US 20200255497A1

(19) **United States**

(12) **Patent Application Publication**

**Ouzounov et al.**

(10) **Pub. No.: US 2020/0255497 A1**

(43) **Pub. Date: Aug. 13, 2020**

(54) **RECOMBINANT COLLAGEN AND ELASTIN MOLECULES AND USES THEREOF**

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(21) Appl. No.: **16/839,044**

(22) Filed: **Apr. 2, 2020**

**Related U.S. Application Data**

(63) Continuation of application No. 16/144,914, filed on Sep. 27, 2018.

(60) Provisional application No. 62/657,591, filed on Apr. 13, 2018, provisional application No. 62/564,964, filed on Sep. 28, 2017.

**Publication Classification**

(51) **Int. Cl.**

| | |
|---|---|
| ***C07K 14/78*** | (2006.01) |
| ***A61K 38/39*** | (2006.01) |
| ***A61K 8/65*** | (2006.01) |
| ***A61Q 17/04*** | (2006.01) |
| ***A61Q 19/08*** | (2006.01) |

(52) **U.S. Cl.**

CPC .............. ***C07K 14/78*** (2013.01); ***A61K 38/39*** (2013.01); ***A61Q 19/08*** (2013.01); ***A61Q 17/04*** (2013.01); ***A61K 8/65*** (2013.01)

(57) **ABSTRACT**

This disclosure provides non-naturally occurring collagen and elastin molecules. The non-naturally occurring collagens and elastins include truncated collagens, truncated elastins, as well as fusion proteins thereof. The non-naturally occurring collagen and elastin are useful in foods, cosmetics and many other products and uses.

**Specification includes a Sequence Listing.**

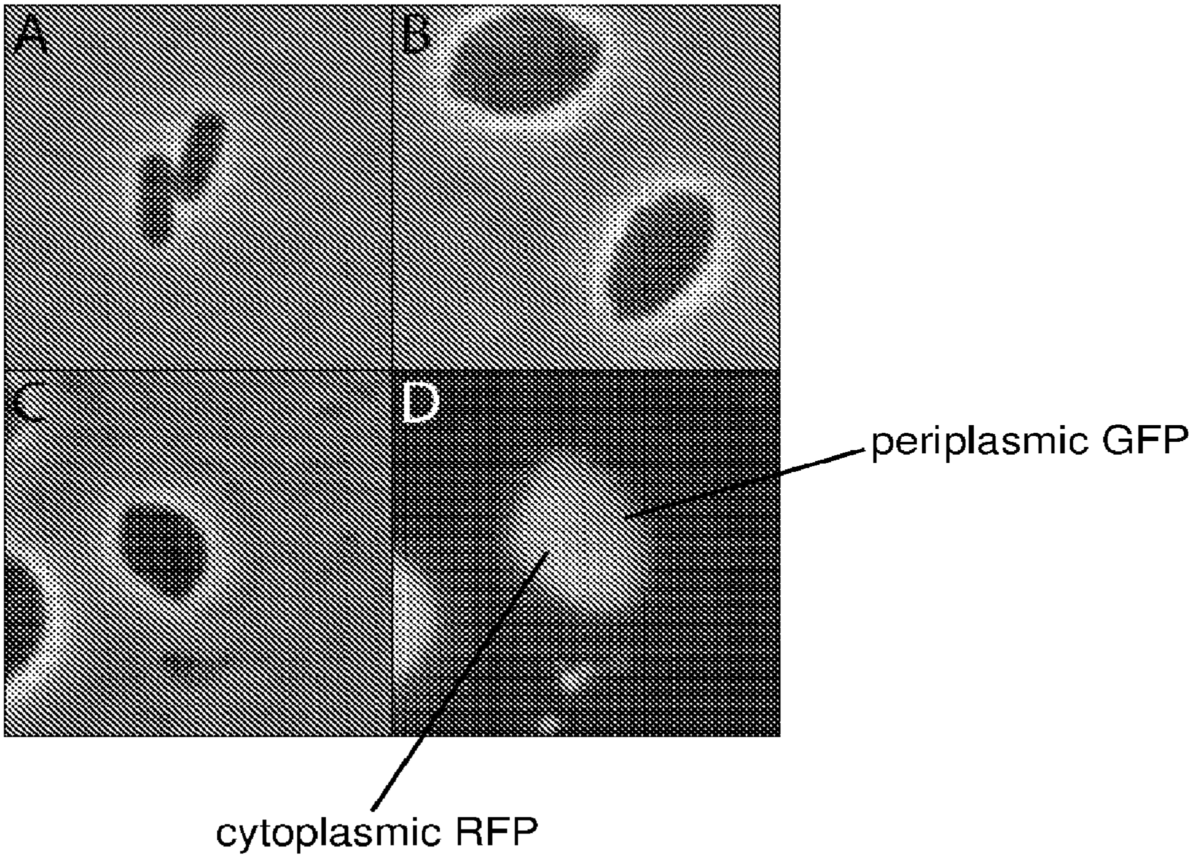


Fig. 1

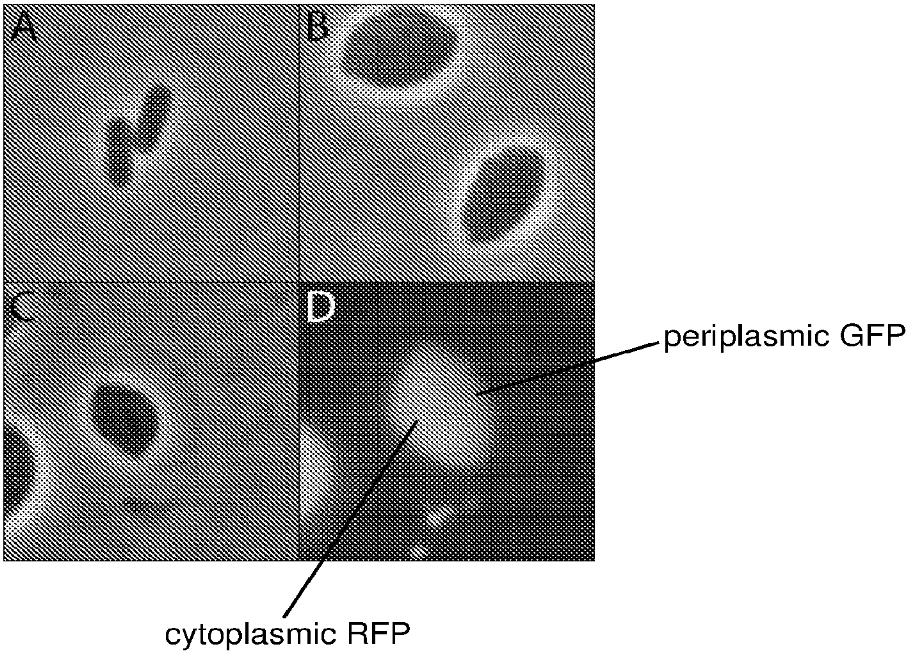


Fig. 2

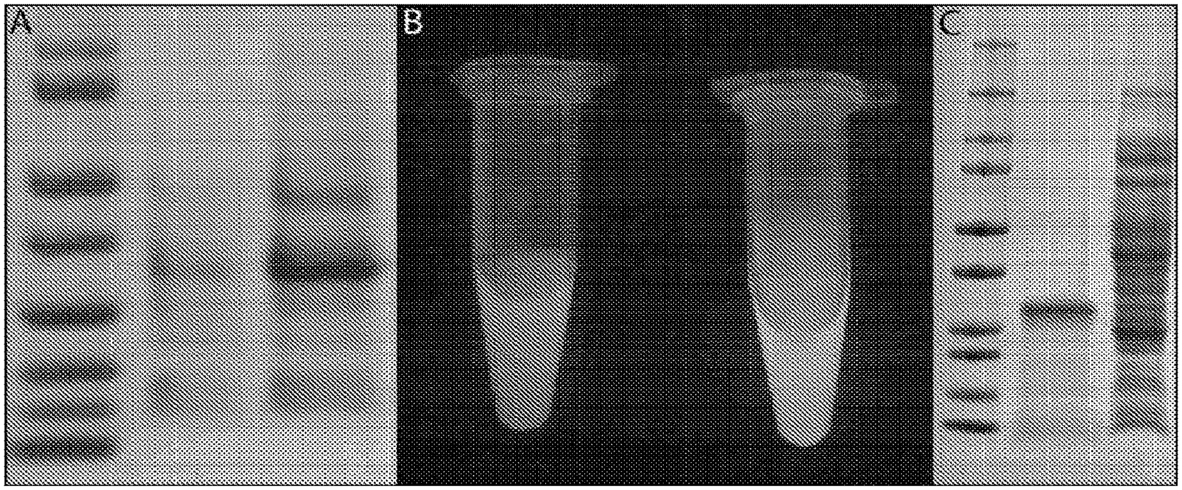


Fig. 3

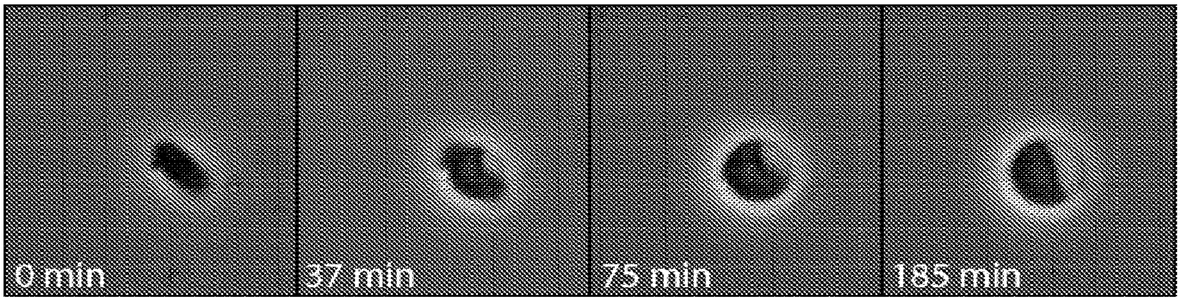


Fig. 4

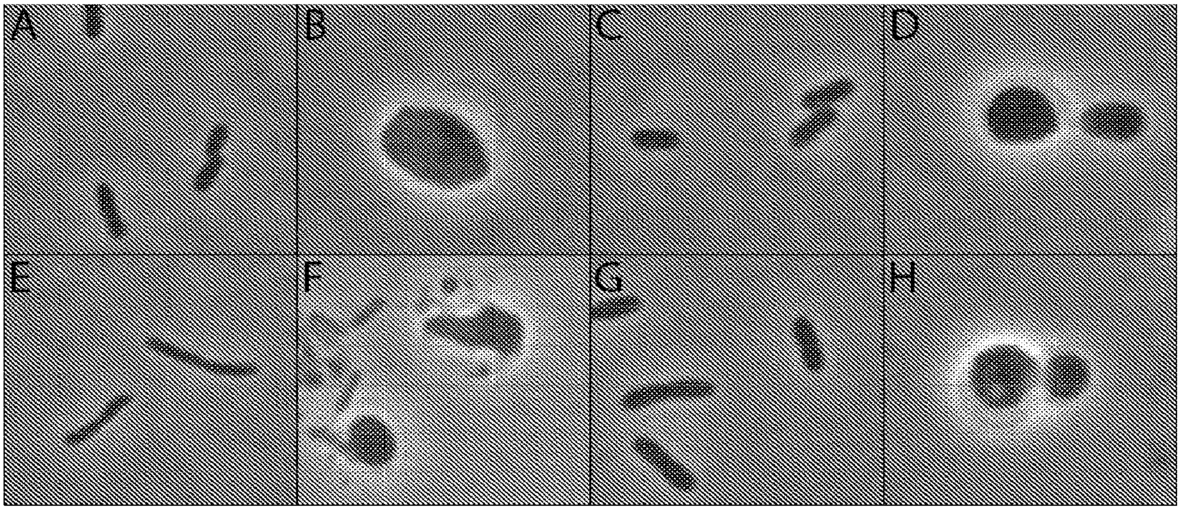
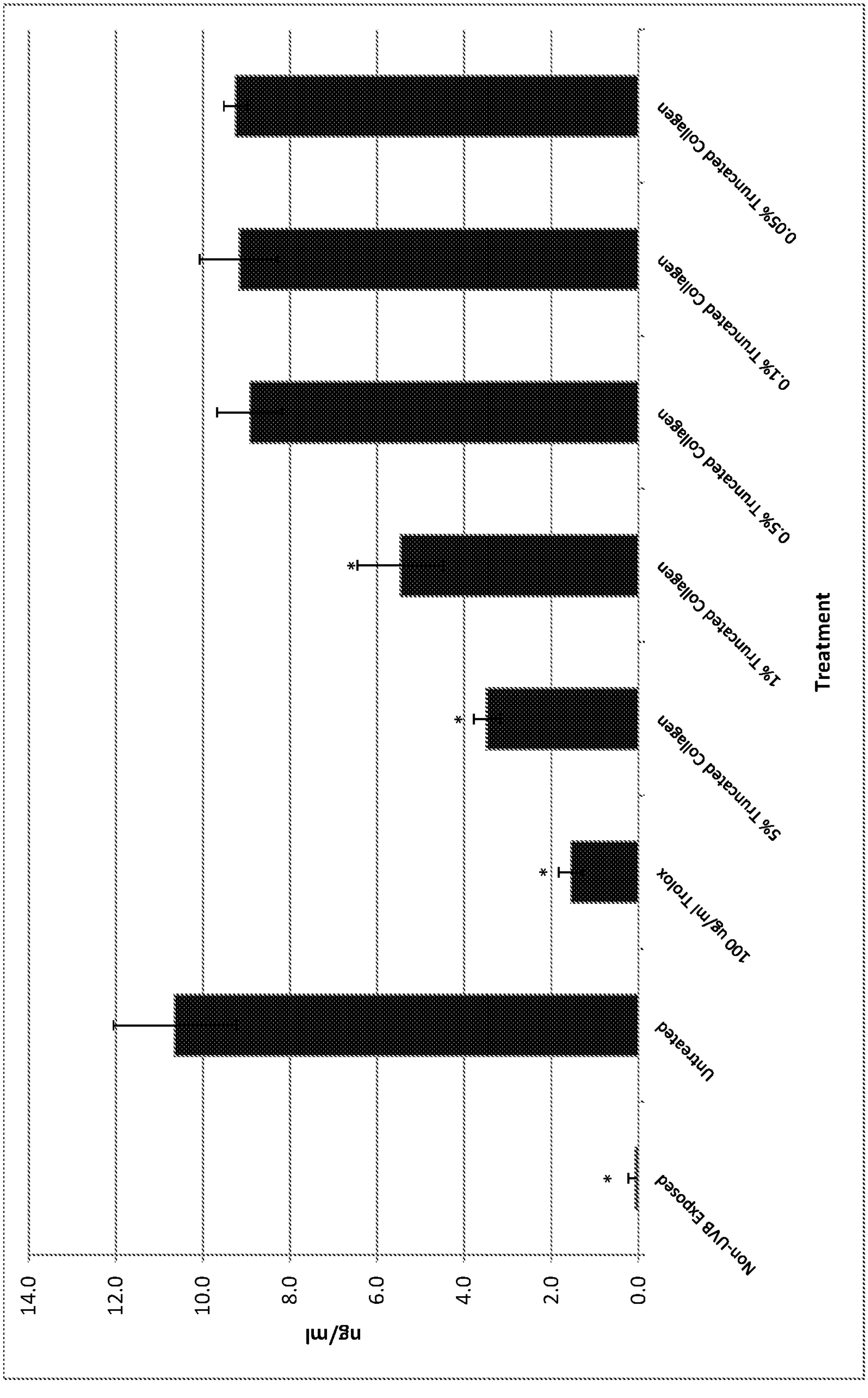


