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(54) Title: ANTI-AGING AND WOUND HEALING COMPOUNDS

(57) Abstract: The invention provides inhibitors of matrix metalloproteinases that are useful for encouraging the development of healthy skin and for treating wounds. The inhibitors are peptides having sequences related to cleavage regions of the proenzyme forms of matrix metalloproteinases. The peptide inhibitors of the invention can be formulated into therapeutic compositions, lotions, creams, skin covering and wound dressings that facilitate healing and healthy skin development, discourage scarring and wrinkling and ameliorate the effects of healing.



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ANTI-AGING AND WOUND HEALING COMPOUNDS

5 This application is a continuation-in-part of U.S. Patent Application Serial No. 10/153,185 filed May 21, 2002, and U.S. Patent Application Serial No. 10/032,376 filed December 21, 2001, both of which claim priority to U.S. Provisional Patent Application Serial No. 60/312,726, filed August 16, 2001, all of which are incorporated herein by reference in their entirety.

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FIELD OF THE INVENTION

 The invention relates to formulations containing inhibitors of matrix metalloproteinases that are useful for healing wounds and for reversing the effects of aging on the skin. The inhibitors are peptides having sequences related to the cleavage site of the proenzyme forms of matrix metalloproteinases.

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BACKGROUND OF THE INVENTION

 The condition of the skin is always affected by factors such as humidity, ultraviolet rays, cosmetic compositions, aging, diseases, stress and eating habits. As the result, various skin troubles can arise. The skin also becomes less resilient with age as illustrated by the formation of wrinkles. Aging is generally associated with the thinning and general degradation of skin. As the skin naturally ages, there is a reduction in the number of cells and blood vessels that supply the skin. There is also a flattening of the dermal-epidermal junction that results in weaker mechanical resistance of this junction. As a consequence, older persons are more susceptible to blister formation in cases of mechanical trauma or disease processes. (See Oikarinen, (1990) "The Aging of Skin: Chronoaging Versus Photoaging", Photodermatal. Photoimmunol. Photomed., Vol. 7, pp 3-4).

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 Skin contains an elaborate network of elastin fibers that is responsible for maintaining its elastic properties. With excessive exposure to sunlight the elastic fiber system becomes hyperplastic, disorganized and ultimately disrupted. This process is known as actinic elastosis and it is a principal cause of wrinkling, discoloration and laxity of the skin in the exposed areas of the body. As new fibroblasts, endothelial cells and keratinocytes form, the skin can repair itself. However, the skin becomes less able to do so

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as it ages. Therefore, agents that can accelerate the growth and repair of prematurely aged skin are needed.

Wound healing is also accelerated by increased cellular proliferation and migration of certain cell types. The mechanisms involved in wound healing are often divided into
5 four phases: hemostasis, inflammation, proliferation and maturation. During inflammation, leucocytes accumulate to combat bacteria and the permeability blood vessel walls increases, leading to swelling. If an infection does not develop the number of leucocytes diminishes. Monocytes replace the leukocytes. Macrophages and lymphocytes release
10 growth factors (cytokines) as well as a number of chemical substances, such as histamine, serotonin, and prostaglandins. These substances help regulate the wound healing process. In the proliferation phase, new fibroblasts, endothelial cells and keratinocytes arise, connective tissue is formed, new blood vessels grow and injured tissue is regenerated. Fibroblasts become dominant after about a week, and the inflammation decreases and the strength of the tissues around the wound site is rapidly increased. During the maturation
15 phase collagen is laid down and scar tissue is formed. This maturation phase might go on for a long time during which tissues of various types are regenerated. In order to obtain an optimal healing of skin and associated tissues, the supply of different vitamins and trace elements as well as nutrients should be sufficient as well as the oxygen supply.

Chronic wounds or indolent, nonhealing wounds may arise from different causes
20 including infection, the presence of foreign bodies or toxic irritants, burns, prolonged cutaneously applied pressure and poor blood supply owing to impaired circulation. In a chronic wound the tissue homeostasis and the wound environment are compromised so that either healing fails to occur or healing begins but is subsequently halted. Factors contributing to the failure of healing in chronic wounds are tissue necrosis, dehydration,
25 chronic wound edema, fibrotic induration and small blood vessel disease.

One of the major reasons that chronic wounds do not heal is that a class of proteinases, called matrix metalloproteinases (MMPs), destroys the newly formed wound bed (Vaalamo et al., 1997; Weckroth et al., 1996; DiColandrea et al., 1998; Moses et al., 1996). These matrix metalloproteinases are normally prevented from destroying the wound
30 bed by the action of four Tissue Inhibitors of MetalloProteinase (TIMPs1-4) that form very specific inhibitory complexes with the matrix metalloproteinases (Olson et al., 1997; Taylor et al., 1996; Howard et al., 1991). That is, each TIMP only inhibits a specific subset of matrix metalloproteinases. In chronic wounds the ratio of matrix metalloproteinase to

TIMP is high, such that most of the matrix metalloproteinases are uninhibited (Vaalamo et al., 1996; Saarialho-Kere, 1998). In fact, with elevated proteinase levels, the TIMP molecules themselves can be hydrolyzed. There is no naturally occurring TIMP molecule that singly inhibits all types of matrix metalloproteinases.

5 Many approaches have been suggested to control matrix metalloproteinase activity, including both small molecule (Levy et al., 1998; Wojtowicz-Praga et al., 1997; Duivenvoorden, et al., 1997) and peptide based inhibitors (Otake et al., 1994) and anti-MMP antibodies (Su et al., 1995). However, an ideal composition for wound healing and reversing the effects of aging would not only provide optimal inhibition of
10 metalloproteinase but would stimulate the growth and regeneration of injured tissues.

SUMMARY OF THE INVENTION

The present invention provides compositions containing peptides that are useful as anti-aging and wound healing agents. The peptides of the invention not only inhibit
15 metalloproteinases but also stimulate cellular proliferation and migration in certain cell types, including fibroblasts, endothelial cells and keratinocytes. Various topical lotions, dressings, and compositions are contemplated, as well as methods of using the peptides to reverse the effects of aging and to heal wounds.

The present invention is therefore directed to peptide inhibitors of matrix
20 metalloproteinases. These peptide inhibitors have amino acid sequences identical or related to the linking region spanning the two globular domains of matrix metalloproteinases. Several types of matrix metalloproteinases and their sequences are known, including matrix metalloproteinase-1, matrix metalloproteinase-2, matrix metalloproteinase-3, matrix metalloproteinase-4, matrix metalloproteinase-4, matrix
25 metalloproteinase-5, matrix metalloproteinase-6, matrix metalloproteinase-7, matrix metalloproteinase-8, and matrix metalloproteinase-9, matrix metalloproteinase-10, matrix metalloproteinase-11, matrix metalloproteinase-12, and matrix metalloproteinase-13. The invention contemplates inhibitors having amino acid sequences from the linking region of any of the matrix metalloproteinases. For example, peptide inhibitors of the invention can
30 have amino acid sequences drawn from any region from about amino acid 70 to about amino acid 120 of the matrix metalloproteinase-2 sequence (SEQ ID NO:14), and analogous regions of all other matrix metalloproteinases.

The invention provides peptides of any one of formulae (I), (II), (III):

Xaa₁-Xaa₂-Xaa₃-Xaa₄-Xaa₅-Xaa₆ Xaa₇-Xaa₈-Xaa₉ (I)

Xaa₁₀-Xaa₁₁-Xaa₁₂ Xaa₁₃-Xaa₁₄-Xaa₁₅-Xaa₁₆-Xaa₁₇-Xaa₁₈-Xaa₁₉ (II)

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Xaa₁-Xaa₂-Xaa₃-Xaa₄-Xaa₅-Xaa₆-Xaa₇-Xaa₈-Xaa₉-Xaa₁₀-Xaa₁₁-
Xaa₁₂-Xaa₁₃-Xaa₁₄-Xaa₁₅-Xaa₁₆-Xaa₁₇-Xaa₁₈-Xaa₁₉ (III)

wherein

- 10 Xaa₁, Xaa₄, and Xaa₆ are separately each apolar amino acids;
Xaa₂ is a basic amino acid;
Xaa₃ is a cysteine-like amino acid;
Xaa₅ is a polar or aliphatic amino acid;
Xaa₇ is an acidic amino acid,
15 Xaa₈ is an aliphatic or polar amino acid;
Xaa₉ is an aliphatic, apolar or basic amino acid; and
Xaa₁₀ is a polar, acidic, basic or apolar amino acid;
Xaa₁₁ is a polar or aromatic amino acid;
Xaa₁₂ is a polar, basic, aliphatic or apolar amino acid;
20 Xaa₁₃ is an aromatic, aliphatic, polar or acidic amino acid;
Xaa₁₄ is an aromatic, apolar or polar amino acid;
Xaa₁₅ is an apolar or acidic amino acid;
Xaa₁₆ is a basic, a polar or an apolar amino acid;
Xaa₁₇ is a basic, a polar, an aliphatic, an apolar or an acidic amino acid;
25 Xaa₁₈ is an apolar or an aliphatic amino acid;
Xaa₁₉ is a basic or an aliphatic amino acid; and

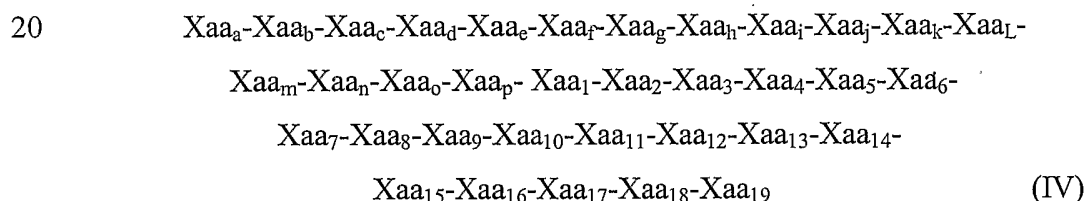
wherein the peptide is capable of inhibiting the activity of matrix metalloproteinase-1, matrix metalloproteinase-2, matrix metalloproteinase-3, matrix metalloproteinase-4, matrix metalloproteinase-4, matrix metalloproteinase-5, matrix metalloproteinase-6, matrix metalloproteinase-7, matrix metalloproteinase-8, or matrix metalloproteinase-9, matrix metalloproteinase-10, matrix metalloproteinase-11, matrix metalloproteinase-12, and matrix metalloproteinase-13. In some embodiments, the peptide can inhibit the activity of

matrix metalloproteinase-2, matrix metalloproteinase-3, matrix metalloproteinase-7, matrix metalloproteinase-8, or matrix metalloproteinase-9.

An apolar amino acid can be, for example, methionine, glycine or proline. A basic amino acid, for example, can be histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, ρ -aminophenylalanine, or 2,4-diaminobutyric acid. Cysteine-like amino acids of the invention include, for example, cysteine, homocysteine, penicillamine, or β -methyl cysteine.

Aliphatic amino acids include, for example, alanine, valine, leucine, isoleucine, t-butylalanine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, β -alanine, N-methylglycine, or α -aminoisobutyric acid. Acidic amino acids include, for example, aspartic acid or glutamic acid. Polar amino acids include, for example, asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or an apolar amino acid such as methionine, glycine or proline. Aromatic amino acids of the invention can be, for example, phenylalanine, tyrosine, tryptophan, phenylglycine, naphthylalanine, β -2-thienylalanine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, pyridylalanine, or 3-benzothienyl alanine.

The invention also provides peptides of formula (IV)(SEQ ID NO:18):



wherein:

Xaa _a is proline;	Xaa ₁ is proline;
Xaa _b is glutamine or glutamic acid;	Xaa ₂ is arginine;
Xaa _c is threonine;	Xaa ₃ is cysteine;
Xaa _d is glycine;	Xaa ₄ is glycine;
Xaa _e is aspartic acid or glutamic acid;	Xaa ₅ is valine or asparagine;
Xaa _f is leucine;	Xaa ₆ is proline;
Xaa _g is aspartic acid;	Xaa ₇ is aspartic acid;
Xaa _h is glutamine or serine;	Xaa ₈ is valine or leucine;

- Xaa_i is asparagine or alanine; Xaa₉ is alanine or glycine;
 Xaa_j is threonine; Xaa₁₀ is asparagine or arginine;
 Xaa_k is isoleucine or leucine; Xaa₁₁ is tyrosine or phenylalanine;
 Xaa_L is glutamic acid or lysine; Xaa₁₂ is asparagine or glutamine;
 5 Xaa_m is threonine or alanine; Xaa₁₃ is phenylalanine or threonine;
 Xaa_n is methionine; Xaa₁₄ is phenylalanine;
 Xaa_o is arginine; Xaa₁₅ is proline or glutamic acid;
 Xaa_p is lysine or threonine; Xaa₁₆ is arginine or glycine;
 Xaa₁₇ is lysine or aspartic acid; Xaa₁₈ is proline or leucine;
 10 Xaa₁₉ is lysine; and

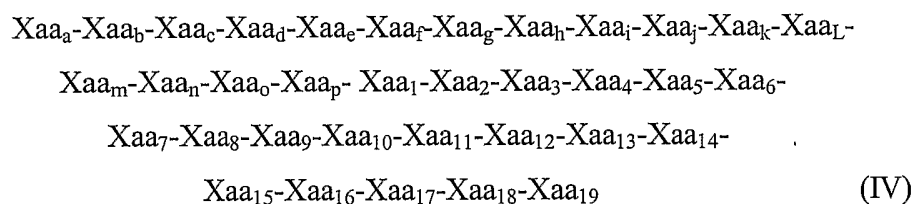
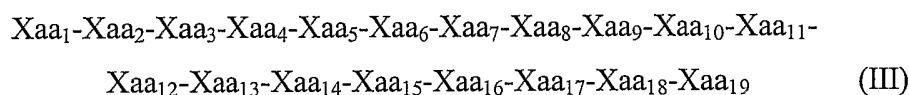
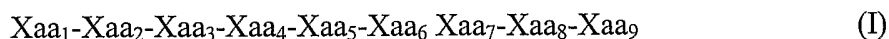
wherein the peptide is capable of inhibiting the activity of a metalloproteinase. For example, the matrix metalloproteinase can be matrix metalloproteinase-1, matrix metalloproteinase-2, matrix metalloproteinase-3, matrix metalloproteinase-4, matrix metalloproteinase-4, matrix metalloproteinase-5, matrix metalloproteinase-6, matrix metalloproteinase-7, matrix metalloproteinase-8, and matrix metalloproteinase-9, matrix metalloproteinase-10, matrix metalloproteinase-11, matrix metalloproteinase-12, or matrix metalloproteinase-13. Desirable peptides inhibit matrix metalloproteinase-2 or matrix metalloproteinase-9.

Linking regions from which peptide inhibitors of the invention can be derived have, for example, amino acid sequences ranging from about position 70 to about position 120 of SEQ ID NO:14, and analogous regions of other matrix metalloproteinases. In some embodiments the peptide inhibitors of the invention have amino acid sequences ranging from about position 77 to about position 110 of SEQ ID NO:14, and analogous regions or other matrix metalloproteinases. Examples of some of the peptide inhibitors include those containing amino acid sequences SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, or SEQ ID NO:13.

Peptides of the invention have varying affinities for the different matrix metalloproteinases. For example, in one embodiment, the peptide inhibitors can inhibit matrix metalloproteinase-2 with a k_i of about 1.0 μM to about 500.0 μM . In another embodiment, the peptide inhibitors can inhibit matrix metalloproteinase-2 with a k_i of about 1.0 μM to about 400.0 μM . In yet another embodiment, the peptide inhibitors can inhibit matrix metalloproteinase-2 with a k_i of about 1.0 μM to about 50.0 μM .

The invention further provides compositions that include a therapeutically effective amount of peptide of the invention and a pharmaceutically acceptable carrier. Wound treatments and skin lotions are also contemplated by the invention.

The invention further provides a method for treating a wound or for reversing the effects on aging that comprises administering a therapeutically effective amount of a peptide of formula I, II, III or IV:



(SEQ ID NO:21)

wherein:

- 20 Xaa₁, Xaa₄, and Xaa₆ are separately each apolar amino acids;
 Xaa₂ is a basic amino acid;
 Xaa₃ is a cysteine-like amino acid;
 Xaa₅ is a polar or aliphatic amino acid;
 Xaa₇ is an acidic amino acid,
 25 Xaa₈ is an aliphatic or polar amino acid;
 Xaa₉ is an aliphatic, apolar or basic amino acid; and
 Xaa₁₀ is a polar, acidic, basic or apolar amino acid;
 Xaa₁₁ is a polar or aromatic amino acid;
 Xaa₁₂ is a polar, basic, aliphatic or apolar amino acid;
 30 Xaa₁₃ is an aromatic, aliphatic, polar or acidic amino acid;
 Xaa₁₄ is an aromatic, apolar or polar amino acid;
 Xaa₁₅ is an apolar or acidic amino acid;
 Xaa₁₆ is a basic, a polar or an apolar amino acid;

- Xaa₁₇ is a basic, a polar, an aliphatic, an apolar or an acidic amino acid;
 Xaa₁₈ is an apolar or an aliphatic amino acid;
 Xaa₁₉ is a basic or an aliphatic amino acid;
 Xaa_a is proline;
 5 Xaa_b is glutamine or glutamic acid;
 Xaa_c is threonine;
 Xaa_d is glycine;
 Xaa_e is aspartic acid or glutamic acid;
 Xaa_f is leucine;
 10 Xaa_g is aspartic acid;
 Xaa_h is glutamine or serine;
 Xaa_i is asparagine or alanine;
 Xaa_j is threonine;
 Xaa_k is isoleucine or leucine;
 15 Xaa_L is glutamic acid or lysine;
 Xaa_m is threonine or alanine;
 Xaa_n is methionine;
 Xaa_o is arginine; and
 Xaa_p is lysine or threonine;
 20 wherein the peptide is capable of inhibiting the activity of a matrix metalloproteinase.

An apolar amino acid in the peptides of the invention can be, for example, methionine, glycine or proline. The basic amino acid can be, for example, histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, ρ -aminophenylalanine, and 2,4-diaminobutyric acid. The cysteine-like amino acid can be, for example, cysteine,
 25 homocysteine, penicillamine, or β -methyl cysteine. The aliphatic amino acid can be, for example, alanine, valine, leucine, isoleucine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, β -alanine, N-methylglycine, or α -aminoisobutyric acid. The acidic amino acid can be, for example, aspartic acid or glutamic acid. A polar amino acid can be asparagine, glutamine, serine,
 30 threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or an apolar amino acid such as methionine, glycine or proline. An aromatic amino acid is phenylalanine, tyrosine, tryptophan, phenylglycine, naphthylalanine, β -2-thienylalanine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-

fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, pyridylalanine, or 3-benzothienyl alanine.

In another embodiment the invention provides a method for treating a wound or ameliorating the effects of aging that comprises administering a therapeutically effective amount of a peptide of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, or SEQ ID NO:13.

DESCRIPTION OF THE FIGURES

Figure 1 provides a CLUSTAL X™ (version 1.8) multiple sequence alignment of the cleavage spanning regions of select MMP proenzymes. Figure 1A provides an alignment that highlights conserved residues where an “*” indicates complete identity among the sequences, a “:” indicates 7/9 conserved positions, and a “.” indicates greater than 80% identical positions with mostly conserved substitutions. Figure 1B indicates the positions of heterogeneity in bold.

Figure 2 provides the structure of proMMP-1 (Protein databank file 1FBL.ENT). The area of SEQ ID NOS:2-10 shown in Table 1 spans the short region between the two large domains. During activation this region is cleaved.

Figure 3 provides a three-dimensional model of MMP-9. The cleavage region that creates the N-terminus of the active proteinase is shown in cross-hatching. The two zinc ions are illustrated as spheres. The cleavage domain peptide may bind to the MMP in the vicinity of its normal location in the proenzyme. This binding (also near the catalytic zinc) sterically blocks a portion of the active site. This blockage prevents substrate binding.

Figure 4 illustrates the inhibition of MMP-9 activity by the 19-mer (SEQ ID NO:11) cleavage domain peptide. MMP-9 was mixed with the 19-mer (SEQ ID NO:11) peptide prior to the FRET assay. The concentrations of the 19-mer (SEQ ID NO:11) peptide were as follows: 0 mM (closed circles), 0.01 mM (open circles), 0.03 mM (closed squares), 0.06 mM (open squares), 0.125 mM (closed triangles), 0.25 mM (open triangles), 0.5 mM (x's), 1 mM (inverted closed triangles), 2 mM (inverted open triangles).

Figure 5 illustrates the inhibition of MMP-9 activity by the 10-mer (SEQ ID NO:13) cleavage domain peptide. MMP-9 was mixed with the 10-mer (SEQ ID NO:13) peptide prior to the FRET assay. The concentrations of the 10-mer (SEQ ID NO:13)

peptide were as follows: 0 mM (closed triangles), 0.25 mM (open triangles), 0.5 mM (open inverted triangles), 1.0 mM (closed inverted triangles), 2.0 mM (x's).

Figure 6 illustrates the inhibition of MMP-9 activity by the 9-mer (SEQ ID NO:12) cleavage domain peptide. MMP-9 was mixed with the 9-mer (SEQ ID NO:12) peptide prior to the FRET assay. The concentrations of the 9-mer (SEQ ID NO:12) peptide were as follows: 0 mM (closed triangles), 0.25 mM (open triangles), 0.5 mM (open inverted triangles), 1.0 mM (closed inverted triangles), 2.0 mM (x's).

Figure 7 illustrates the inhibition of MMP-9 activity by the 19-mer (SEQ ID NO:11) cleavage domain peptide. MMP-9 was mixed with the 19-mer (SEQ ID NO:11) peptide prior to the fluorescent collagen assay. The concentrations of the 19-mer (SEQ ID NO:11) peptide were as follows: 0 mM (closed circles), 0.06 mM (open diamonds), 0.1 mM (open squares), 0.25 mM (open circles), 0.5 mM (x's).

Figure 8 illustrates a longer time course inhibition of MMP-9 activity by the 19-mer (SEQ ID NO:11) cleavage domain peptide. MMP-9 was mixed with the 19-mer (SEQ ID NO:11) peptide prior to the fluorescent collagen assay. The concentrations of the 19-mer (SEQ ID NO:11) peptide were as follows: 0 mM (closed circles), 0.06 mM (open diamonds), 0.1 mM (open squares), 0.25 mM (open circles), 0.5 mM (x's).

Figure 9 illustrates a longer time course inhibition of MMP-9 activity by the 10-mer (SEQ ID NO:13) cleavage domain peptide. MMP-9 was mixed with the 10-mer (SEQ ID NO:13) peptide prior to the fluorescent collagen assay. The concentrations of the 10-mer (SEQ ID NO:13) peptide were as follows: 0 mM (open circles), 0.1 mM (open diamonds), 0.2 mM (open squares), 0.4 mM (x's).

Figure 10 illustrates a longer time course of inhibition of MMP-9 activity by the 9-mer (SEQ ID NO:12) cleavage domain peptide. MMP-9 was mixed with the 9-mer (SEQ ID NO:12) peptide prior to the fluorescent collagen assay. The concentrations of the 9-mer (SEQ ID NO:12) peptide were as follows: 0 mM (closed circles), 0.06 mM (open diamonds), 0.1 mM (open squares), 0.25 mM (open circles), 0.5 mM (x's).

Figure 11 provides the HPLC elution profiles of a typical splicing reaction. The arrows indicate that the first peak decreases in area over the course of the reaction (pro-MMP-9 peak), while the second two peaks (mature MMP-9 and N-terminal cleavage product, respectively) increase in area.

Figure 12 illustrates the conversion of pro-MMP-9 into N-terminal and C-terminal domains by stromilysin. Pro-MMP-9 was reacted with stromilysin in the presence of zero

(closed circles), 0.5 μM (open squares) or 1.0 μM (closed squares) 19-mer (SEQ ID NO:11) peptide. At the times indicated, an aliquot was removed and subjected to HPLC. The pro-MMP peak area was integrated and was set to 100 percent for the zero time point sample. Open circles represent pro-MMP incubated in buffer without stromilysin or 19-mer (SEQ ID NO:11) peptide.

Figure 13A provides an isothermal titration calorimetry analysis of the interaction of the 19-mer (SEQ ID NO:11) inhibitor peptide with MMP-9. Each peak shows the heat produced by the injection and subsequent binding reaction. Figure 13B provides a binding isotherm produced by integrating the value of each injection peak from Figure 13A with respect to time.

Figure 14 provides an isothermal titration calorimetry analysis of the interaction of the 19-mer (SEQ ID NO:11) inhibitor peptide with MMP-2. Figure 14A provides the raw isothermal calorimetry data for the titration of 19-mer (SEQ ID NO:11) (1 mM) into MMP-2 (20 μM) in 20 mM cacodylate (pH 6.8), 10 mM NaCl at 25 °C. Each peak shows the heat produced by the injection and subsequent binding reaction. Figure 14B provides a binding isotherm produced by integrating the value of each injection peak from Figure 14A with respect to time.

Figure 15 provides a surface plasmon resonance binding isotherm generated when the 19-mer (SEQ ID NO:11) peptide is flowed over a surface of immobilized MMP-9.

Figure 16 provides a bar graph showing the percent living cells, relative to a positive control, in a skin model after treatment with two concentrations of peptide. The first sample, treated with phosphate buffered saline (PBS), is the positive control used to establish the cell count representing 100% viability. The second sample is a negative control where cells were exposed to 1% Triton-X100, showing that the assay can detect cell death. The next three samples are the 19-mer (SEQ ID NO:11), the 10-mer (SEQ ID NO:13), and the 9-mer (SEQ ID NO:12) peptides used at a concentration of 500 μM . The final three samples are the 19-mer (SEQ ID NO:11), the 10-mer (SEQ ID NO:13), and the 9-mer (SEQ ID NO:12) peptides used at a concentration of 2 mM. Data shown represent the average of three tests.

Figure 17 graphically depicts the time course of wound healing in db/db diabetic mice. The plot shows the relative average wound area versus days post wounding for mice treated with either normal saline (open circles) or 20 $\mu\text{g}/\text{mL}$ of the 19-mer peptide (SEQ ID

NO:11) (closed circles). Data presented show the mean relative wound diameter derived from 10 subject animals.

Figure 18 graphically depicts the proliferation of normal human dermal fibroblasts (Clonetics, CC-2509) in the presence and absence of the 19-mer (SEQ ID NO:11). Cell growth was detected by optical density (OD) measurements at 490 nm. in three different concentrations. The bar labeled "19mer6" reflects cell growth in the presence of the 19-mer (SEQ ID NO:11) at a concentration of 1×10^{-6} M. The bar labeled "19mer5" reflects cell growth in the presence of the 19-mer (SEQ ID NO:11) at a concentration of 1×10^{-5} M. The bar labeled "19mer4" reflects cell growth in the presence of the 19-mer (SEQ ID NO:11) at a concentration of 1×10^{-4} M. The "control" cells were grown with no added peptide.

Figure 19 graphically depicts the proliferation of normal human keratinocytes in the presence and absence of the 19-mer peptide (SEQ ID NO:11). As illustrated, the 19-mer peptide (SEQ ID NO:11) leads to increased growth of keratinocytes in a dose-dependent manner. Control cells with no added 19-mer peptide had the lowest cellular density. Cells receiving as little as 1×10^{-5} M of the 19-mer (SEQ ID NO:11, labeled 19mer5 in Fig. 19), exhibited significantly greater cell density ($P > 0.01$) than cells received no 19-mer peptide. Cells receiving 1×10^{-4} M of the 19-mer (labeled "19mer4" in Figure 19) exhibited even greater cell growth ($P > 0.001$). However, cells receiving 1×10^{-6} M of the 19-mer (labeled "19mer6" in Figure 19) exhibited only a small amount of cell proliferation ($P > 0.05$) that was found to be statistically non-significant.

Figure 20 depicts the 48-well chemotaxis chamber (Neuroprobe, Inc.) used for migration assays of normal human dermal fibroblasts (NHDF).

Figure 21A and B illustrate the migration of normal human dermal fibroblasts (NHDF). Figure 21A shows the membrane for the migration assay with $8 \mu\text{m}$ pores (which appear as circles) with no NHDF present (300X magnification). Figure 21B picture shows the membrane after NHDF migration due to addition of a positive control compound ($1.25 \mu\text{g/mL}$ plasma fibronectin). This photograph was taken using 300X magnification. The nuclei of NHDF are stained purple. Some NHDF have migrated through the membrane while others appear to be trapped in the $8 \mu\text{m}$ pore.

Figure 22 provides a bar graph illustrating the percentage of normal human dermal fibroblast (NHDF) migration relative to the migration of NHDF when exposed to a positive control (plasma fibronectin) at various concentrations of the 19-mer peptide (SEQ ID

NO:11). Because some chemotactic substances have very narrow ranges of active concentrations, ten-fold dilutions of 19-mer were used for initial experiments. The average of three separate experiments is shown (the 100 µg/mL data are the average of six experiments). Concentrations of 1000 and 100 µg/mL of 19-mer peptide (SEQ ID NO:11) were chemotactic to fibroblasts ($55 \pm 3\%$ and $46 \pm 3\%$ of the positive control, respectively). Fibroblast migration experiments using concentrations of 19-mer (SEQ ID NO:11) less than 100 µg/mL were only approximately two-fold higher than the negative control and were not considered significant.

Figure 23 provides a bar graph illustrating the percentage of normal human dermal fibroblast (NHDF) migration relative to the migration of NHDF when exposed to a positive control (fibronectin) at various concentrations of the 19-mer peptide (SEQ ID NO:11) and its derivatives. At 100 µg/mL, the acetylated 19-mer (SEQ ID NO:11) peptide (Ac-19-mer) triggered NHDF migration to about the same extent as the 19-mer, but at higher concentrations, the Ac-19-mer is not as effective. The 9-mer (SEQ ID NO:12) and 10-mer (SEQ ID NO:13) peptides trigger NHDF migration only at 1000 µg/mL. Interestingly, the 14-mer TMRKPRCGNPDVAN (SEQ ID NO:19) and the 17-mer TLKAMRKPRCGNPDVAN (SEQ ID NO:20) peptides are not chemotactic to NHDF at any concentration (data not shown). The peptide sequences of the 14-mer TMRKPRCGNPDVAN (SEQ ID NO:19) and the 17-mer TLKAMRKPRCGNPDVAN (SEQ ID NO:20) are derived from MMP enzymes, beginning only slightly further down toward the N-terminus. Therefore, the amino acid sequence of the peptide is important to the induction of NHDF migration.

