpha C-terminal amino acid.

53. A composition comprising an isolated peptide according to any one of claims 38-52 and an excipient.

54. A pharmaceutical composition comprising an isolated peptide according to any one of claims 38-52 and a pharmaceutically acceptable carrier.

55. The pharmaceutical composition according to claim 54, wherein said composition is sterile, sterilizable or sterilized.

56. A kit comprising at least one isolated peptide according to any one of claims 38-52.

57. The method of any one of claims 1-37, wherein said administration of said peptide reducesMARCKS-related mucus hypersecretion from at least one mucus secreting cell or tissue in said subject, whereby mucus hypersecretion in the subject is reduced compared to that which would occur in the absence of said administration of said peptide.