Fig. 5


ng/ml
14.0
12.0
10.0
8.0
6.0
4.0
2.0
0.0
*
Non-UVB Exposed
Untreated
*
100 ug/ml Trolox
*
5% Truncated Collagen
*
1% Truncated Collagen
0.5% Truncated Collagen
0.1% Truncated Collagen
0.05% Truncated Collagen
Treatment

# RECOMBINANT COLLAGEN AND ELASTIN MOLECULES AND USES THEREOF

## CROSS-REFERENCE

**[0001]** This application is a continuation application of U.S. patent application Ser. No. 16/144,914, filed Sep. 27, 2018, which application claims priority from U.S. Provisional Patent Application No. 62/564,964, filed Sep. 28, 2017, and U.S. Provisional Patent Application No. 62/657,591, filed Apr. 13, 2018, the disclosures of which are incorporated by reference herein in their entirety.

## SEQUENCE LISTING

**[0002]** The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Nov. 21, 2018, is named 57607702SL.txt and is 320,570 bytes in size.

## FIELD

**[0003]** The present disclosure relates to non-naturally occurring full-length and truncated collagen molecules and full-length and truncated elastin molecules and uses thereof.

## BACKGROUND

**[0004]** Collagens and similar proteins are the most abundant proteins in the biosphere. Collagens and elastins are structural proteins found in the skin, connective tissue and bone of animals and other tissues. In humans, the amount of collagen present in the body is approximately one third of the total proteins and accounts for about three fourths of the dry weight of skin. Elastin is a highly elastic protein found in connective tissue and other types of tissue.

**[0005]** The structure of collagen is a triple helix in which three polypeptide strands together form a helical coil. The individual polypeptide strands are composed of repeating triplet amino acid sequences designated as GLY-X-Y. X and Y can be any amino acid and the third amino acid is glycine. The amino acids proline and hydroxyproline are found in high concentrations in collagen. The most common triplet is proline-hydroxyproline-glycine (Gly-Pro-Hyp) accounting for approximately 10.5% of the triplets in collagen.

**[0006]** Gelatin is a product obtained by partial hydrolysis of collagen. Typically, gelatin is produced by acid hydrolysis, alkaline hydrolysis, and enzymatic hydrolysis or by exposing collagen to heat in an aqueous solution (e.g., boiling the bones and skins of animal, boiling fish scales, etc.).

**[0007]** Gelatin is used in many products including cosmetics, foods, pharmaceuticals, medical devices, photographic films, adhesives, binders and many others. The physical and chemical properties of gelatin are tuned to the particular application. These physical/chemical properties include gel strength, melting point temperature, viscosity, color, turbidity, pH, isoelectric point and others.

**[0008]** Elastin is an elastic protein that is crucial for the proper functioning of arteries, lung, tendons, ligament, skin and other tissue. Elastin provides the tissues with the ability to stretch and return to its original shape. The protein tropoelastin is the building block of elastin. In contrast to collagen that include a family of genes, there is one tropoelastin gene in humans. When expressed, the single elastin gene is spliced to produce different forms of the tropoelastin protein. Many tropoelastin molecules associate together to form elastin.

**[0009]** L-form bacteria, or L-forms, are bacterial strains derived from parent species (N-forms) that are able to grow as cell wall-deficient (spheroplast type) or as cell wall-less (protoplast type) cells. See, Madoff S (Ed): The Bacterial L-Forms. New York: Marcel Dekker Inc., 1986; Mattmann L H (Ed): Cell Wall Deficient Forms. Boca Raton: CRC Press; 1993; and Gumpert J, Taubeneck U: Characteristic properties and biological significance of stable protoplast type L-forms. In Protoplasts, Lecture Proceedings of the 6th International Protoplast Symposium: Basel. Experientia 1983, 46(suppl):227-241.

**[0010]** Protoplast type L-forms have been cultivated in the cell wall-less state and represent genetically stable mutants showing extreme pleiotropic changes, including the inability to form cell walls, capsules, flagella, pili, spores and mesosomes, altered colony and cell morphology, qualitative and quantitative changes in the lipid and protein components of the cytoplasmic membrane, the absence of extracellular proteolytic activities, resistance against bacteriophages and the incapability to propagate outside laboratory conditions. See, Gumpert and Taubeneck (supra); and Hoischen et al., Lipid and fatty acid composition of cytoplasmic membranes from *Streptomyces* hygroscopic and its stable protoplast type L-form. J Bacteriol 1997, 179:3430-3436.

## SUMMARY

**[0011]** In one aspect, a non-naturally occurring collagen produced by a host cell is provided. The non-naturally occurring collagen is jellyfish (Hydrozoan) collagen, human collagen, *Chondrosia reniformis* (kidney sponge) collagen, or *Rhincodon typus* (whale shark) collagen. In an embodiment, the non-naturally occurring collagen is a full-length or a truncated collagen. In one embodiment, the collagen is truncated by an internal truncation of between 50 amino acids and 500 amino acids. In another embodiment, the truncation is at the C-terminal end or the N-terminal end of the collagen polypeptide. The non-naturally occurring collagens are SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 89 SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO:110, or SEQ ID NO: 112.

**[0012]** In another aspect, the non-naturally occurring collagen further comprises amino acid sequences including a secretion tag, a histidine tag, a green fluorescent protein tag, a protease cleavage site, a Beta-lactamase and/or GEK amino acid trimer repeats and/or GDK amino acid trimer repeats. When the non-naturally occurring collagen comprises one or more amino acid trimer repeats of the sequence glycine-glutamic acid-lysine (GEK) and/or glycine-aspartic acid-lysine (GDK), the number of GEK and/or GDK trimer repeats can range from 2 to 50 trimer repeats (SEQ ID NOS: 130-131, respectively). In one aspect, the secretion tag is DsbA, PelB, OmpA, TolB, MalE, lpp, TorA, or HylA, or a hybrid secretion tag that comprises a portion of one secretion tag fused to a portion of a second secretion tag. An exemplary secretion tag is DsbA.

**[0013]** In one aspect, provided are compositions that comprise between 0.005% and 30% w/w non-naturally occurring collagen. The compositions can further comprise at least one additional ingredient comprising a topical carrier or a preservative.

**[0014]** Compositions comprising non-naturally occurring collagen are in one aspect topical compositions for applying to skin. The topical compositions are used for decreasing skin damage or promoting the repair of damaged skin.

**[0015]** One aspect provides methods for decreasing skin damage or promoting the repair of damaged skin. The method comprises applying the composition comprising elastin to the skin of a subject. The method increases the viability of the fibroblast cells or keratinocytes of the skin of the subject. In another aspect the application of the composition increases the synthesis of procollagen by the fibroblast cells of the subject's skin. In another aspect the topical application of the composition protects skin or keratinocytes against UV damage. In yet another embodiment, thymine-thymine (TT) dimer formation is decreased by the collagens or elastins disclosed herein.

**[0016]** Another aspect provided herein are methods of increasing the viability of skin cells. The method comprises applying collagen or elastin molecules to the skin or skin cell. The collagen or elastin as provided increases the viability of keratinocytes and/or fibroblasts is increased upon exposure to UV radiation, urban dust or other damaging stimuli.

**[0017]** In another aspect provided herein are methods for decreasing the production of inflammatory cytokines in a skin cell. In one embodiment the skin cell is a keratinocyte. The method comprises applying a collagen or elastin molecule to a skin cell. The production of inflammatory cytokines including TNFα, IL-1α, IL-1β, IL-3, IL-6, IL-7, IL-8, IL-10, IL-18, and IL-1RA.

**[0018]** In another aspect, provided are methods of protecting skin cells against the effect of exposure to urban dust. The method comprises the step of applying the collagen or elastin disclosed herein to the skin cell. The exposure of skin cell to collagen or elastin increases the viability of the skin cell. In an embodiment, the skin cell is a keratinocyte or a fibroblast.

**[0019]** In one aspect, a non-naturally occurring elastin produced by a host cell is provided. The non-naturally occurring elastin is jellyfish elastin, human elastin, *Chondrosia reniformis* (kidney sponge) elastin, or *Rhincodon typus* elastin. In an embodiment, the non-naturally occurring elastin is a full-length or truncated elastin. In one embodiment, the elastin is truncated by an internal truncation of between 50 amino acids and 500 amino acids. In another embodiment, the truncation is at the C-terminal end or the N-terminal end of the elastin polypeptide. The non-naturally occurring elastins are SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55 SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 98, or SEQ ID NO: 110.

**[0020]** In another aspect, the non-naturally occurring elastin further comprises amino acid sequences including a secretion tag, a histidine tag, a green fluorescent protein tag, a protease cleavage site, a Beta-lactamase and/or GEK amino acid trimer repeats and/or GDK amino acid trimer repeats. When the non-naturally occurring collagen comprises one or more amino acid trimer repeats of the sequence glycine-glutamic acid-lysine (GEK) and/or glycine-aspartic acid-lysine (GDK), the number of GEK and/or GDK trimer repeats can range from 2 to 50 trimer repeats (SEQ ID NOS: 130-131, respectively). In one aspect, the secretion tag is DsbA, PelB, OmpA, TolB, MalE, lpp, TorA, or HylA, or a hybrid secretion tag that comprises a portion of one secretion tag fused to a portion of a second secretion tag. An exemplary secretion tag is DsbA.

**[0021]** In another embodiment, compositions that comprise between 0.005% and 30% w/w non-naturally occurring elastin are provided. The compositions can further comprise at least one additional ingredient comprising a topical carrier or a preservative.

**[0022]** Compositions comprising non-naturally occurring elastin are in one aspect topical compositions for applying to skin. The topical compositions are used for decreasing skin damage or promoting the repair of damaged skin.

**[0023]** One embodiment provides methods for decreasing skin damage or promoting the repair of damaged skin. The method comprises applying the composition comprising elastin to the skin of a subject. The method increases the viability of the fibroblast cells of the skin of the subject. In another aspect the application of the composition increases the synthesis of procollagen by the fibroblast cells of the subject's skin. In another aspect the topical application of the compositions protects skin or keratinocytes against UV damage. In yet another embodiment, thymine-thymine (TT) dimer formation is decreased by the collagens or elastins disclosed herein.

**[0024]** Another embodiment provides polynucleotides that encode a non-naturally occurring collagen or a non-naturally occurring elastin. The polynucleotides encode collagen or elastin from jellyfish, human, *Chondrosia reniformis* (kidney sponge), or *Rhincodon typus*. The encoded collagen or elastin may be full length or truncated. In one embodiment, the collagen or elastin is truncated by an internal truncation of between 50 amino acids and 500 amino acids.

**[0025]** In one embodiment polynucleotides that encode fusion proteins comprising a secretion tag, a histidine tag, a green fluorescent protein tag, a protease cleavage site, a Beta-lactamase along and/or GEK amino acid trimer repeat and/or GDK amino acid trimer repeats together with collagen or elastin are provided. The non-naturally occurring collagen or elastin may comprise one or more amino acid trimer repeats of the sequence glycine-glutamic acid-lysine (GEK) and/or glycine-aspartic acid-lysine (GDK), the number of GEK and/or GDK trimer repeats can range from 2 to 50 trimer repeats (SEQ ID NOS: 130-131, respectively). In one aspect, the secretion tag is DsbA, PelB, OmpA, TolB, MalE, lpp, TorA, or HylA, or a hybrid secretion tag that comprises a portion of one secretion tag fused to a portion of a second secretion tag. An exemplary embodiment secretion tag is DsbA.

**[0026]** The polynucleotides and vectors can be used to transform host cells and express the polynucleotides. Polynucleotides encoding a non-naturally occurring collagen, wherein the polynucleotide is SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19 SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO:

95, SEQ ID NO: 97, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO:111, SEQ ID NO: 113, or SEQ ID NO: 105 are provided. Polynucleotides encoding a non-naturally occurring elastin, wherein the polynucleotide is SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, and SEQ ID NO: 72, SEQ ID NO: 99, or SEQ ID NO: 101 provided.