Figure 24 provides a bar graph illustrating that addition of the 19-mer peptide (SEQ ID NO:11) leads to increased collagen production in human skin fibroblasts. Control human skin fibroblast, with no added 19-mer (SEQ ID NO:11) peptide, produced only low amounts of collagen. In contrast, cells receiving as little as 1×10^{-6} M of the 19-mer (SEQ ID NO:11, labeled 19mer6 in Fig. 24) or 1×10^{-5} M of the 19-mer (SEQ ID NO:11, labeled 19mer5 in Fig. 24), exhibited significantly greater cell density ($P > 0.001$) than cells received no 19-mer peptide.

30

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides inhibitors of matrix metalloproteinases that are useful for counteracting the effects of aging on skin and for promoting wound healing. In

general, the present inhibitors and compositions promote wound healing, prevent scarring, improve skin tone, reduce wrinkling, and stimulate the development of a smooth, healthy skin.

Matrix metalloproteinases are produced *in vivo* as inactive proenzymes. Proteolytic cleavage of the proenzyme results in activation and formation of the mature matrix metalloproteinase. The peptide sequence that is cleaved off is a proenzyme leader sequence of approximately 100 to 110 amino acids in length that is found at the extreme amino terminus of the protein. According to the invention, these proenzyme leader peptides can block the matrix metalloproteinases active site and inhibit the activity of the matrix metalloproteinase. Administration of matrix metalloproteinase proenzyme leader peptides reduces the rate of extracellular matrix destruction and provides a faster rate of wound healing.

Most inhibition strategies involve preventing enzymatic activity of matrix metalloproteinases with organic small molecules. These compounds are often toxic to the body and are not naturally occurring molecules. Use of natural peptides to inhibit activated matrix metalloproteinases provides a high degree of proteinase control without toxic side effects. Unlike small molecule inhibition strategies, the peptides of the invention can be used to inhibit activation of individual or all matrix metalloproteinase classes simultaneously. The peptides can be freely introduced onto the skin, into the wound environment or they can be tethered to, or delivered by, a skin covering or wound dressing.

The invention provides a high degree of control over the level of proteinase activity for healing chronic wounds and ameliorating the effects of aging. For example, as some amount of proteinase level is required during chronic wound healing (Agren et al., 1999), one of skill in the art may choose to only partially inhibit proteinase activity. By modulating the type and amount of inhibitor peptide applied, the degree of matrix metalloproteinase inhibition can be controlled.

Peptides

According to the present invention, peptides having sequences related to a matrix metalloproteinase proenzyme leader in the region of the cleavage site are useful for wound healing and for promoting development of healthy skin. These peptides inhibit the activity of many types of matrix metalloproteinases and promote the cell growth and migration of fibroblasts and keratinocytes.

The position at which the matrix metalloproteinase proenzyme leader is cleaved is at about amino acid position 110 of the proenzyme amino acid sequence. Peptide inhibitors of the invention have sequences related to any region within proenzyme amino acid position 70 to about amino acid position 120. Such peptides inhibit the activity of many types of matrix metalloproteinases. The present peptides can also prevent the activation of proenzyme matrix metalloproteinases, as well as inhibit the enzymatic activity of mature matrix metalloproteinases. Peptides containing sequences that are more conserved in a variety of matrix metalloproteinases, for example, sequences toward the N-terminal side of the cleavage region, can be used to provide inhibitors that are generally effective against a variety of matrix metalloproteinases. However, peptides containing sequences are less conserved, for example, sequences toward the C-terminal side of the cleavage region, can be used to provide inhibitors that are specific for individual matrix metalloproteinases.

Hence, peptides with sequences from any proenzyme leader region of a matrix metalloproteinase are contemplated by the invention as inhibitors of matrix metalloproteinases, as well as variant peptides that have one or more amino acids substituted for the amino acids that are naturally present in the matrix metalloproteinase. Mixtures of peptides with different sequences are also contemplated.

In general, the peptide sequences, peptide variants and mixtures of peptides are formulated and used in a manner that optimizes wound healing, the regeneration of skin, the prevention of scarring or the reversal and prevention of wrinkling. Hence, the composition and formulations of the present peptides can be varied so that lesser or greater levels of inhibition are achieved so long as healing and anti-aging is promoted.

The size of a peptide inhibitor can vary. In general, a peptide of only about five amino acids can be too small to provide optimal inhibition. However, peptides of more than about eight to nine amino acids are sufficiently long to provide inhibition. Therefore, while the overall length is not critical, peptides longer than eight amino acids are often employed in the invention. Other peptides employed in the invention are longer than nine amino acids. Still other peptides employed in the invention are longer than ten amino acids. Moreover, peptides are longer than about fifteen amino acids are also used in the invention. There is no particular upper limit on peptide size. However, it is generally cheaper to make shorter peptides than longer peptides. Hence, the peptide inhibitors of the invention are generally shorter than about one hundred amino acids. Many peptide

inhibitors used in the invention are shorter than about fifty amino acids. Other peptide inhibitors used in the invention are shorter than about thirty amino acids. Peptides shorter than about twenty five amino acids can also be used. Similarly, peptides shorter than about twenty three amino acids are also used in the invention. An example of a peptide useful for practicing the invention has SEQ ID NO:11, with nineteen amino acids.

The sequences of several representative matrix metalloproteinases from about proenzyme amino acid position 70 to about amino acid position 120 are provided in Table 1.

Table 1: Sequences of Matrix Metalloproteinase Cleavage Regions

MMP	Sequence	SEQ ID
mmp2	MQKFFGLPQTGDLDQNTIETMRK PRCGNPDVA NYNFFPRKPKWD	NO:2
mmp13	MQSFFGLEVTGKLDDNTLDVMKK PRCGVPDV GEYNVFPRTLKWSKMNLTY	NO:3
mmp7	MQKFFGLPETGKLSRVMEIMQK PRCGVPDVA EFSLMPNSPKWHSRTVTVYRIVSYT	NO:4
mmp3	MQKFLGLEVTGKLSDTLEVMRK PRCGVPDV GHFRTFPGIPKWRKTHLTYRIVN	NO:5
mmp10	MQKFLGLEVTGKLDTDTLEVMRK PRCGVPDV GHFSSFPGMPKWRKTHLTYRIVNY	NO:6
mmp12	MQHFLGLKVTGQLDTSTLEMMHAP PRCGVPDV HHFREMPGGPVWRKHYYTYRINN	NO:7
mmp9	LQKQLSLPETGELDSATLKAMRT PRCGVPDLG RFQTFEGDLKWHHHN	NO:8
mmp1	MQEFFGLKVTGKPDAETLKVMKQ PRCGVPDV AQFVLTEGNPRWEQTHLTYRIEN	NO:9
mmp8	MQRFFGLNVTGKPNEETLDMMKK PRCGVPDS GGFMLTPGNPKWERTNLTYRIRNY	NO:10

10

Each of the peptides listed in Table 1, as well as peptides with SEQ ID NO:1, 11, 12 and 13, are contemplated as peptide inhibitors of the invention. Moreover, peptide variants and derivatives of the peptides having any of SEQ ID NO: 1-13 are also useful as peptide inhibitors. Such peptide variants and derivatives can have one or more amino acid

substitutions, deletions, insertions or other modifications so long as the peptide variant or derivative can inhibit a matrix metalloproteinase.

Amino acid residues of the isolated peptides can be genetically encoded L-amino acids, naturally occurring non-genetically encoded L-amino acids, synthetic L-amino acids or D-enantiomers of any of the above. The amino acid notations used herein for the twenty
5 genetically encoded L-amino acids and common non-encoded amino acids are conventional and are as shown in Table 2.

Table 2

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

Amino Acid	One-Letter Symbol	Common Abbreviation
2,3-Diaminopropionic acid		Dpr
α -Aminoisobutyric acid		Aib
N-Methylglycine (sarcosine)		MeGly
Ornithine		Orn
Citrulline		Cit
t-Butylalanine		t-BuA
t-Butylglycine		t-BuG
N-methylisoleucine		Melle
Phenylglycine		Phg
Cyclohexylalanine		Cha
Norleucine		Nle
Naphthylalanine		Nal
Pyridylalanine		
3-Benzothienyl alanine		
4-Chlorophenylalanine		Phe(4-Cl)
2-Fluorophenylalanine		Phe(2-F)
3-Fluorophenylalanine		Phe(3-F)
4-Fluorophenylalanine		Phe(4-F)
Penicillamine		Pen
1,2,3,4-Tetrahydro-isoquinoline-3-carboxylic acid		Tic
β -2-thienylalanine		Thi
Methionine sulfoxide		MSO
Homoarginine		hArg
N-acetyl lysine		AcLys

Amino Acid	One-Letter Symbol	Common Abbreviation
2,4-Diamino butyric acid		Dbu
ρ -Aminophenylalanine		Phe(pNH ₂)
N-methylvaline		MeVal
Homocysteine		hCys
Homoserine		hSer
ϵ -Amino hexanoic acid		Aha
δ -Amino valeric acid		Ava
2,3-Diaminobutyric acid		Dab

Peptides that are encompassed within the scope of the invention can have one or more amino acids substituted with an amino acid of similar chemical and/or physical properties, so long as these variant or derivative peptides retain the ability to inhibit the activity of a matrix metalloproteinase, stimulate cellular growth of fibroblasts or keratinocytes, or stimulate the cellular migration of fibroblasts.

Amino acids that are substitutable for each other generally reside within similar classes or subclasses. As known to one of skill in the art, amino acids can be placed into three main classes: hydrophilic amino acids, hydrophobic amino acids and cysteine-like amino acids, depending primarily on the characteristics of the amino acid side chain. These main classes may be further divided into subclasses. Hydrophilic amino acids include amino acids having acidic, basic or polar side chains and hydrophobic amino acids include amino acids having aromatic or apolar side chains. Apolar amino acids may be further subdivided to include, among others, aliphatic amino acids. The definitions of the classes of amino acids as used herein are as follows:

“Hydrophobic Amino Acid” refers to an amino acid having a side chain that is uncharged at physiological pH and that is repelled by aqueous solution. Examples of genetically encoded hydrophobic amino acids include Ile, Leu and Val. Examples of non-genetically encoded hydrophobic amino acids include t-BuA.

“Aromatic Amino Acid” refers to a hydrophobic amino acid having a side chain containing at least one ring having a conjugated π -electron system (aromatic group). The aromatic group may be further substituted with substituent groups such as alkyl, alkenyl, alkynyl, hydroxyl, sulfonyl, nitro and amino groups, as well as others. Examples of genetically encoded aromatic amino acids include phenylalanine, tyrosine and tryptophan. Commonly encountered non-genetically encoded aromatic amino acids include phenylglycine, 2-naphthylalanine, β -2-thienylalanine, 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine and 4-fluorophenylalanine.

“Apolar Amino Acid” refers to a hydrophobic amino acid having a side chain that is generally uncharged at physiological pH and that is not polar. Examples of genetically encoded apolar amino acids include glycine, proline and methionine. Examples of non-encoded apolar amino acids include Cha.

“Aliphatic Amino Acid” refers to an apolar amino acid having a saturated or unsaturated straight chain, branched or cyclic hydrocarbon side chain. Examples of genetically encoded aliphatic amino acids include Ala, Leu, Val and Ile. Examples of non-encoded aliphatic amino acids include Nle.

“Hydrophilic Amino Acid” refers to an amino acid having a side chain that is attracted by aqueous solution. Examples of genetically encoded hydrophilic amino acids include Ser and Lys. Examples of non-encoded hydrophilic amino acids include Cit and hCys.

“Acidic Amino Acid” refers to a hydrophilic amino acid having a side chain pK value of less than 7. Acidic amino acids typically have negatively charged side chains at physiological pH due to loss of a hydrogen ion. Examples of genetically encoded acidic amino acids include aspartic acid (aspartate) and glutamic acid (glutamate).

“Basic Amino Acid” refers to a hydrophilic amino acid having a side chain pK value of greater than 7. Basic amino acids typically have positively charged side chains at physiological pH due to association with hydronium ion. Examples of genetically encoded basic amino acids include arginine, lysine and histidine. Examples of non-genetically encoded basic amino acids include the non-cyclic amino acids ornithine, 2,3-diaminopropionic acid, 2,4-diaminobutyric acid and homoarginine.

“Polar Amino Acid” refers to a hydrophilic amino acid having a side chain that is uncharged at physiological pH, but which has a bond in which the pair of electrons shared

in common by two atoms is held more closely by one of the atoms. Examples of genetically encoded polar amino acids include asparagine and glutamine. Examples of non-genetically encoded polar amino acids include citrulline, N-acetyl lysine and methionine sulfoxide.

5 “Cysteine-Like Amino Acid” refers to an amino acid having a side chain capable of forming a covalent linkage with a side chain of another amino acid residue, such as a disulfide linkage. Typically, cysteine-like amino acids generally have a side chain containing at least one thiol (SH) group. Examples of genetically encoded cysteine-like amino acids include cysteine. Examples of non-genetically encoded cysteine-like amino
10 acids include homocysteine and penicillamine.

As will be appreciated by those having skill in the art, the above classifications are not absolute. Several amino acids exhibit more than one characteristic property, and can therefore be included in more than one category. For example, tyrosine has both an aromatic ring and a polar hydroxyl group. Thus, tyrosine has dual properties and can be
15 included in both the aromatic and polar categories. Similarly, in addition to being able to form disulfide linkages, cysteine also has apolar character. Thus, while not strictly classified as a hydrophobic or apolar amino acid, in many instances cysteine can be used to confer hydrophobicity to a peptide.

Certain commonly encountered amino acids that are not genetically encoded and
20 that can be present, or substituted for an amino acid, in the peptides and peptide analogues of the invention include, but are not limited to, β -alanine (b-Ala) and other omega-amino acids such as 3-aminopropionic acid (Dap), 2,3-diaminopropionic acid (Dpr), 4-aminobutyric acid and so forth; α -aminoisobutyric acid (Aib); ϵ -aminohexanoic acid (Aha); δ -aminovaleric acid (Ava); methylglycine (MeGly); ornithine (Orn); citrulline (Cit); t-butylalanine (t-BuA); t-butylglycine (t-BuG); N-methylisoleucine (MeIle); phenylglycine
25 (Phg); cyclohexylalanine (Cha); norleucine (Nle); 2-naphthylalanine (2-Nal); 4-chlorophenylalanine (Phe(4-Cl)); 2-fluorophenylalanine (Phe(2-F)); 3-fluorophenylalanine (Phe(3-F)); 4-fluorophenylalanine (Phe(4-F)); penicillamine (Pen); 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid (Tic); β -2-thienylalanine (Thi); methionine
30 sulfoxide (MSO); homoarginine (hArg); N-acetyl lysine (AcLys); 2,3-diaminobutyric acid (Dab); 2,3-diaminobutyric acid (Dbu); p-aminophenylalanine (Phe(pNH₂)); N-methyl valine (MeVal); homocysteine (hCys) and homoserine (hSer). These amino acids also fall into the categories defined above.

The classifications of the above-described genetically encoded and non-encoded amino acids are summarized in Table 3, below. It is to be understood that Table 3 is for illustrative purposes only and does not purport to be an exhaustive list of amino acid residues that may comprise the peptides and peptide analogues described herein. Other amino acid residues that are useful for making the peptides and peptide analogues described herein can be found, e.g., in Fasman, 1989, CRC Practical Handbook of Biochemistry and Molecular Biology, CRC Press, Inc., and the references cited therein. Amino acids not specifically mentioned herein can be conveniently classified into the above-described categories on the basis of known behavior and/or their characteristic chemical and/or physical properties as compared with amino acids specifically identified.

TABLE 3

Classification	Genetically Encoded	Genetically Non-Encoded
Hydrophobic		
Aromatic	F, Y, W	Phg, Nal, Thi, Tic, Phe(4-Cl), Phe(2-F), Phe(3-F), Phe(4-F), Pyridyl Ala, Benzothienyl Ala
Apolar	M, G, P	
Aliphatic	A, V, L, I	t-BuA, t-BuG, Melle, Nle, MeVal, Cha, bAla, MeGly, Aib
Hydrophilic		
Acidic	D, E	
Basic	H, K, R	Dpr, Orn, hArg, Phe(p-NH ₂), DBU, A ₂ BU
Polar	Q, N, S, T, Y	Cit, AcLys, MSO, hSer
Cysteine-Like	C	Pen, hCys, β -methyl Cys

Peptides of the invention can have any amino acid substituted by any similarly classified amino acid to create a variant or derivative peptide, so long as the peptide variant or derivative retains an ability to inhibit the activity of a matrix metalloproteinase.

In one embodiment, the peptide inhibitors of the invention include any one of peptide formulae I, II or III.

Xaa₁-Xaa₂-Xaa₃-Xaa₄-Xaa₅-Xaa₆ Xaa₇-Xaa₈-Xaa₉ (I)

Xaa₁₀-Xaa₁₁-Xaa₁₂ Xaa₁₃-Xaa₁₄-Xaa₁₅-Xaa₁₆-Xaa₁₇-Xaa₁₈-Xaa₁₉ (II)

5

Xaa₁-Xaa₂-Xaa₃-Xaa₄-Xaa₅-Xaa₆-Xaa₇-Xaa₈-Xaa₉-Xaa₁₀-Xaa₁₁-
Xaa₁₂-Xaa₁₃-Xaa₁₄-Xaa₁₅-Xaa₁₆-Xaa₁₇-Xaa₁₈-Xaa₁₉ (III)

wherein

10 Xaa₁, Xaa₄, and Xaa₆ are separately each apolar amino acids, for example, methionine, glycine or proline;

Xaa₂ is a basic amino acid, for example, histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, *p*-aminophenylalanine, and 2,4-diaminobutyric acid;

15 Xaa₃ is a cysteine-like amino acid, for example, cysteine, homocysteine, penicillamine, or *β*-methyl cysteine;

Xaa₅ is a polar or aliphatic amino acid, for example, a polar amino such as asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or an aliphatic amino acid such as alanine, valine, leucine,
20 isoleucine, t-butylalanine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, *β*-alanine, N-methylglycine, or *α*-aminoisobutyric acid;

Xaa₇ is an acidic amino acid, for example, aspartic acid or glutamic acid;

Xaa₈ is an aliphatic or polar amino acid, for example an aliphatic amino acid such as alanine, valine, leucine, isoleucine, t-butylalanine, t-butylalanine, methylisoleucine,
25 norleucine, N-methylvaline, cyclohexylalanine, *β*-alanine, N-methylglycine, or *α*-aminoisobutyric acid, or a polar amino acid such as asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine;

Xaa₉ is an aliphatic, apolar or basic amino acid, for example, an aliphatic amino acid such as alanine, valine, leucine, isoleucine, t-butylalanine, t-butylalanine, N-
30 methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, *β*-alanine, N-methylglycine, or *α*-aminoisobutyric acid, an apolar amino acid such as methionine, glycine or proline, or a basic amino acid such as histidine, lysine, arginine, 2,3-

diaminopropionic acid, ornithine, homoarginine, ρ -amino-phenylalanine, and 2,4-diaminobutyric acid;

Xaa₁₀ is a polar, acidic, basic or apolar amino acid, for example, a polar amino acid such as asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, an acidic amino acid such as aspartic acid or
5 glutamic acid, a basic amino acid such as histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, ρ -amino-phenylalanine, and 2,4-diaminobutyric acid, or an apolar amino acid such as methionine, glycine or proline;

Xaa₁₁ is a polar or aromatic amino acid, for example, a polar amino acid such as
10 asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or an aromatic amino acid such as phenylalanine, tyrosine, tryptophan, phenylglycine, naphthylalanine, β -2-thienylalanine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, pyridylalanine, or 3-benzothienyl alanine;

Xaa₁₂ is a polar, basic, aliphatic or apolar amino acid, for example, a polar amino
15 acid such asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or a basic amino acid such as histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, ρ -amino-phenylalanine, and 2,4-diaminobutyric acid, or an aliphatic amino acid such as alanine, valine, leucine,
20 isoleucine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, β -alanine, N-methylglycine, or α -aminoisobutyric acid, or an apolar amino acid such as methionine, glycine or proline ;

Xaa₁₃ is an aromatic, aliphatic, polar or acidic amino acid, for example, an aromatic
25 amino acid such as phenylalanine, tyrosine, tryptophan, phenylglycine, naphthylalanine, β -2-thienylalanine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, pyridylalanine, or 3-benzothienyl alanine, or an aliphatic amino acid such as alanine, valine, leucine, isoleucine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, β -alanine, N-methylglycine, or α -aminoisobutyric acid, or a polar amino
30 acid such as asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or an acidic amino acid such as aspartic acid or glutamic acid;

Xaa₁₄ is an aromatic, apolar or polar amino acid, for example, an aromatic amino acid such as phenylalanine, tyrosine, tryptophan, phenylglycine, naphthylalanine, β -2-thienylalanine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, pyridylalanine, or 3-benzothienyl alanine, or an apolar amino acid such as methionine, glycine or proline, or a polar amino acid such as asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine;

Xaa₁₅ is an apolar or acidic amino acid, for example, an apolar amino acid such as methionine, glycine or proline, or an acidic amino acid such as aspartic acid or glutamic acid;

Xaa₁₆ is a basic, a polar or an apolar amino acid, for example, a basic amino acid such as histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, ρ -amino-phenylalanine, and 2,4-diaminobutyric acid; or a polar amino acid such as asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or an apolar amino acid such as methionine, glycine or proline;

Xaa₁₇ is a basic, a polar, an aliphatic, an apolar or an acidic amino acid, for example, a basic amino acid such as histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, ρ -amino-phenylalanine, and 2,4-diaminobutyric acid, or a polar amino acid such as asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or an aliphatic amino acid such as alanine, valine, leucine, isoleucine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, β -alanine, N-methylglycine, or α -aminoisobutyric acid, or an apolar amino acid such as methionine, glycine or proline, an acidic amino acid such as aspartic acid or glutamic acid;

Xaa₁₈ is an apolar or an aliphatic amino acid, for example, an apolar amino acid such as methionine, glycine or proline, or an aliphatic amino acid such as alanine, valine, leucine, isoleucine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, β -alanine, N-methylglycine, or α -aminoisobutyric acid; and

Xaa₁₉ is a basic or an aliphatic amino acid, for example, a basic amino acid such as histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, ρ -amino-phenylalanine, and 2,4-diaminobutyric acid, or an aliphatic amino acid such as alanine,

valine, leucine, isoleucine, t-butylalanine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, β -alanine, N-methylglycine, or α -aminoisobutyric acid.

In some embodiments:

- 5 Xaa₁ is proline,
Xaa₂ is arginine,
Xaa₃ is cysteine,
Xaa₄ is glycine,
Xaa₅ is valine or asparagine,
Xaa₆ is proline,
10 Xaa₇ is aspartic acid,
Xaa₈ is valine, leucine, or serine,
Xaa₉ is alanine, glycine or histidine,
Xaa₁₀ is asparagine, aspartic acid, histidine, arginine, glutamine
or glycine,
15 Xaa₁₁ is tyrosine or phenylalanine,
Xaa₁₂ is asparagine, serine, arginine, glutamine, valine or
methionine,
Xaa₁₃ is phenylalanine, valine, leucine, threonine, serine, or
glutamic acid,
20 Xaa₁₄ is phenylalanine, methionine or threonine,
Xaa₁₅ is proline or glutamic acid,
Xaa₁₆ is arginine, asparagine or glycine,
Xaa₁₇ is lysine, threonine, serine, isoleucine, methionine, glycine,
aspartic acid or asparagine,
25 Xaa₁₈ is proline or leucine, and
Xaa₁₉ is lysine, valine or arginine.

Desirable peptides of the invention also include the sequences defined by SEQ ID NO:1-13. For example, a nineteen amino acid peptide having SEQ ID NO:11 (PRCGNPDVANYNFFPRKPK) is desirable. This peptide (SEQ ID NO:11) spans the
30 cleavage site of MMP-2. Two smaller peptides (PRCGNPDVA (SEQ ID NO:12) and NYNFFPRKPK (SEQ ID NO:13)), that represent halves of the SEQ ID NO:11 peptide, are also desirable peptides. All three peptides inhibit MMP-9 activity and other matrix metalloproteinase enzymes to a varying degree.

A single peptide having a sequence identical to that of a matrix metalloproteinase cleavage region can be used to inhibit the activity of a single or only a few matrix metalloproteinases. A formulation of such a single peptide will inhibit one or more, but generally not all, matrix metalloproteinase. Such partial inhibition of matrix metalloproteinase activity may facilitate healing. Alternatively, two or more peptides can be combined to target two or more matrix metalloproteinases that may provide more complete inhibition of matrix metalloproteinase activity.

One of skill in the art can design an appropriate peptide inhibitor or combination of peptide inhibitors to achieve the quality and quantity of inhibition desired using available teachings in combination with the teachings provided herein. "Quality" of inhibition refers to the type of matrix metalloproteinase inhibited. Different matrix metalloproteinases can have somewhat different substrates and sites of activity. "Quantity" of inhibition refers to the overall amount of inhibition from all matrix metalloproteinases. By modulating the type and quantity of peptide inhibitor used, the quality and quantity of inhibition can be modulated. One of skill in the art can readily make modifications to the peptides provided by the invention and observe the type and degree to which a given matrix metalloproteinase is inhibited.

For example, one of skill in the art can compare and align the peptide sequences shown in Figure 1 and design a peptide inhibitor to achieve the quality and quantity of inhibition desired. In one embodiment, provided by way of example, the aligned amino acid sequences for three wound site matrix metalloproteinases, mmp2, mmp9 and mmp1, are compared to identify regions of homology and regions of divergence in sequence.

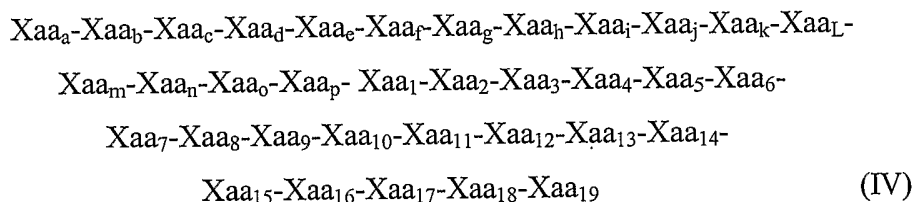
<u>MMP</u>	<u>SEQUENCE</u>	<u>SEQ ID NO</u>
mmp2 :	MQKFFGLPQTGDLDQNTIETMRKPRCGNPDVANYNFFPRKPKW	NO : 15
mmp9 :	LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKW	NO : 16
mmp1 :	<u>MQEFFGLKVTGKPD</u> <u>AE</u> <u>TLKVMKQ</u> PRCGVPDVA <u>QFVLT</u> <u>TEGNPRW</u>	NO : 17

In this sequence alignment, bold denotes amino acids found in MMP-1 that are not found in MMP-2 or MMP-9, and underlining shows amino acids found in MMP-1 and only in MMP-2 or MMP-9.

In one embodiment, it is desirable to inhibit MMPs-2 and 9, but to keep the level of MMP-1 relatively unregulated in order to heal chronic wounds. Based on the sequence

alignment above one of skill in the art can design a peptide with amino acids that are found in MMP2 and MMP9 proenzyme sequences but not in the MMP1 proenzyme sequence, to produce a peptide that will inhibit MMPs-2 and 9, while leaving MMP-1 uninhibited. Such a peptide is provided by formula IV.

5



10

(SEQ ID NO:18)

wherein:

	Xaa _a is proline;	Xaa ₁ is proline;
	Xaa _b is glutamine or glutamic acid;	Xaa ₂ is arginine;
	Xaa _c is threonine;	Xaa ₃ is cysteine;
15	Xaa _d is glycine;	Xaa ₄ is glycine;
	Xaa _e is aspartic acid or glutamic acid;	Xaa ₅ is valine or asparagine, desirably asparagine;
	Xaa _f is leucine;	Xaa ₆ is proline;
	Xaa _g is aspartic acid;	Xaa ₇ is aspartic acid;
20	Xaa _h is glutamine or serine;	Xaa ₈ is valine or leucine, desirably leucine;
	Xaa _i is asparagine or alanine;	Xaa ₉ is alanine or glycine, desirably glycine;
	Xaa _j is threonine;	Xaa ₁₀ is asparagine or arginine;
25	Xaa _k is isoleucine or leucine, desirably isoleucine;	Xaa ₁₁ is tyrosine or phenylalanine, desirably tyrosine;
	Xaa _l is glutamic acid or lysine, desirably glutamic acid;	Xaa ₁₂ is asparagine or glutamine;
	Xaa _m is threonine or alanine;	Xaa ₁₃ is phenylalanine or threonine;
30	Xaa _n is methionine;	Xaa ₁₄ is phenylalanine;
	Xaa _o is arginine;	Xaa ₁₅ is proline or glutamic acid, desirably proline;
		Xaa ₁₆ is arginine or glycine, desirably arginine;

Xaa_p is lysine or threonine;

Xaa₁₈ is proline or leucine,

Xaa₁₇ is lysine or aspartic acid;

desirably leucine; and

Xaa₁₉ is lysine.

5 Peptide Modifications

The invention also contemplates modifying the peptide inhibitors to stabilize them, to facilitate their uptake and absorption and to improve any other characteristic or property of the peptides that is known to one of skill in art. For example, the peptide inhibitors can be cyclized, charges on the peptide inhibitors can be neutralized, and the peptides can be
10 linked to other chemical moieties.

Peptides can be cyclized by any method available to one of skill in the art. For example, the N-terminal and C-terminal ends can be condensed to form a peptide bond by known procedures. Functional groups present on the side chains of amino acids in the peptides can also be joined to cyclize the peptides of the invention. For example,
15 functional groups that can form covalent bonds include --COOH and --OH; --COOH and --NH₂; and --COOH and --SH. Pairs of amino acids that can be used to cyclize a peptide include Asp and Lys; Glu and Lys; Asp and Arg; Glu and Arg; Asp and Ser; Glu and Ser; Asp and Thr; Glu and Thr; Asp and Cys; and Glu and Cys. Other examples of amino acid residues that are capable of forming covalent linkages with one another include cysteine-
20 like amino acids such Cys, hCys, β -methyl-Cys and Pen, which can form disulfide bridges with one another. Desired cysteine-like amino acid residues include Cys and Pen. Other pairs of amino acids that can be used for cyclization of the peptide will be apparent to those skilled in the art.

The groups used to cyclize a peptide need not be amino acids. Examples of
25 functional groups capable of forming a covalent linkage with the amino terminus of a peptide include carboxylic acids and esters. Examples of functional groups capable of forming a covalent linkage with the carboxyl terminus of a peptide include --OH, --SH, --NH₂ and --NHR where R is (C₁ - C₆) alkyl, (C₁ - C₆) alkenyl and (C₁ - C₆) alkynyl.

The variety of reactions between two side chains with functional groups suitable for
30 forming such interlinkages, as well as reaction conditions suitable for forming such interlinkages, will be apparent to those of skill in the art. Desired reaction conditions used to cyclize the peptides are sufficiently mild so as not to degrade or otherwise damage the peptide. Suitable groups for protecting the various functionalities as necessary are well

known in the art (see, e.g., Greene & Wuts, 1991, 2nd ed., John Wiley & Sons, NY), as are various reaction schemes for preparing such protected molecules.

In one embodiment the charges at the N-terminal and C-terminal ends are effectively removed. This can be done by any method available to one of skill in the art, for example, by acetylating the N-terminus and amidating the C-terminus.

Methods for preparing cyclic peptides and modifying peptide in other ways are well-known in the art (see, e.g., Spatola, 1983, Vega Data 1(3) for a general review); Spatola, 1983, "Peptide Backbone Modifications" In: Chemistry and Biochemistry of Amino Acids Peptides and Proteins (Weinstein, ed.), Marcel Dekker, New York, p. 267 (general review); Morley, 1980, Trends Pharm. Sci. 1:463-468; Hudson et al., 1979, Int. J. Prot. Res. 14:177-185 (--CH₂ NH--, --CH₂ CH₂ --); Spatola et al., 1986, Life Sci. 38:1243-1249 (--CH₂ --S); Hann, 1982, J. Chem. Soc. Perkin Trans. I. 1:307-314 (--CH = CH--, cis and trans); Almquist et al., 1980, J. Med. Chem. 23:1392-1398 (--CO CH₂ --); Jennings-White et al., Tetrahedron. Lett. 23:2533 (--CO CH₂ --); European Patent Application EP 45665 (1982) CA:97:39405 (--CH(OH) CH₂ --); Holladay et al., 1983, Tetrahedron Lett. 24:4401-4404 (--C(OH)CH₂--); and Hruby, 1982, Life Sci. 31:189-199 (-CH₂ --S--).

Wound Healing and Anti-aging

Peptides of the invention can be used to heal wounds, to ameliorate the effects of aging on skin and are particularly beneficial for chronic wound healing. Individual peptides, peptide variants, peptide derivatives and mixtures thereof (e.g. those with different sequences) can be combined in a formulation to promote wound healing and to prevent or treat skin problems associated with aging. Optimal healing and skin regeneration may require some matrix metalloproteinase activity. Hence, the compositions and formulations of the present invention do not necessarily promote maximal inhibition of matrix metalloproteinases. Instead, the activity of the peptide inhibitor formulation is varied as needed to optimize healing and promote healthy skin development. Lesser or greater levels of inhibition can be achieved by varying the type, content and amount of inhibitor peptides so that healing and healthy skin development is promoted.

To promote healthy skin development and/or treat wounds, peptides of the invention are introduced onto the skin or into wounds in any manner chosen by one of skill in the art. For example, peptides can be formulated into a therapeutic composition

containing a therapeutically effective amount of one or more peptides and a pharmaceutical carrier. Such a composition can be introduced onto skin or into the wound as a cream, spray, foam, gel or in the form of any other formulation. In another embodiment, peptides of the invention can be formulated into a skin covering or dressing containing a

5 therapeutically effective amount of one or more peptides impregnated into, covalently attached or otherwise associated with a covering or dressing material. In one embodiment, the skin covering or dressing permits release of the peptide inhibitor. Release of the peptide inhibitor can be in an uncontrolled or a controlled manner. Hence, the skin coverings or wound dressings of the invention can provide slow or timed release of the

10 peptide inhibitor into a wound. Skin coverings and dressing materials can be any material used in the art including bandage, gauze, sterile wrapping, hydrogel, hydrocolloid and similar materials.

A therapeutically effective amount of a peptide of the invention is an amount of peptide that inhibits a matrix metalloproteinase to a degree needed to promote healthy skin

15 development and/or wound healing. For example, when present in a therapeutic or pharmaceutical composition, the amount of peptides of the invention can be in the range of about 0.001% to about 35% by weight of the composition. The peptides can form about 0.5% to about 20% by weight of the composition. Alternately, the peptides form about 1.0% to about 10% by weight of the composition. The therapeutically effective amount of

20 peptide inhibitor necessarily varies with the route of administration. For example, a therapeutic amount between 30 to 112,000 μg per kg of body weight can be effective for intravenous administration. However, the amount of the peptide inhibitor required for healthy skin development or wound treatment will vary not only with the route of administration, but also the nature of the condition being treated and the age and condition

25 of the patient and will be ultimately at the discretion of the attendant physician or clinician.

The dosage and method of administration can vary depending upon the location of the skin or tissue to be treated and/or upon severity of the wound. Useful dosages of the peptides and peptide conjugates can be determined by correlating their in vitro activity, and in vivo activity in animal models described herein. The compound can conveniently be

30 administered in unit dosage form; for example, containing about 0.001 μg to about 10 mg, conveniently about 0.01 μg to about 5 mg, more conveniently, about 0.10 μg to about 1 mg, and even more conveniently about 1.0 μg to 500 μg of peptide per unit dosage form. The desired dose may be presented in a single dose, as divided doses, or as a continuous

infusion. The desired dose can also be administered at appropriate intervals, for example, as two, three, four or more sub-doses per day. One of skill in the art can readily prepare and administer an effective formulation from available information using the teachings provided herein.

5 The peptide inhibitors of the invention can be formulated as pharmaceutical compositions and administered to a mammalian host, such as a human patient in a variety of dosage forms adapted to the chosen route of administration, i.e., orally or parenterally, by intravenous, intramuscular, topical or subcutaneous routes.

10 Thus, the peptide inhibitors may be systemically administered, for example, intravenously or intraperitoneally by infusion or injection. Solutions of the peptide inhibitor can be prepared in water, optionally mixed with a nontoxic surfactant. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, triacetin, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

15 The pharmaceutical dosage forms suitable for injection or infusion or topical application can include sterile aqueous solutions or dispersions or sterile powders comprising the active ingredient that are adapted for the extemporaneous preparation of sterile injectable or infusible solutions or dispersions, optionally encapsulated in liposomes. In all cases, the ultimate dosage form must be sterile, fluid and stable under the conditions
20 of manufacture and storage. The liquid carrier or vehicle can be a solvent or liquid dispersion medium comprising, for example, water, ethanol, a polyol (for example, glycerol, propylene glycol, liquid polyethylene glycols, and the like), vegetable oils, nontoxic glyceryl esters, and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the formation of liposomes, by the maintenance of the required
25 particle size in the case of dispersions or by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In some cases, one of skill in the art may choose to include isotonic agents, for example, sugars, buffers or sodium chloride. Prolonged absorption of the injectable compositions
30 can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

 Sterile injectable solutions are prepared by incorporating the peptide or peptide conjugate in the required amount in the appropriate solvent with various of the other

ingredients enumerated above, as required, followed by filter sterilization. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation include vacuum drying and the freeze-drying techniques, which yield a powder of the active ingredient plus any additional desired ingredient present in the previously sterile-
5 filtered solutions.

In some instances, the peptide inhibitors can also be administered orally, in combination with a pharmaceutically acceptable vehicle such as an inert diluent or an assimilable edible carrier. They may be enclosed in hard or soft shell gelatin capsules, may be compressed into tablets, or may be incorporated directly with the food of the patient's
10 diet. For oral therapeutic administration, the peptide inhibitor may be combined with one or more excipients and used in the form of ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, wafers, and the like. Such compositions and preparations should contain at least 0.1% of active compound. The percentage of the compositions and preparations may, of course, be varied and may conveniently be between
15 about 2 to about 60% of the weight of a given unit dosage form. The amount of active compound in such therapeutically useful compositions is such that an effective dosage level will be obtained.

The tablets, troches, pills, capsules, and the like may also contain the following: binders such as gum tragacanth, acacia, corn starch or gelatin; excipients such as dicalcium
20 phosphate; a disintegrating agent such as corn starch, potato starch, alginic acid and the like; a lubricant such as magnesium stearate; and a sweetening agent such as sucrose, fructose, lactose or aspartame or a flavoring agent such as peppermint, oil of wintergreen, or cherry flavoring may be added. When the unit dosage form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier, such as a vegetable oil or a
25 polyethylene glycol. Various other materials may be present as coatings or to otherwise modify the physical form of the solid unit dosage form. For instance, tablets, pills, or capsules may be coated with gelatin, wax, shellac or sugar and the like. A syrup or elixir may contain the active compound, sucrose or fructose as a sweetening agent, methyl and propylparabens as preservatives, a dye and flavoring such as cherry or orange flavor. Of
30 course, any material used in preparing any unit dosage form should be pharmaceutically acceptable and substantially non-toxic in the amounts employed. In addition, the peptide inhibitor may be incorporated into sustained-release preparations and devices.

Useful solid carriers include finely divided solids such as talc, clay, microcrystalline cellulose, silica, alumina and the like. Useful liquid carriers include water, alcohols or glycols or water-alcohol/glycol blends, in which the present compounds can be dissolved or dispersed at effective levels, optionally with the aid of non-toxic surfactants.

5 Adjuvants such as fragrances and additional antimicrobial agents can be added to optimize the properties for a given use.

Thickeners such as synthetic polymers, fatty acids, fatty acid salts and esters, fatty alcohols, modified celluloses or modified mineral materials can also be employed with liquid carriers to form spreadable pastes, gels, ointments, soaps, and the like, for
10 application directly to the skin of the user.

In general, the peptides of the invention are administered topically for wound treatment and for promoting healthy skin development. The active peptides may be administered topically by any means either directly or indirectly to the selected tissue as sprays, foams, powders, creams, jellies, pastes, suppositories or solutions. The term paste
15 used in this document should be taken to include creams and other viscous spreadable compositions such as are often applied directly to the skin or spread onto a bandage or dressing. Peptides of the invention can be covalently attached, stably adsorbed or otherwise applied to a skin covering or wound dressing material. To facilitate healing after surgery, the active peptides of the invention can be applied directly to target tissues or to
20 prosthetic devices or implantable sustained released devices. The compositions can be administered by aerosol, as a foam or as a mist, with or without other agents, directly onto the skin or wound.

The peptides can be administered in a formulation that can include an emulsion of the peptide in a wax, oil, an emulsifier, water, and/or a substantially water-insoluble
25 material that forms a gel in the presence of water. The formulation provides the desirable properties of an emulsion, in that it is spreadable and has the creamy consistency of an emulsion, yet that does not break down when subjected to normal sterilization procedures, e.g. steam sterilization, because the gel stabilizes the emulsion. It also exhibits better water retention properties than a conventional gel because water is held both in the emulsion and
30 in the gel.

The formulation can also contain a humectant to reduce the partial vapor pressure of the water in the cream or lotion to reduce the rate at which the cream or lotion dries out. Suitable humectants are miscible with water to a large extent and are generally suitable for

application to the skin. Polyols are especially suitable for the purpose and suitable polyols may include monopropylene glycol or glycerine (glycerol). The polyol may be present in proportions of 20-50% (by weight) of the total formulation; alternatively the range is 30-40%. This relatively high proportion of polyol also ensures that if the paste should dry out to any degree, the resulting paste remains soft and flexible because the glycerine may act as a plasticiser for the polymer. When the paste is applied on a bandage, for example, it may therefore still be removed easily from the skin when the paste has lost water without the need to cut the bandage off. The polyol also has the advantage of functioning to prevent the proliferation of bacteria in the paste when it is in contact with the skin or wound, particularly infected wounds.

The formulation can include other ingredients. Ingredients that may be used include: zinc oxide, ichthammol, calamine, silver sulphadiazine, chlorhexidine acetate, coal tar, chlorhexidine gluconate, salicylic acid, metronidazole or other antibacterial agents, or a combination thereof. Other ingredients may also be found suitable for incorporation into the cream.

These ingredients can be included in beneficial amounts, for example, up to about 15 wt %, of zinc oxide may be added; typically 6-10% of zinc oxide is used, possibly in combination with another ingredient such as ichthammol (0-3 wt %) and/or calamine (0-15% wt). Ichthammol or calamine may also be used alone. Chlorhexidine acetate can be used at a concentration of up to 1% by weight; 0.5 wt % is typical.

An example of a wax for the emulsion is glyceryl monostearate, or a combination of glyceryl monostearate and PEG100 stearate that is available commercially as CITHROL GMS/AS/NA from Croda Universal Ltd. This combination provides both a wax and an emulsifier (PEG 100 stearate) that is especially compatible with the wax, for forming an emulsion in water. A second emulsifier can be included in the formulation to increase the stability of the emulsion, for example, a PEG20 stearate, such as CITHROL 1OMS that is supplied by Croda Universal Ltd. The total concentration of emulsifier in the cream should normally be in the range of from 3-15%. Where two emulsifiers are used, one may be present in a greater concentration than the other.

The water-insoluble material forms a gel with the water of the formulation. The material is therefore hydrophilic but does not dissolve in water to any great extent. The material can be a polymeric material, for example, a water-absorbing non water-soluble polymer. However, non-polymeric materials that form gels with water and that are stable

at elevated temperatures could also be used, e.g. clays such as kaolin or bentonite. Some polymers used in the invention are super-absorbent polymers such as those disclosed in WO-92/16245 and that comprise hydrophilic cellulose derivatives that have been partially cross-linked to form a three dimensional structure. Suitable cross-linked cellulose derivatives include those of the hydroxy lower alkyl celluloses, wherein the alkyl group contains from 1 to 6 carbon atoms, e.g. hydroxyethyl cellulose or hydroxypropylcellulose, or the carboxy-celluloses e.g. carboxymethyl hydroxyethyl cellulose or carboxymethylcellulose. An example of a polymer that may be used in the invention is a partially cross-linked sodium carboxymethylcellulose polymer supplied as AKUCCELL X181 by Akzo Chemicals B.V. This polymer is a superabsorbent polymer in that it may absorb at least ten times its own weight of water. The cross-linked structure of the polymer prevents it from dissolving in water but water is easily absorbed into and held within the three-dimensional structure of the polymer to form a gel. Water is lost less rapidly from such a gel than from a solution and this is advantageous in slowing or preventing the drying out of the cream formulation. The polymer content of the formulation is normally less than 10%, for example, the polymer content can range from about 0.5 to about 5.0% by weight, or from about 1.0% to about 2% by weight.

The formulation may be sterilized and components of the formulation should be selected, by varying the polymer content, to provide the desired flow properties of the finished product. That is, if the product to be sterilized, then the formulation should be chosen to give a product of relatively high viscosity/elasticity before sterilization. If certain components of the formulation are not to be sterilized, the formulation can be sterilized before addition of those components, or each component can be sterilized separately. The formulation can then be made by mixing each sterilized ingredients under sterile conditions. When components are separately sterilized and then mixed together, the polymer content can be adjusted to give a product having the desired flow properties of the finished product. The emulsion content determines the handling properties and feel of the formulation, higher emulsion content leading to increased spreadability and creaminess.

The formulation may be packaged into tubes, tubs or other suitable forms of containers for storage or it may be spread onto a substrate and then subsequently packaged. Suitable substrates include dressings, including film dressings, and bandages.

The following examples are intended to illustrate but not limit the invention.

EXAMPLE 1: Peptide Inhibitors

General Materials

All peptides were synthesized by Sigma-Genosys, Inc. The released peptides were purified to >95% homogeneity via RP-HPLC by the company. The pooled eluted peak material was desalted and lyophilized. Mass Spectroscopy analysis confirmed the peptide molecular weight and purity. Unless otherwise noted, all chemicals were purchased from Sigma Chemical Corp. or from Fluka Chemical Co. Active MMP-9 enzyme was purchased from Calbiochem.

10

Molecular Modeling

Molecular modeling utilized two visualization programs, Swiss PDB Viewer (Guex and Peitsch, 1997) and Rasmol (Sayle and Milner-White, 1995). Model work was performed on a Compaq PC running Windows 95, as well as a Silicon Graphics, Inc.

15 Octane UNIX workstation. Additionally, the Cerius2 molecular package from Molecular Simulations, Inc. was utilized on the Octane. Three dimensional structure files were downloaded from the Protein Databank as follows (filename, reference): MMP-1 (1FBL, Li et al., 1995), MMP-2 (1GEN, Libson et al., 1995), MMP-8 (1JAO, 1JAN, Grams, et al., 1995; Reinemer et al., 1994), MMP-9 (1MMQ, Browner et al., 1995), TIMP-2/MT-1 MMP
20 complex (1BUV, Fernandez-Catalan et al., 1998), TIMP-2 (1BR9, Tuuttila et al., 1998), and TIMP-1/MMP complex (1UEA, Gomis-Ruth et al., 1997; Huang et al., 1996; Becker et al., 1995). These files were used to analyze the three-dimensional structure of the proteins, as well as being the source of primary sequence data.

25 Inhibition Assays

Two enzymatic assays were performed. The first assay measured the enzymatic hydrolysis of fluoresceinated collagen by MMP-9 as a function of time. Fluoresceinated collagen (Molecular Probes, Inc.), at a concentration of 5 μ M was added to reaction buffer (50 mM Tris- HCl (pH 7.6), 150 mM NaCl, 5 mM CaCl₂, 0.1 mM NaN₃) and was placed
30 into a Spectrosil quartz fluorometer cuvette. MMP, at a concentration of 0.1 μ M, was mixed with varying amounts of peptide and incubated at 25 °C for 10 minutes in order to effect binding. The protein mixture was added to the collagen substrate, and was quickly mixed. Fluorescence emission intensity at 520 nm was measured as a function of time

(excitation wavelength 495 nm) in a Shimadzu RF5301 fluorometer (Lakowicz, 1983). The fluorescein release assay was used to determine the inhibitory constant (K_i) of the peptide inhibitor ($[I]$) according to Segel (1993) via the use of Dixon plots ($1/v$ vs. $[I]$), such that:

5

$$\text{slope} = K_m / (V_{\max} K_i [S]) \quad (1)$$

where K_m is the Michaelis constant, V_{\max} is the reaction maximum velocity, and $[S]$ is the substrate concentration.

10 The second assay utilized the technique of fluorescence resonance energy transfer (FRET). The substrate peptide (Calbiochem) of seven amino acids was coupled to a carboxyl terminal dinitrophenyl acceptor, and an amino terminal 2-aminobenzo-anthraniloyl (Abz) moiety donor. Cleavage of this substrate by MMP-9 resulted in the liberation of a fluorescent product (365 nm excitation, 450 nm emission). Peptide at a
15 concentration of 5 μM was added to reaction buffer (50 mM Tris- HCl (pH 7.6), 150 mM NaCl, 5 mM CaCl_2 , 0.1 mM NaN_3) and was placed into a black 96-well microtiter plate well that had been previously blocked with 1% BSA. MMP at a concentration of 0.1 μM was mixed with varying amounts of either the 9-mer (SEQ ID NO:12), the 10-mer (SEQ ID NO:13), or the 19-mer (SEQ ID NO:11) peptide and incubated at 25 °C for 10 minutes in
20 order to effect binding. The protein mixture was added to the fluorescent peptide substrate, and was quickly mixed. Fluorescence intensity as a function of time was measured with a Dynex MFX fluorescence microtiter plate reader. Fluorescence intensity was related back to moles of peptide cleaved by producing a standard curve with an Abz containing non-FRET peptide. Inhibitory constants were derived from the curves as above. Other matrix
25 metalloproteinase enzymes were tested in a similar manner utilizing specific substrate FRET peptides (all from Calbiochem).

Anti-activation Assay

The assay measures how much proenzyme is converted into mature matrix
30 metalloproteinase. Proenzyme pro-MMP-9 (100 μg) was mixed with 0.5 μg of stromilysin in PBS. The reaction was incubated at 35 °C. Aliquots were removed from the reaction over an 80 minute time course. Each aliquot is mixed with EDTA to a final concentration of 1 mM, injected onto a BioSelect 125 HPLC column and chromatographed in PBS. The

zero (injection) time point was a single peak that elutes from the column in approximately 750 seconds. This peak reduces in size as a function of time, and two new peaks appear. The first peak elutes at approximately 800 seconds, and represents the mature form of MMP-9. The second peak elutes at approximately 1100 seconds, and corresponds to the N-terminal pro-domain fragment. Peak areas were determined by integrating over the elution profile, and the percent area changes were plotted.

Isothermal titration calorimetry

Isothermal titration calorimetry (ITC) was performed with a VP-ITC instrument from MicroCal, Inc. Titrations were carried out by injecting 5 μ L of an inhibitor peptide solution (at concentration ranges from 0.5 mM to 2.0 mM) into the 1.4 mL stirred reaction cell. MMP-9 ranged in concentration from 50 to 80 μ M in the cell. Both the inhibitor and the enzyme were in 20 mM sodium cacodylate (pH 5.5-7.0), 40 mM NaCl, or 20 mM Tris-HCl (pH 7.0-7.5), 40 mM NaCl. Titrations were conducted between 20 °C and 40 °C. Typical experimental conditions for the titrations were a 10 second injection period followed by a 240 second delay between injections for a total of 40 injections. Blank titrations of inhibitor peptide into buffer were performed in order to correct for heats of dilution and mixing.

The independent set of multiple binding sites is the most common model for binding experiment evaluations. The analytical solution for the total heat is determined by (Freire et al., 1990):

$$Q = V \Delta H \times \left[[L] + \frac{1 + [M] nK - \sqrt{(1 + [M] nK - [L]K)^2 + 4K[L]}}{2K} \right] \quad (2)$$

where Q is the total heat, V is the cell volume, ΔH is the enthalpy, M is the macromolecule concentration (the binding partner in the cell), n is the binding stoichiometry, L is the ligand concentration (the binding partner in the syringe), and K is the association constant. Data were fit to this model using Origin version 5 (MicroCal, Inc.).

Surface Plasmon Resonance

The BiaCore-X surface plasmon resonance (SPR) device (BiaCore, Inc.) was utilized to measure the interaction between the 19-mer (SEQ ID NO:11) peptide (P) and MMP-9. For these experiments a carboxymethyl dextran sensor chip (CM-5, Lofas et al., 1993) was activated with 50 mM N-hydroxysuccinimide, 0.2 M N-ethyl-N'-(dimethylaminopropyl)-carbodiimide at a flow rate of 10 μ L per minute for ten minutes. MMP-9 at a concentration of 75 ng/ μ L was coupled to the activated surface at a flow rate of 10 μ L per minute for ten minutes. The final surface was inactivated by flowing 1 M ethanolamine-HCl at a rate of 10 μ L per minute for five minutes over the sensor surface. The 19-mer (SEQ ID NO:11) peptide was flowed over the sensor surface at a rate of 20 μ L per minute, and at concentrations that ranged from 10 to 50 nM. The association and dissociation phases of the binding isotherms were smoothed by an automated FFT routine prior to modeling rate constants. Binding isotherms were evaluated by simultaneously fitting the forward (k_a) and reverse (k_d) rate constants to:

15

$$d[\text{P}\sim\text{MMP-9}] / dt = (k_a [\text{P}] [\text{MMP-9}]) - (k_d [\text{P}\sim\text{MMP-9}]) \quad (3)$$

(Karlsson and Falt, 1997) where [P], [MMP-9], and [P~MMP-9] are the concentrations of free peptide, free MMP-9, and the complex respectively. The equilibrium affinity constant (K_A) is then defined as:

20

$$K_A = k_a / k_d \quad (4)$$

Equation 3 is properly expressed in terms of the SPR signal (Morton et al., 1995) as:

25

$$dR/dt = k_a C R_{\text{max}} - (k_a C + k_d)R \quad (5)$$

where R is the SPR signal (in response units, RU) at time t, R_{max} is the maximum MMP-9 binding capacity in RU, and C is the chelating peptide concentration. Kinetic analysis (O'Shannessy et al., 1993) was performed using Origin from Microcal, Inc.

30

Viability Assays

The relative toxicity of the 9-mer (SEQ ID NO:12), the 10-mer (SEQ ID NO:13) and the 19-mer (SEQ ID NO:11) peptides was assayed using the skin model Epiderm from

MatTek Corp. The individual skin sample containers were preincubated in culture medium at 37 °C, 5% CO₂ for two hours prior to the addition of the peptides. The sample containers were transferred to 6 well plates that contained fresh media. All peptides were dissolved in PBS at a final concentration of 10 mM, and 100 μL each peptide solution was pipetted onto the surface of the Epiderm sample container. Incubation was continued for 12 hours at 37 °C, 5% CO₂. After the incubation period, the sample containers were washed three times with PBS and the sample containers were transferred to a 24 well plate that contained 300 μL of MTT assay media per well (MTT concentration was 1 mg/mL). The colorimetric assay was allowed to develop for three hours (incubation at 37 °C, 5% CO₂). Sample containers were then transferred to a 24 well culture plate that contained 2 mL of isopropanol per well. Extraction of the colored precipitate occurred over a period of four hours at room temperature. Absorbance readings were taken at 570 nm and 650 nm for each sample. The percent viability of each sample relative to a PBS control was calculated as:

15

$$100 \times (OD_{570}^{sam} - OD_{650}^{sam}) / (OD_{570}^{con} - OD_{650}^{con}) \quad (6)$$

Routinely, the peptide sample was assayed in triplicate.

20 Results

The sequence of matrix metalloproteinase-2 (SEQ ID NO:14) is provided below to facilitate definition of the various domains and regions in matrix metalloproteinases.

```

1 MEALMARGAL TGPLRALCLL GCLLSHAAAA PSPIIKFPGD
25 41 VAPKTDKELA VQYLNTFYGC PKESCNLFVL KDTLKKMQKF
81 FGLPQTGDL D QNTIETMRKP RCGNPDVANY NFFPRKPKWD
121 KNQITYRIIG YTPDLDPETV DDAFARAFQV WSDVTPLRFS
161 RIHDGEADIM INFGRWEHGD GYPFDGKDGL LAHAFAPGTG
201 VGGDSHFDDD ELWTLGEGQV VRVKYGNADG EYCKFPFLFN
30 241 GKEYNSCTDT GRSDGFLWCS TTYNFEKD GK YGFCPHEALF
281 TMGGNAEGQP CKFPFRFQGT SYDSCTTEGR TDGYRWC GTT
321 EDYDRDKKYG FCPETAMSTV GGNSEGAPCV FPF TFLGNKY
361 ESCTSAGRSD GKMWCATTAN YDDDRKWGFC PDQGYSLFLV

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401 AAHEFGHAMG LEHSQDPGAL MAPIYTYTKN FRLSQDDIKG
441 IQELYGASPD IDLGTGPTPT LGPVTPEICK QDIVFDGIAQ
481 IRGEIFFFKD RFIWRTVTPR DKPMGPLLVA TFWPELPEKI
521 DAVYEAPQEE KAVFFAGNEY WIYSASTLER GYPKPLTSLG
5 541 LPPDVQRVDA AFNWSKNKKT YIFAGDKFWR YNEVKKKMDP
601 GFPKLIADAW NAIPDNLDAV VDLQGGGHSY FFKGAYYLKL
641 ENQSLKSVKF GSIKSDWLGC

```

A robust pairwise alignment of the cleavage region of nine MMP amino acid sequences was calculated using the program CLUSTAL™ (Higgins et al., 1992). This alignment defined the positions of both conserved and nonconserved amino acids that flanked the activation proteinase cleavage site. An arbitrary number of N-terminal amino acids, as well as the number of amino acids C-terminal to the activation cleavage site were picked for the alignment. The alignment of MMP sequences (Table 1) shown in Figure 1 indicates that all of the MMP activation regions can be aligned in a statistically significant manner. The regions chosen for the alignment roughly correspond to amino acids 70-120, assuming an average MMP structure of signal sequence is amino acids 1-20, the propeptide domain is amino acids 21-100, and the mature active enzyme is from amino acids 101 to the end. The 19-mer (SEQ ID NO:11) sequence that was chosen for study is contained within the alignment region. Specifically, in MMP-2 the 19-mer (SEQ ID NO:11) corresponds to amino acids 100-118.

Alignment of the MMP sequences indicates that the central region of the activation domain, PRCGVDPDV (SEQ ID NO:1), is highly conserved and there is a larger degree of sequence variation flanking this area. The sequence heterogeneity can be used to design peptide sequences that inhibit specific MMP enzymes, or combinations of MMP's, simply by choice of amino acids (based on this alignment). In addition the length of a particular peptide can be varied in order to modulate potency.

The three dimensional structure of proMMP-1 is provided in Figure 2, indicating that the activation regions shown in Table 1 and Figure 1 each constitute a bridge that interconnects two large globular domains. The cleavage region is defined as a short unstructured domain that connects the propeptide domain to the active enzyme domain. This sequence is cleaved in two as part of the activation step. It is also the region that is sensitive to HgCl₂ mediated activation *in vitro*.

Activation removes the steric block (that was the propeptide domain) uncovering the mature enzyme active site. The N-terminal end is in proximity to the catalytic zinc ion, which is generally required for enzymatic activity. The structure of active MMP-9 is shown in Figure 3, with the zinc ions depicted as solid balls. The second zinc is a structural ion, that is, it contributes to protein stability, but not to catalysis. The C-terminal half of the 19-mer (SEQ ID NO:11) peptide is now the enzyme's extreme amino terminus, shown to the left of Figure 3 as an ascending portion of the last loop (crosshatching). Modeling of the activation domain peptide to the surface of the activated MMPs indicates that the peptide (especially if longer N-terminal regions are included) can interact with the active site region, in effect, blocking substrate access to the active site. In that manner it may act as a mini pro-domain or enzymatic "cap."

It is known that enzymes can be proteolyzed into fragments and these fragments can be reconstituted to regenerate active enzyme. The various peptide domains reassemble and are held together by noncovalent intermolecular forces. A classic example of such a peptide-protein interaction involves the ribonuclease S-peptide/ribonuclease S-protein interaction (Levit and Berger, 1976). The ribonuclease S-peptide binds to the S-protein in its proper position and the resulting complex restores the enzymatic activity of RNASE-S.