**[0027]** Host cells that express the polynucleotides of the invention are disclosed. Host cells can be any host cell including bacterial cells, yeast cells, fungal cells, insect cells, mammalian cells, plant cells and any other cells used to express exogenous polynucleotides.

**[0028]** Bacterial host cells in which the cells have been modified to inhibit cell division and the periplasmic space is increased are provided. An exemplary host cell is *E. coli.*

**[0029]** One embodiment provides a method of producing a non-naturally occurring collagen or a non-naturally occurring elastin. The method comprises the steps of inoculating a culture medium with a recombinant host cell comprising polynucleotides that encode the collagen or elastin, cultivating the host cell, and isolating the non-naturally occurring collagen or the non-naturally occurring elastin from the host cell.

## BRIEF DESCRIPTION OF THE DRAWINGS

**[0030]** FIG. **1** depicts the physiological state difference between switched and unswitched cells. A) Unswitched *Escherichia coli* cells. B) Same *Escherichia coli* population as figure A but has undergone the physiological switch. C) Phase contrast of switched *Escherichia coli* cell containing cytoplasmic RFP and periplasmic GFP. D) Fluorescent imaging of cell in figure C illustrates targeted protein localization.

**[0031]** FIG. **2** depicts enhanced protein production in switched cells. A-B) Target protein for T7 inducible protein production is periplasmic expressed GFP, produced in *Escherichia coli* BL21. The same population of cells was used and induced at OD 1.1. A) Protein ladder (lane 1), IPTG induced protein production (lane 2), IPTG induced protein production with physiological switch (lane 3). B) Two vials of the cell GFP induced cultures with IPTG only on left and IPTG+Switch on right. C) Expression of a 22 kDa collagen using switched cells showing protein ladder (lane 1), supernatant after protein production (lane 2), cell pellet (lane 3).

**[0032]** FIG. **3** depicts a time-lapse of *Escherichia coli* cell switching over time.

**[0033]** FIG. **4** illustrates other organisms undergoing the physiological switch. A) *Agrobacterium tumefaciens* normal physiology. B) *Agrobacterium tumefaciens* switched physiology. C) *Pseudomonas aeruginosa* PAO1 normal physiology. D) *Pseudomonas aeruginosa* PAO1 switched physiology. E) *Brevundimonas diminuta* normal physiology. F) *Brevundimonas diminuta* switched physiology. G) *Agrobacterium tumefaciens* normal physiology. H) *Agrobacterium tumefaciens* switched physiology.

**[0034]** FIG. **4** illustrates other organisms undergoing the physiological switch. A) *Agrobacterium tumefaciens* normal physiology. B) *Agrobacterium tumefaciens* switched physiology. C) *Pseudomonas aeruginosa* PAO1 normal physiology. D) *Pseudomonas aeruginosa* PAO1 switched physiology. E) *Brevundimonas diminuta* normal physiology. F) *Brevundimonas diminuta* switched physiology. G) *Agrobacterium tumefaciens* normal physiology. H) *Agrobacterium tumefaciens* switched physiology.

**[0035]** FIG. **5** illustrates the reduction in TT dimer formation by treatment of human keratinocytes with truncated collagen.

## DESCRIPTION

**[0036]** In the following description, certain specific details are set forth in order to provide a thorough understanding of various embodiments of the disclosure. However, one skilled in the art will understand that the disclosure may be practiced without these details.

**[0037]** As used herein the term "about" refers to +10%.

**[0038]** The term "consisting of" means "including and limited to".

**[0039]** The term "consisting essentially of" means that the composition, method or structure may include additional ingredients, steps and/or parts, but only if the additional ingredients, steps and/or parts do not materially alter the basic and novel characteristics of the claimed composition, method or structure.

**[0040]** As used herein, the singular form "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a compound" or "at least one compound" may include a plurality of compounds, including mixtures thereof.

**[0041]** Throughout this application, various embodiments of this disclosure may be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the disclosure. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 3, 4, 5, and 6. This applies regardless of the breadth of the range.

**[0042]** Whenever a numerical range is indicated herein, it is meant to include any cited numeral (fractional or integral) within the indicated range. The phrases "ranging/ranges between" a first indicate number and a second indicate number and "ranging/ranges from" a first indicate number "to" a second indicate number are used herein interchangeably and are meant to include the first and second indicated numbers and all the fractional and integral numerals there between.

**[0043]** As used herein the term "method" refers to manners, means, techniques and procedures for accomplishing a given task including, but not limited to, those manners, means, techniques and procedures either known to, or readily developed from known manners, means, techniques and procedures by practitioners of the chemical, pharmacological, biological, biochemical and medical arts.

**[0044]** The term "collagen" or "collagen-like" as used herein refers to a monomeric polypeptide that can associate with one or more collagen or collagen-like polypeptides to form a quaternary structure. Collagen can be treated with acid, base or heat to prepare gelatin. The quaternary structure of natural collagen is a triple helix typically composed of three polypeptides. Of the three polypeptides that form natural collagen, two are usually identical and are designated as the alpha chain. The third polypeptide is designated as the beta chain. Thus a typical natural collagen can be designated as AAB, wherein the collagen is composed of two alpha ("A") strands and one beta ("B") strand. The term "procollagen" as used herein refers to polypeptides produced by cells that can be processed to naturally occurring collagen.

**[0045]** The terms "elastin" as used herein refers to a polypeptide that is elastic and functions to stretch or contract and return to its original shape. Elastin is found naturally in connective tissue.

**[0046]** The term "expression vector" or "vector" as used herein refers to a nucleic acid assembly which is capable of directing the expression of the exogenous gene. The expression vector may include a promoter which is operably linked to the exogenous gene, restriction endonuclease sites, nucleic acids that encode one or more selection markers, and other nucleic acids useful in the practice of recombinant technologies.

**[0047]** The term "fibroblast" as used herein refers to a cell that synthesizes procollagen and other structural proteins. Fibroblasts are widely distributed in the body and found in skin, connective tissue and other tissues.

**[0048]** The term "fluorescent protein" is a protein that is commonly used in genetic engineering technologies used as a reporter of expression of an exogenous polynucleotide. The protein when exposed to ultraviolet or blue light fluoresces and emits a bright visible light. Proteins that emit green light is green fluorescent protein (GFP) and proteins that emit red light is red fluorescent protein (RFP).

**[0049]** The term "gelatin" as used herein refers to collagen that has been further processed by exposure to acid, base or heat. While not wishing to be bound by theory or mechanism, treatment of collagen with acid, base or heat is thought to denature the collagen polypeptides. Aqueous denatured collagen solutions form reversible gels used in foods, cosmetics, pharmaceuticals, industrial products, medical products, laboratory culture growth media, and many other applications.

**[0050]** The term "gene" as used herein refers to a polynucleotide that encodes a specific protein, and which may refer to the coding region alone or may include regulatory sequences preceding (5' non-coding sequences) and following (3' non-coding sequences) the coding sequence.

**[0051]** The term "histidine tag" is a 2-30 contiguous series of histidine residues on a recombinant polypeptide.

**[0052]** The term "host cell" is a cell that is engineered to express an introduced exogenous polynucleotide.

**[0053]** The term"keratinocyte" is a cell that produces keratins found in the epidermal layer of the skin.

**[0054]** The term "lactamase" as used herein refer to enzymes that hydrolyze antibiotics that contain a lactam (cyclic amide) moiety. "Beta-lactamase" or "β-lactamase" are enzymes that hydrolyze antibiotics that contain a β-lactam moiety.

**[0055]** The term "non-naturally occurring" as used herein refers to collagen or elastin that is not normally found in nature. The non-naturally occurring collagen or elastin are recombinantly prepared. The non-naturally occurring collagen or elastin is a recombinant collagen or recombinant elastin. The non-naturally occurring collagen is in one embodiment a truncated collagen. Other non-naturally occurring collagen polypeptides include chimeric collagens. A chimeric collagen is a polypeptide wherein one portion of a collagen polypeptide is contiguous with a portion of a second collagen polypeptide. For example, a collagen molecule comprising a portion of a jellyfish collagen contiguous with a portion of a human collagen is a chimeric collagen. In another embodiment, the non-naturally occurring collagen comprises a fusion polypeptide that includes additional amino acids such as a secretion tag, histidine tag, green fluorescent protein, protease cleavage site, GEK repeats, GDK repeats, and/or beta-lactamase. The non-naturally occurring elastin in one embodiment a truncated elastin. Other non-naturally occurring elastin polypeptides include chimeric elastins. A chimeric elastin is a polypeptide wherein one portion of an elastin polypeptide is contiguous with a portion of a second elastin polypeptide. For example, a collagen molecule comprising a portion of a jellyfish elastin contiguous with a portion of a human elastin is a chimeric elastin. In another embodiment, the non-naturally occurring elastin comprises a fusion polypeptide that includes additional amino acids such as a secretion tag, histidine tag, green fluorescent protein, protease cleavage site and/or beta-lactamase. The chimeric gelatin or the chimeric elastin can comprise additional amino acids such as a secretion tag, histidine tag, green fluorescent protein, protease cleavage site, GEK repeats, GDK repeats, and/or beta-lactamase.

**[0056]** The term "protease cleavage site" is an amino acid sequence that is cleaved by a specific protease.

**[0057]** The term "secretion tag" or "signal peptide" refers to an amino acid sequence that recruits the host cell's cellular machinery to transport an expressed protein to a particular location or cellular organelle of the host cell.

**[0058]** The term "truncated collagen" refers to a monomeric polypeptide that is smaller than a full-length collagen wherein one or more portions of the full-length collagen is not present. Collagen polypeptides are truncated at the C-terminal end, the N-terminal end, or truncated by removal of internal portion(s) of the full-length collagen polypeptide.

**[0059]** The term "truncated elastin" refers to a monomeric polypeptide that is smaller than a full-length elastin wherein one or more portions of the full-length elastin is not present. Elastin polypeptides are truncated at the C-terminal end, the N-terminal end, or truncated by removal of internal portion (s) of the full-length elastin polypeptide.

**[0060]** In co-owned application PCT/US17/24857, incorporated by reference, an expression system that uses modified bacterial cells (switched cells) in which cell division is inhibited and growth of the periplasmic space is greatly enhanced was disclosed. In this expression system, the expressed proteins are targeted to the periplasmic space. Recombinant protein production in these switched cells is dramatically increased compared with that in non-switched cells. Structurally, the cells comprise both inner and outer membranes but lack a functional peptidoglycan cell wall, while the cell shape is spherical and increases in volume over time. Notably, while the periplasmic space normally comprises only 10-20% of the total cell volume, the periplasmic compartment of the switched state described herein can comprise more than 20%, 30%, 40% or 50% and up to 60%, 70%, 80% or 90% of the total cell volume.

**[0061]** The modified bacterial cells of PCT/US17/24857 are derived from Gram-negative bacteria, e.g. selected from: gammaproteobacteria and alphaproteobacteria. In some embodiments, the bacterium is selected from: *Escherichia* *coli, Vibrio natriegens, Pseudomonas fluorescens, Caulobacter crescentus, Agrobacterium tumefaciens*, and *Brevundimonas diminuta*. In specific embodiments, the bacterium is *Escherichia coli*, e.g. strain BL21(DE3).

**[0062]** In another aspect, the host bacterial cells have an enlarged periplasmic space in a culture medium comprising a magnesium salt, wherein the concentration of magnesium ions in the medium is at least about 3, 4, 5 or 6 mM. In further embodiments, the concentration of magnesium ions in the medium is at least about 7, 8, 9 or 10 mM. In some embodiments, the concentration of magnesium ions in the medium is between about 5 mM and 25 mM, between about 6 mM and/or about 20, 15 or 10 mM. In some embodiments, the magnesium salt is selected from: magnesium sulfate and magnesium chloride.

**[0063]** In other embodiments, the culture medium further comprises an osmotic stabilizer, including, e.g. sugars (e.g., arabinose, glucose, sucrose, glycerol, sorbitol, mannitol, fructose, galactose, saccharose, maltotrioseerythritol, ribitol, pentaerythritol, arabitol, galactitol, xylitol, iditol, maltotriose, and the like), betaines (e.g., trimethylglycine), proline, sodium chloride, wherein the concentration of the osmotic stabilizer in the medium is at least about 4%, 5%, 6%, or 7% (w/v). In further embodiments, the concentration of osmotic stabilizer is at least about 8%, 9%, or 10% (w/v). In some embodiments, the concentration of the osmotic stabilizer in the medium is between about 5% to about 20% (w/v).

**[0064]** In some embodiments, the cell culture may further comprise ammonium chloride, ammonium sulfate, calcium chloride, amino acids, iron(II) sulfate, magnesium sulfate, peptone, potassium phosphate, sodium chloride, sodium phosphate, and yeast extract.

**[0065]** The host bacterial cell may be cultured continuously or discontinuously; in a batch process, a fed-batch process or a repeated fed-batch process.

**[0066]** In some embodiments, the antibiotic is selected from: β-lactam antibiotics (e.g. penicillins, cephalosporins, carbapenems, and monobactams), phosphonic acid antibiotics, polypeptide antibiotics, and glycopeptide antibiotics. In particular embodiments, the antibiotic is selected from alafosfalin, amoxicillin, ampicillin, aztreonam, bacitracin, carbenicillin, cefamandole, cefotaxime, cefsulodin, cephalothin, fosmidomycin, methicillin, nafcillin, oxacillin, penicillin g, penicillin v, fosfomycin, primaxin, and vancomycin.