According to the invention, the activation domain peptides may rebind to the activated MMP in the area where they occur in the proMMP forming an inactive complex. Such binding can be measured (see below). Moreover, the 19-mer (SEQ ID NO:11) peptide may ligand the zinc through its cysteine residue, again preventing catalysis.

Inhibition of MMP enzymatic activity

The first inhibition studies were performed with a 19 amino acid peptide (SEQ ID NO:11) that was derived from the MMP-2 cleavage domain region. This peptide was selected from the area of the CLUSTAL alignment that demonstrated the highest degree of conservation. The selected 19-mer (SEQ ID NO:11) is strictly conserved at the N-terminal, but shows a high degree of variability in the C-terminal portion. Two smaller peptides that represent the N-terminal and C-terminal halves of this peptide were also tested. The two halves roughly divide the peptide into the conserved N-terminal portion (9-mer (SEQ ID NO:12)) and the non conserved C-terminal portion (10-mer (SEQ ID NO:13)). This will allow for testing not only the overall efficacy of inhibition, but selectivity.

19-mer:	PRCGNPDVANYNFFPRKPK	(SEQ ID NO:11)
9-mer:	PRCGNPDVA	(SEQ ID NO:12)
10-mer:	NYNFFPRKPK	(SEQ ID NO:13)

5 All three peptides were capable of inhibiting MMP-9 in either fluorescence based assay. In all cases studied, the 19-mer (SEQ ID NO:11) was a better enzymatic inhibitor than were the two half peptides. The 9-mer (SEQ ID NO:12) was a more effective inhibitor than is the C-terminal 10-mer (SEQ ID NO:13) peptide. These results indicate that the cysteine may be needed because it acts as a zinc ligand or that N-terminal regions are required to
10 effect the steric blocking of the enzyme active site. This hypothesis could be tested by producing inhibitor peptides that contain more N-terminal sequence (meaning amino acids before residue 100). A typical inhibition plot of MMP-9 titrated with the 19-mer (SEQ ID NO:11) is shown in Figure 4.

Similar inhibition analyses performed with the 10-mer (SEQ ID NO:13) and the 9-
15 mer (SEQ ID NO:12) peptides are shown in Figures 5 and 6 respectively. Each peptide is capable of inhibiting MMP-9 in the FRET-based assay, with inhibitor constants (K_i 's) ranging from 45.2 to 327.7 μ M (see Table 4). The choice of substrate (FRET peptide or fluoresceinated collagen) makes little difference in the relative inhibition of the three peptides, with a consistent trend as follows: 19-mer (SEQ ID NO:11) > 9-mer (SEQ ID
20 NO:12) > 10-mer (SEQ ID NO:13). Typical reaction plots for titrating MMP-9 with the peptides are shown in Figures 7-9.

Inhibitor constants were slightly lower overall for the collagen substrate, ranging from 30.3 to 221.3 μ M for collagen and 45.2 to 327.7 μ M for the FRET-peptide. These data indicate that the peptides are somewhat more effective inhibitors when a collagen
25 substrate is utilized, suggesting that the inhibitor peptide blocks the active site and that, because collagen is significantly larger than the FRET-peptide substrate, it is easier to prevent its access to the enzyme active site. The smaller FRET-peptide substrate can more readily gain access the active site, even in the presence of an inhibitor peptide.

The typical enzymatic assay (shown in Figures 4-7) were typically conducted for
30 30-40 minutes. Extended time assays show that the 19-mer (SEQ ID NO:11) effectively inhibits the MMP-9 catalyzed hydrolysis of collagen to beyond 1000 minutes (Figure 8). The 10-mer (SEQ ID NO:13) peptide is less effective at preventing the destruction of collagen at long time points (Figure 9) than is the 9-mer (SEQ ID NO:12) peptide

(Figure 10). Again the 19-mer (SEQ ID NO:11) peptide shows the greatest degree of inhibition.

Similar enzymatic studies were performed on other MMP enzymes to test the effectiveness of the 19-mer (SEQ ID NO:11) peptide. These assays utilized FRET peptides that incorporated specific MMP cleavage sites into their sequence. The 19-mer (SEQ ID NO:11) peptide is capable of potently inhibiting multiple MMP's. The effectiveness of the 19-mer (SEQ ID NO:11) peptide against the various MMPs is as follows: MMP-2 > MMP-3 > MMP-8 > MMP-7 > MMP-9 > MMP-1, with inhibitor constants that range from 3.1 μ M (MMP-2) to 41.1 μ M (MMP-1). These data are summarized in Table 2.

10

Table 4. Summary of inhibitor data

Peptide	Enzyme	Substrate	Ki (μ M)
19-mer (SEQ ID NO:11)	MMP-9	Collagen	30.3
9-mer (SEQ ID NO:12)	MMP-9	Collagen	185.9
10-mer (SEQ ID NO:13)	MMP-9	Collagen	221.3
19-mer (SEQ ID NO:11)	MMP-9	FRET peptide	45.2
9-mer (SEQ ID NO:12)	MMP-9	FRET peptide	232.8
10-mer (SEQ ID NO:13)	MMP-9	FRET peptide	327.7
19-mer (SEQ ID NO:11)	MMP-1	FRET peptide	41.1
19-mer (SEQ ID NO:11)	MMP-2	FRET peptide	3.1
19-mer (SEQ ID NO:11)	MMP-3	FRET peptide	6.4
19-mer (SEQ ID NO:11)	MMP-7	FRET peptide	22.8
19-mer (SEQ ID NO:11)	MMP-8	FRET peptide	12.5

Anti Splicing activity of the 19-mer (SEQ ID NO:11) peptide:

MMPs are biosynthetically produced in an inactive proenzyme form. Proteolytic cleavage of the proenzyme, often by a separate class of membrane bound MMPs, results in MMP activation. The proenzyme leader sequence is approximately 100 amino acids in length (it varies somewhat from MMP to MMP) and is found at the extreme amino terminus of the protein. Inhibition of proenzyme activation may be a fruitful method of lowering the activity of MMP enzymes in chronic wounds. If these enzymes are incapable of functioning, the rate of ECM degradation will be reduced, that in turn may result in faster rates of chronic wound healing.

20

Clearly the activation domain peptides (the 19-mer (SEQ ID NO:11), the 9-mer (SEQ ID NO:12), and the 10-mer (SEQ ID NO:13)) inhibit the enzymatic activity of a variety of MMPs. In addition to this activity, the 19-mer (SEQ ID NO:11) peptide prevents the activation of the pro (inactive) form of MMP-9. Thus the 19-mer (SEQ ID NO:11) peptide can lower the overall level of MMP activity in the skin and within chronic wound exudate by inhibiting already activated MMPs or by preventing the activation of newly synthesized pro-MMPs.

Figure 11 shows a typical splicing assay. The first peak, eluting at approximately 700 seconds, is pro-MMP-9. As the splicing reaction proceeds, this peak decreases in intensity (as marked with the downwards arrow), and two new peaks appear. The first new peak, eluting at approximately 800 seconds, is mature and active MMP-9. The second new peak, eluting at approximately 1050 seconds, is the prodomain. As the splicing reaction proceeds, the intensity of these two peaks increases (as marked with the upwards arrows). When the reaction is complete, there is no detectable pro-MMP-9 remaining. Titrating the standard splicing reaction with the 19-mer (SEQ ID NO:11) peptide prevents the conversion of pro-MMP-9 into the prodomain and the active enzyme. Figure 12 shows the results of this titration. Splicing can be inhibited in a dose dependent manner with micromolar 19-mer (SEQ ID NO:11) peptide.

20 Isothermal Titration Calorimetry

Calorimetry was utilized to determine whether or not the 19-mer (SEQ ID NO:11) peptide formed a stable non-covalent complex with active MMP-9. These data provide an understanding of the mechanism of enzyme inhibition and anti activation properties of the 19-mer (SEQ ID NO:11) peptide. Figure 13 shows an isothermal calorimetry experiment for the interaction between the 19-mer (SEQ ID NO:11) MMP inhibitor and MMP-9. The peptide was dissolved in 20 mM cacodylate (pH 6.8), 20 mM NaCl at a final concentration of 1 mM. MMP-9 was dialyzed into the same buffer at a final concentration of 20 μ M. A series of standard injections were performed as described above. Results for the interaction between MMP-9 and the 19-mer (SEQ ID NO:11) are as follows:

30

Stoichiometry:	0.975 ± 0.02
ΔH (kcal/mol):	-26.1 ± 1.45
ΔS (cal mol ⁻¹ K ⁻¹):	-11.6 ± 2.2

$$K_A (M^{-1}): \quad 1.65 \times 10^6 \pm 4.5 \times 10^4$$

These results indicate that the interaction between the 19-mer (SEQ ID NO:11) peptide and MMP-9 is enthalpically driven, that is ΔH is negative. The reaction is not favored entropically as evidenced by the negative value of ΔS . However, the enthalpic term is larger in magnitude than the term, $T\Delta S$, hence the overall free energy (ΔG) is negative.

The 19-mer (SEQ ID NO:11) reaction with MMP-2 was observed and found to be enthalpically driven and entropically unfavorable. The isothermal calorimetry analysis shown in Figure 14 was produced by titration of the 19-mer (SEQ ID NO:11) with MMP-2. The following values were obtained from these experiments.

Stoichiometry:	0.99 ± 0.03
ΔH (kcal/mol):	-15.4 ± 2.05
ΔS (cal mol ⁻¹ K ⁻¹):	-21.1 ± 1.8
K_A (M ⁻¹):	$2.40 \times 10^6 \pm 3.7 \times 10^4$

Hence, the binding reactions are entropically unfavorable. This presumably arises from the loss of configurational entropy upon binding. Remember that a fully flexible peptide contains a large numbers of degrees of freedom. In all binding cases, the peptide to MMP stoichiometry is 1:1, that indicates that a single 19-mer (SEQ ID NO:11) peptide interacts with a single MMP molecule.

Surface Plasmon Resonance

The binding of the 19-mer (SEQ ID NO:11) to MMP-9 was kinetically studied using the technique of surface plasmon resonance (SPR). A sensor chip was constructed by tethering active MMP-9 to the surface of a BIACore, Inc. CM-5 chip following the standard chemistries that are recommended by the manufacturer. The 19-mer (SEQ ID NO:11) was flowed over the MMP-9 surface in a BIACore-X™ instrument and binding and dissociation were monitored in real time. A typical binding isotherm is shown in Figure 15. The association phase (30- 430 seconds) was best fit to a single binding site model and resulted in an association rate constant (k_a) of $2.2 \times 10^4 M^{-1}s^{-1}$. The dissociation phase (440- 700 seconds) was similarly fit and resulted in a dissociation rate constant (k_d) of $4.1 \times 10^{-3} s^{-1}$. The calculated equilibrium association constant ($K_a = k_a/k_d$) of 5.3×10^6 is in

close agreement with the thermodynamic data. There was an observed bulk transport effect of approximately 100 response units at the start of the dissociation phase that was not modeled. Thus binding of the 19-mer (SEQ ID NO:11) peptide to MMP-9 is both kinetically and thermodynamically favorable.

5

Viability Assays

Unlike many small molecule MMP inhibitors, the three peptides in this study are not toxic to cells when dosed onto the EpiDerm™ skin model. Figure 16 shows that peptide at two concentrations (500 μ M and 2 mM) results in only a slight reduction in viability compared to a PBS control. The total average viability of the peptides is 97.6% (for the 19-mer (SEQ ID NO:11)), 89.6% (for the 10-mer (SEQ ID NO:13)), and 95.8% (for the 9-mer (SEQ ID NO:12)). These results indicate that this peptide therapeutic approach to chronic wound healing is not toxic to mammalian cells. The data plotted in Figure 16 is an average of triplicate samples. The standard deviation for the viability ranged from 2.2 to 3.7 for the study and showed no correlation to dose or peptide identity. Viability was slightly lower at the higher peptide concentrations.

10

15

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These results show that the peptides are not toxic in an EpiDerm™ skin model, that they are kinetically and entropically favored to form binding complexes with MMPs, and that they inhibit enzymatic activity and prevent activation of matrix metalloproteinases.

EXAMPLE 2: Wound Healing by Peptide Inhibitors

Methods

Wounds were created in C57BL6/KsJ db/db mice with a 4 mm biopsy punch. The mice were obtained from The Jackson Laboratories and were aged 3-7 months before the onset of the wounding protocol. All mice were anesthetized prior to wounding. Two wounds were introduced onto the upper back of each animal by pulling the skin away from underlying structures and pushing the punch through the isolated skin. Typically, wounds were created to an average depth of 1.7 mm, with a range of 1.3 to 2.2 mm. No muscle involvement occurred during the course of wounding. Immediately post-wounding the wounds were either treated with normal saline (to serve as the non treated control group) or with 5 μ L of 20 μ g/mL 19-mer peptide (SEQ ID NO:11).

25

30

Each day the wounds were digitally photographed and wound areas were determined by computer integration of the photographs. All wound treatments and the

subsequent data analyses were performed in a blind manner (see e.g., Brown et al., 1994). Wound area at the time of wounding (day 0) is arbitrarily set to a relative value of 1 for all wounds; such that subsequent wound areas are converted to relative wound areas by dividing the wound area at day n by the wound area at day zero.

5

Results:

As can be seen in Figure 17, the application of a single dose of the 19-mer peptide (at the time of wounding, day zero) greatly accelerates the time to full wound closure in the diabetic mouse model. On average wounds treated with the 19-mer peptide closed in 9
10 days post wounding compared to 14 days in the saline treated control. In addition, wounds treated with the 19-mer peptide (SEQ ID NO:11) showed a reduction in wound inflammation at day one post wounding. Also of note is the observation that the 19-mer peptide (SEQ ID NO:11) treated wounds began the contraction process faster than did the saline treated control wounds (day 5 versus day 8).

15

**EXAMPLE 3: Stimulation of Fibroblast Growth
by Peptide Inhibitors**

This Example provides data showing that peptides of the invention stimulate fibroblast proliferation.

20

Materials and Methods

A human skin fibroblast cell line (Clonetics, Walkersville, MD, normal human dermal fibroblasts, neonatal, catalog number CC-2509) was tested to ascertain whether exposure to a peptide of the invention would stimulate cellular proliferation. The
25 proliferative response of the human skin fibroblast cell line to the 19mer peptide (SEQ ID NO:11) was measured in a 96-well assay system using serum-free medium as a control. A stock solution containing 0.5 g/L of the 19-mer peptide (SEQ ID NO:11) was prepared in water and then diluted with serum-free Dulbecco's Modified Eagle's Medium (DMEM, Sigma Chemical Co., St. Louis, MO) to form solutions containing the peptide at 1×10^{-4} M,
30 1×10^{-5} M and 1×10^{-6} M. Cells were seeded into 96 well plates at a concentration of 1×10^3 cells in 100 μ l of DMEM containing 10% fetal bovine serum (FBS, Sigma Chemical Co., St. Louis, MO). Plates were incubated for 24 hours at 37° C in a humidified 5% CO₂ atmosphere. After incubation, the medium was aspirated and the wells were rinsed twice

with 100 μ l of serum-free DMEM. The final rinse was aspirated and 100 μ l of the 1×10^{-4} M, 1×10^{-5} M or 1×10^{-6} M solutions of the 19-mer (SEQ ID NO:11) were added to 20 wells. In addition, 100 μ l of vehicle (serum-free DMEM) was added to 10 wells as control. All wells were incubated for 28 hours at 37°C in a humidified, 5% CO₂ atmosphere. After
5 incubation, 20 μ l of Cell Titer 96 Aqueous One Solution was added to all wells. The plates were swirled gently and placed back in the incubator for 45 minutes and spectrophotometric absorbance was read at 490 nm. Results were analyzed statistically using one-way ANOVA.

10 **Results:**

As can be seen in Figure 18, the addition of the 19-mer peptide (SEQ ID NO:11) leads to increased growth of fibroblasts in a dose-dependent manner. The control, with no added 19-mer peptide, had the lowest cellular density. Cells receiving as little as 1×10^{-5} M of the 19-mer (SEQ ID NO:11, labeled 19mer5 in Fig. 18), exhibited significantly
15 greater cell density ($P > 0.01$) than cells received no 19-mer peptide. Cells receiving 1×10^{-4} M of the 19-mer (labeled "19mer4" in Figure 18) exhibited even greater cell growth ($P > 0.001$). However, cells receiving 1×10^{-6} M of the 19-mer (labeled "19mer6" in Figure 18) exhibited a small amount of cell proliferation ($P < 0.05$) that was found to be statistically not very significant.

20 A statistically significant difference in cell growth was therefore observed between the control cells and cells treated with the 19-mer peptide (SEQ ID NO:11). Based on these statistically significant differences, the 19-mer peptide (SEQ ID NO:11) appears to be a good cell proliferating agent for fibroblasts.

25 **EXAMPLE 4: Stimulation of Keratinocyte Growth by Peptide Inhibitors**

This Example provides data showing that peptides of the invention stimulate keratinocyte proliferation.

30 **Materials and Methods**

A human skin keratinocyte cell line from Clonetics (Walkersville, MD, normal human epidermal keratinocytes, neonatal, catalog number cc-2503) was exposed to the 19-mer (SEQ ID NO:11) to ascertain whether this peptide could stimulate proliferation of

keratinocytes. The proliferative response of these human skin keratinocytes to the 19-mer peptide (SEQ ID NO:11) was measured in a 96-well assay system using keratinocyte basal medium (KBM, Clonetics, catalog number CC-3103) as a control. A stock solution containing 0.5 g/L of the 19-mer peptide was prepared in water and then diluted with KBM to form solutions containing the peptide at 1×10^{-4} M, 1×10^{-5} M and 1×10^{-6} M. Cells were seeded into a 96 well plate at a concentration of 2.5×10^3 cells in 100 μ l of KBM. The plates were incubated for 24 hours at 37° C in a humidified 5% CO₂ atmosphere. After incubation, 100 μ l of the 1×10^{-4} M, 1×10^{-5} M or 1×10^{-6} M solutions of the 19-mer (SEQ ID NO:11) were added to 10 wells each. In addition, 100 μ l of vehicle KBM was added to 10 wells as control. The plate was incubated for 48 hours at 37°C in a humidified, 5% CO₂ atmosphere. After incubation, 20 μ l of Cell Titer 96 Aqueous One Solution was added to all wells. The plate was swirled gently and placed back in the incubator for 3 hours. The spectrophotometric absorbance of each well was read at 490 nm. Results were analyzed statistically using one-way ANOVA.

15

Results

As can be seen in Figure 19, the addition of the 19-mer peptide (SEQ ID NO:11) leads to increased growth of keratinocytes in a dose-dependent manner. Control cells with no added 19-mer peptide had the lowest cellular density. Cells receiving as little as 1×10^{-5} M of the 19-mer (SEQ ID NO:11, labeled 19mer5 in Fig. 19), exhibited significantly greater cell density ($P > 0.01$) than cells received no 19-mer peptide. Cells receiving 1×10^{-4} M of the 19-mer (labeled "19mer4" in Figure 19) exhibited even greater cell growth ($P > 0.001$). However, cells receiving 1×10^{-6} M of the 19-mer (labeled "19mer6" in Figure 19) exhibited only a small amount of cell proliferation ($P > 0.05$) that was found to be statistically non-significant.

25

A statistically significant difference was therefore observed between the control cells and keratinocyte cells treated with the 19-mer peptide (SEQ ID NO:11). Therefore, the 19-mer peptide (SEQ ID NO:11) appears to be a good proliferating agent for keratinocytes.

30

EXAMPLE 5: Peptide Inhibitors Stimulate Fibroblast Migration

This Example provides data illustrating that peptides of the invention can stimulate fibroblast migration.

5 **Materials and Methods**

Normal, human dermal fibroblasts (NHDF) were obtained from Biowhittaker, (Walkersville, MD) and propagated in T75 flasks in FBM media (500 mL, Biowhittaker) containing insulin, hFGF-b, GA-1000, and fetal bovine serum (10 mL) for up to 12 passages. For the migration assay, NHDF were washed once with 10 mL of Hank's
10 buffered saline solution (HBSS). Three milliliters of trypsin (0.25%) in EDTA were added to the T75 flask for no more than five minutes to remove NHDF from the flask. NHDF in trypsin solution were added to 7 mL of FBM with no supplements added. NHDF were centrifuged for 5 minutes, and the supernatant was removed. NHDF were resuspended in
15 10 mL of FBM for counting. NHDF were centrifuged for another 5 minutes, and the supernatant was removed. NHDF were resuspended at 1×10^6 cells per mL in FBM without supplements. It was important to use FBM media only in migration assays because the complete media contains fibroblast growth factor and serum, both of which will trigger migration of fibroblasts.

Peptides were synthesized and purified by the Microchemical Facility at Emory
20 University or by SigmaGenesis. All peptides were analyzed by mass spectrometry after HPLC to assess purity. Approximately 0.5-2.0 milligrams of peptide were used to make fresh stock solutions (5 mg/mL in PBS) for each migration assay. The peptide stock solutions in PBS were used to make more dilute solutions (1 mg/mL, 100 μ g/mL, 10
25 μ g/mL, 1 μ g/mL, 100 ng/mL, 10 ng/mL) in FBM (without supplements) for the migration assays.

Polyvinylpyrrolidone-free polycarbonate membranes with 8 mm pores (Neuroprobe, Inc., Gaithersburg, MD) were washed with 90% ethanol for 15 minutes and rinsed four times with deionized water. Membranes were then placed into a glass dish containing an aqueous solution of 5 μ g/mL gelatin. The glass dish was placed in to a water
30 bath at about 90 °C for one hour. Membranes were removed from the gelatin solution and were allowed to dry for one hour in the 37 °C incubator.

A 48-well chemotaxis chamber (Neuroprobe, Inc., Gaithersburg, MD) (see Figure 20) was used for the migration assays. Twenty-eight μ L of each test solution were added to

the bottom wells of the chamber in quadruplicate. A gelatin-treated membrane was placed carefully on top of the bottom wells. The gasket and top part of chamber were then placed carefully on top of the membrane. The apparatus was tightened using six thumbscrews. A solution of NHDF containing an estimated cell density (2×10^5 cells per mL) was made by adding 320 μL of the 1×10^6 cells per mL solution to 1.28 mL of FBM (no supplements). Fifty microliters of the 2×10^5 cells per mL NHDF solution were added to the top part of each well in the chamber. The chamber was placed in the incubator at $37^\circ\text{C}/5\% \text{CO}_2$ for three hours. The chamber was removed, the thumbscrews were removed, and the chamber was turned upside down on a paper towel. The bottom part of the chamber was removed, revealing the membrane with the NHDF that migrated through the membrane facing up. The membrane was carefully removed. The cells that did not migrate through the membrane were scraped off the membrane by moistening one side of the membrane with PBS and using a cell scraper (Neuroprobe, Inc.). The membrane was fixed with methanol and stained using the Diff-Quik Staining Solutions I and II. The nuclei of NHDF are stained purple. The membrane was mounted on a glass slide using cedarwood immersion oil and a cover slip. Cells on three separate fields on each of three areas corresponding to different chambers were counted using a Zeiss light microscope (25X objective x 10X eyepiece x 1.25X). The average number of migrated NHDF in the negative control was subtracted from the experimental (peptide) data and positive control data. The data is then expressed in terms of percent of migrated NHDF compared to the plasma fibronectin positive control ($1.25 \mu\text{g}/\text{mL}$), which is defined below.

$$\text{Percent NDHF migration} = \frac{\text{avg. \# of NHDF per field} - \text{avg. \# of NHDF per field (neg control)}}{\text{avg. \# of NHDF per field (pos control)} - \text{avg. \# of NHDF per field (neg control)}} \times 100\%$$

Results

The membrane used for fibroblast (NHDF) migration had $8 \mu\text{m}$ pores as shown in Figure 21A (top). The chemoattractant solution signals for the migration of fibroblasts through the membrane. Once fibroblasts move through the membrane, they adhere to the membrane on the chemoattractant side. As shown in Figure 21B (bottom), the nuclei of the fibroblasts are stained purple for visual counting. Cells that are trapped inside the pore (pore appears to have a dark purple color) were included in the total cell count. The migration of NHDF due to the positive control resulted in cell counts that ranged from 27

to 60 NHDF per field. The positive control that was used in the NHDF migration assays was plasma fibronectin (1.25 $\mu\text{g}/\text{mL}$ dissolved in FBM media). Fibronectin is a molecule that helps to make up the ECM during wound repair. Fibronectin, which binds to the $\alpha_4\beta_1$ integrin receptor of fibroblasts, is chemotactic in a very narrow concentration range (0.8-
5 1.6 $\mu\text{g}/\text{mL}$). Postlethwaite, A.E.; Kang, A.H. "Fibroblast Chemoattractants" in Methods of Enzymology, vol. 163, Academic Press: New York, 1988, pp. 694-707. The negative control (FBM media without supplements) cell counts were between 1 to 7 NHDF per field (<10% of the positive control) (see Figure 22).

Several concentrations of 19-mer peptide were used in the NHDF migration assay.
10 Because of the narrow concentration range in which plasma fibronectin is chemotactic to NHDF, 10-fold dilutions of peptide were used so a large range of concentrations could be examined. As shown in Figure 23, a significant number of NHDF had migrated through the membrane at concentrations of 19-mer above 0.1 mg/mL ($55\% \pm 3\%$ and $46\% \pm 3\%$ for 1000 $\mu\text{g}/\text{mL}$ and 100 $\mu\text{g}/\text{mL}$, respectively). Concentrations of 19-mer below 100 $\mu\text{g}/\text{mL}$
15 were only slightly chemotactic. Because these concentrations of 19-mer induced about 20% NHDF migration, which was only approximately two times the NHDF migration of the negative control, these data were not considered significant. There was no difference in the migration induced by 19-mer stocks made from two different commercial sources (data not shown).

20 Different variations of the 19-mer sequence were synthesized and purified to determine whether amino acid sequence alterations influenced fibroblast migration. The following peptides were tested: the 9-mer PRCGNPDVA (SEQ ID NO:12), the 10-mer NYNFFPRKPK (SEQ ID NO:13), the 14-mer TMRKPRCGNPDVAN (SEQ ID NO:19), and the 17-mer TLKAMRKPRCGNPDVAN (SEQ ID NO:20). The 14-mer and 17-mer
25 peptide sequences are based upon the sequence further toward the N-terminus of MMP-2 and MMP-9, respectively. The 9-mer (SEQ ID NO:12) and 10-mer (SEQ ID NO:13) peptides inhibit MMP activity. The 19-mer (SEQ ID NO:11) peptide was also synthesized with protective acetyl and amide groups (Ac-19-mer) at the N and C termini, respectively, to determine if the addition of these groups would change the effect on fibroblast
30 migration. The Ac-19-mer was chemotactic for fibroblasts both at 100 ($44 \pm 3\%$) and 1000 ($40 \pm 6\%$) $\mu\text{g}/\text{mL}$ as shown in Figure 23. The 10-mer (SEQ ID NO:13) peptide was chemotactic at 1000 $\mu\text{g}/\text{mL}$ ($30 \pm 2\%$) but not at 100 $\mu\text{g}/\text{mL}$ ($11 \pm 0\%$, on the order of the negative control as shown in Figure 22). The 9-mer (SEQ ID NO:12) was chemotactic at

1000 $\mu\text{g/mL}$ ($32 \pm 2\%$) but not at 100 $\mu\text{g/mL}$ ($16 \pm 0\%$). Interestingly, the addition of amino acids to the N-terminus of the 9-mer resulted in the absence of NHDF migration. The 14-mer TMRKPRCGNPDVAN (SEQ ID NO:19) and the 17-mer TLKAMRKPRCGNPDVAN (SEQ ID NO:20) did not induce NHDF migration at
5 concentrations ranging from 1000 $\mu\text{g/mL}$ to 10 ng/mL (data not shown). Because of the large variation in NHDF migration between the different peptides, the amino acid sequence may be important to the activation of NHDF to migrate.

The migration of fibroblasts to a wound site is crucial for proper healing. The chemotactic properties of the 19-mer peptide ($\geq 100 \mu\text{g/mL}$) and the Ac-19-mer, 9-mer, and
10 10-mer derivatives have been demonstrated using the NHDF migration assay. Because the 9-mer and 10-mer both induce NHDF migration to approximately the same extent, it is difficult to assess whether particular amino acids are crucial to activation. Interestingly, the 14-mer TMRKPRCGNPDVAN (SEQ ID NO:19) and the 17-mer TLKAMRKPRCGNPDVAN (SEQ ID NO:20) have no effect on fibroblast mobility.
15 While the exact mechanism of the 19-mer chemoattraction is unknown, the amino acid sequence of the peptide is important to the activation of fibroblasts.

EXAMPLE 6: Peptide Inhibitors Do Not Stimulate Neutrophil Migration

This Example provides data illustrating that a peptide of the invention does not
20 stimulate neutrophil migration.

Materials and Methods

Peptides were synthesized and purified by the Microchemical Facility at Emory University or by SigmaGenesis. All peptides were analyzed by mass spectrometry after
25 HPLC to assess purity. Approximately 0.5-2.0 milligrams of peptide were used to make fresh stock solutions (5 mg/mL in HBSS/HSA) for each migration assay. The peptide stock solutions were used to make more dilute solutions (1 mg/mL , 100 $\mu\text{g/mL}$, 10 $\mu\text{g/mL}$, 1 $\mu\text{g/mL}$, 100 ng/mL , and 10 ng/mL) in HBSS/HSA for the assays.

Neutrophils were isolated from human blood (collected in Vacutainer™ tubes
30 containing EDTA) by layering the blood/EDTA mixture (about 20 mL) on top of two layers of Histopaque™ 1119 (bottom layer, 18 mL) and 1077 (top layer, 7 mL) in 50 mL Falcon tubes. The tubes were centrifuged at 1800 rpm for 30 minutes (no brake). Four layers appeared in the tubes after the spin (from top to bottom layers): plasma, 1077, 1119,

and red blood cells. The buffy coat between the plasma and 1077 layers contained lymphocytes, monocytes, and some platelets. The plasma layer, the buffy coat, and most of the 1077 layer was removed and discarded. The 1119 layer that contained the neutrophils was removed and was placed into a clean 50 mL tube. Dulbecco's Phosphate Buffered Saline (DPBS) was added to bring the volume to 50 mL. The cells were centrifuged for 15 minutes at 2100 rpm. The cells were resuspended in 10 mL of DPBS, transferred to 15 mL tubes, and centrifuged again for 10 minutes at 2000 rpm. This process was repeated to wash the cells a second time. After the supernatant was removed, the red blood cells were lysed by adding 6 mL of cold sterile water to each 15 mL of supernatant. Cells were mixed in the water for only 30 seconds. Six mL of cold 2% sterile saline was then added. Cells were centrifuged again for 10 minutes at 2000 rpm. The red supernatant (containing hemoglobin from red blood cells) was removed. This process of red blood cell lysis was repeated two more times to remove all of the red blood cells. After most of the red blood cells were removed, neutrophils were resuspended in 10 mL of HBSS/HSA for counting with trypan blue. Cells were centrifuged and resuspended in HBSS/HSA at a concentration of 1.25×10^6 cells/mL.

A neutrophil migration assay was performed in duplicate using a 24-well transwell plate (3 μ m pore size for membrane). Transwell membranes were pre-moistened with 20-40 μ L of HBSS/HSA (0.04-0.4%). Chemotactic solutions (500 μ L) were added to the bottom of each well. Neutrophils (200 μ L of 1.25×10^6 cells/mL solution) were added to the membranes on the transwell. Transwells were then placed into the chemotactic solutions. The plate was placed into the incubator (37 °C, 5% CO₂) for one hour. Cells that migrated through the membrane were counted using trypan blue.

25 Results

In the neutrophil migration experiments, neutrophils that were isolated were approximately 95% viable. Neutrophils were resuspended in HBSS/0.4%HSA for this experiment. IL-8 (10 nM in the HBSS/0.4%HSA buffer) was used as a positive control for neutrophil migration. Concentrations of 19-mer used were 1 mg/mL, 100, 10, and 1 μ g/mL.

The second column in Table 5 describes the results from the first experiment. The negative and positive controls were HBSS/HSA and IL-8, respectively.

Table 5. Percent neutrophil migration of each chemotactic substrate.

Chemotactic Substrate	Percent Neutrophil Migration exp.1	Percent Neutrophil Migration exp. 2
HBSS/HSA*	29%	0%
10 nM IL-8	81%	51%
1 mg/mL 19-mer	23%	4%
100 µg/mL 19-mer	29%	0%
10 µg/mL 19-mer	22%	-
1 µg/mL 19-mer	32%	-

* HSA concentration was 0.4% for exp.1 and 0.04% for exp. 2.

5

The 19-mer peptide (SEQ ID NO:11) induced a similar neutrophil migration as the negative control. The addition of IL-8 resulted in 81% of the added neutrophils migrating through the membrane. While the positive control appeared to work well, the negative control (29%) seemed to be quite high. Therefore in the second experiment, the amount of HSA was decreased ten-fold to 0.04%. As shown in the third column of Table 5, the negative control had dropped dramatically to 0% neutrophil migration. The IL-8 positive control also dropped but still showed a large amount of neutrophil migration (51%). As in the first experiment, the 19-mer did not have an effect on neutrophil migration.

The migration of fibroblasts to a wound site is crucial for proper healing. The chemotactic properties of the 19-mer peptide (SEQ ID NO:11) have been demonstrated using the NHDF migration assay. However, the 19-mer appeared to have no effect on migration of neutrophils. Perhaps there is a receptor that is inherent to fibroblasts and not to neutrophils that is involved with 19-mer recognition, binding, and chemotactic signaling.

EXAMPLE 7: Stimulation of Collagen Production

The stimulation response of the 19mer peptide (SEQ ID NO:11) on collagen production in the human skin fibroblast cell line (Clonetics, Walkersville, MD, normal human dermal fibroblasts, neonatal, catalog number CC-2509) was measured using Takara Biomedicals EIA assay kit (TAK MK101) sold by Panvera (Madison, WI). The cells were first grown in a 96-well assay system using Dulbecco's Modified Eagle's Medium (DMEM) with 10% fetal bovine serum (FBS) both purchased from Sigma Chemical Co, St. Louis, MO. Serum-free DMEM was used as a control. A stock solution containing 0.5 g/L of the 19-mer peptide (SEQ ID NO:11) was prepared in water and then diluted with serum-free DMEM to form solutions containing the peptide at 1×10^{-5} M and 1×10^{-6} M. Cells were seeded into 96 well plates at a concentration of 5×10^3 cells in 100 μ l of DMEM containing 10% fetal bovine serum (FBS, Sigma Chemical Co., St. Louis, MO). Plates were incubated for 24 hours at 37° C in a humidified 5% CO₂ atmosphere. After incubation, the medium was aspirated and the wells were rinsed twice with 100 μ l of serum-free DMEM. The final rinse was aspirated and 100 μ l of the 1×10^{-5} M or 1×10^{-6} M solutions of the 19-mer (SEQ ID NO:11) were added to the wells (n=2 for each concentration). In addition, 100 μ l of vehicle (serum-free DMEM) was added to 4 wells as control. All wells were incubated for 48 hours at 37°C in a humidified, 5% CO₂ atmosphere.

The assay was performed using the recommended 20ul of the supernatant from each well of the 96-well plate. Standard buffer and stop solutions were freshly prepared before running the assay. 100ul of antibody-POD conjugate solution (supplied with the kit) was added into the wells using pre antibody coated 96 well plate (supplied with the kit). 20ul of standard and test solutions (from the other 96-well plate containing fibroblasts) were added to appropriate wells. Plate was mixed gently, sealed and incubated for three hrs. at 37°C.

After incubation each well was washed carefully four times with PBS buffer (400ul). All the wells were completely emptied at the end of washing from any liquid. 100ul of substrate solution (hydrogen peroxide and tetramethylbenzidine in a buffer solution, supplied with the kit) was added to each well and the plate was incubated for 15 minutes. At this point 100ul of stop solution (freshly prepared 1N H₂SO₄) was added to each well in the same order as substrate. The plate was gently mixed and absorbance was read at 450nm. Results were analyzed statistically using one-way ANOVA.

Results:

As can be seen in Figure 24 and Table 6, the addition of the 19-mer peptide (SEQ ID NO:11) leads to increased collagen production at both concentrations employed. Control cells with no added 19-mer peptide (SEQ ID NO:11) had the lowest amount of collagen. At concentrations of 10^{-5} and 10^{-6} M, 19mer peptide (SEQ ID NO:11) produced statistically significant amounts ($P < 0.001$) of collagen. These results indicate that the 19-mer peptide (SEQ ID NO:11) stimulates collagen production.

Table 6: Summary of Data

10

Group	Number of Points	Mean	Standard Derivation	Standard Error of the Mean	Median
19mer5	2	0.8365	0.02051	0.01450	0.8365
19mer6	2	0.8315	0.01202	0.008500	0.8315
Control	4	0.7388	0.01431	0.007157	0.7330

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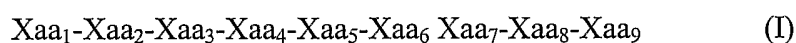
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WHAT IS CLAIMED:

1. A peptide comprising SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:16, or SEQ ID NO:17, wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes.
2. The peptide of claim 1 wherein the peptide is a chemoattractant for fibroblasts or keratinocytes.
3. The peptide of claim 1 wherein the peptide can stimulate collagen production in fibroblasts.
4. A composition comprising a therapeutically effective amount of peptide of formula I and a pharmaceutically acceptable carrier:



wherein:

- Xaa₁, Xaa₄, and Xaa₆ are separately each apolar amino acids;
 Xaa₂ is a basic amino acid;
 Xaa₃ is a cysteine-like amino acid;
 Xaa₅ is a polar or aliphatic amino acid;
 Xaa₇ is an acidic amino acid;
 Xaa₈ is an aliphatic or polar amino acid;
 Xaa₉ is an aliphatic, apolar or basic amino acid; and

wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes.

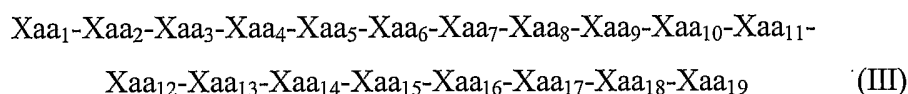
5. A composition comprising a therapeutically effective amount of peptide of formula II and a pharmaceutically acceptable carrier:



wherein:

- Xaa₁₀ is a polar, acidic, basic or apolar amino acid;
 Xaa₁₁ is a polar or aromatic amino acid;
 Xaa₁₂ is a polar, basic, aliphatic or apolar amino acid;
 5 Xaa₁₃ is an aromatic, aliphatic, polar or acidic amino acid;
 Xaa₁₄ is an aromatic, apolar or polar amino acid;
 Xaa₁₅ is an apolar or acidic amino acid;
 Xaa₁₆ is a basic, a polar or an apolar amino acid;
 Xaa₁₇ is a basic, a polar, an aliphatic, an apolar or an acidic amino acid;
 10 Xaa₁₈ is an apolar or an aliphatic amino acid;
 Xaa₁₉ is a basic or an aliphatic amino acid; and
- wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes.

- 15 6. A composition comprising a therapeutically effective amount of peptide of formula III and a pharmaceutically acceptable carrier:



wherein

- 20 Xaa₁, Xaa₄, and Xaa₆ are separately each apolar amino acids;
 Xaa₂ is a basic amino acid;
 Xaa₃ is a cysteine-like amino acid;
 Xaa₅ is a polar or aliphatic amino acid;
 Xaa₇ is an acidic amino acid;
 25 Xaa₈ is an aliphatic or polar amino acid;
 Xaa₉ is an aliphatic, apolar or basic amino acid;
 Xaa₁₀ is a polar, acidic, basic or apolar amino acid;
 Xaa₁₁ is a polar or aromatic amino acid;
 Xaa₁₂ is a polar, basic, aliphatic or apolar amino acid;
 30 Xaa₁₃ is an aromatic, aliphatic, polar or acidic amino acid;
 Xaa₁₄ is an aromatic, apolar or polar amino acid;
 Xaa₁₅ is an apolar or acidic amino acid;
 Xaa₁₆ is a basic, a polar or an apolar amino acid;

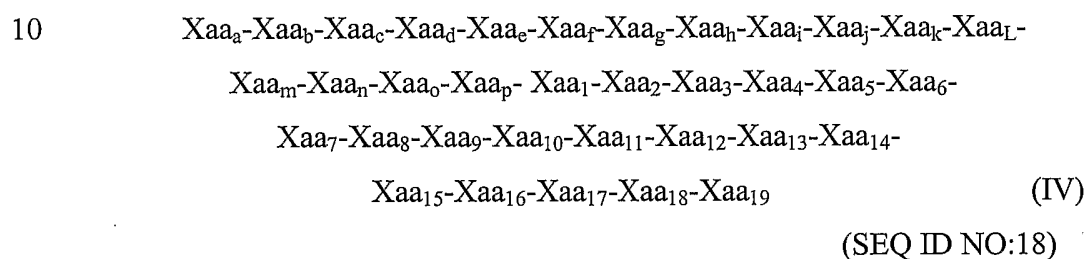
Xaa₁₇ is a basic, a polar, an aliphatic, an apolar or an acidic amino acid;

Xaa₁₈ is an apolar or an aliphatic amino acid;

Xaa₁₉ is a basic or an aliphatic amino acid; and

wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate
5 cellular proliferation of fibroblasts or keratinocytes.

7. A composition that comprises a therapeutically effective amount of peptide of formula IV and a pharmaceutically acceptable carrier:



15

- | | |
|--|--|
| Xaa _a is proline; | Xaa ₁ is proline; |
| Xaa _b is glutamine or glutamic acid; | Xaa ₂ is arginine; |
| Xaa _c is threonine; | Xaa ₃ is cysteine; |
| Xaa _d is glycine; | Xaa ₄ is glycine; |
| 20 Xaa _e is aspartic acid or glutamic acid; | Xaa ₅ is valine or asparagine; |
| Xaa _f is leucine; | Xaa ₆ is proline; |
| Xaa _g is aspartic acid; | Xaa ₇ is aspartic acid; |
| Xaa _h is glutamine or serine; | Xaa ₈ is valine or leucine; |
| Xaa _i is asparagine or alanine; | Xaa ₉ is alanine or glycine; |
| 25 Xaa _j is threonine; | Xaa ₁₀ is asparagine or arginine; |
| Xaa _k is isoleucine or leucine; | Xaa ₁₁ is tyrosine or phenylalanine; |
| Xaa _l is glutamic acid or lysine; | Xaa ₁₂ is asparagine or glutamine; |
| Xaa _m is threonine or alanine; | Xaa ₁₃ is phenylalanine or threonine; |
| Xaa _n is methionine; | Xaa ₁₄ is phenylalanine; |
| 30 Xaa _o is arginine; | Xaa ₁₅ is proline or glutamic acid; |
| Xaa _p is lysine or threonine; | Xaa ₁₆ is arginine or glycine; |
| Xaa ₁₇ is lysine or aspartic acid; | Xaa ₁₈ is proline or leucine; |
| Xaa ₁₉ is lysine; and | |

wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes.

8. The composition of any one of claims 4-7, wherein an apolar amino acid is methionine, glycine or proline.
9. The composition of any one of claims 4-7, wherein a basic amino acid is histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, ρ -aminophenylalanine, and 2,4-diaminobutyric acid.
10. The composition of any one of claims 4-7, wherein a cysteine-like amino acid is cysteine, homocysteine, penicillamine, or β -methyl cysteine.
11. The composition of any one of claims 4-7, wherein an aliphatic amino acid is alanine, valine, leucine, isoleucine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, β -alanine, N-methylglycine, or α -aminoisobutyric acid.
12. The composition of any one of claims 4-7, wherein an acidic amino acid is aspartic acid or glutamic acid.
13. The composition of any one of claims 4-7, wherein a polar amino acid is asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or an apolar amino acid such as methionine, glycine or proline.
14. The composition of any one of claims 4-7, wherein an aromatic amino acid is phenylalanine, tyrosine, tryptophan, phenylglycine, naphthylalanine, β -2-thienylalanine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, pyridylalanine, or 3-benzothieryl alanine.
15. The composition of any one of claims 4-7, wherein the peptide can also inhibit proteinase activity of any one of matrix metalloproteinase-1, matrix metalloproteinase-3,

matrix metalloproteinase-4, matrix metalloproteinase-5, matrix metalloproteinase-6, matrix metalloproteinase-7, matrix metalloproteinase-8, and matrix metalloproteinase-9, matrix metalloproteinase-10, matrix metalloproteinase-11, matrix metalloproteinase-12, or matrix metalloproteinase-13.

5

16. The composition of any one of claims 4-7, wherein the peptide is a chemoattractant for fibroblasts or keratinocytes.

17. The composition of any one of claims 4-7, wherein the peptide can stimulate
10 collagen production in fibroblasts.

18. A composition that comprises a therapeutically effective amount of peptide that comprises SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID
15 NO:11, SEQ ID NO:12, or SEQ ID NO:13, and a pharmaceutically acceptable carrier.

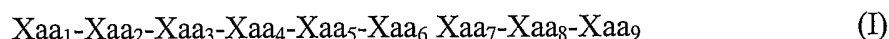
19. The composition of claim 18 wherein the peptide can inhibit proteinase activity of any one of matrix metalloproteinase-1, matrix metalloproteinase-2, matrix metalloproteinase-3, matrix metalloproteinase-4, matrix metalloproteinase-4, matrix
20 metalloproteinase-5, matrix metalloproteinase-6, matrix metalloproteinase-7, matrix metalloproteinase-8, and matrix metalloproteinase-9, matrix metalloproteinase-10, matrix metalloproteinase-11, matrix metalloproteinase-12, or matrix metalloproteinase.

20. The composition of claim 18 wherein the peptide can stimulate cellular growth of
25 fibroblasts or keratinocytes.

21. The composition of claim 18, wherein the peptide is a chemoattractant for fibroblasts or keratinocytes.

30 22. The composition of claim 18, wherein the peptide can stimulate collagen production in fibroblasts.

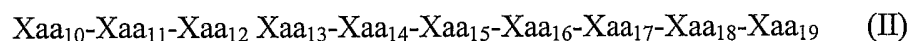
23. A wound dressing that comprises a peptide of the formula I:



wherein:

- 5 Xaa₁, Xaa₄, and Xaa₆ are separately each apolar amino acids;
 Xaa₂ is a basic amino acid;
 Xaa₃ is a cysteine-like amino acid;
 Xaa₅ is a polar or aliphatic amino acid;
 Xaa₇ is an acidic amino acid;
 Xaa₈ is an aliphatic or polar amino acid;
 10 Xaa₉ is an aliphatic, apolar or basic amino acid; and
- wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes.

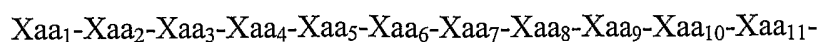
24. A wound dressing that comprises a peptide of the formula II:
 15

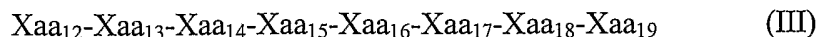


wherein:

- 20 Xaa₁₀ is a polar, acidic, basic or apolar amino acid;
 Xaa₁₁ is a polar or aromatic amino acid;
 Xaa₁₂ is a polar, basic, aliphatic or apolar amino acid;
 Xaa₁₃ is an aromatic, aliphatic, polar or acidic amino acid;
 Xaa₁₄ is an aromatic, apolar or polar amino acid;
 Xaa₁₅ is an apolar or acidic amino acid;
 25 Xaa₁₆ is a basic, a polar or an apolar amino acid;
 Xaa₁₇ is a basic, a polar, an aliphatic, an apolar or an acidic amino acid;
 Xaa₁₈ is an apolar or an aliphatic amino acid;
 Xaa₁₉ is a basic or an aliphatic amino acid; and
- wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate
 30 cellular proliferation of fibroblasts or keratinocytes.

25. A wound dressing that comprises a peptide of formula III:

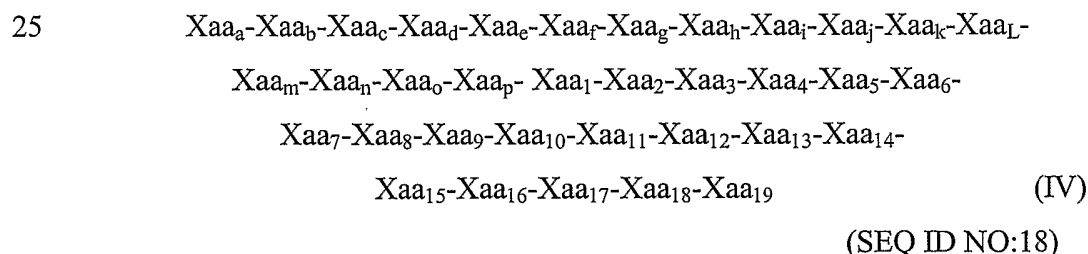




wherein:

- Xaa₁, Xaa₄, and Xaa₆ are separately each apolar amino acids;
 Xaa₂ is a basic amino acid;
 5 Xaa₃ is a cysteine-like amino acid;
 Xaa₅ is a polar or aliphatic amino acid;
 Xaa₇ is an acidic amino acid;
 Xaa₈ is an aliphatic or polar amino acid;
 Xaa₉ is an aliphatic, apolar or basic amino acid;
 10 Xaa₁₀ is a polar, acidic, basic or apolar amino acid;
 Xaa₁₁ is a polar or aromatic amino acid;
 Xaa₁₂ is a polar, basic, aliphatic or apolar amino acid;
 Xaa₁₃ is an aromatic, aliphatic, polar or acidic amino acid;
 Xaa₁₄ is an aromatic, apolar or polar amino acid;
 15 Xaa₁₅ is an apolar or acidic amino acid;
 Xaa₁₆ is a basic, a polar or an apolar amino acid;
 Xaa₁₇ is a basic, a polar, an aliphatic, an apolar or an acidic amino acid;
 Xaa₁₈ is an apolar or an aliphatic amino acid;
 Xaa₁₉ is a basic or an aliphatic amino acid; and
 20 wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes.

26. A wound dressing that comprises a peptide of formula IV:



30

wherein:

- Xaa_a is proline; Xaa₁ is proline;
 Xaa_b is glutamine or glutamic acid; Xaa₂ is arginine;

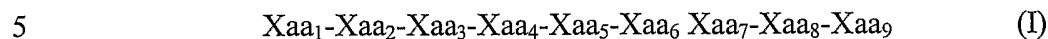
- | | | |
|----|---|--|
| | Xaa _c is threonine; | Xaa ₃ is cysteine; |
| | Xaa _d is glycine; | Xaa ₄ is glycine; |
| | Xaa _e is aspartic acid or glutamic acid; | Xaa ₅ is valine or asparagine; |
| | Xaa _f is leucine; | Xaa ₆ is proline; |
| 5 | Xaa _g is aspartic acid; | Xaa ₇ is aspartic acid; |
| | Xaa _h is glutamine or serine; | Xaa ₈ is valine or leucine; |
| | Xaa _i is asparagine or alanine; | Xaa ₉ is alanine or glycine; |
| | Xaa _j is threonine; | Xaa ₁₀ is asparagine or arginine; |
| | Xaa _k is isoleucine or leucine; | Xaa ₁₁ is tyrosine or phenylalanine; |
| 10 | Xaa _L is glutamic acid or lysine; | Xaa ₁₂ is asparagine or glutamine; |
| | Xaa _m is threonine or alanine; | Xaa ₁₃ is phenylalanine or threonine; |
| | Xaa _n is methionine; | Xaa ₁₄ is phenylalanine; |
| | Xaa _o is arginine; | Xaa ₁₅ is proline or glutamic acid; |
| | Xaa _p is lysine or threonine; | Xaa ₁₆ is arginine or glycine; |
| 15 | Xaa ₁₇ is lysine or aspartic acid; | Xaa ₁₈ is proline or leucine; |
| | Xaa ₁₉ is lysine; and | |

wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes.

- 20 27. The wound dressing of any one of claims 23-26, wherein an apolar amino acid is methionine, glycine or proline.
28. The wound dressing of any one of claims 23-26, wherein a basic amino acid is histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, ρ -aminophenylalanine, and 2,4-diaminobutyric acid.
- 25
29. The wound dressing of any one of claims 23-26, wherein a cysteine-like amino acid is cysteine, homocysteine, penicillamine, or β -methyl cysteine.
- 30 30. The wound dressing of any one of claims 23-26, wherein an aliphatic amino acid is alanine, valine, leucine, isoleucine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, β -alanine, N-methylglycine, or α -aminoisobutyric acid.

31. The wound dressing of any one of claims 23-26, wherein an acidic amino acid is aspartic acid or glutamic acid.
- 5 32. The wound dressing of any one of claims 23-26, wherein a polar amino acid is asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or an apolar amino acid such as methionine, glycine or proline.
- 10 33. The wound dressing of any one of claims 23-26, wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes., wherein an aromatic amino acid is phenylalanine, tyrosine, tryptophan, phenylglycine, naphthylalanine, β -2-thienylalanine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, pyridylalanine, or 3-benzothienyl alanine.
- 15 34. A wound dressing that comprises a peptide comprising SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, or SEQ ID NO:13, wherein the peptide can inhibit a matrix metalloproteinase or the peptide can
- 20 stimulate cellular proliferation of fibroblasts or keratinocytes.
35. The wound dressing of any one of claims 23-26 or 34, wherein the peptide can stimulate cellular growth of fibroblasts or keratinocytes.
- 25 36. The wound dressing of any one of claims 23-26 or 34, wherein the peptide is a chemoattractant for fibroblasts or keratinocytes.
37. The wound dressing of any one of claims 23-26 or 34, wherein the peptide can stimulate collagen production in fibroblasts.
- 30 38. The wound dressing of any one of claims 23-26 or 34, wherein the dressing promotes wound healing, prevents scarring, improve skin tone, reduces wrinkling, or stimulates the development of a smooth, healthy skin.

39. A lotion for treating skin to reduce the effects of aging that comprises a peptide of the formula I:



wherein:

Xaa₁, Xaa₄, and Xaa₆ are separately each apolar amino acids;

Xaa₂ is a basic amino acid;

Xaa₃ is a cysteine-like amino acid;

10 Xaa₅ is a polar or aliphatic amino acid;

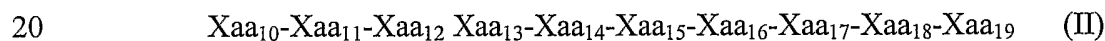
Xaa₇ is an acidic amino acid;

Xaa₈ is an aliphatic or polar amino acid;

Xaa₉ is an aliphatic, apolar or basic amino acid; and

15 wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes.

40. A lotion for treating skin to reduce the effects of aging that comprises a peptide of the formula II:



wherein:

Xaa₁₀ is a polar, acidic, basic or apolar amino acid;

Xaa₁₁ is a polar or aromatic amino acid;

25 Xaa₁₂ is a polar, basic, aliphatic or apolar amino acid;

Xaa₁₃ is an aromatic, aliphatic, polar or acidic amino acid;

Xaa₁₄ is an aromatic, apolar or polar amino acid;

Xaa₁₅ is an apolar or acidic amino acid;

Xaa₁₆ is a basic, a polar or an apolar amino acid;

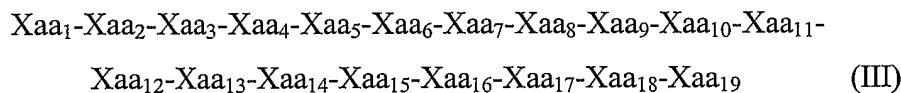
30 Xaa₁₇ is a basic, a polar, an aliphatic, an apolar or an acidic amino acid;

Xaa₁₈ is an apolar or an aliphatic amino acid;

Xaa₁₉ is a basic or an aliphatic amino acid; and

wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes.

41. A lotion for treating skin to reduce the effects of aging that comprises a peptide of
5 formula III:

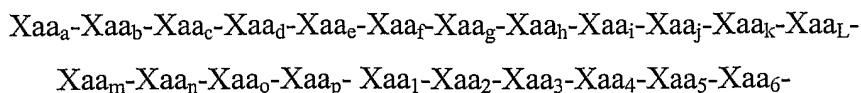


wherein:

- Xaa₁, Xaa₄, and Xaa₆ are separately each apolar amino acids;
10 Xaa₂ is a basic amino acid;
Xaa₃ is a cysteine-like amino acid;
Xaa₅ is a polar or aliphatic amino acid;
Xaa₇ is an acidic amino acid;
Xaa₈ is an aliphatic or polar amino acid;
15 Xaa₉ is an aliphatic, apolar or basic amino acid;
Xaa₁₀ is a polar, acidic, basic or apolar amino acid;
Xaa₁₁ is a polar or aromatic amino acid;
Xaa₁₂ is a polar, basic, aliphatic or apolar amino acid;
Xaa₁₃ is an aromatic, aliphatic, polar or acidic amino acid;
20 Xaa₁₄ is an aromatic, apolar or polar amino acid;
Xaa₁₅ is an apolar or acidic amino acid;
Xaa₁₆ is a basic, a polar or an apolar amino acid;
Xaa₁₇ is a basic, a polar, an aliphatic, an apolar or an acidic amino acid;
Xaa₁₈ is an apolar or an aliphatic amino acid;
25 Xaa₁₉ is a basic or an aliphatic amino acid; and

wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes.

42. A lotion for treating skin to reduce the effects of aging that comprises a peptide of
30 formula IV:



Xaa₇-Xaa₈-Xaa₉-Xaa₁₀-Xaa₁₁-Xaa₁₂-Xaa₁₃-Xaa₁₄-

Xaa₁₅-Xaa₁₆-Xaa₁₇-Xaa₁₈-Xaa₁₉

(IV)

(SEQ ID NO:18)

- 5 wherein:
- | | |
|--|--|
| Xaa _a is proline; | Xaa ₁ is proline; |
| Xaa _b is glutamine or glutamic acid; | Xaa ₂ is arginine; |
| Xaa _c is threonine; | Xaa ₃ is cysteine; |
| Xaa _d is glycine; | Xaa ₄ is glycine; |
| 10 Xaa _e is aspartic acid or glutamic acid; | Xaa ₅ is valine or asparagine; |
| Xaa _f is leucine; | Xaa ₆ is proline; |
| Xaa _g is aspartic acid; | Xaa ₇ is aspartic acid; |
| Xaa _h is glutamine or serine; | Xaa ₈ is valine or leucine; |
| Xaa _i is asparagine or alanine; | Xaa ₉ is alanine or glycine; |
| 15 Xaa _j is threonine; | Xaa ₁₀ is asparagine or arginine; |
| Xaa _k is isoleucine or leucine; | Xaa ₁₁ is tyrosine or phenylalanine; |
| Xaa _l is glutamic acid or lysine; | Xaa ₁₂ is asparagine or glutamine; |
| Xaa _m is threonine or alanine; | Xaa ₁₃ is phenylalanine or threonine; |
| Xaa _n is methionine; | Xaa ₁₄ is phenylalanine; |
| 20 Xaa _o is arginine; | Xaa ₁₅ is proline or glutamic acid; |
| Xaa _p is lysine or threonine; | Xaa ₁₆ is arginine or glycine; |
| Xaa ₁₇ is lysine or aspartic acid; | Xaa ₁₈ is proline or leucine; |
| Xaa ₁₉ is lysine; and | |
- wherein the peptide can inhibit matrix metalloproteinase-2 or the peptide can stimulate
- 25 cellular proliferation of fibroblasts or keratinocytes.

43. The lotion of any one of claims 39-42, wherein an apolar amino acid is methionine, glycine or proline.

30 44. The lotion of any one of claims 39-42, wherein a basic amino acid is histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, *p*-aminophenylalanine, and 2,4-diaminobutyric acid.

45. The lotion of any one of claims 39-42, wherein a cysteine-like amino acid is cysteine, homocysteine, penicillamine, or β -methyl cysteine.
46. The lotion of any one of claims 39-42, wherein an aliphatic amino acid is alanine, valine, leucine, isoleucine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, β -alanine, N-methylglycine, or α -aminoisobutyric acid.
47. The lotion of any one of claims 39-42, wherein an acidic amino acid is aspartic acid or glutamic acid.
48. The lotion of any one of claims 39-42, wherein a polar amino acid is asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or an apolar amino acid such as methionine, glycine or proline.
49. The lotion of any one of claims 39-42, wherein an aromatic amino acid is phenylalanine, tyrosine, tryptophan, phenylglycine, naphthylalanine, β -2-thienylalanine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, pyridylalanine, or 3-benzothienyl alanine.
50. The lotion of any one of claims 39-42, wherein the dressing improve skin tone, reduces wrinkling, or stimulates the development of a smooth, healthy skin.
51. The lotion of any one of claims 39-42, wherein the peptide can stimulate cellular growth of fibroblasts or keratinocytes.
52. The lotion of any one of claims 39-42, wherein the peptide is a chemoattractant for fibroblasts or keratinocytes.
53. The lotion of any one of claims 39-42, wherein the peptide can stimulate collagen production in fibroblasts.
54. A lotion that comprises a peptide comprising SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8,

SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, or SEQ ID NO:13,
wherein the peptide can inhibit a matrix metalloproteinase.