**[0067]** Without being bound by theory, the cell morphology that promotes recombinant protein production and inhibits cell division appears to be driven by the removal of the cell wall under the media conditions stated above. In some embodiments, the methods for removal/inhibition of cell wall synthesis can be through the use of antibiotics that inhibit peptidoglycan synthesis (such as ampicillin, carbenicillin, penicillins or fosfomycin), or other methods known in the art.

**[0068]** When having an appropriate periplasmic targeting signal sequence, recombinantly produced polypeptides can be secreted into the periplasmic space of bacterial cells. Joly, J. C. and Laird, M. W., in The Periplasm ed. Ehrmann, M., ASM Press, Washington D.C., (2007) 345-360. In the chemically oxidizing environment of the periplasm the formation of disulfide bonds and thereby the functionally correct folding of polypeptides is favored.

**[0069]** In general, the signal sequence may be a component of the expression vector, or it may be a part of the exogenous gene that is inserted into the vector. The signal sequence selected should be one that is recognized and processed (i.e., cleaved by a signal peptidase) by the host cell. For bacterial host cells that do not recognize and process the native signal sequence of the exogenous gene, the signal sequence is substituted by any commonly known bacterial signal sequence. In some embodiments, recombinantly produced polypeptides can be targeted to the periplasmic space using the DsbA signal sequence. Dinh and Bernhardt, J Bacteriol, September 2011, 4984-4987.

**[0070]** In one aspect, t a non-naturally occurring collagen or elastin is produced by a host cell is provided. The non-naturally occurring collagen or elastin is jellyfish collagen or elastin, t, human collagen or elastin, or *Chondrosia reniformis* (kidney sponge) collagen or elastin, or *Rhincodon typus* collagen or elastin. The non-naturally occurring collagen or elastin is a truncated collagen. The truncation is an internal truncation, a truncation at the N-terminal portion of the collagen or elastin, or a truncation at the C-terminal portion of the collagen or elastin. The collagen or elastin is truncated by a truncation of between 50 amino acids and 1000 amino acids, between, 50 amino acids and 950 amino acids, between 50 amino acids and 900 amino acids, between 50 amino acids and 850 amino acids, between 50 amino acids and 800 amino acids, between 50 amino acids and 850 amino acids, between 50 amino acids and 800 amino acids, between 50 amino acids and 750 amino acids, between 50 amino acids and 700 amino acids, between 50 amino acids and 650 amino acids, between 50 amino acids and 600 amino acids, between 50 amino acids and 650 amino acids, between 50 amino acids and 500 amino acids, between 50 amino acids and 450 amino acids, between 50 amino acids and 400 amino acids, between 50 amino acids and 350 amino acids, between 50 amino acids and 300 amino acids, between 50 amino acids and 250 amino acids, between 50 amino acids and 200 amino acids, between 50 amino acids and 150 amino acids, or between 50 amino acids and 100 amino acids. In another embodiment, the collagen or elastin is truncated by 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 650, 700, 750, 800, 850, 900, 950, or 1000 amino acids. The non-naturally occurring collagen or elastin are encoded by a portion of a polynucleotide sequence or the entire polynucleotide sequence disclosed herein.

**[0071]** The non-naturally occurring collagen or elastin further comprises amino acid sequences including a secretion tag. The secretion tag directs the collagen or elastin to the periplasmic space of the host cell. In particular embodiments, the signal peptide is derived from DsbA, PelB, OmpA, TolB, MalE, lpp, TorA, or HylA, or a hybrid secretion tag that comprises a portion of one secretion tag fused to a portion of a second secretion tag. In one aspect the secretion tag is attached to the non-naturally occurring collagen or elastin. In another aspect the secretion tag is cleaved from the non-naturally occurring collagen or elastin.

**[0072]** The non-naturally occurring collagen or the non-naturally occurring elastin o further comprises a histidine tag. The histidine tag or polyhistidine tag is a sequence of 2 to 20 histidine residues (SEQ ID NO: 117) that are attached to the collagen or elastin. The histidine tag comprises 2 to 20 histidine residues (SEQ ID NO: 117), 5 to 15 histidine residues (SEQ ID NO: 118), 5 to 18 histidine residues (SEQ

ID NO: 119), 5 to 16 histidine residues (SEQ ID NO: 120), 5 to 15 histidine residues (SEQ ID NO: 118), 5 to 14 histidine residues (SEQ ID NO: 121), 5 to 13 histidine residues (SEQ ID NO: 122), 5 to 12 histidine residues (SEQ ID NO: 123), 5 to 11 (SEQ ID NO: 124), 5 to 10 histidine residues (SEQ ID NO: 125), 6 to 12 histidine residues (SEQ ID NO: 126), 6 to 11 histidine residues (SEQ ID NO: 127), or 7 to 10 histidine residues (SEQ ID NO: 128). The histidine tags are useful in purification of proteins by chromatographic methods utilizing nickel based chromatographic media. Exemplary fluorescent proteins include green fluorescent protein (GFP) or red fluorescent protein (RFP). Fluorescent proteins are well known in the art. In one embodiment the non-naturally occurring collagen or the on-naturally occurring elastin comprises a GFP and/or RFP. In one embodiment a superfolder GFP is fused to the on-naturally occurring collagen or elastin. The superfolder GFP is a GFP that folds properly even when fused to a poorly folded polypeptide. In one aspect the histidine tag is attached to the non-naturally occurring collagen or elastin. In another aspect the histidine tag is cleaved from the non-naturally occurring collagen or elastin.

**[0073]** The non-naturally occurring collagen or non-naturally occurring elastin further comprises a protease cleavage site. The protease cleavage site is useful to cleave the recombinantly produced collagen or elastin to remove portions of the polypeptide. The portions of the polypeptide that may be removed include the secretion tag, the histidine tag, the fluorescent protein tag and/or the Beta-lactamase. The proteases comprise endoproteases, exoproteases, serine proteases, cysteine proteases, threonine proteases, aspartic proteases, glutamic proteases, and metalloproteases. Exemplary protease cleavage sites include amino acids that are cleaved by Thrombin, TEV protease, Factor Xa, Enteropeptidase, and Rhinovirus 3C Protease. In one aspect the cleavage tag is attached to the non-naturally occurring collagen or elastin. In another aspect the cleavage tag is removed by an appropriate protease from the non-naturally occurring collagen or elastin.

**[0074]** The non-naturally occurring collagen or non-naturally occurring elastin further comprises an enzyme that is a Beta-lactamase. The beta-lactamase is useful as a selection marker. In one aspect the beta-lactamase is attached to the non-naturally occurring collagen or elastin. In another aspect the beta-lactamase is cleaved from the non-naturally occurring collagen or elastin.

**[0075]** The non-naturally occurring collagen or non-naturally occurring elastin further comprises GEK amino acid trimer repeats and/or GDK amino acid trimer repeats. The GEK and the GDK trimer repeats facilitate the gelling of the collagen and/or the gelatin. In one embodiment, the non-naturally occurring collagen or the non-naturally occurring elastin comprises 2-50 GEK and/or 2-50 GDK trimer repeats (SEQ ID NOS: 130-131, respectively), 2-40 GEK and/or 2-40 GDK trimer repeats (SEQ ID NOS: 132-133, respectively), 2-30 GEK and/or 2-30 GDK trimer repeats (SEQ ID NOS: 134-135, respectively), 2-20 GEK and/or 2-20 GDK trimer repeats (SEQ ID NOS: 136-137, respectively), 2-15 GEK and/or 2-15 GDK trimer repeats (SEQ ID NOS: 138-139, respectively). 2-10 GEK and/or 2-10 GDK trimer repeats (SEQ ID NOS: 140-141, respectively), 2-9 GEK and/or 2-9 GDK trimer repeats (SEQ ID NOS: 142-143, respectively), 2-8 GEK and/or 2-8 GDK trimer repeats (SEQ ID NOS: 144-145, respectively), 2-7 GEK and/or 2-7 GDK trimer repeats (SEQ ID NOS: 146-147, respectively), 2-6 GEK and/or 2-6 GDK trimer repeats (SEQ ID NOS: 148-149, respectively), 2-5 GEK and/or 2-5 GDK trimer repeats (SEQ ID NOS: 150-151, respectively), or 2-4 GEK and/or 2-4 GDK trimer repeats (SEQ ID NOS: 152-153, respectively). In one aspect the GEK trimer repeat or the GDK trimer repeat is attached to the non-naturally occurring collagen or elastin. In another aspect the GEK trimer repeat or the GDK trimer repeat is cleaved from the non-naturally occurring collagen or elastin.

**[0076]** Provided herein are compositions that comprise between 0.005% and 30% w/w non-naturally occurring collagen and/or non-naturally occurring elastin. The composition comprises between 0.005% and 20% w/w non-naturally occurring collagen and/or non-naturally occurring elastin, between 0.005% and 10% w/w non-naturally occurring collagen and/or non-naturally occurring elastin, between 0.005% and 5% w/w non-naturally occurring collagen and/or non-naturally occurring elastin, between 0.005% and 2% w/w non-naturally occurring collagen and/or non-naturally occurring elastin, between 0.005% and 1% w/w non-naturally occurring collagen and/or non-naturally occurring elastin, between 0.005% and 0.5% w/w non-naturally occurring collagen and/or non-naturally occurring elastin, and between 0.005% and 0.2% w/w non-naturally occurring collagen and/or non-naturally occurring elastin.

**[0077]** The compositions that comprise the between non-naturally occurring collagen and/or non-naturally occurring elastin are personal care products. In some embodiments the compositions are formulated for topical administration. The compositions can contain other cosmetic ingredients suitable for human use. The personal care products are useful for preventing or treating ultraviolet radiation damage to human skin or hair. The personal care products are applied to skin or hair. The compositions include, for example, masks, skin cleaners such as soap, cleansing creams, cleansing lotions, cleansing milks, cleansing pads, facial washes, hair shampoo, hair conditioner and body shampoos.

**[0078]** The compositions that comprise the non-naturally occurring collagen and/or non-naturally occurring elastin can further comprise at least one additional ingredient comprising a topical carrier or a preservative. The topical carrier comprises a topical carrier selected from the group consisting of liposome, biodegradable microcapsule, lotion, spray, aerosol, dusting powder, biodegradable polymer, mineral oil, triglyceride oil, silicone oil, glycerin, glycerin monostearate, alcohols, emulsifying agents, liquid petroleum, white petrolatum, propylene glycol, polyoxyethylene, polyoxypropylene, wax, sorbitan monostearate, polysorbate, cetyl ester wax, cetearyl alcohol, 2-octyldodecanol, benzyl alcohol, cyclomethicone, cyclopentasiloxane, and water. The preservative comprises a preservative selected from the group consisting of tocopherol, diiodomethyl-p-tolylsulfone, 2-Bromo-2-nitropropane-1,3-diol, cis isomer 1-(3-chloroallyl)-3,5,7-triaza-1-azoniaadamantane chloride, glutaraldehyde, 4,4-dimethyl oxazolidine, 7-Ethylbicyclooxazolidine, methyl paraben, sorbic acid, Germaben II, rosemary extract, and EDTA

**[0079]** Provided are methods of decreasing skin damage, promoting the repair of damaged skin, protecting skin against UV damage, protecting skin cells against the effects of exposure to urban dust. The method comprises the step of applying the composition comprising the non-naturally occurring collagen and/or non-naturally occurring elastin to the skin of a subject. Without being bound to a particular theory or mechanism, the collagen and/or the elastin in the composition decrease skin damage by protecting against UV damage, and/or promotes the repair of damaged skin by increasing the viability of cells and/or increasing procollagen synthesis when applied to skin, and/or promotes the viability of skin cells. The collagens and elastins in one aspect decrease the formation of thymine-thymine (TT) dimer formation.

**[0080]** One aspect provides polynucleotides that encode a non-naturally occurring collagen or a non-naturally occurring elastin. The polynucleotides encode collagen or elastin from jellyfish, human, *Chondrosia reniformis* (kidney sponge), or *Rhincodon typus*. The polynucleotides encode for collagen or elastin that is full length or truncated.

**[0081]** Another aspect provides polynucleotides that encode collagen or elastin fusion proteins. The elastin or collagen fusion proteins comprise a secretion tag, a histidine tag, a fluorescent protein tag, a protease cleavage site, a Beta-lactamase along and/or GEK amino acid trimer repeats and/or GDK amino acid trimer repeats together with collagen or elastin.

**[0082]** The polynucleotides are in one aspect vectors used to transform host cells and express the polynucleotides. The polynucleotides further comprise nucleic acids that encode enzymes that permit the host organism to grow in the presence of a selection agent. The selection agents include certain sugars including galactose containing sugars or antibiotics including ampicillin, hygromycin, G418 and others. Enzymes that are used to confer resistance to the selection agent include β-galactosidase or a β-lactamase.

**[0083]** In one aspect host cells that express the polynucleotides of the invention are provided. Host cells can be any host cell including gram negative bacterial cells, gram positive bacterial cells, yeast cells, insect cells, mammalian cells, plant cells or any other cells used to express exogenous polynucleotides. An exemplary gram-negative host cell is *E. coli.*

**[0084]** Bacterial host cells in which the cells have been modified to inhibit cell division and the periplasmic space is increased are taught. As discussed herein and taught in example 1, Beta-lactam antibiotics are useful as a switch to convert wild-type bacterial cells to a modified bacterial cell in which cell replication is inhibited and the periplasmic space is increased. Exemplary Beta-lactam antibiotics including penicillins, cephalosporins, carbapenems, and monobactams.

**[0085]** The switched form of bacteria (L-form) are cultivated in culture media that include certain salts and other nutrients. Salts and media compositions that support the physiological switch physiology that have been tested are M63 salt media, M9 salt media, PYE media, and Luria-Bertani (LB) media. Any necessary supplements besides carbon, nitrogen, and inorganic phosphate sources may also be included at appropriate concentrations introduced alone or as a mixture with another supplement or medium such as a complex nitrogen source. In certain embodiments, the medium further comprises one or more ingredients selected from: ammonium chloride, ammonium sulfate, calcium chloride, casamino acids, iron(II) sulfate, magnesium sulfate, peptone, potassium phosphate, sodium chloride, sodium phosphate, and yeast extract.

**[0086]** Beta-lactamases are enzymes that confer resistance to lactam antibiotics in prokaryotic cells. Typically when Beta-lactamases are expressed in bacterial host cells, the expressed Beta-lactamase protein also includes targeting sequences (secretion tag) that direct the Beta-lactamase protein to the periplasmic space. Beta-lactamases are not functional unless they are transported to the periplasmic space. Beta-lactamase targeted to the periplasmic without the use of an independent secretion tag that targets the enzyme to the periplasmic space are provided. By creating a fusion protein in which a periplasmic secretion tag added to the N-terminus of a protein such as GFP, collagen, or GFP/collagen chimeras, the functionality of the Beta-lactamase lacking a native secretion tag can be used to select for full translation and secretion of the N-terminal fusion proteins. Using this approach, we have used a DsbA-GFP-Collagen-Beta-lactamase fusion to select for truncation products in the target collagens that favor translation and secretion.

**[0087]** Another embodiment provides methods of producing a non-naturally occurring collagen or a non-naturally occurring elastin. The method comprises the steps of inoculating a culture medium with a recombinant host cell comprising polynucleotides that encode the collagen or elastin, cultivating the host cell, and isolating the non-naturally occurring collagen or the non-naturally occurring elastin from the host cell.

**[0088]** A process for fermentative preparation of a protein is provided. The process comprises the steps of:

**[0089]** a) culturing a recombinant Gram-negative bacterial cell in a medium comprising a magnesium salt, wherein the concentration of magnesium ions in the medium is at least about 6 mM, and wherein the bacterial cell comprises an exogenous gene encoding the protein;

**[0090]** b) adding an antibiotic to the medium, wherein the antibiotic inhibits peptidoglycan biogenesis in the bacterial cell; and

**[0091]** c) harvesting the protein from the medium.

**[0092]** The bacteria may be cultured continuously—as described, for example, in WO 05/021772—or discontinuously in a batch process (batch cultivation) or in a fed-batch or repeated fed-batch process for the purpose of producing the target protein. In some embodiments, protein production is conducted on a large-scale. Various large-scale fermentation procedures are available for production of recombinant proteins. Large-scale fermentations have at least 1,000 liters of capacity, preferably about 1,000 to 100,000 liters of capacity. These fermentors use agitator impellers to distribute oxygen and nutrients, especially glucose (the preferred carbon/energy source). Small-scale fermentation refers generally to fermentation in a fermentor that is no more than approximately 20 liters in volumetric capacity.

**[0093]** For accumulation of the target protein, the host cell is cultured under conditions sufficient for accumulation of the target protein. Such conditions include, e.g., temperature, nutrient, and cell-density conditions that permit protein expression and accumulation by the cell. Moreover, such conditions are those under which the cell can perform basic cellular functions of transcription, translation, and passage of proteins from one cellular compartment to another for the secreted proteins, as are known to those skilled in the art.

**[0094]** The bacterial cells are cultured at suitable temperatures. For *E. coli* growth, for example, the typical temperature ranges from about 20° C. to about 39° C. In one embodiment, the temperature is from about 20° C. to about

37° C. In another embodiment, the temperature is at about 30° C. In one embodiment, the host cells, in the non-switched state or switched state are cultivated at one temperature and switched to a different temperature to induce protein production. The host cells are cultivated first at one temperature to propagate the cells, then to induce protein production the cell are cultivated at a lower temperature. The first temperature is 23°, 24°, 25°, 26°, 27°, 28°, 29°, 30°, 31°, 32°, 33°, 34°, 35°, 36°, or 37° C. The second temperature is 20°, 21°, 22°, 23°, 24°, 25°, 26°, 27°, 28°, 29°, 30°, 31°, 32°, 33°, 34°, 35° or 36° C. The cultivation at the second temperature is conducted between 1 hour and 100 hours, between 5 hours and 90 hours, between 5 hours and 80 hours, between 5 hours and 80 hours, between 5 hours and 70 hours, between 10 hours and 70 hours, between 15 hours and 70 hours, between 15 hours and 65 hours, between 15 hours and 60 hours, between 20 hours and 60 hours, between 20 hours and 55 hours, between 20 hours and 50 hours, between 24 hours and 50 hours, between 24 hours and 48 hours, between 30 hours and 50 hours, between 30 hours and 45 hours, or between 30 hours and 40 hours.

**[0095]** The pH of the culture medium may be any pH from about 5-9, depending mainly on the host organism. For *E. coli*, the pH is from about 6.8 to about 7.4, or about 7.0.

**[0096]** For induction of gene expression, typically the cells are cultured until a certain optical density is achieved, e.g., an OD600 of about 1.1, at which point induction is initiated (e.g., by addition of an inducer, by depletion of a repressor, suppressor, or medium component, etc.) to induce expression of the exogenous gene encoding the target protein. In some embodiments, expression of the exogenous gene is inducible by an inducer selected from, e.g. isopropyl-β-d-1-thiogalactopyranoside, lactose, arabinose, maltose, tetracycline, anhydrotetracycline, vavlycin, xylose, copper, zinc, and the like. The induction of gene expression can also be accomplished by decreasing the dissolved oxygen levels during fermentation. The dissolved oxygen levels of the fermentation during cell propagation is between 10% and 30%. To induce gene expression the dissolved oxygen level is reduced to below 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or 0%. In host cells, in either the physiological state or the switched state, protein production can be induced by lowering the temperature of the fermentation as disclosed herein.

**[0097]** After product accumulation, the cells are vortexed and centrifuged in order to induce lysis and release of recombinant proteins. The majority of the proteins is found in the supernatant but any remaining membrane bound proteins can be released using detergents (such as triton X-100).

**[0098]** In a subsequent step, the target protein, as a soluble or insoluble product released from the cellular matrix, is recovered in a manner that minimizes co-recovery of cellular debris with the product. The recovery may be done by any means, but in one embodiment, can comprise histidine tag purification through a nickel column. See, e.g., Purification of Proteins Using Polyhistidine Affinity Tags, Methods Enzymology. 2000; 326: 245-254.

## EXAMPLES

### Example 1: Expression System

Materials and Methods:

Strains:

**[0099]** Tested Physiological Switch and Protein Production:
*E. coli* BL21(DE3)—From NEB, product # c2527
*E. coli* K12 NCM3722—From The *Coli* Genetic Stock Center, CGSC #12355
**[0100]** Tested Physiological Switch:

Gammaproteobacteria:

**[0101]** *Vibrio natriegens*—From ATCC, product #14048
*Pseudomonas fluorescens*—From ATCC, product #31948
*Pseudomonas aeruginosa* PAO1—From ATCC, product # BAA-47
**[0102]** Alphaproteobacteria:
*Caulobacter crescentus*—From ATCC, product #19089
*Agrobacterium tumefaciens/Rhizobium radiobacter*—From ATCC, product #33970
*Brevundimonas diminuta*—From ATCC, product #13184
**[0103]** Media Compositions:
**[0104]** 1 liter 5×m63 salts:
10 g (NH4)2SO4—From P212121, product #7783-20-2
68 g KH2PO4—From P212121, product #7778-77-0
2.5 mg FeSO4.7H2O—From Sigma Aldrich, product # F7002
Bring volume up to 1 liter with milliQ water
Adjust to pH 7 with KOH (From P212121, product #1310-58-3)
Autoclave mixture
**[0105]** 1 liter of 1M MgSO4:
246.5 g MgSO4.7H2O—From P212121, (Sigma Aldrich, product #10034-99-8) Bring volume up to 1 liter with milliQ water.
Autoclave mixture.
**[0106]** 1 Liter of Switch Media 1:
133.4 mL 5×m63 salts

10 mL 1M MgSO4

**[0107]** 38.6 g Glucose—From P212121, product #50-99-7
66.6 g Sucrose—From P212121, product #57-50-1
8.33 g LB mix—From P212121, product # lb-miller
Bring volume up to 1 liter with milliQ water.
Filter sterilize mixture through a 0.22 μM pore vacuum filter (Sigma Aldrich, product # CLS430517).
**[0108]** 1 Liter of Switch Media 2:
133.4 mL 5×m63 salts

10 mL 1M MgSO4

**[0109]** 38.6 g Glucose—From P212121, product #50-99-7
66.6 g Sucrose—From P212121, product #57-50-1
10 g Yeast Extract—From FisherSci.com, product # J60287A1
Bring volume up to 1 liter with milliQ water.
Filter sterilize mixture through a 0.22 μM pore vacuum filter (Sigma Aldrich, product # CLS430517).

**[0110]** For Bioreactor Growth:
5 liter of bioreactor media MGZ12:
1) Autoclave 1 L of Glucose at concentration of 500 g/L in DI water. (VWR, product #97061-170).
2) Autoclave 1 L of Sucrose at concentration of 500 g/L in DI water. (Geneseesci.com, product #62-112).
3) Autoclave in 3946 mL of DI water:
20 g (NH4)2HP04. (VWR, product #97061-932).
66.5 g KH2PO4. (VWR, product #97062-348).
22.5 g H3C6H507. (VWR, product # BDH9228-2.5KG).
2.95 g MgSO4.7H2O. (VWR, product #97062-134).
10 mL Trace Metals (Teknova), 1000×. (Teknova, product # T1001).
After autoclaving add 400 mL of (1) to (3), 65 mL of 10M NaOH (VWR, product #97064-480) to (3), and 666 mL of (2) to (3).
A feed of 500 g/L of glucose can be used during fermentation run as needed.
At induction add:
50 mL of 1M MgSO4.7H2O to a 5 L bioreactor
1 to 10 mM concentration of IPTG. (carbosynth.com, product # EI05931).
Add Fosfomycin (50 μg/mL or higher) and Carbenicillin (100 μg/mL or higher).

Physiological Switch:

**[0111]** The physiological switch is optimally flipped at an OD 600 of 1 to 1.1 for *E. coli* for growth in shake flasks at volumes up to 1 L. For the other species tested, cultures were grown in switch media and subcultured once cultures reached maximal OD 600. In all cases the physiological switch is flipped through the addition of 100-200 ug/mL Carbenicillin (From P212121, product #4800-94-6) and 50-100 ug/mL Fosfomycin (From P212121, product #26016-99-9). The majority of the population is in the switched state within a few hours. To confirm that cells underwent a physiological switch, cells were imaged on a Nikon Ti-E with perfect focus system, Nikon CFI60 Plan Apo 100×NA 1.45 objective, Prior automated filter wheels and stage, LED-CFP/YFP/mCherry and LED-DA/FI/TX filter sets (Semrock), a Lumencor Sola II SE LED illumination system, and a Hamamatsu Flash 4.0 V2 CMOS camera.

Image Analysis of Physiological Switch:

**[0112]** Images were analyzed using ImageJ to measure dimensions. In the switched state, the spherical outline of the outer membrane is treated as a sphere to calculate total volume (V=(4/3)πr3). The cytoplasmic volume is calculated as an ellipsoid that exists within the sphere (V=(4/3)π*(longest radius)*(short radius)2). To calculate the periplasmic volume, the cytoplasmic volume is subtracted from the total volume of the cell.

Protein Expression and Quantification:

**[0113]** *E. coli* BL21(DE3) (NEB product # c2527) containing pET28a (emd Millipore product #69864) and its derivatives carrying GFP or collagen derivatives were grown in a shaking incubator at 37° C. overnight in switch media containing 50 mg/mL kanamycin (p212121 product #2251180). Next day, subcultures are started with a 1:10 dilution of the overnight culture into fresh switch media containing 50 mg/mL kanamycin. The culture is then physiologically switched and protein production is induced simultaneously at an OD 600 of 1 to 1.1 (Read on a Molecular Devices Spectramax M2 microplate reader). The physiologically switch and protein production are flipped through the addition of 100 ug/mL Carbenicillin, 50 ug/mL Fosfomycin, and 100 ug/mL IPTG (p212121 product #367-93-1). Protein expression is continued in the switched state from between 8 hours to overnight at room temperature (approximately 22° C.) on an orbital shaker. In order to quantify total protein levels, Quick Start™ Bradford Protein Assay was used on mixed portion of culture and standard curves are quantitated on a Molecular Devices Spectramax M2 microplate reader. In order to quantitate the relative intensity of target protein production relative to the rest of the protein population the mixed portion of the cultures were run on Mini-PROTEAN® TGX™ Gels and stained with Bio-Safe™ Coomassie Stain.

Induction of Protein Production:

**[0114]** Standard procedures have been followed to induce protein production in the physiological state. We have been using the strain BL21(DE3) containing the plasmid pET28a driving the IPTG/lactose inducible production of recombinant proteins and targeting them to the periplasmic space using the DsbA signal sequence. Using the GFP protein, targeted to the periplasmic space as described above, we have demonstrated the ability to gain and increase of 5-fold in protein production when compared to un-switched cell populations induced at the same optical density, for the same amount of time (figures). The induction was optimal at an OD600 of 1.1 and induction was continued for 10 hours at which point the protein produced was measured at about 200 mg/mL.