55. The lotion of claim 54 wherein the peptide can stimulate cellular proliferation of
5 fibroblasts or keratinocytes.

56. The lotion of claim 54, wherein the peptide is a chemoattractant for fibroblasts or
keratinocytes.

10 57. The lotion of claim 54, wherein the peptide can stimulate collagen production in
fibroblasts.

58. A method for promoting healthy skin development that comprises administering a
therapeutically effective amount of a peptide of formula I:

15



wherein:

Xaa₁, Xaa₄, and Xaa₆ are separately each apolar amino acids;

20 Xaa₂ is a basic amino acid;

Xaa₃ is a cysteine-like amino acid;

Xaa₅ is a polar or aliphatic amino acid;

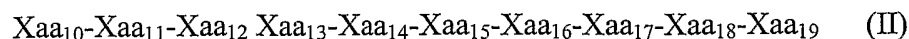
Xaa₇ is an acidic amino acid;

Xaa₈ is an aliphatic or polar amino acid;

25 Xaa₉ is an aliphatic, apolar or basic amino acid; and

wherein the peptide is capable of inhibiting the activity of a matrix
metalloproteinase or of promoting the growth of fibroblasts or keratinocytes.

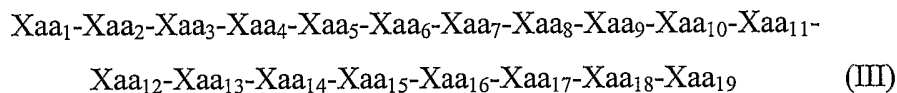
59. A method for promoting healthy skin development that comprises administering a
30 therapeutically effective amount of a peptide of formula II:



wherein:

- Xaa₁₀ is a polar, acidic, basic or apolar amino acid;
 Xaa₁₁ is a polar or aromatic amino acid;
 Xaa₁₂ is a polar, basic, aliphatic or apolar amino acid;
 5 Xaa₁₃ is an aromatic, aliphatic, polar or acidic amino acid;
 Xaa₁₄ is an aromatic, apolar or polar amino acid;
 Xaa₁₅ is an apolar or acidic amino acid;
 Xaa₁₆ is a basic, a polar or an apolar amino acid;
 Xaa₁₇ is a basic, a polar, an aliphatic, an apolar or an acidic amino acid;
 10 Xaa₁₈ is an apolar or an aliphatic amino acid;
 Xaa₁₉ is a basic or an aliphatic amino acid; and
 wherein the peptide is capable of inhibiting the activity of a matrix metalloproteinase or of promoting the growth of fibroblasts or keratinocytes.

- 15 60. A method for promoting healthy skin development that comprises administering a therapeutically effective amount of a peptide of formula III:



20 wherein:

- Xaa₁, Xaa₄, and Xaa₆ are separately each apolar amino acids;
 Xaa₂ is a basic amino acid;
 Xaa₃ is a cysteine-like amino acid;
 Xaa₅ is a polar or aliphatic amino acid;
 25 Xaa₇ is an acidic amino acid;
 Xaa₈ is an aliphatic or polar amino acid;
 Xaa₉ is an aliphatic, apolar or basic amino acid;
 Xaa₁₀ is a polar, acidic, basic or apolar amino acid;
 Xaa₁₁ is a polar or aromatic amino acid;
 30 Xaa₁₂ is a polar, basic, aliphatic or apolar amino acid;
 Xaa₁₃ is an aromatic, aliphatic, polar or acidic amino acid;
 Xaa₁₄ is an aromatic, apolar or polar amino acid;
 Xaa₁₅ is an apolar or acidic amino acid;

Xaa₁₆ is a basic, a polar or an apolar amino acid;

Xaa₁₇ is a basic, a polar, an aliphatic, an apolar or an acidic amino acid;

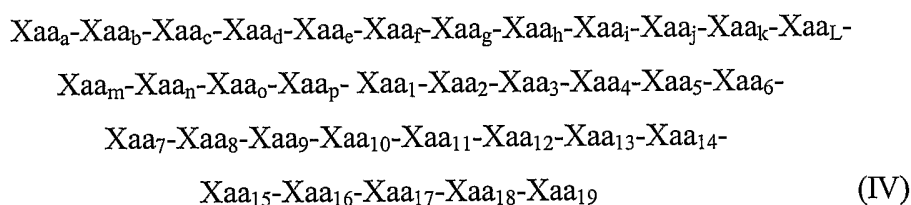
Xaa₁₈ is an apolar or an aliphatic amino acid;

Xaa₁₉ is a basic or an aliphatic amino acid; and

- 5 wherein the peptide is capable of inhibiting the activity of a matrix metalloproteinase or of promoting the growth of fibroblasts or keratinocytes.

61. A method for promoting healthy skin development that comprises administering a therapeutically effective amount of a peptide of formula IV:

10



15

(SEQ ID NO:18)

wherein:

- | | |
|---|--|
| Xaa _a is proline; | Xaa ₁ is proline; |
| Xaa _b is glutamine or glutamic acid; | Xaa ₂ is arginine; |
| Xaa _c is threonine; | Xaa ₃ is cysteine; |
| 20 Xaa _d is glycine; | Xaa ₄ is glycine; |
| Xaa _e is aspartic acid or glutamic acid; | Xaa ₅ is valine or asparagine; |
| Xaa _f is leucine; | Xaa ₆ is proline; |
| Xaa _g is aspartic acid; | Xaa ₇ is aspartic acid; |
| Xaa _h is glutamine or serine; | Xaa ₈ is valine or leucine; |
| 25 Xaa _i is asparagine or alanine; | Xaa ₉ is alanine or glycine; |
| Xaa _j is threonine; | Xaa ₁₀ is asparagine or arginine; |
| Xaa _k is isoleucine or leucine; | Xaa ₁₁ is tyrosine or phenylalanine; |
| Xaa _l is glutamic acid or lysine; | Xaa ₁₂ is asparagine or glutamine; |
| Xaa _m is threonine or alanine; | Xaa ₁₃ is phenylalanine or threonine; |
| 30 Xaa _n is methionine; | Xaa ₁₄ is phenylalanine; |
| Xaa _o is arginine; | Xaa ₁₅ is proline or glutamic acid; |
| Xaa _p is lysine or threonine; | Xaa ₁₆ is arginine or glycine; |
| Xaa ₁₇ is lysine or aspartic acid; | Xaa ₁₈ is proline or leucine; |

Xaa₁₉ is lysine; and

wherein the peptide is capable of inhibiting the activity of a matrix metalloproteinase or of promoting the growth of fibroblasts or keratinocytes.

5 62. The method of any one of claims 58-61, that promotes wound healing, prevents scarring, improves skin tone, reduces wrinkling, or stimulates the development of a smooth, healthy skin.

10 63. The method of any one of claims 58-61, wherein the peptide comprises SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, or SEQ ID NO:13.

15 64. The method of any one of claims 58-61, wherein wherein an apolar amino acid is methionine, glycine or proline.

20 65. The method of any one of claims 58-61, wherein a basic amino acid is histidine, lysine, arginine, 2,3-diaminopropionic acid, ornithine, homoarginine, *p*-aminophenylalanine, and 2,4-diaminobutyric acid.

66. The method of any one of claims 58-61, wherein a cysteine-like amino acid is cysteine, homocysteine, penicillamine, or β -methyl cysteine.

25 67. The method of any one of claims 58-61, wherein an aliphatic amino acid is alanine, valine, leucine, isoleucine, t-butylalanine, N-methylisoleucine, norleucine, N-methylvaline, cyclohexylalanine, β -alanine, N-methylglycine, or α -aminoisobutyric acid.

68. The method of any one of claims 58-61, wherein an acidic amino acid is aspartic acid or glutamic acid.

30 69. The method of any one of claims 58-61, wherein a polar amino acid is asparagine, glutamine, serine, threonine, tyrosine, citrulline, N-acetyl lysine, methionine sulfoxide, or homoserine, or an apolar amino acid such as methionine, glycine or proline.

70. The method of any one of claims 58-61, wherein an aromatic amino acid is phenylalanine, tyrosine, tryptophan, phenylglycine, naphthylalanine, β -2-thienylalanine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, 4-chlorophenylalanine, 2-
5 fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, pyridylalanine, or 3-benzothienyl alanine.
71. The method of any one of claims 58-61, wherein the peptide can stimulate cellular proliferation of fibroblasts or keratinocytes.
10
72. The method of any one of claims 58-61, wherein the peptide is a chemoattractant for fibroblasts or keratinocytes.
73. The method of any one of claims 58-61, wherein the peptide can stimulate collagen
15 production in fibroblasts.

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Fig. 1A

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Fig. 1B

2/22

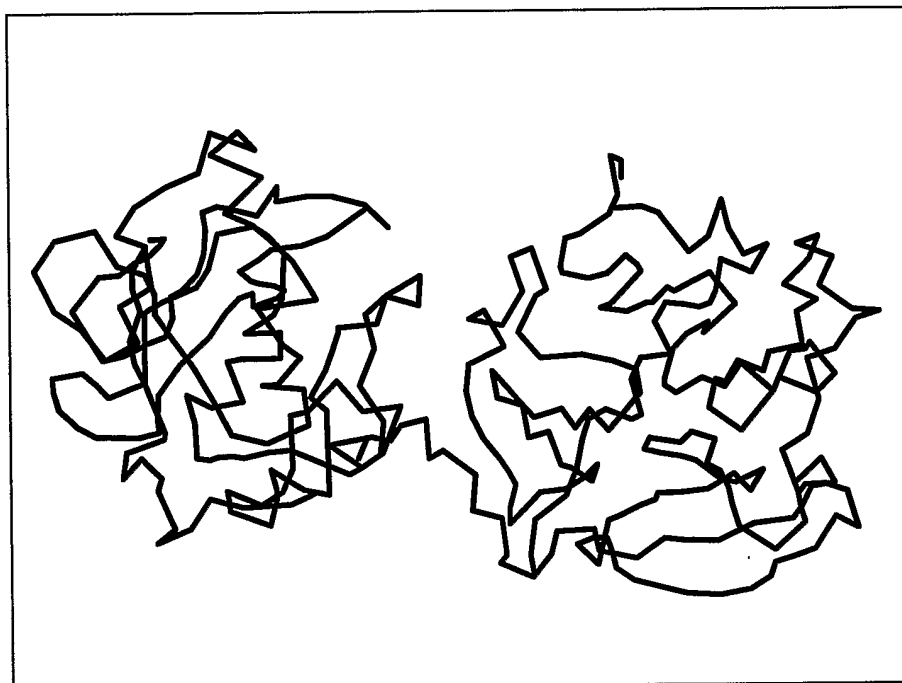


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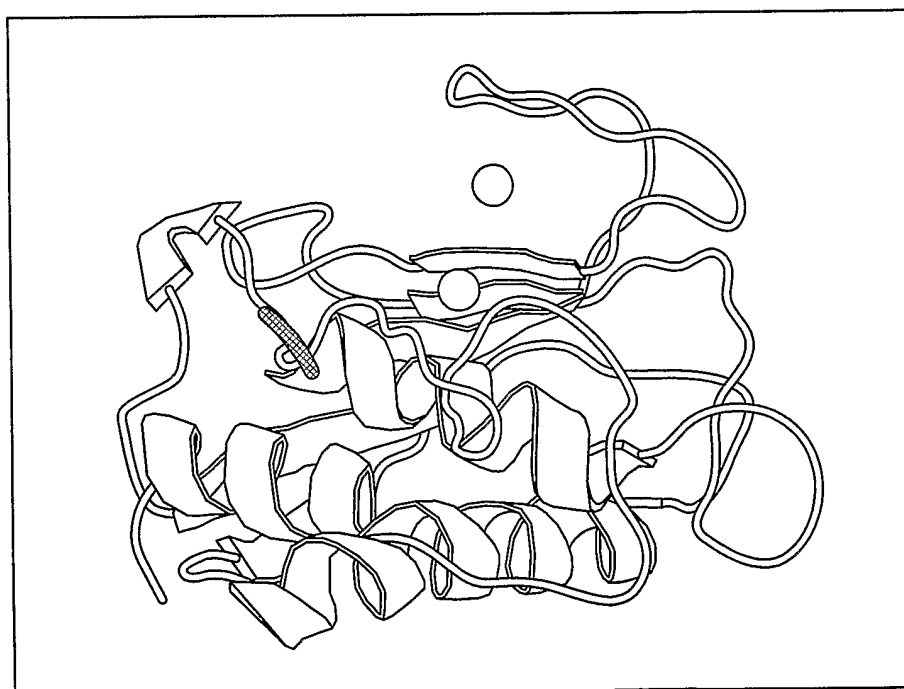