## Example 2: Production of Full-Length Collagen

**[0115]** Full length jellyfish collagen was produced using the expression system discussed in Example 1 herein. The wild-type, full length amino acid sequence of *Podocoryna carnea* (jellyfish or Hydrozoan) collagen is provided in SEQ ID NO: 1.

```
                                         (SEQ ID NO: 1)
GPQGVVGADGKDGTPGEKGEQGRTGAAGKQGSPGADGARGPLGSIGQQGAR

GEPGDPGSPGLRGDTGLAGVKGVAGPSGRPGQPGANGLPGVNGRGGLRGKP

GAKGIAGSDGEAGESGAPGQSGPTGPRGQRGPSGEDGNPGLQGLPGSDGEP

GEEGQPGRSGQPGQQGPRGSPGEVGPRGSKGPSGDRGDRGERGVPGQTGSA

GNVGEDGEQGGKGVDGASGPSGALGARGPPGSRGDTGAVGPPGPTGRSGLP

GNAGQKGPSGEPGSPGKAGSAGEQGPPGKDGSNGEPGSPGKEGERGLAGPP

GPDGRRGETGSPGIAGALGKPGLEGPKGYPGLRGRDGTNGKRGEQGETGPD

GVRGIPGNDGQSGKPGIDGIDGTNGQPGEAGYQGGRGTRGQLGETGDVGQN

GDRGAPGPDGSKGSAGRPGLR
//www.ncbi.nlm.nih.gov/protein/4379341?report=
genbank&log$=protalign&blast_rank=1&RID=T1N9ZEUW014
```

**[0116]** The non-codon optimized polynucleotide sequence encoding the full length jellyfish collagen is disclosed in SEQ ID NO: 2.

(SEQ ID NO: 2)
ggaccacaaggtgttgtaggagctgatggcaaagatggaacaccgggagag

aaaggtgagcaaggacgaaccggagctgcaggaaaacagggaagccctgga

gcagatggagcaagaggccctcttggatcaattggacaacaaggtgctcgt

ggagaacctggtgatccaggatctcccggcttaagaggagatactggattg

gctggagtcaaaggagtagcaggaccatctggtcgacctggacaacccggt

gcaaatggattacctggtgtgaatggcagaggcggtttgagaggcaaacct

ggtgctaaaggaattgctggcagtgatggagaagcgggagaatctggcgca

cctggacagtccggacctaccggtccacgtggtcaacgaggaccaagtggt

gaggatggtaatcctggattacagggattgcctggttctgatggagagccc

ggagaggaaggacaacctggaagatctggtcaaccaggacagcaaggacca

cgtggttcccctggagaggtaggaccaagaggatctaaaggtccatcagga

gatcgtggtgacaggggagagagaggtgttcctggacaaacaggttcggct

ggaaatgtaggagaagatggagagcaaggaggcaaaggtgtcgatggagcg

agtggaccaagtggagctcttggtgctcgtggtcccccaggaagtagaggt

gacaccggggcagtgggacctcccggacctactgggcgatctggtttacct

ggaaacgcaggacaaaagggaccaagtggtgaaccaggtagtccaggaaaa

gcaggatcagctggtgaacagggtcctcctggtaaagacggatcaaatggt

gaacctggatctcctggcaaagagggtgaacgtggtcttgctggtccacca

ggtccagatggcagacgtggtgaaacgggatctccaggtatcgctggtgct

cttggtaaaccaggtttggaaggacctaaaggttatccaggattaagagga

agagatggaaccaatggcaaacgaggagaacaaggagaaactggtcctgat

ggagtcagaggtattcctggaaatgatggacaatctggcaaaccaggtatt

gatggtattgacggaacaaatggtcaaccaggtgaggctggataccaaggt

ggtagaggtacacgtggtcagttaggtgaaactggtgatgtcggacagaat

ggagatcgaggagctcctggtcctgatggatctaaaggttctgctggtaga

ccaggacttcgtgg
https://www.ncbi.nlm.nih.gov/nucleotide/
3355656?report=genbank&log$=nuclalign&
blast_rank=1&RID=TSYP7CMV014

**[0117]** Two different codon optimized polynucleotide sequences encoding the wild-type, full-length jellyfish collagen were synthesized. The two polynucleotide sequences were slightly different due to slightly different codon optimization methods. In addition to the non-truncated, full-length jellyfish collagen, the polynucleotides also encoded a secretion tag, a 9 amino acid his tag (SEQ ID NO: 129), a short linker, and a thrombin cleavage site. The DsbA secretion tag is encoded by nucleotides 1-71. The histidine tag comprising 9 histidine residues (SEQ ID NO: 129) is encoded by nucleotides 73-99 and encodes amino acids 25-33. The linker is encoded by nucleotides 100-111. The thrombin cleavage tag is encoded by nucleotides 112-135 and encodes amino acids 38-45. The truncated collagen is encoded by nucleotides 136-1422. The two polynucleotides are disclosed below in SEQ ID NO: 3 and 4.

(SEQ ID NO: 3)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGCA

TCGGCGGCGCAGTATGAAGATCACCATCACCACCACCACCATCACCACTCT

GGCTCGAGCCTGGTGCCGCGCGGCAGCCATATGGGTCCGCAGGGTGTTGTT

GGTGCAGATGGTAAAGACGGTACCCCGGGTGAAAAAGGAGAACAGGGACGT

ACAGGTGCAGCAGGTAAACAGGGCAGCCCGGGTGCCGATGGTGCCCGTGGC

CCGCTGGGTAGCATTGGTCAGCAGGGTGCAAGAGGCGAACCGGGCGATCCG

GGTAGTCCGGGCCTGCGTGGTGATACGGGTCTGGCCGGTGTTAAAGGCGTT

GCAGGTCCTTCAGGTCGTCCAGGTCAACCGGGTGCAAATGGTCTGCCGGGT

GTTAATGGTCGTGGCGGTCTGCGTGGCAAACCGGGAGCAAAAGGTATTGCA

GGTAGCGATGGAGAAGCCGGTGAAAGCGGTGCCCCGGGTCAGAGTGGTCCG

ACCGGTCCGCGCGGTCAGCGTGGTCCGTCTGGTGAAGATGGCAATCCGGGT

CTGCAGGGTCTGCCTGGTAGTGATGGCGAACCAGGTGAAGAAGGTCAGCCG

GGTCGTTCAGGCCAGCCGGGCCAGCAGGGCCCGCGTGGTAGCCCGGGCGAA

GTTGGCCCGCGGGGTAGTAAAGGTCCTAGTGGCGATCGCGGTGATCGTGGT

GAACGCGGTGTTCCTGGTCAGACCGGTAGCGCAGGTAATGTTGGCGAAGAT

GGTGAACAGGGTGGCAAAGGTGTTGATGGTGCAAGCGGTCCGAGCGGTGCA

CTGGGTGCACGTGGTCCTCCGGGCAGCCGTGGTGACACCGGTGCAGTTGGT

CCGCCTGGCCCGACCGGCCGTAGTGGCTTACCGGGTAATGCAGGTCAGAAA

GGTCCGTCAGGTGAACCTGGCAGCCCTGGTAAAGCAGGTAGTGCCGGTGAG

CAGGGTCCGCCGGGCAAAGATGGTAGTAATGGTGAGCCGGGTAGCCCTGGC

AAAGAAGGTGAACGTGGTCTGGCAGGACCGCCGGGTCCTGATGGTCGCCGC

GGTGAAACGGGTTCACCGGGTATTGCCGGTGCCCTGGGTAAACCAGGTCTG

GAAGGTCCGAAAGGTTATCCTGGTCTGCGCGGTCGTGATGGTACCAATGGC

AAACGTGGCGAACAGGGCGAAACCGGTCCAGATGGTGTTCGTGGTATTCCG

GGTAACGATGGTCAGAGCGGTAAACCGGGCATTGATGGTATTGATGGCACC

AATGGTCAGCCTGGCGAAGCAGGTTATCAGGGTGGTCGCGGTACCCGTGGT

CAGCTGGGTGAAACAGGTGATGTTGGTCAGAATGGTGATCGCGGCGCACCG

GGTCCGGATGGTAGCAAAGGTAGCGCCGGTCGTCCGGGTTTACGTtaa

(SEQ ID NO: 4)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGCA

TCGGCGGCGCAGTATGAAGATCACCATCACCACCACCACCATCACCACTCT

GGCTCGAGCCTGGTGCCGCGCGGCAGCCATATGGGTCCGCAGGGTGTTGTT

GGTGCAGATGGTAAAGACGGTACCCCGGGTGAAAAAGGtGAACAGGGtCGT

ACcGGTGCAGCAGGTAAACAGGGCAGCCCGGGTGCCGATGGTGCCCGTGGC

CCGCTGGGTAGCATTGGTCAGCAGGGTGCAcgtGGCGAACCGGGCGATCCG

GGTAGcCCGGGCCTGCGTGGTGATACGGGTCTGGCCGGTGTTAAAGGCGTT

GCAGGTCCTTCtGGTCGTCCAGGTCAACCGGGTGCAAATGGTCTGCCGGGT

GTTAATGGTCGTGGCGGTCTGCGTGGCAAACCGGGtGCAAAAGGTATTGCA

GGTAGCGATGGcGAAGCCGGTGAAAGCGGTGCCCCGGGTCAGAGcGGTCCG

-continued

ACCGGTCCGCGCGGTCAGCGTGGTCCGTCTGGTGAAGATGGCAATCCGGGT

CTGCAGGGTCTGCCTGGTagcGATGGCGAACCAGGTGAAGAAGGTCAGCCG

GGTCGTTCtGGCCAGCCGGGCCAGCAGGGCCCGCGTGGTAGCCCGGGCGAA

GTTGGCCCGCGcGGTtcTAAAGGTCCTAGcGGCGATCGCGGTGATCGTGGT

GAACGCGGTGTTCCTGGTCAGACCGGTAGCGCAGGTAATGTTGGCGAAGAT

GGTGAACAGGGTGGCAAAGGTGTTGATGGTGCAAGCGGTCCGAGCGGTGCA

CTGGGTGCACGTGGTCCTCCGGGCAGCCGTGGTGACACCGGTGCAGTTGGT

CCGCCTGGCCCGACCGGCCGTAGcGGCctgCCGGGTAATGCAGGTCAGAAA

GGTCCGTCtGGTGAACCTGGCAGCCCTGGTAAAGCAGGTAGcGCCGGTGAG

CAGGGTCCGCCGGGCAAAGATGGTAGcAATGGTGAGCCGGGTAGCCCTGGC

AAAGAAGGTGAACGTGGTCTGGCAGGtCCGCCGGGTCCTGATGGTCGCCGC

GGTGAAACGGGTTCtCCGGGTATTGCCGGTGCCCTGGGTAAACCAGGTCTG

GAAGGTCCGAAAGGTTATCCTGGTCTGCGCGGTCGTGATGGTACCAATGGC

AAACGTGGCGAACAGGGCGAAACCGGTCCAGATGGTGTTCGTGGTATTCCG

GGTAACGATGGTCAGAGCGGTAAACCGGGCATTGATGGTATTGATGGCACC

AATGGTCAGCCTGGCGAAGCAGGTTATCAGGGTGGTCGCGGTACCCGTGGT

CAGCTGGGTGAAACcGGTGATGTTGGTCAGAATGGTGATCGCGGCGCACCG

GGTCCGGATGGTAGCAAAGGTAGCGCCGGTCGTCCGGGTctgCGTtaa

**[0118]** The amino acid sequence encoded by the polynucleotides of SEQ ID NO: 3 and SEQ ID NO:4 is disclosed in SEQ ID NO:5 below. In SEQ ID NO: 5 the DsbA secretion tag is encoded by nucleotides 1-71 and encodes amino acids 1-24; the histidine tag comprising 9 histidine residues (SEQ ID NO: 129) is encoded by nucleotides 73-99 and encodes amino acids 25-33; the linker is encoded by nucleotides 100-111 and encodes amino acids 34-37; the thrombin cleavage tag is encoded by nucleotides 112-135 and encodes amino acids 38-45; the full-length collagen is encoded by nucleotides 136-1422 and encodes amino acids 46-474.

(SEQ ID NO: 5)

MKKIWLALAGLVLAFSASAAQYEDHHHHHHHHHSGSSLVPRGSHMGPQGVV

GADGKDGTPGEKGEQGRTGAAGKQGSPGADGARGPLGSIGQQGARGEPGDP

GSPGLRGDTGLAGVKGVAGPSGRPGQPGANGLPGVNGRGGLRGKPGAKGIA

GSDGEAGESGAPGQSGPTGPRGQRGPSGEDGNPGLQGLPGSDGEPGEEGQP

GRSGQPGQQGPRGSPGEVGPRGSKGPSGDRGDRGERGVPGQTGSAGNVGED

GEQGGKGVDGASGPSGALGARGPPGSRGDTGAVGPPGPTGRSGLPGNAGQK

GPSGEPGSPGKAGSAGEQGPPGKDGSNGEPGSPGKEGERGLAGPPGPDGRR

GETGSPGIAGALGKPGLEGPKGYPGLRGRDGTNGKRGEQGETGPDGVRGIP

GNDGQSGKPGIDGIDGTNGQPGEAGYQGGRGTRGQLGETGDVGQNGDRGAP

GPDGSKGSAGRPGLR

**[0119]** The full length jellyfish collagen without the DsbA secretion tag, the histidine tag, linker and thrombin cleavage site is disclosed in SEQ ID NO: 89.

(SEQ ID NO: 89)

GPQGVVGADGKDGTPGEKGEQGRTGAAGKQGSPGADGARGPLGSIGQQGAR

GEPGDPGSPGLRGDTGLAGVKGVAGPSGRPGQPGANGLPGVNGRGGLRGKP

GAKGIAGSDGEAGESGAPGQSGPTGPRGQRGPSGEDGNPGLQGLPGSDGEP

GEEGQPGRSGQPGQQGPRGSPGEVGPRGSKGPSGDRGDRGERGVPGQTGSA

GNVGEDGEQGGKGVDGASGPSGALGARGPPGSRGDTGAVGPPGPTGRSGLP

GNAGQKGPSGEPGSPGKAGSAGEQGPPGKDGSNGEPGSPGKEGERGLAGPP

GPDGRRGETGSPGIAGALGKPGLEGPKGYPGLRGRDGTNGKRGEQGETGPD

GVRGIPGNDGQSGKPGIDGIDGTNGQPGEAGYQGGRGTRGQLGETGDVGQN

GDRGAPGPDGSKGSAGRPGLR

**[0120]** The polynucleotides of SEQ ID NO: 3 and SEQ ID NO: 4 were synthesized by Gen9 DNA, now Ginkgo Bioworks internal synthesis. Overlaps between the pET28 vector and SEQ ID NO: 3 and SEQ ID NO: 4 were designed to be between 30 and 40 bp long and added using PCR with the enzyme PrimeStar GXL polymerase (http://www.clontech.com/US/Products/PCR/GC_Rich/PrimeSTAR_GXL_DNA_Polymerase?sitex=10020:22372:US). The opened pET28a vector and insert DNA (SEQ ID NO: 3 or SEQ ID NO: 4) were then assembled together into the final plasmid using SGI Gibson assembly (https://us.vwr.com/store/product/17613857/gibson-assembly-hifi-1-step-kit-synthetic-genomics-inc). Sequence of plasmid was then verified through sanger sequencing through Eurofins Genomics (www.eurofinsgenomics.com).

**[0121]** The transformed cells were cultivated in minimal media and frozen in 1.5 aliquots with glycerol at a ratio of 50:50 of cells to glycerol. One vial of this frozen culture was revived in 50 ml of minimal media overnight at 37° C., 200 rpm. Cells were transferred into 300 ml of minimal media and grown for 6-9 hours to reach an OD600 of 5-10.

**[0122]** Minimal media used in this example and throughout this application is prepared as follows. The minimal media (Table 1) was autoclaved in several separate fractions, Salts mix (Ammonium Phosphate dibasic, Potassium phosphate monobasic, Citric acid anhydrous, Magnesium sulfate heptahydrate), the Sucrose at 500 g/L, the Glucose at 55%, the Trace Metals TM5 (table 2), and Sodium Hydroxide 10M. The minimal media was then mixed together at the above concentrations post-autoclaving in the hood.

TABLE 1

Minimal media recipe for shake flask cultures

| chemical | Formula | MW | Conc (g/L) |
|---|---|---|---|
| Ammonium Phosphate dibasic | $(NH_4)_2HPO_4$ | 133 | 4 |
| Potassium phosphate monobasic | $KH_2PO_4$ | 137 | 13.3 |
| Citric acid anhydrous | $H_3C_6H_5O_7$ | 192.14 | 4.5 |
| Magnesium sulfate heptahydrate | $MgSO_4 \bullet 7H_2O$ | 246 | 0.59 |
| Trace Metals TM5 | | | 2 |
| Glucose | $C_6H_{12}O_6$ | 500 | 40 |
| Sodium Hydroxide 10M | NaOH | 400 | 5.2 |
| Sucrose 500 g/L | $C_{12}H_{22}O_{11}$ | 500 | 66.6 |

TABLE 2

Trace Metals TM5 composition

| chemical | Formula | MW | Conc (g/L) |
|---|---|---|---|
| Ferrous Sulfate Heptahydrate | $FeSO_4 \bullet 7H_20$ | 278.02 | 27.8 |
| Calcium Chloride | $CaC_{12} \bullet 2H_20$ | 147 | 2.94 |
| Manganese Chloride | $MnC_{12}$ | 125.84 | 1.26 |
| Zinc Sulfate | $ZnSO_4 \bullet H_20$ | 179.5 | 1.8 |
| Nickel Chloride | $NiC_{12} \bullet 6H_20$ | 237.69 | 0.48 |
| Sodium Molybate | $Na_2MoO_4 \bullet 2H_20$ | 241.95 | 0.48 |
| Sodium Selenite | $Na_2SeO_3$ | 172.94 | 0.35 |
| Boric Acid | $H_3BO_3$ | 61.83 | 0.12 |

**[0123]** The harvested cells were disrupted in a homogenizer at 14,000 psi pressure in 2 passes. Resulting slurry contained the collagen protein along with other proteins.

**[0124]** The collagen was purified by acid treatment of homogenized cell broth. The pH of the homogenized slurry was decreased to 3 using 6M Hydrochloric acid. Acidified cell slurry was incubated overnight at 4° C. with mixing, followed by centrifugation. Supernatant of the acidified slurry was tested on a polyacrylamide gel and found to contain collagen in relatively high abundance compared to starting pellet. The collagen slurry thus obtained was high in salts. To obtain volume and salt reduction, concentration and diafiltration steps were performed using an EMD Millipore Tangential Flow Filtration system with ultrafiltration cassettes of 0.1 $m^2$ each. Total area of filtration was 0.2 $m^2$ using 2 cassettes in parallel. A volume reduction of 5× and a salt reduction of 19× was achieved in the TFF stage. Final collagen slurry was run on an SDS-PAGE gel to confirm presence of the collagen. This slurry was dried using a multi-tray lyophilizer over 3 days to obtain a white, fluffy collagen powder.

**[0125]** The purified collagen was analyzed on an SDS-PAGE gel and a thick and clear band was observed at the expected size of 42 kilodaltons. The purified collagen was also analyzed by mass spectrometry and it was confirmed that the 42 kilodalton protein was jellyfish collagen.

**[0126]** The fermentations were performed at various temperature ranging from 25° to 28° C. For some fermentations, the temperature of the fermentation was maintained at a constant temperature and immediately upon completion of fermentation (OD600 of 5-10) the collagen was purified. For other fermentations, the temperature of the fermentations was maintained for a desired period of time and when cell densities of OD600 of 5-10 were reached, the temperature was reduced to induce protein production. Typically, the temperature was reduced from 28° C. to 25° C. After the fermentation at 25° C. was continued for 40-60 hours, the collagen was isolated.

Additional Full Length Jellyfish Collagens

**[0127]** A full length jellyfish collagen without a His tag, linker, and thrombin cleavage site is disclosed below. Two codon-optimized nucleotide sequence encoding this collagen are provided in SEQ ID NO: 6 and SEQ ID NO: 7. The differences in the nucleotide sequences are due to different codon-optimization strategies but encode the same protein. The amino acid sequence is disclosed in SEQ ID NO: 8. The DsbA secretion tag is encoded by nucleotides 1-72 and encodes amino acids 1-24. The collagen sequence is encoded by nucleotides 73-1359 and encodes amino acids 25-453.

(SEQ ID NO: 6)

ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGCA

TCGGCGGCGCAGTATGAAGATGGTCCGCAGGGTGTTGTTGGTGCAGATGGT

AAAGACGGTACCCCGGGTGAAAAAGGAGAACAGGGACGTACAGGTGCAGCA

GGTAAACAGGGCAGCCCGGGTGCCGATGGTGCCCGTGGCCCGCTGGGTAGC

ATTGGTCAGCAGGGTGCAAGAGGCGAACCGGGCGATCCGGGTAGTCCGGGC

CTGCGTGGTGATACGGGTCTGGCCGGTGTTAAAGGCGTTGCAGGTCCTTCA

GGTCGTCCAGGTCAACCGGGTGCAAATGGTCTGCCGGGTGTTAATGGTCGT

GGCGGTCTGCGTGGCAAACCGGGAGCAAAAGGTATTGCAGGTAGCGATGGA

GAAGCCGGTGAAAGCGGTGCCCCGGGTCAGAGTGGTCCGACCGGTCCGCGC

GGTCAGCGTGGTCCGTCTGGTGAAGATGGCAATCCGGGTCTGCAGGGTCTG

CCTGGTAGTGATGGCGAACCAGGTGAAGAAGGTCAGCCGGGTCGTTCAGGC

CAGCCGGGCCAGCAGGGCCCGCGTGGTAGCCCGGGCGAAGTTGGCCCGCGG

GGTAGTAAAGGTCCTAGTGGCGATCGCGGTGATCGTGGTGAACGCGGTGTT

CCTGGTCAGACCGGTAGCGCAGGTAATGTTGGCGAAGATGGTGAACAGGGT

GGCAAAGGTGTTGATGGTGCAAGCGGTCCGAGCGGTGCACTGGGTGCACGT

GGTCCTCCGGGCAGCCGTGGTGACACCGGTGCAGTTGGTCCGCCTGGCCCG

ACCGGCCGTAGTGGCTTACCGGGTAATGCAGGTCAGAAAGGTCCGTCAGGT

GAACCTGGCAGCCCTGGTAAAGCAGGTAGTGCCGGTGAGCAGGGTCCGCCG

GGCAAAGATGGTAGTAATGGTGAGCCGGGTAGCCCTGGCAAAGAAGGTGAA

CGTGGTCTGGCAGGACCGCCGGGTCCTGATGGTCGCCGCGGTGAAACGGGT

TCACCGGGTATTGCCGGTGCCCTGGGTAAACCAGGTCTGGAAGGTCCGAAA

GGTTATCCTGGTCTGCGCGGTCGTGATGGTACCAATGGCAAACGTGGCGAA

CAGGGCGAAACCGGTCCAGATGGTGTTCGTGGTATTCCGGGTAACGATGGT

CAGAGCGGTAAACCGGGCATTGATGGTATTGATGGCACCAATGGTCAGCCT

GGCGAAGCAGGTTATCAGGGTGGTCGCGGTACCCGTGGTCAGCTGGGTGAA

ACAGGTGATGTTGGTCAGAATGGTGATCGCGGCGCACCGGGTCCGGATGGT

AGCAAAGGTAGCGCCGGTCGTCCGGGTTTACGTtaa

(SEQ ID NO: 7)

ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGCA

TCGGCGGCGCAGTATGAAGATGGTCCGCAGGGTGTTGTTGGTGCAGATGGT

AAAGACGGTACCCCGGGTGAAAAAGGtGAACAGGGtCGTACcGGTGCAGCA

GGTAAACAGGGCAGCCCGGGTGCCGATGGTGCCCGTGGCCCGCTGGGTAGC

ATTGGTCAGCAGGGTGCAcgtGGCGAACCGGGCGATCCGGGTAGcCCGGGC

CTGCGTGGTGATACGGGTCTGGCCGGTGTTAAAGGCGTTGCAGGTCCTTCt

GGTCGTCCAGGTCAACCGGGTGCAAATGGTCTGCCGGGTGTTAATGGTCGT

GGCGGTCTGCGTGGCAAACCGGGtGCAAAAGGTATTGCAGGTAGCGATGGc

GAAGCCGGTGAAAGCGGTGCCCCGGGTCAGAGcGGTCCGACCGGTCCGCGC

GGTCAGCGTGGTCCGTCTGGTGAAGATGGCAATCCGGGTCTGCAGGGTCTG

CCTGGTagcGATGGCGAACCAGGTGAAGAAGGTCAGCCGGGTCGTTCtGGC

-continued

CAGCCGGGCCAGCAGGGCCCGCGTGGTAGCCCGGGCGAAGTTGGCCCGCGc

GGTtcTAAAGGTCCTAGcGGCGATCGCGGTGATCGTGGTGAACGCGGTGTT

CCTGGTCAGACCGGTAGCGCAGGTAATGTTGGCGAAGATGGTGAACAGGGT

GGCAAAGGTGTTGATGGTGCAAGCGGTCCGAGCGGTGCACTGGGTGCACGT

GGTCCTCCGGGCAGCCGTGGTGACACCGGTGCAGTTGGTCCGCCTGGCCCG

ACCGGCCGTAGcGGCctgCCGGGTAATGCAGGTCAGAAAGGTCCGTCtGGT

GAACCTGGCAGCCCTGGTAAAGCAGGTAGcGCCGGTGAGCAGGGTCCGCCG

GGCAAAGATGGTAGcAATGGTGAGCCGGGTAGCCCTGGCAAAGAAGGTGAA

CGTGGTCTGGCAGGtCCGCCGGGTCCTGATGGTCGCCGCGGTGAAACGGGT

TCtCCGGGTATTGCCGGTGCCCTGGGTAAACCAGGTCTGGAAGGTCCGAAA

GGTTATCCTGGTCTGCGCGGTCGTGATGGTACCAATGGCAAACGTGGCGAA

CAGGGCGAAACCGGTCCAGATGGTGTTCGTGGTATTCCGGGTAACGATGGT

CAGAGCGGTAAACCGGGCATTGATGGTATTGATGGCACCAATGGTCAGCCT

GGCGAAGCAGGTTATCAGGGTGGTCGCGGTACCCGTGGTCAGCTGGGTGAA

ACcGGTGATGTTGGTCAGAATGGTGATCGCGGCGCACCGGGTCCGGATGGT

AGCAAAGGTAGCGCCGGTCGTCCGGGTctgCGTtaa

(SEQ ID NO: 8)

MKKIWLALAGLVLAFSASAAQYEDGPQGVVGADGKDGTPGEKGEQGRTGAA

GKQGSPGADGARGPLGSIGQQGARGEPGDPGSPGLRGDTGLAGVKGVAGPS

GRPGQPGANGLPGVNGRGGLRGKPGAKGIAGSDGEAGESGAPGQSGPTGPR

GQRGPSGEDGNPGLQGLPGSDGEPGEEGQPGRSGQPGQQGPRGSPGEVGPR

GSKGPSGDRGDRGERGVPGQTGSAGNVGEDGEQGGKGVDGASGPSGALGAR

GPPGSRGDTGAVGPPGPTGRSGLPGNAGQKGPSGEPGSPGKAGSAGEQGPP

GKDGSNGEPGSPGKEGERGLAGPPGPDGRRGETGSPGIAGALGKPGLEGPK

GYPGLRGRDGTNGKRGEQGETGPDGVRGIPGNDGQSGKPGIDGIDGTNGQP

GEAGYQGGRGTRGQLGETGDVGQNGDRGAPGPDGSKGSAGRPGLR

## Example 3: Production of Truncated Collagen

**[0128]** A codon optimized DNA sequence, optimized for expression in *E. coli*, encoding a jellyfish collagen with a truncation of 240 internal amino acids was synthesized and expressed. The DNA sequence is shown below in SEQ ID NO: 9. In SEQ ID NO: 9, The DsbA secretion tag is encoded by nucleotides 1-72 and encodes amino acids 1-24 of SEQ ID NO: 10. The histidine tag comprising 9 histidine (SEQ ID NO: 129) residues is encoded by nucleotides 73-99 and encodes amino acids 25-33 of SEQ ID NO: 10. The linker is encoded by nucleotides 100-111 and encodes amino acids 34-37 of SEQ ID NO: 10. The thrombin cleavage site is encoded by nucleotides 112-135 and encodes amino acids 38-45 of SEQ ID NO: 10. The truncated collagen is encoded by nucleotides 136-822 and encodes amino acids 46-274 of SEQ ID NO: 10.