Fig. 3

3/22

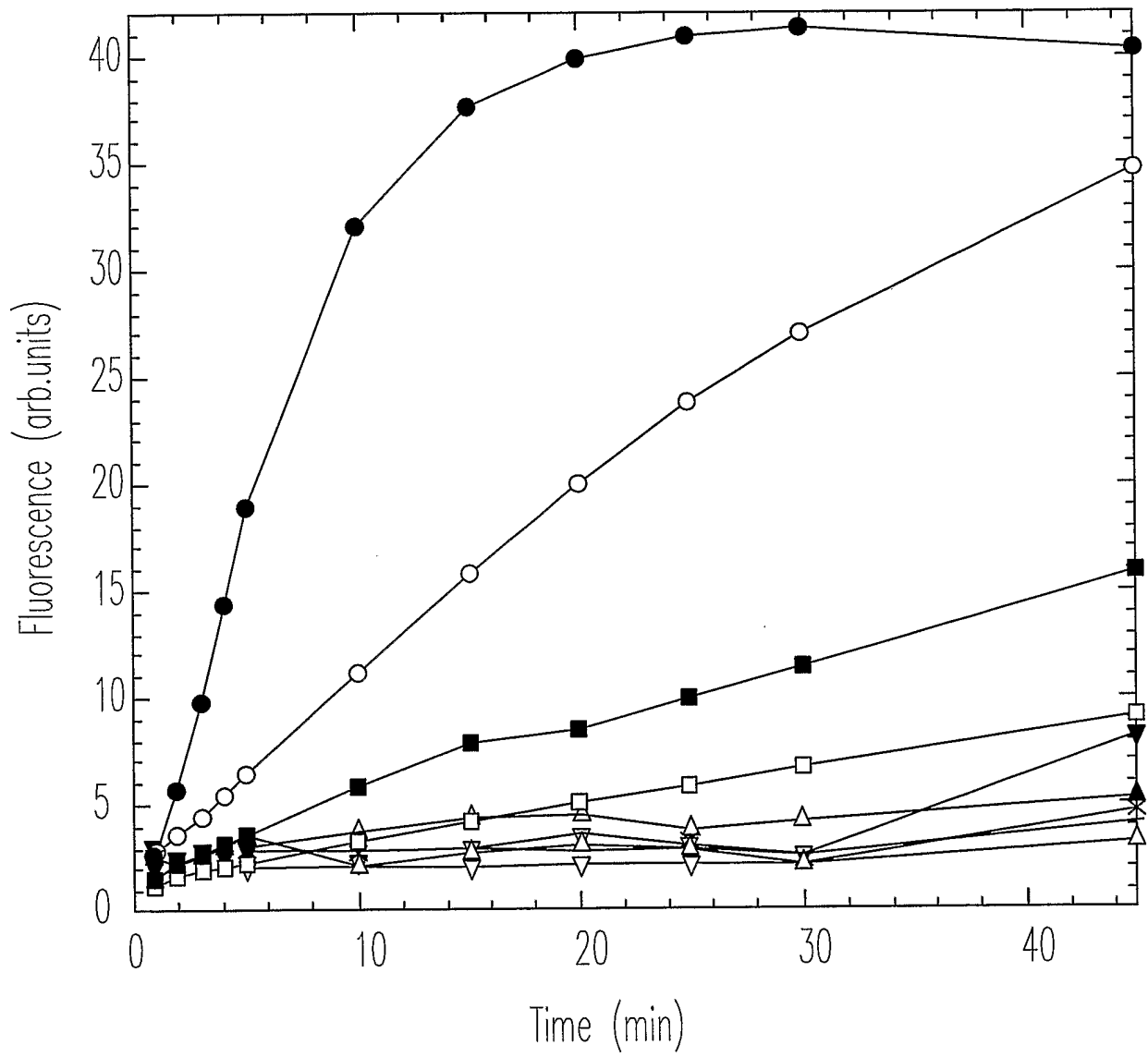


Fig. 4

4/22

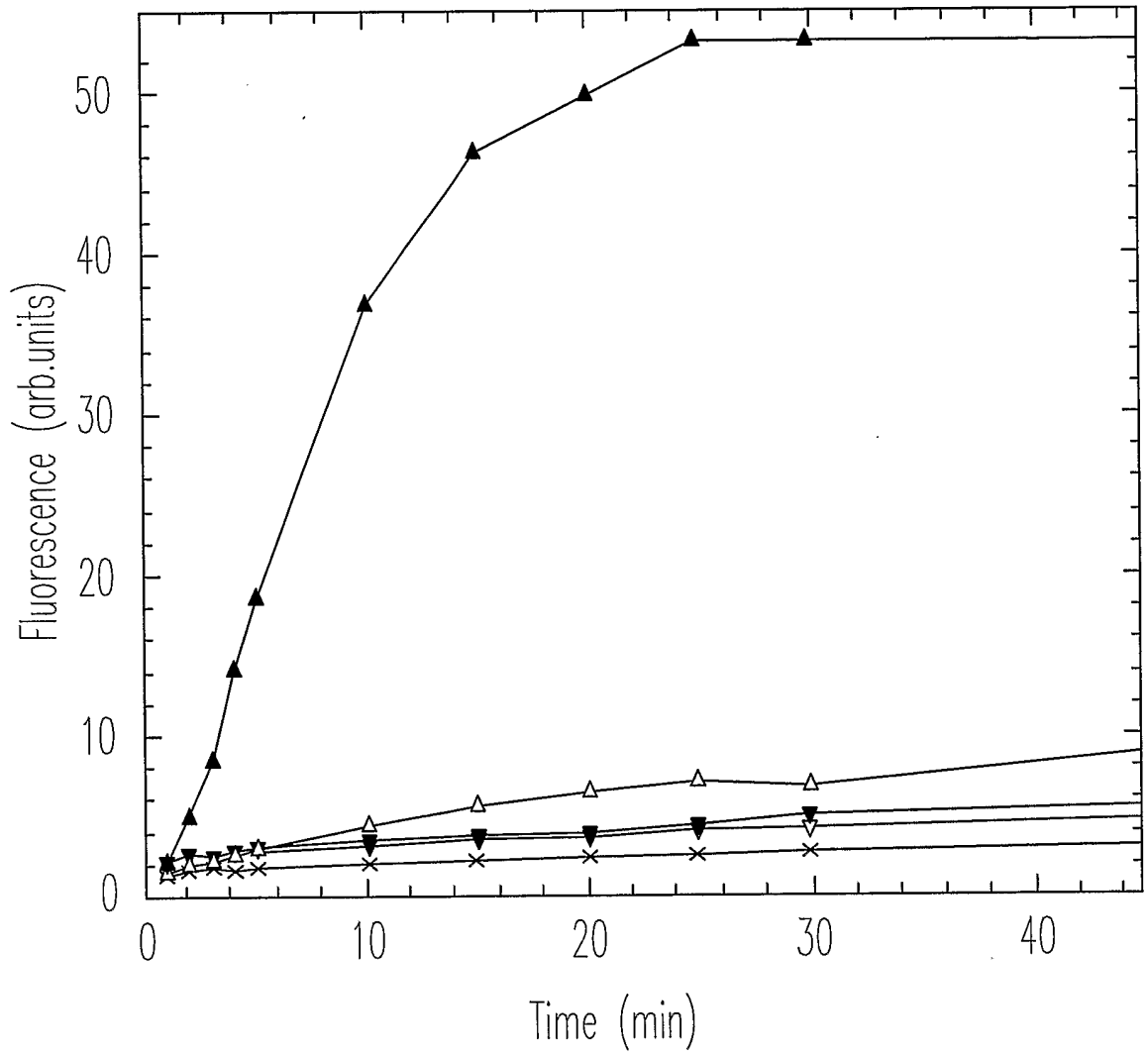


Fig. 5

5/22

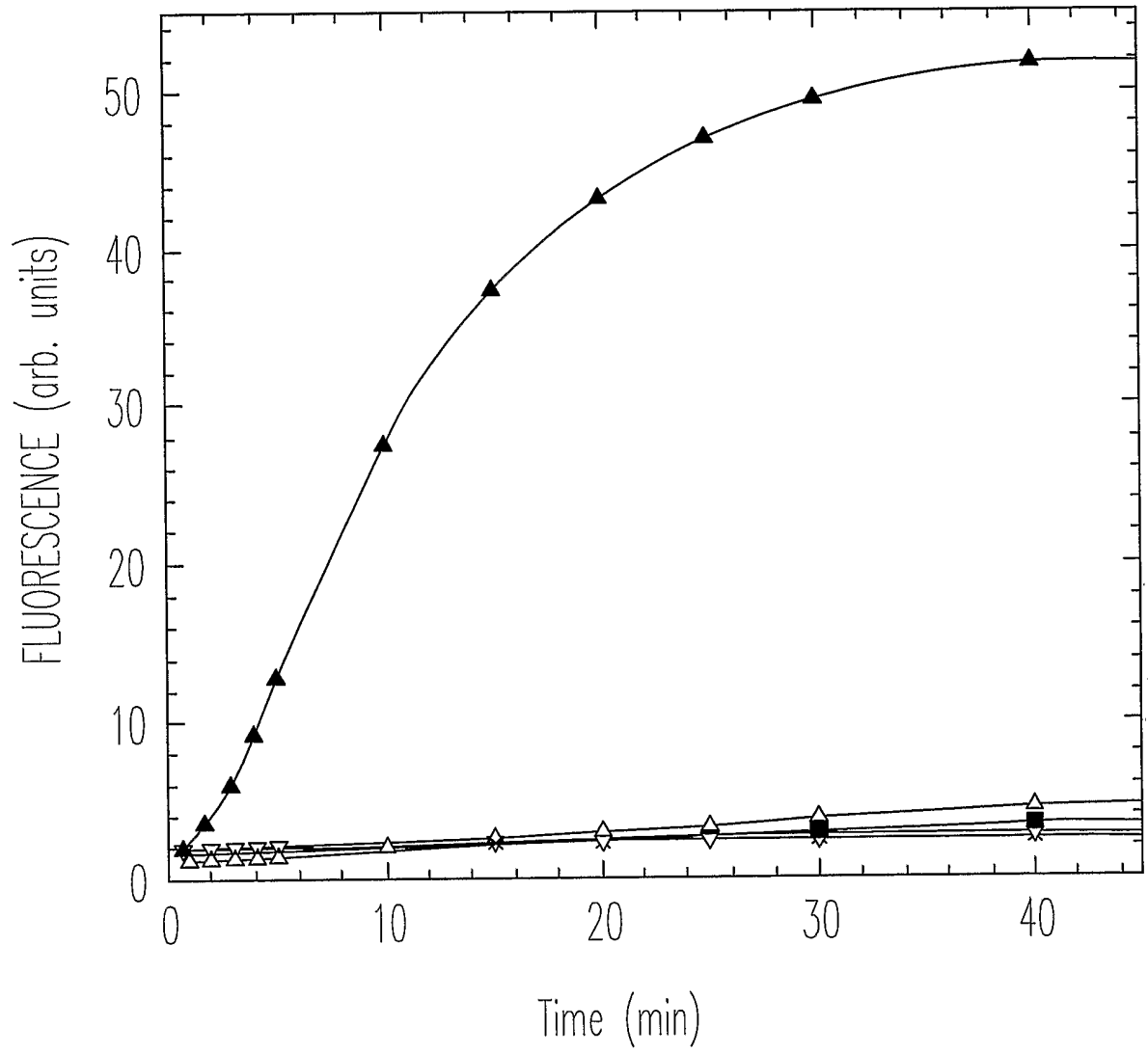


Fig. 6

6/22

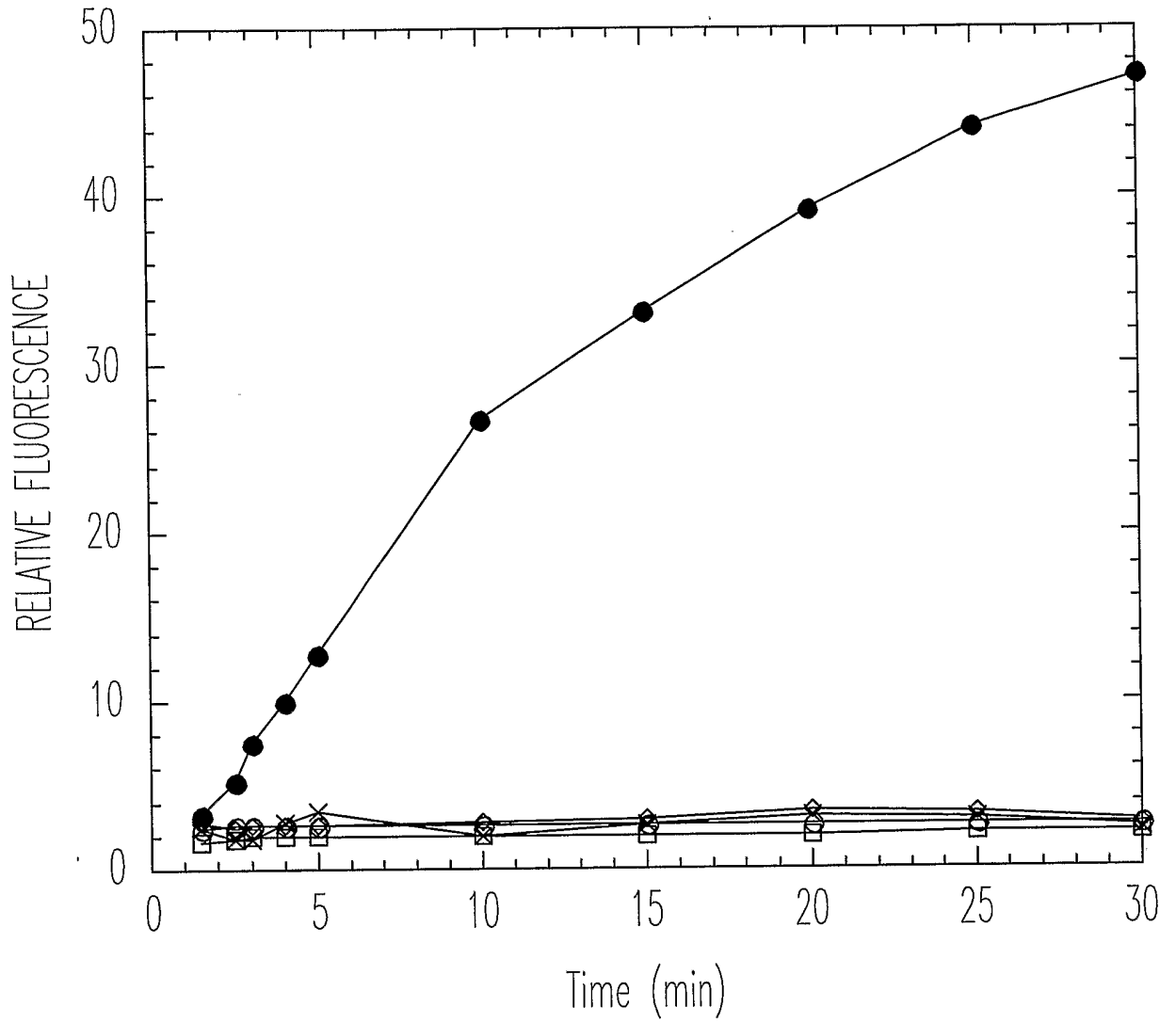


Fig. 7

7/22

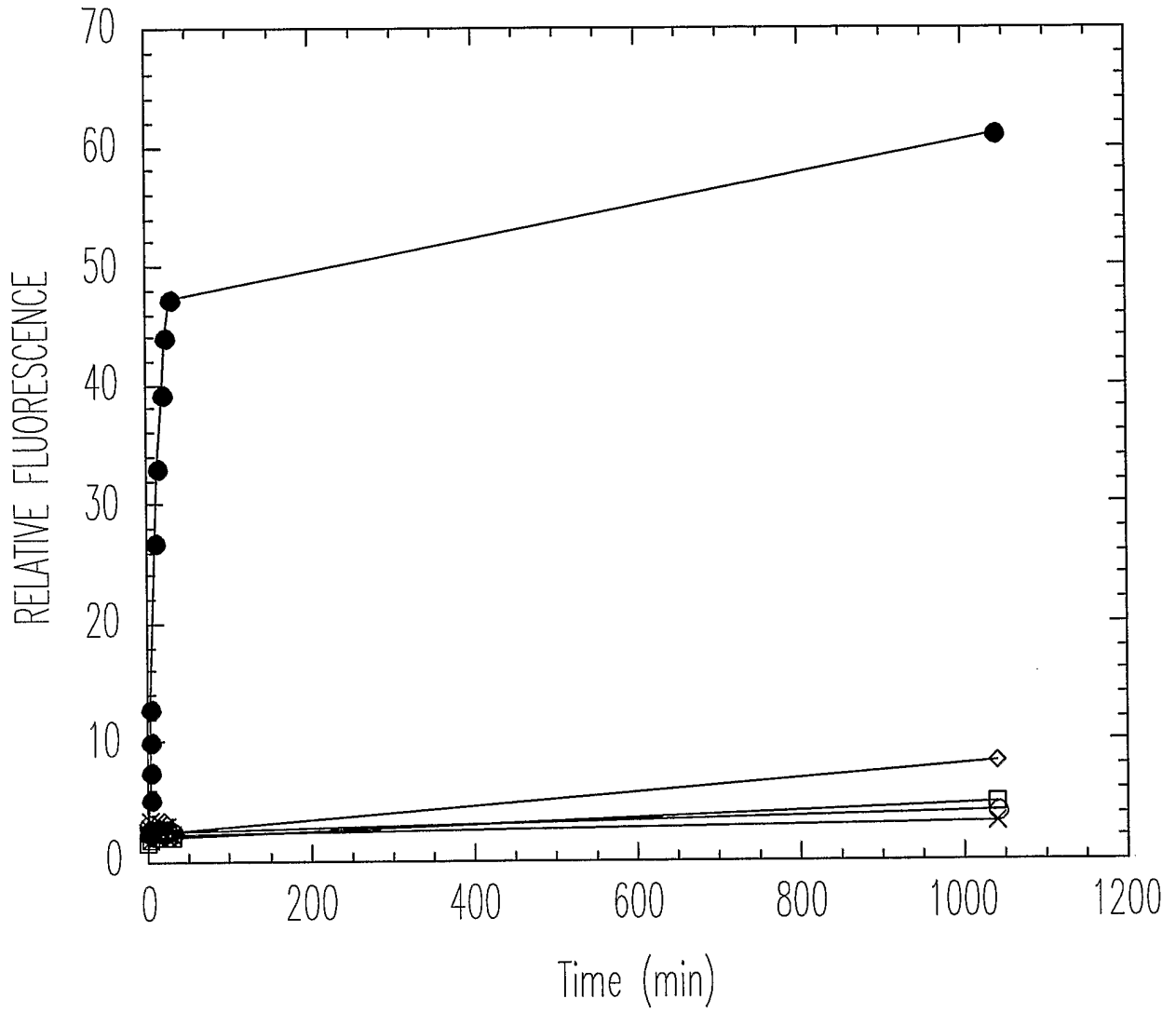


Fig. 8

8/22

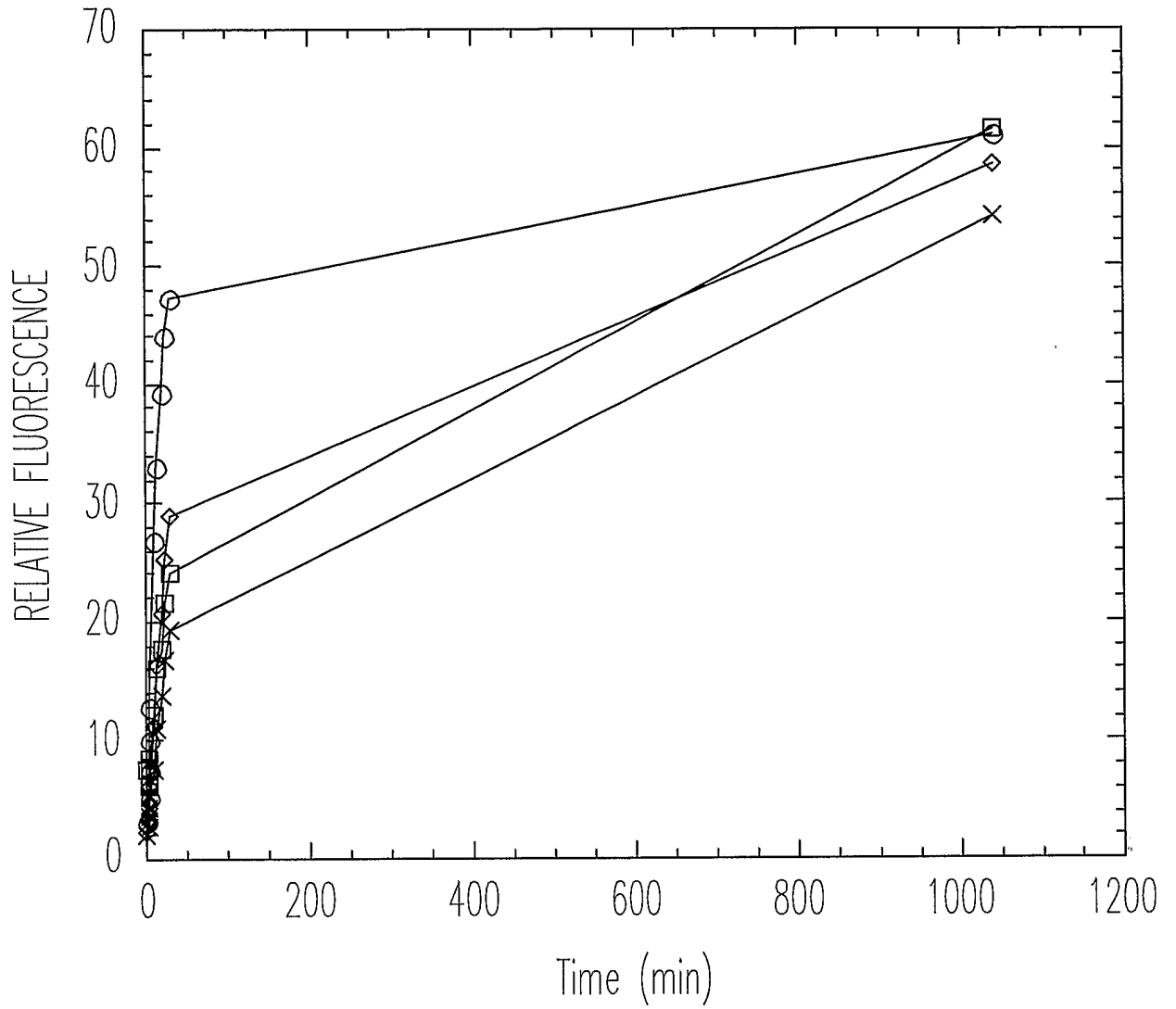


Fig. 9

9/22

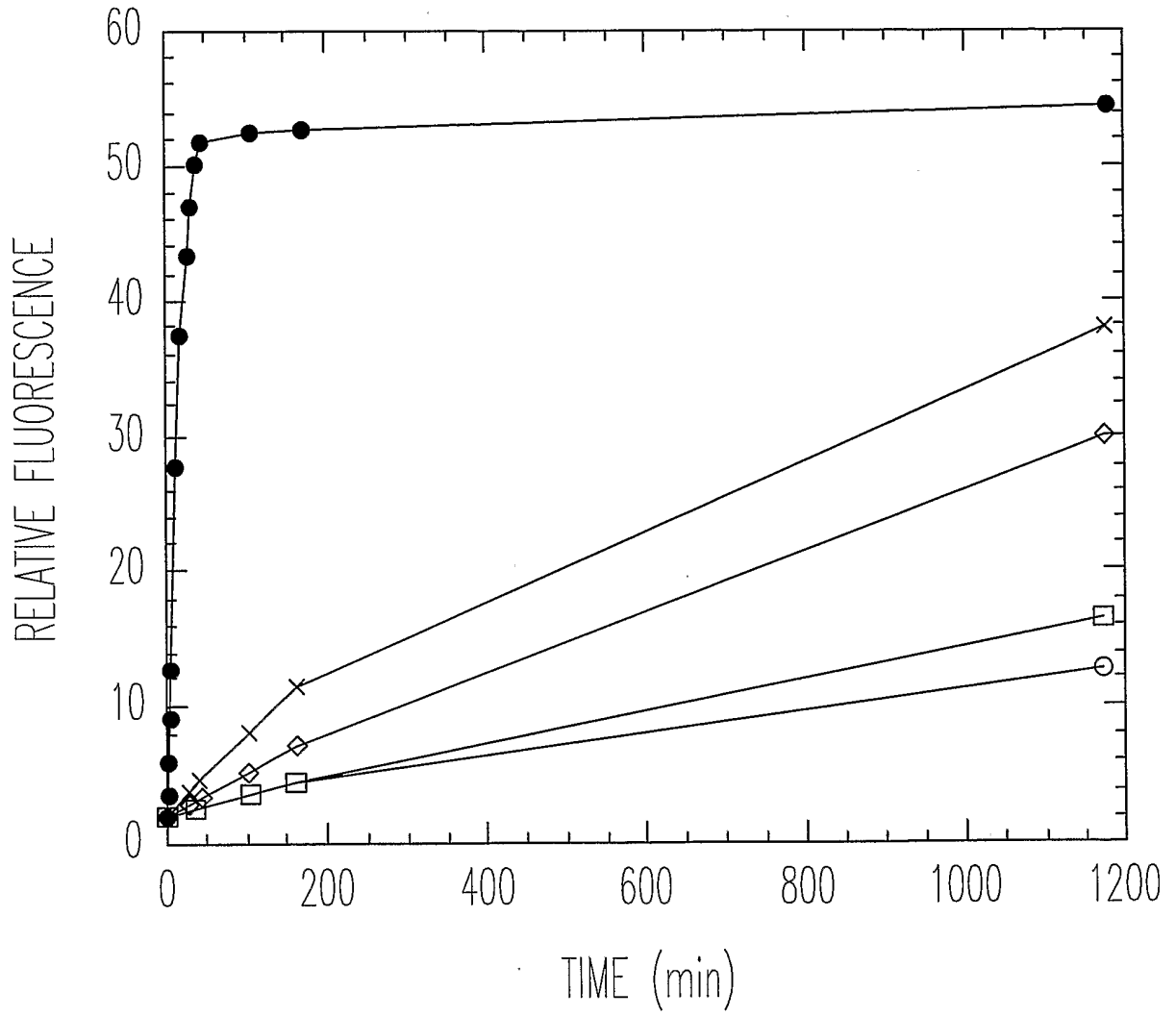


Fig. 10

10/22

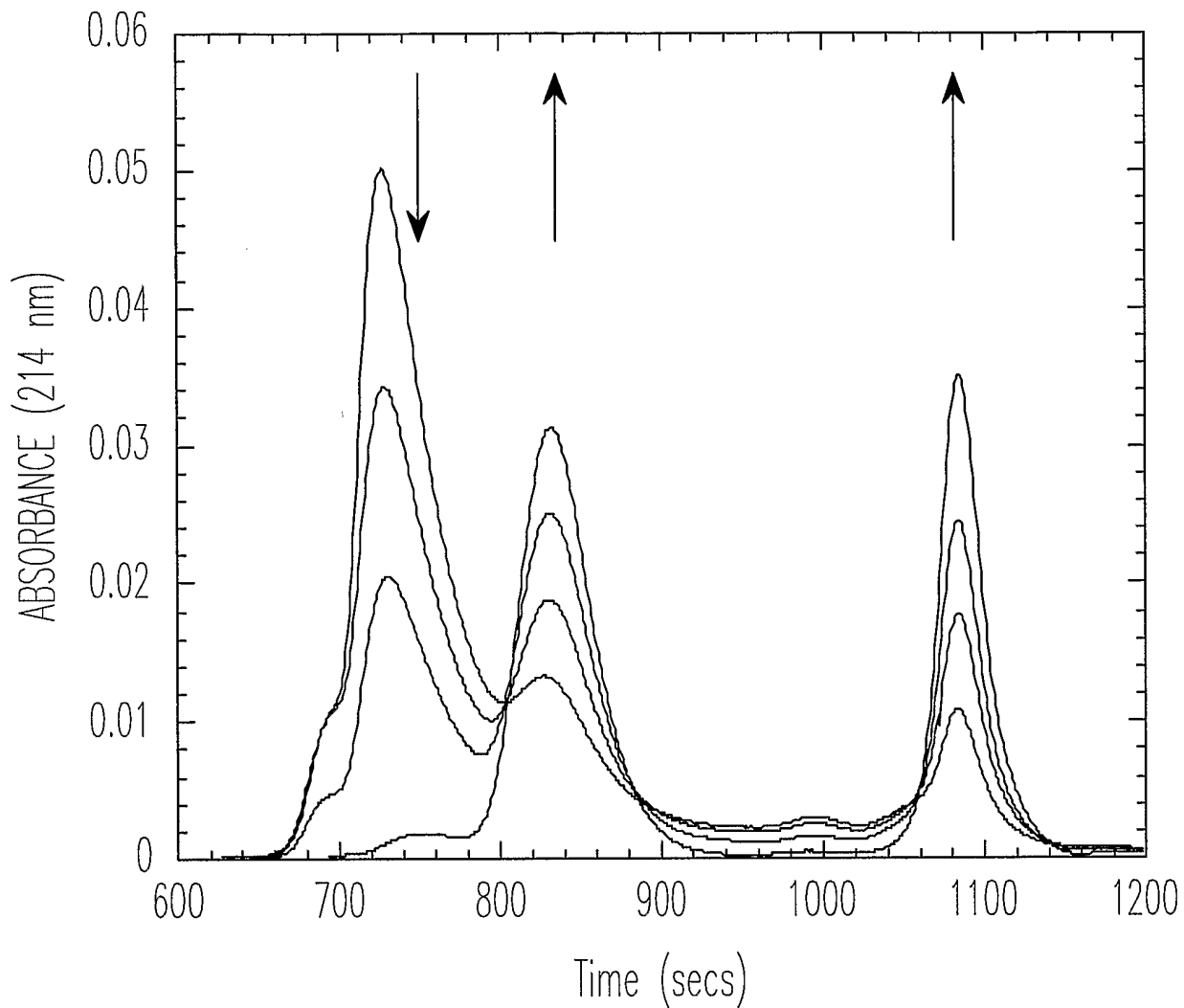


Fig. 11

11/22

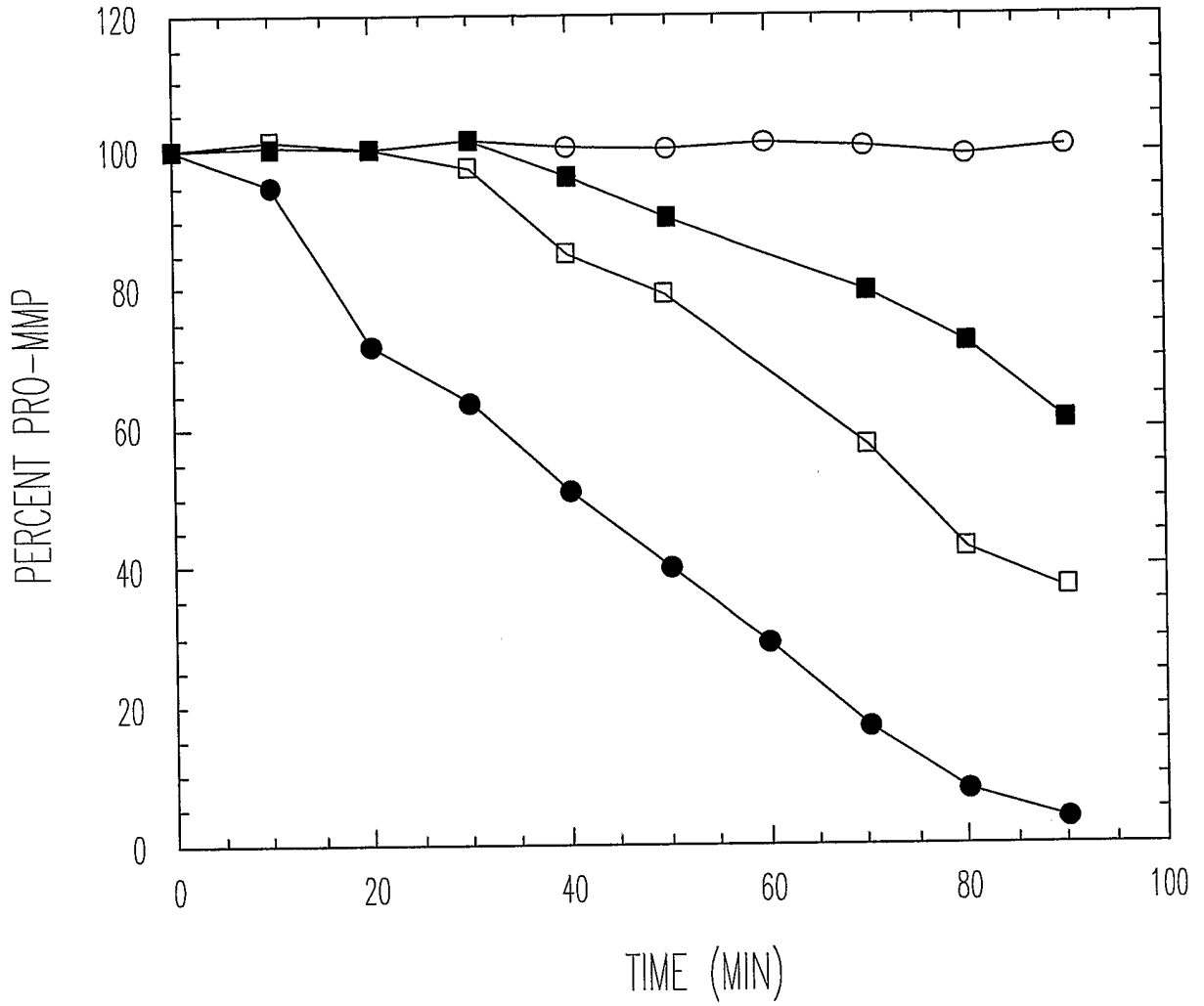


Fig. 12

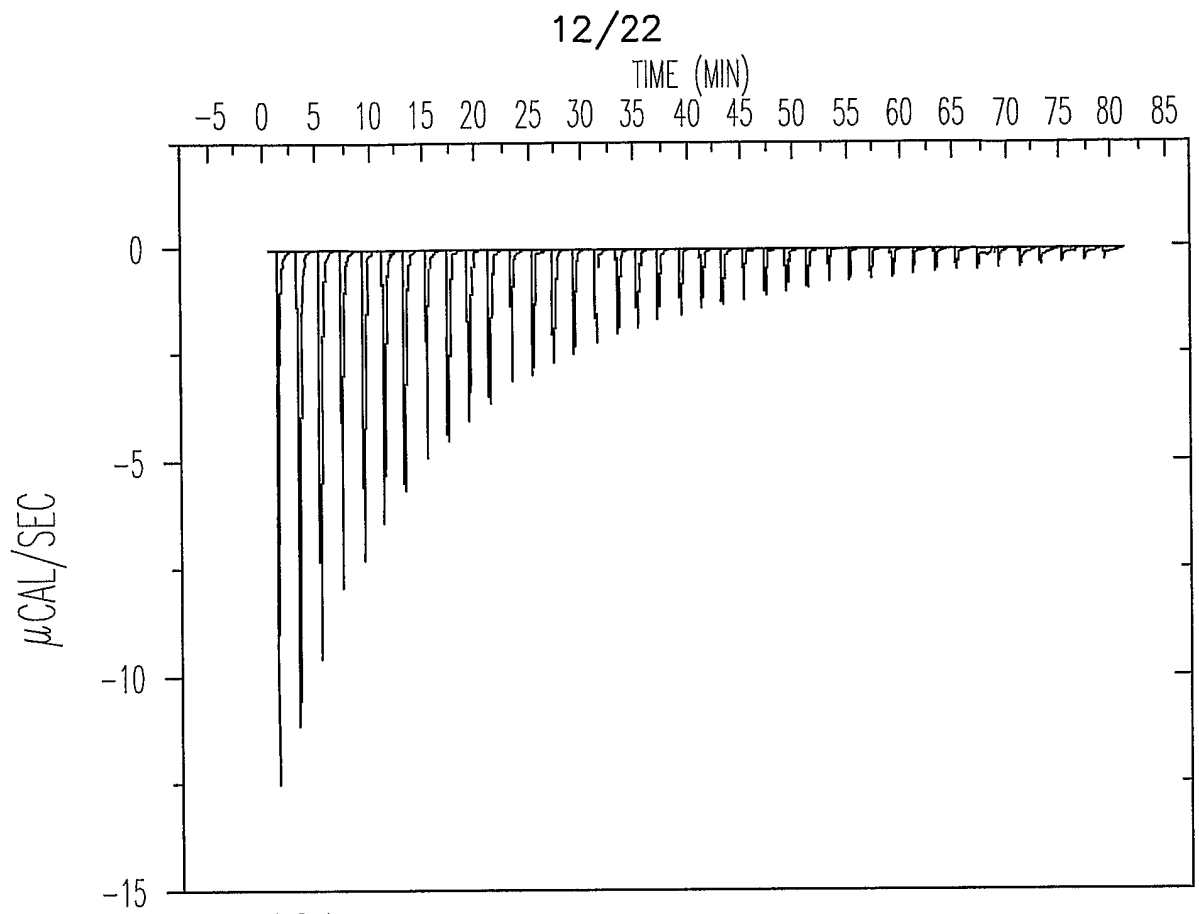


Fig. 13A

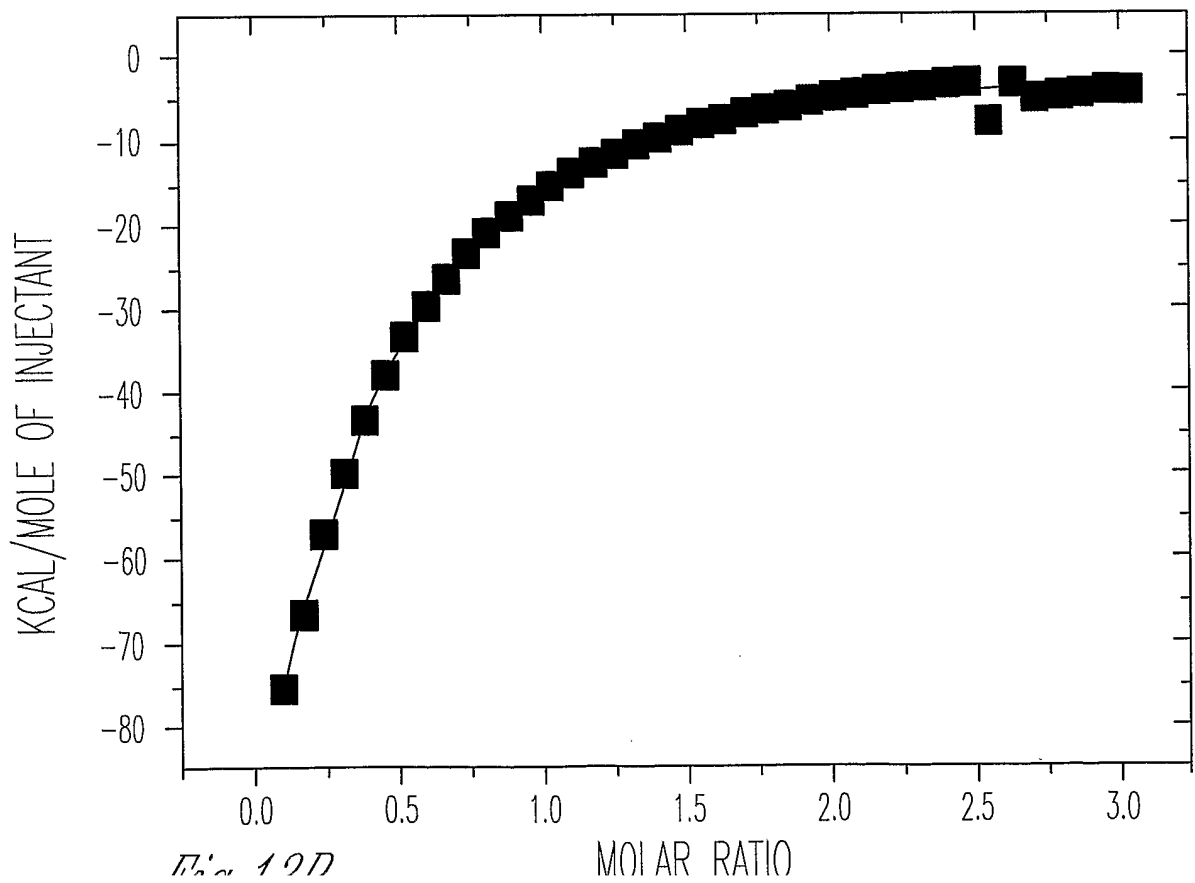


Fig. 13B

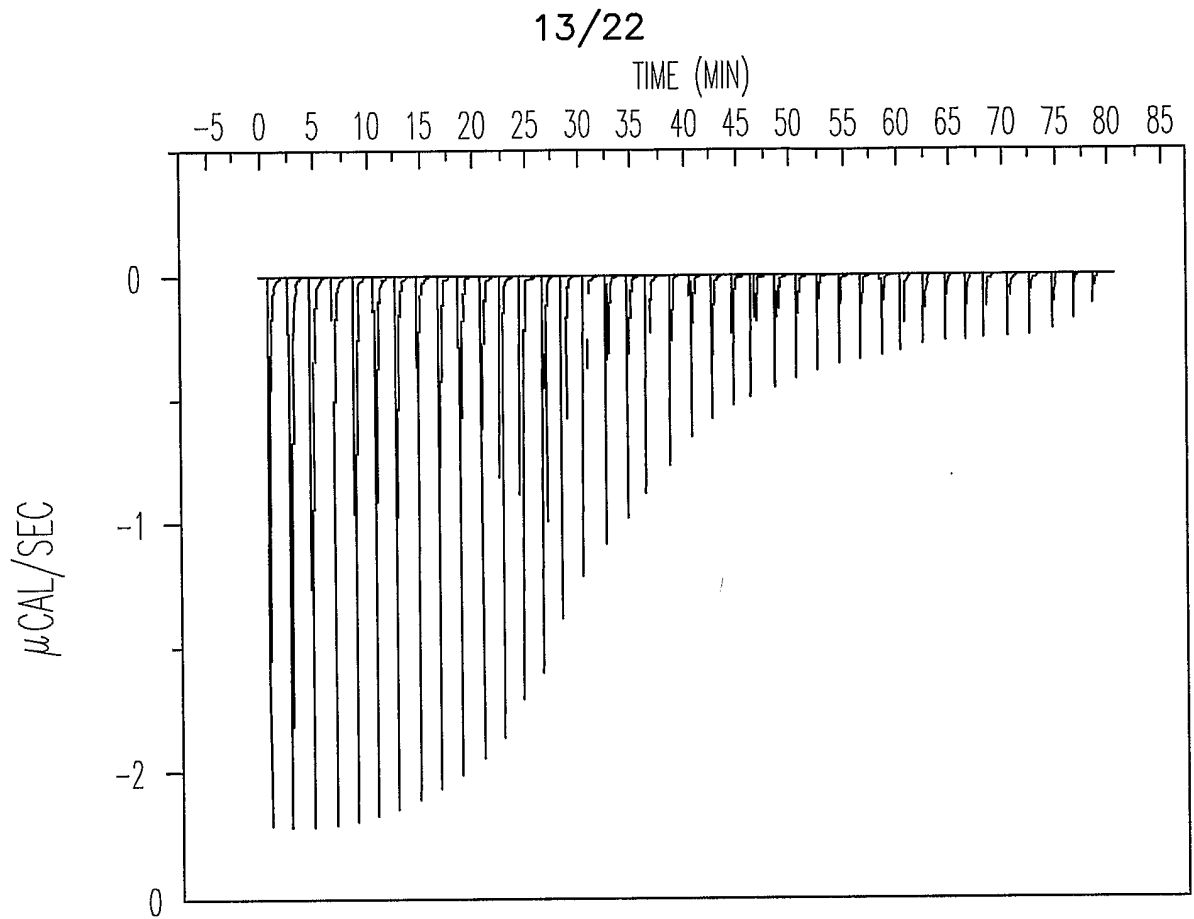


Fig. 14A

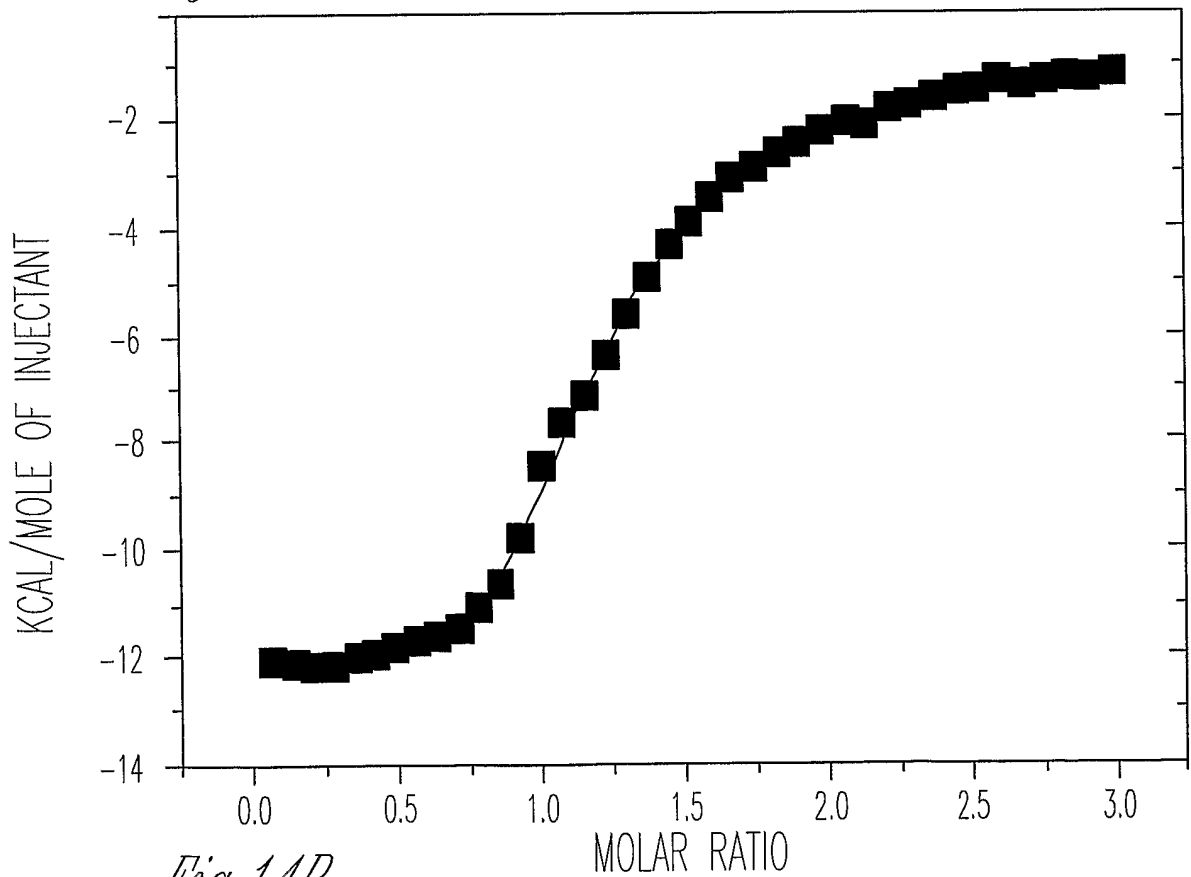


Fig. 14B

14/22

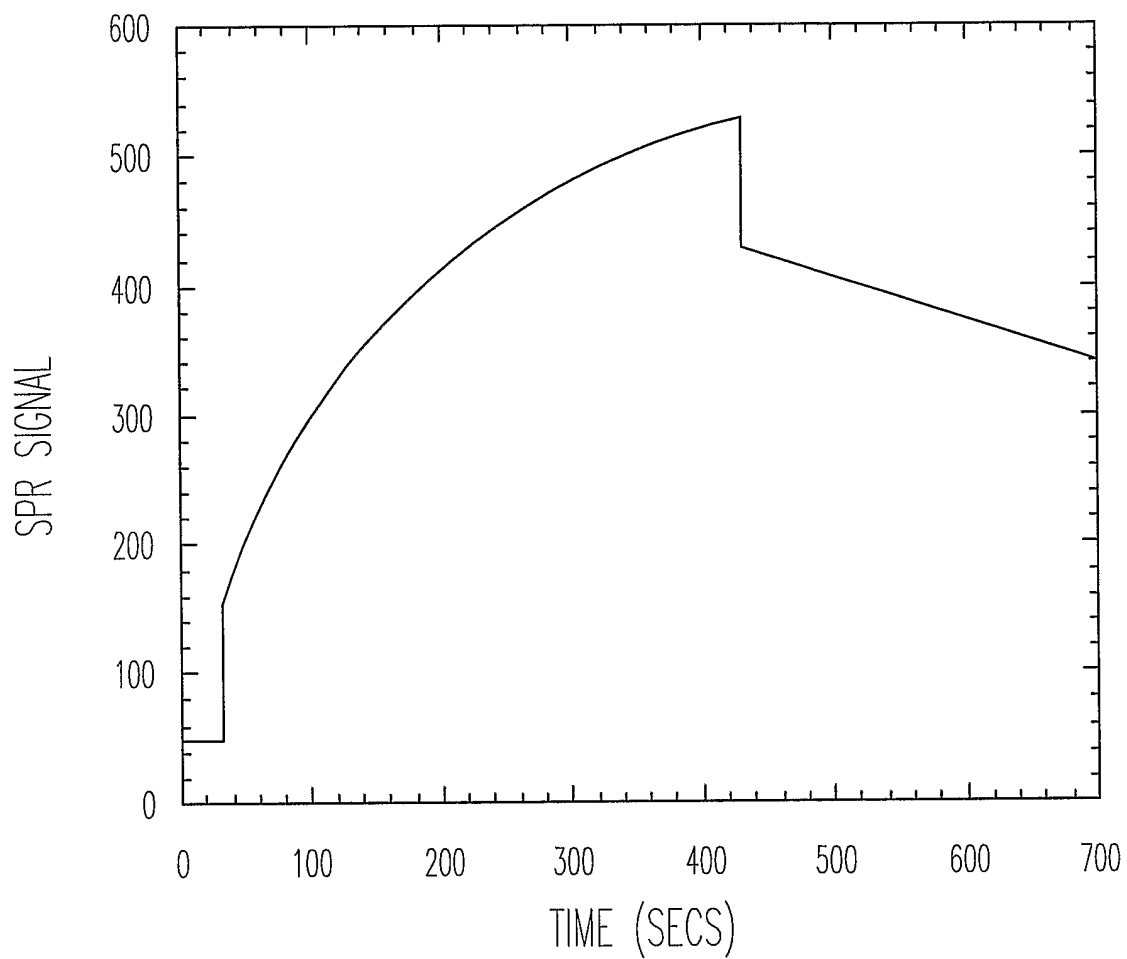


Fig. 15

15/22

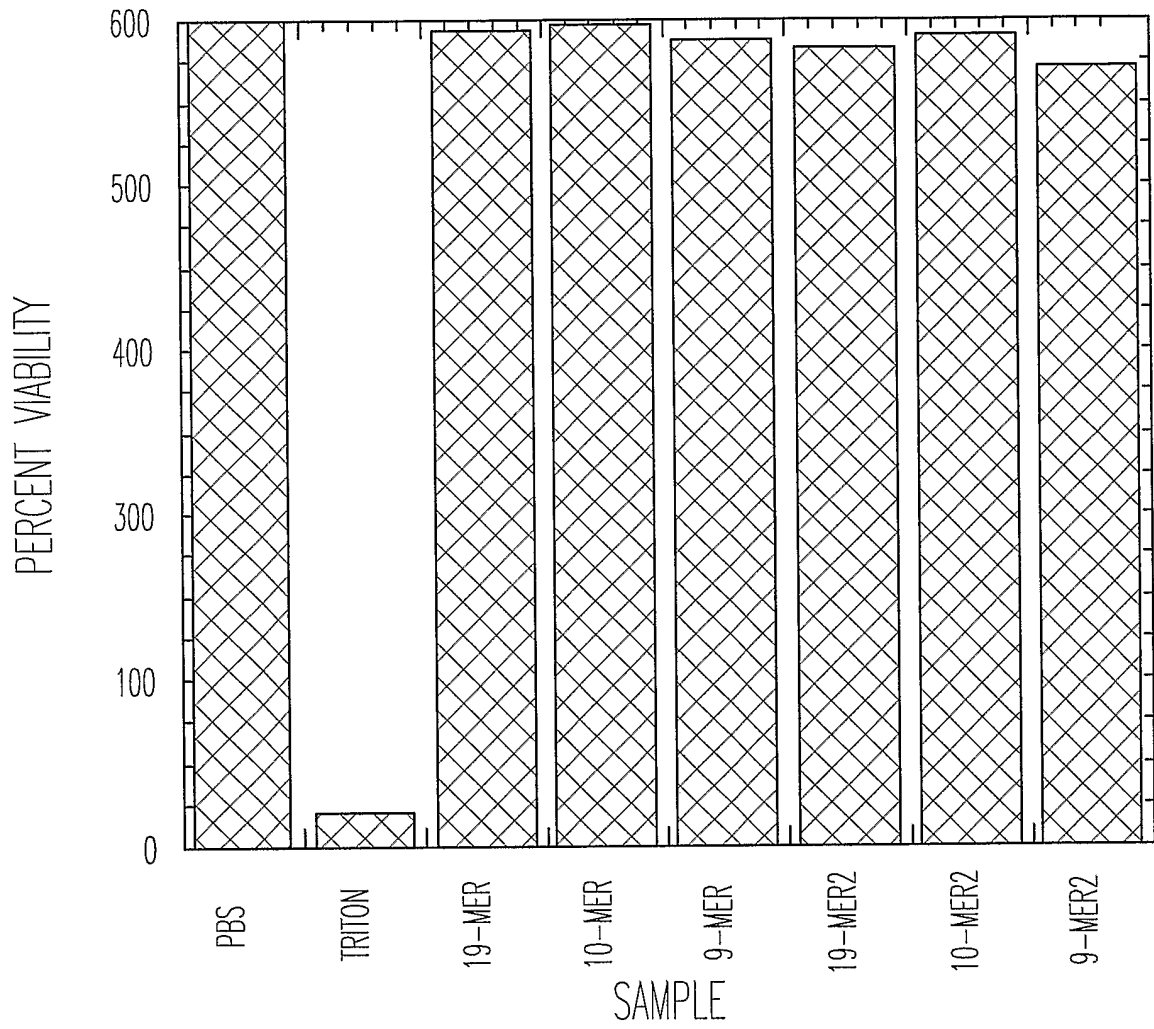


Fig. 16

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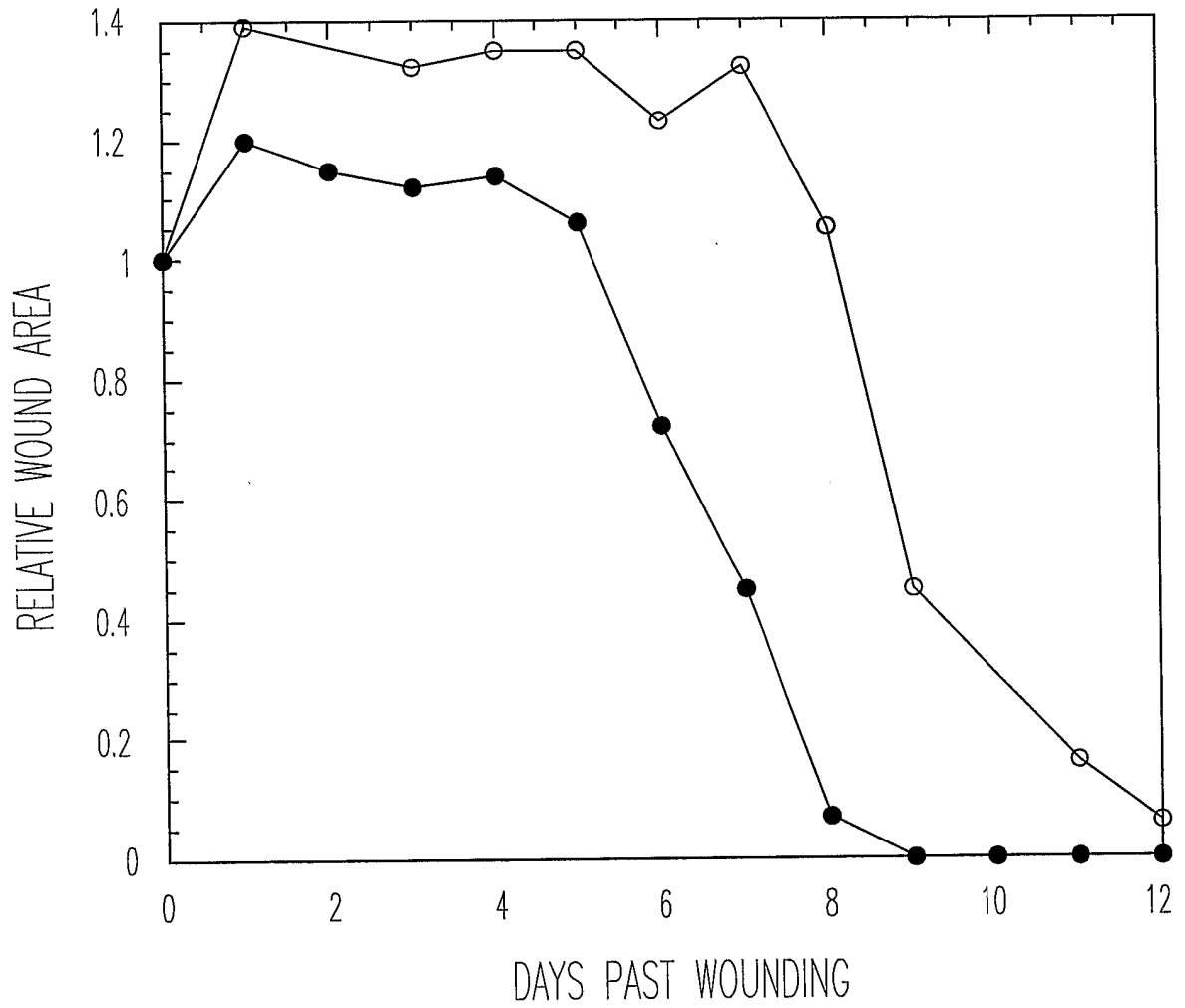


Fig. 17

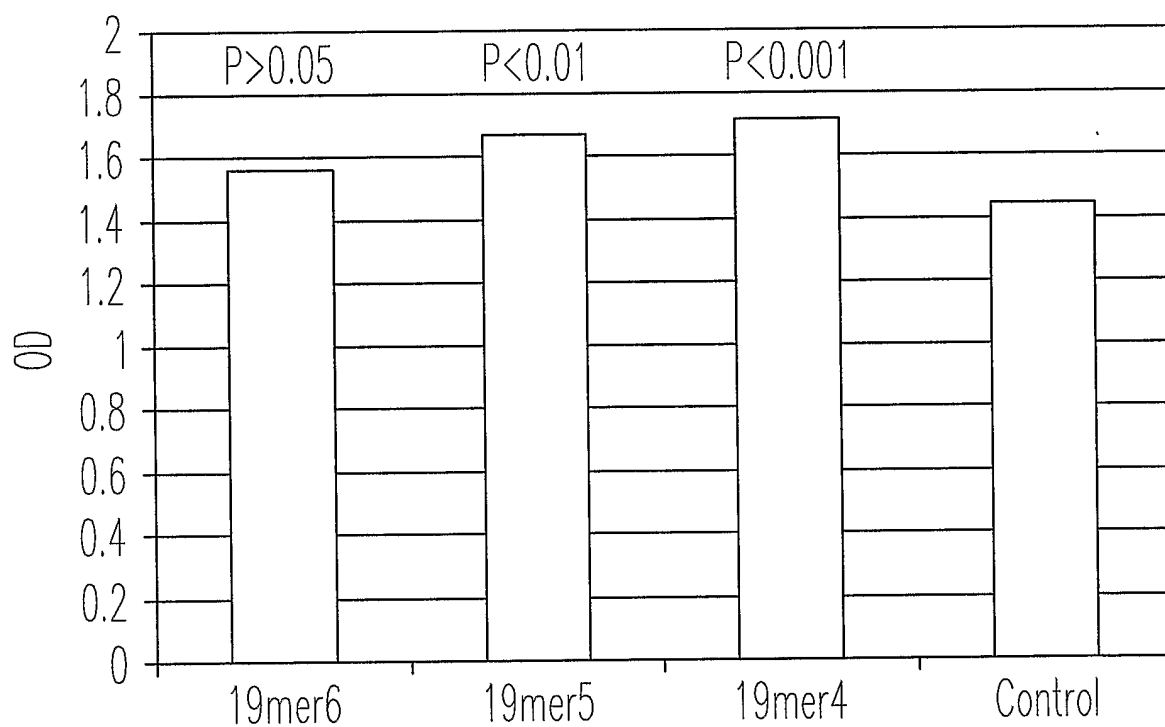


Fig. 18

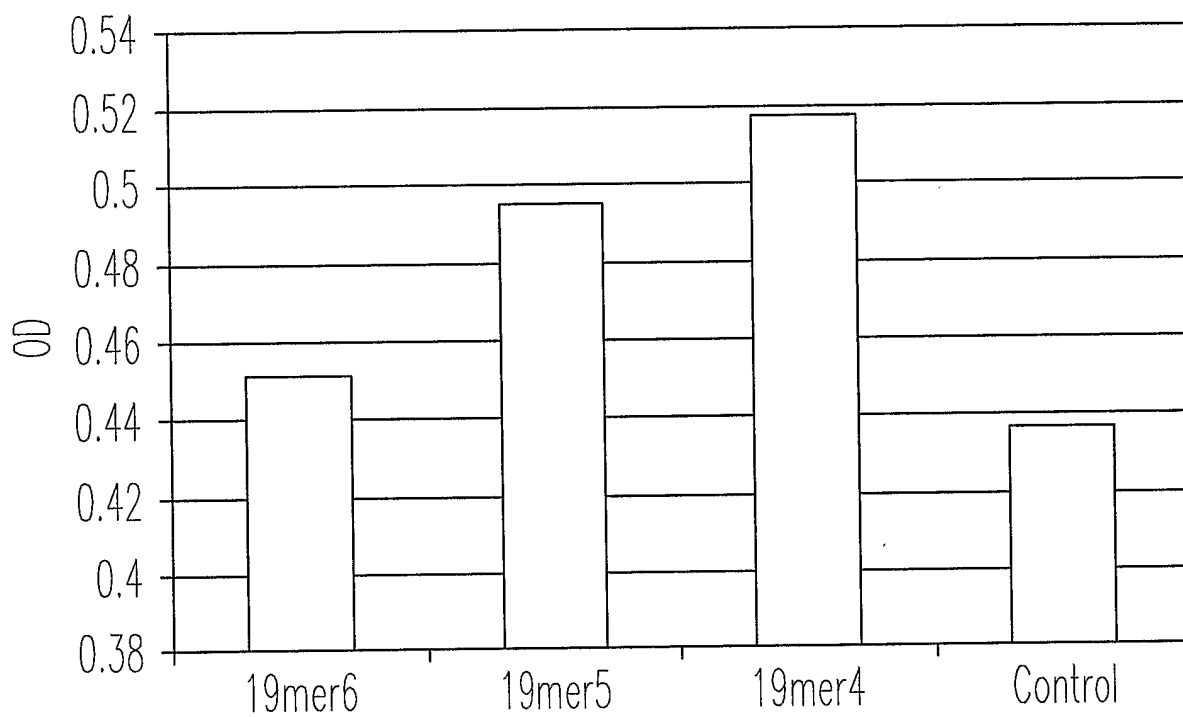


Fig. 19

19/22

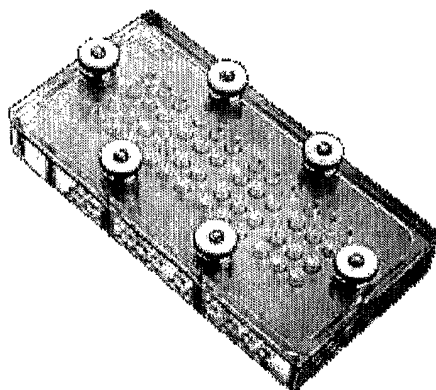


Fig. 20

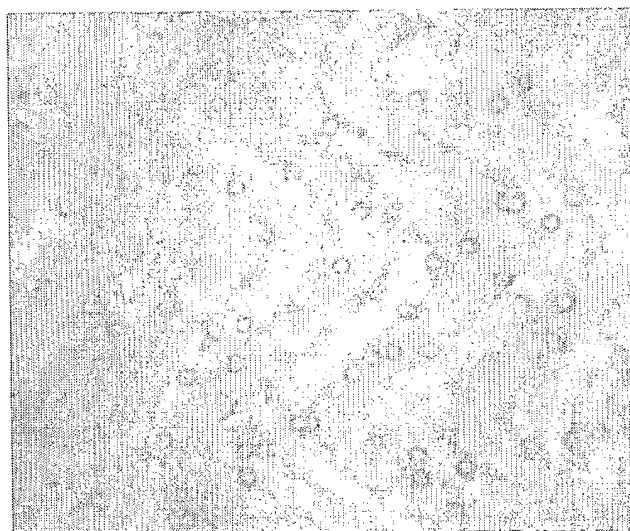


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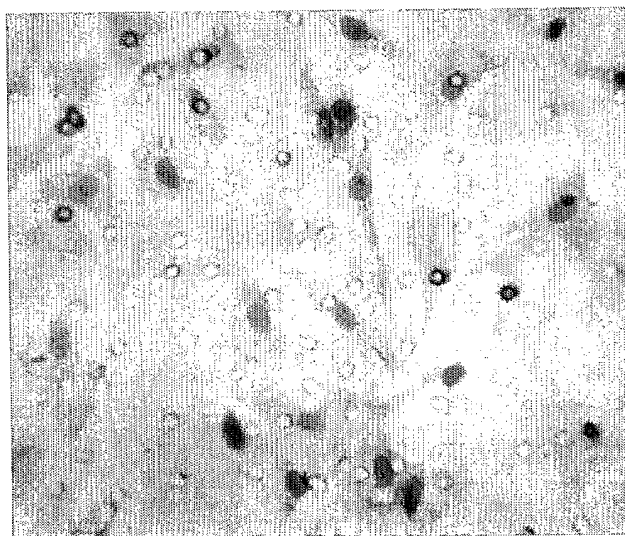


Fig. 21B

20/22

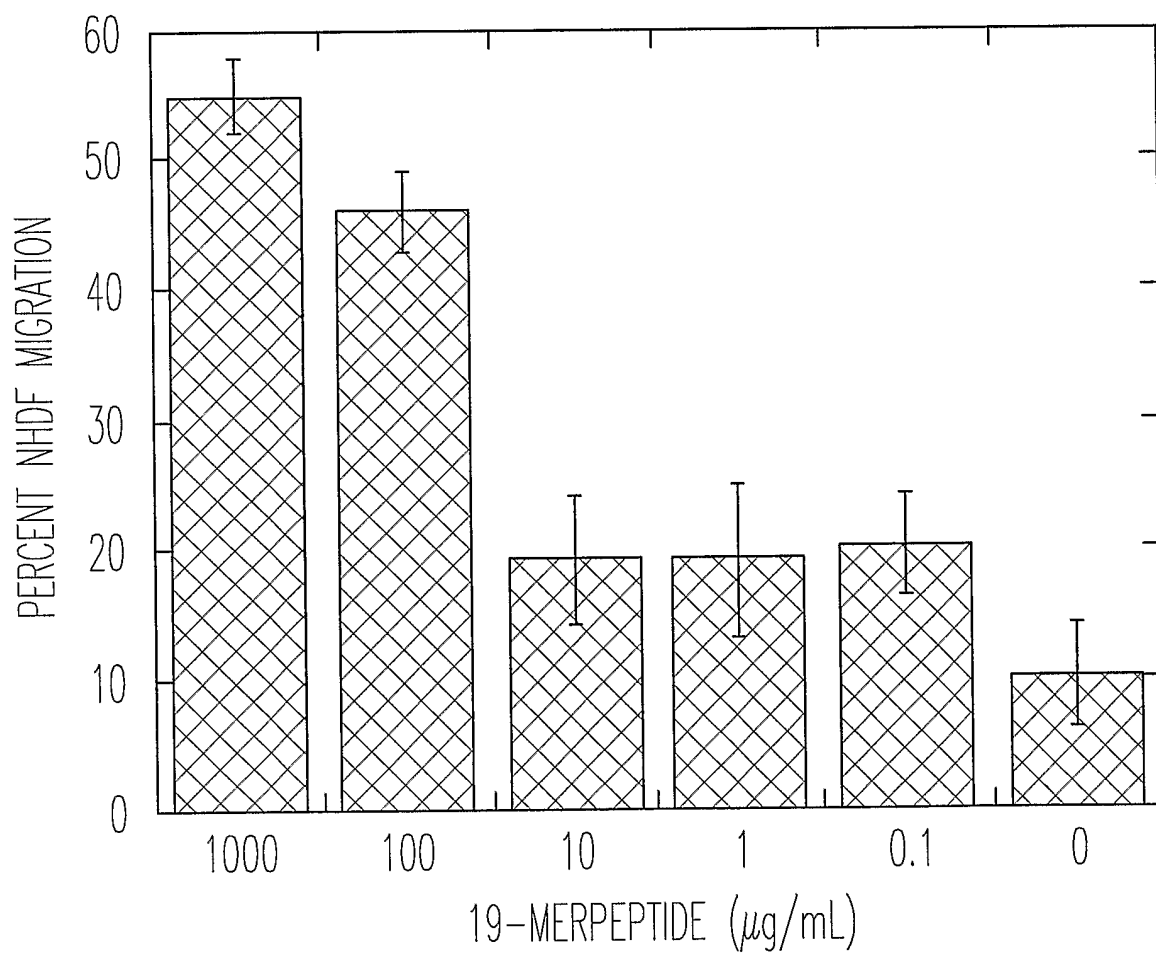


Fig. 22

21/22

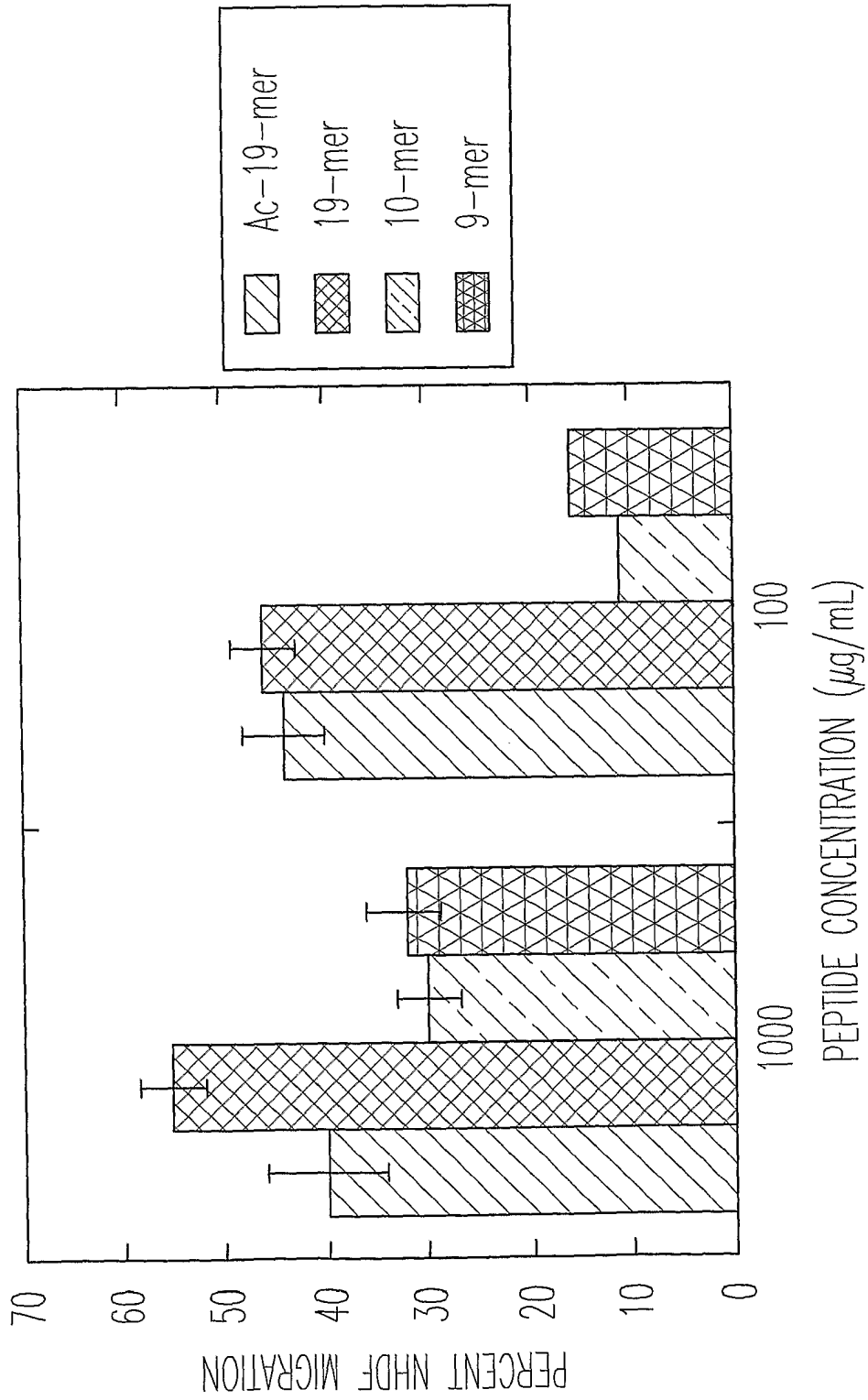


Fig. 23

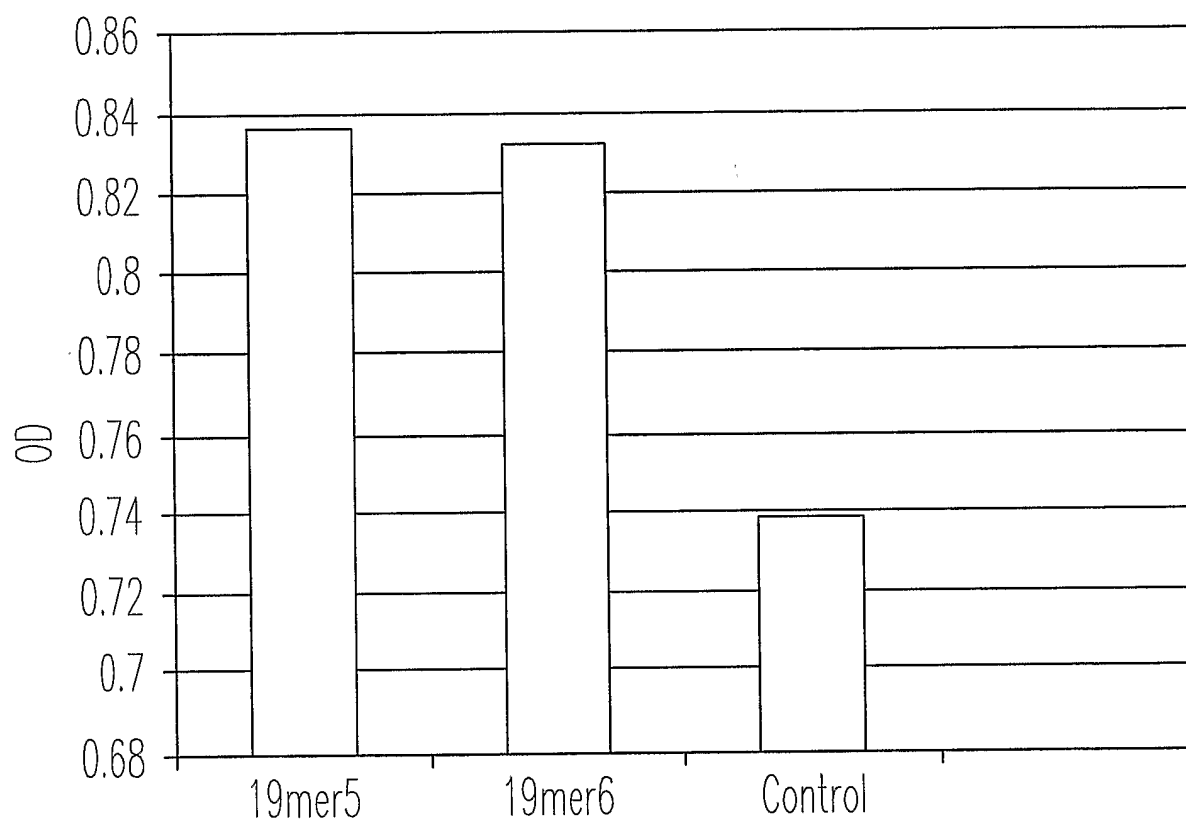


Fig. 24

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/26198

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12N 9/99
 US CL : 435/184

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 U.S. : 435/184

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
 WEST

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99/31969 A2 (AMERICAN HOME PRODUCTS CORPORATION) 01 July 1999 (01.07.99), abstract, claims.	1-73

Further documents are listed in the continuation of Box C.

See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

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