(SEQ ID NO: 9)

ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGCA

TCGGCGGCGCAGTATGAAGATCACCATCACCACCACCACCATCACCACTCT

-continued

GGCTCGAGCCTGGTGCCGCGCGGCAGCCATATGGGTCCGCAGGGTGTTGTT

GGTGCAGATGGTAAAGACGGTACCCCGGGTGAAAAAGGAGAACAGGGACGT

ACAGGTGCAGCAGGTAAACAGGGCAGCCCGGGTGCCGATGGTGCCCGTGGC

CCGCTGGGTAGCATTGGTCAGCAGGGTGCAAGAGGCGAACCGGGCGATCCG

GGTAGTCCGGGCCTGCGTGGTGATACGGGTCTGGCCGGTGTTAAAGGCGTT

GCAGGTCCTTCAGGTCGTCCAGGTCAACCGGGTGCAAATGGTCTGCCGGGT

GTTAATGGTCGTGGCGGTCTGGAACGTGGTCTGGCAGGACCGCCGGGTCCT

GATGGTCGCCGCGGTGAAACGGGTTCACCGGGTATTGCCGGTGCCCTGGGT

AAACCAGGTCTGGAAGGTCCGAAAGGTTATCCTGGTCTGCGCGGTCGTGAT

GGTACCAATGGCAAACGTGGCGAACAGGGCGAAACCGGTCCAGATGGTGTT

CGTGGTATTCCGGGTAACGATGGTCAGAGCGGTAAACCGGGCATTGATGGT

ATTGATGGCACCAATGGTCAGCCTGGCGAAGCAGGTTATCAGGGTGGTCGC

GGTACCCGTGGTCAGCTGGGTGAAACAGGTGATGTTGGTCAGAATGGTGAT

CGCGGCGCACCGGGTCCGGATGGTAGCAAAGGTAGCGCCGGTCGTCCGGGT

TTACGTtaa

**[0129]** The truncated collagen is approximately 54% of the full length collagen and is disclosed below in SEQ ID NO: 10.

(SEQ ID NO: 10)

MKKIWLALAGLVLAFSASAAQYEDHHHHHHHHHSGSSLVPRGSHMGPQGVV

GADGKDGTPGEKGEQGRTGAAGKQGSPGADGARGPLGSIGQQGARGEPGDP

GSPGLRGDTGLAGVKGVAGPSGRPGQPGANGLPGVNGRGGLERGLAGPPGP

DGRRGETGSPGIAGALGKPGLEGPKGYPGLRGRDGTNGKRGEQGETGPDGV

RGIPGNDGQSGKPGIDGIDGTNGQPGEAGYQGGRGTRGQLGETGDVGQNGD

RGAPGPDGSKGSAGRPGLR

**[0130]** The polynucleotide encoding the truncated jellyfish collagen without the DsbA secretion tag, the histidine tag, linker and thrombin cleavage site is disclosed in SEQ ID NO: 85

(SEQ ID NO: 85)

GTCCGCAGGGTGTTGTTGGTGCAGATGGTAAAGACGGTACCCCGGGTGAAA

AAGGAGAACAGGGACGTACAGGTGCAGCAGGTAAACAGGGCAGCCCGGGTG

CCGATGGTGCCCGTGGCCCGCTGGGTAGCATTGGTCAGCAGGGTGCAAGAG

GCGAACCGGGCGATCCGGGTAGTCCGGGCCTGCGTGGTGATACGGGTCTGG

CCGGTGTTAAAGGCGTTGCAGGTCCTTCAGGTCGTCCAGGTCAACCGGGTG

CAAATGGTCTGCCGGGTGTTAATGGTCGTGGCGGTCTGGAACGTGGTCTGG

CAGGACCGCCGGGTCCTGATGGTCGCCGCGGTGAAACGGGTTCACCGGGTA

TTGCCGGTGCCCTGGGTAAACCAGGTCTGGAAGGTCCGAAAGGTTATCCTG

GTCTGCGCGGTCGTGATGGTACCAATGGCAAACGTGGCGAACAGGGCGAAA

-continued

CCGGTCCAGATGGTGTTCGTGGTATTCCGGGTAACGATGGTCAGAGCGGTA

AACCGGGCATTGATGGTATTGATGGCACCAATGGTCAGCCTGGCGAAGCAG

GTTATCAGGGTGGTCGCGGTACCCGTGGTCAGCTGGGTGAAACAGGTGATG

TTGGTCAGAATGGTGATCGCGGCGCACCGGGTCCGGATGGTAGCAAAGGTA

GCGCCGGTCGTCCGGGTTTACGTtaa

**[0131]** The truncated jellyfish collagen without the DsbA secretion tag, the histidine tag, linker and thrombin cleavage site is disclosed in SEQ ID NO: 86

(SEQ ID NO: 86)

GPQGVVGADGKDGTPGEKGEQGRTGAAGKQGSPGADGARGPLGSIGQQGAR

GEPGDPGSPGLRGDTGLAGVKGVAGPSGRPGQPGANGLPGVNGRGGLERGL

AGPPGPDGRRGETGSPGIAGALGKPGLEGPKGYPGLRGRDGTNGKRGEQGE

TGPDGVRGIPGNDGQSGKPGIDGIDGTNGQPGEAGYQGGRGTRGQLGETGD

VGQNGDRGAPGPDGSKGSAGRPGLR

**[0132]** The polynucleotides of SEQ ID NO: 9 was codon optimized and synthesized by Gen9 DNA, now Ginkgo Bioworks internal synthesis. Overlaps between the pET28 vector and SEQ ID NO: 9 were designed to be between 30 and 40 bp long and added using PCR with the enzyme PrimeStar GXL polymerase (http://www.clontech.com/US/Products/PCR/GC_Rich/PrimeSTAR_GXL_DNA_Polymerase?sitex=10020:22372:US). The opened pET28a vector and insert DNA (SEQ ID NO: 9) was then assembled together into the final plasmid using SGI Gibson assembly (https://us.vwr.com/store/product/i7613857/gibson-assembly-hifi-1-step-kit-synthetic-genomics-inc). Sequence of plasmid was then verified through sanger sequencing through Eurofins Genomics (www.eurofinsgenomics.com).

**[0133]** The transformed cells were cultivated in minimal media and frozen in 1.5 aliquots with glycerol at a ratio of 50:50 of cells to glycerol. One vial of this frozen culture was revived in 50 ml of minimal media overnight at 37° C., 200 rpm. Cells were transferred into 300 ml of minimal media and grown for 6-9 hours to reach an OD600 of 5-10.

**[0134]** A bioreactor was prepared with 2.7 L of minimal media+glucose and 300 ml of OD600 of 5-10 culture was added to bring the starting volume to 3 L. Cells were grown at 28° C., pH7 with Dissolved Oxygen maintained at 20% saturation using a cascade containing agitation, air and oxygen. pH was controlled using 28% w/w Ammonium hydroxide solution. Fermentation was run in a fed-batch mode using a DO-stat based feeding algorithm once the initial bolus of 40 g/L was depleted around 13 hours. After 24-26 hours of initial growth, the OD600 reached above 100. At this point, 300 mL of 500 g/L sucrose was added and temperature was reduced to 25 C. High density culture was induced for protein production using 1 mM IPTG. Fermentation was continued for another 20-24 hours and cells were harvested using a bench top centrifuge at 9000 rcf, 15 C for 60 minutes. Cell pellet recovered from centrifugation was resuspended in a buffer containing 0.5M NaCl and 0.1M KH2PO4 at pH8 in a weight by weight ratio of 2× buffer to 1× cells.

**[0135]** The harvested cells were disrupted in a homogenizer at 14,000 psi pressure in 2 passes. Resulting slurry contained the collagen protein along with other proteins.

**[0136]** The fermentations were performed at various temperature ranging from 25° to 28° C. For some fermentations, the temperature of the fermentation was maintained at a constant temperature and immediately upon completion of fermentation (OD600 of 5-10) the collagen was purified. For other fermentations, the temperature of the fermentations was maintained for a desired period of time and when cell densities of OD600 of 5-10 were reached, the temperature was reduced to induce protein production. Typically, the temperature was reduced from 28° C. to 25° C. After the fermentation at 25° C. was continued for 40-60 hours, the collagen was isolated.

**[0137]** The collagen was purified by acid treatment of homogenized cell broth. Additionally, acid treatment was also performed on non-homogenized whole cells recovered from the bioreactor after centrifugation and resuspension in the buffer described above. The pH of either the homogenized slurry of the resuspended whole cells was decreased to 3 using 6M Hydrochloric acid. Acidified cell slurry was incubated overnight at 4° C. with mixing, followed by centrifugation. Supernatant of the acidified slurry was tested on a polyacrylamide gel and found to contain collagen in relatively high abundance compared to starting pellet. The collagen slurry thus obtained was high in salts. To obtain volume and salt reduction, concentration and diafiltration steps were performed using an EMD Millipore Tangential Flow Filtration system with ultrafiltration cassettes of 0.1 $m^2$ each. Total area of filtration was 0.2 $m^2$ using 2 cassettes in parallel. A volume reduction of 5× and a salt reduction of 19× was achieved in the TFF stage. Final collagen slurry was run on an SDS-PAGE gel to confirm presence of the collagen. This slurry was dried using a multi-tray lyophilizer over 3 days to obtain a white, fluffy collagen powder.

**[0138]** The purified truncated collagen obtained from homogenized cell broth or non-homogenized cells were analyzed on an SDS-PAGE gel and a thick and clear band was observed at the expected size of 27 kilodaltons. The purified collagen was also analyzed by mass spectrometry and it was confirmed that the 27 kilodalton protein was jellyfish collagen.

**[0139]** An alternative purification method of the full length and truncated collagens is provided below.

**[0140]** The fermentation broth was mixed with 0.3-0.5% w/v of Poly Ethyl Imine (PEI). After 15 minutes of incubation with PEI, the fermentation broth was centrifuged at 9000 rcf for 15 minutes to recover the supernatant, which contained the collagen protein. The pellet containing the cells was discarded and the PEI-treated collagen containing supernatant was mixed with Sodium Bentonite (0.2% final w/v) (Wyopure®, Wyoming Bentonite) and centrifuged. The bentonite containing pellet was discarded and the supernatant was recovered.

**[0141]** The Bentonite treated supernatant was concentrated between 3-6 fold on a tangential flow filtration system (TFF) (EMD Millipore) using a 5 kDa cassette. The collagen was retained with almost no losses in the permeate stream. To remove salts, the retentate from the concentration step was diafiltered using the same TFF set-up. Final conductivity of the protein solution was <10 milliSiemens. The typical conductivity was between 400 microsiemens and 1.5 millisiemens. Highly concentrated collagen solutions had higher conductivities approaching 4 milliSiemens. A skilled artisan will understand that conductivities higher than 10 milliSiemens may be observed depending on the concentration of the collagen. Next, the desalted and concentrated protein was subjected to treatment with activated carbon using the W-L 9000 10×40 granulated resin (Carbon Activated Corporation). 5% w/v of the carbon resin was mixed with collagen containing protein feed and mixed at 45-50° C. with mild agitation. The carbon-treated slurry was filtered using a Buchner funnel lined with an Ertel Filter Press Pad M-953 (Ertel Alsop) in presence or absence of a filtration aid such as Diatomaceous Earth (Sigma Aldrich). Post-filtration, the collagen solution was filtered through a 0.2 micron filter followed by one to several hours of treatment with Sodium Bentonite (0.2% w/v final) (Wyopure®, Wyoming Bentonite) and centrifuged at 9000 rcf, 15-30 minutes to obtain a highly pure, clear and particulate free collagen solution. When removal of endotoxin proteins was desired, the protein was passed through a chromatographic filter like Sartobind-Q (Sartorius-Stedim) to specifically remove endotoxin proteins.

**[0142]** The purified collagen was analyzed on an SDS-PAGE gel and a thick and clear band was observed at 30 kilodaltons. The upshift in size is due to the structure of the collagen molecule and the high glycine/proline amino acid content. The purified collagen was also analyzed by mass spectrometry and it was confirmed that the 30 kilodalton protein was the truncated collagen.

**[0143]** The truncated collagens were further analyzed by HPLC using an Agilent 1100 series HPLC. The column was the 50 mm Agilent PLRP-S reverse phase column with an inner diameter of 4.6 mm, M particle size and 1000 Angstrom pore size.

**[0144]** The sample was prepared by diluting 1:1 in a 0.04% sodium azide solution in HPLC-grade water. After dilution, the resulting mixture was filtered through a 0.45 um filter to remove any large particles that can clog the HPLC column. For analysis, the samples are diluted appropriately with a 20 mM ammonium acetate buffer in HPLC-grade water at a pH of about 4.5. After mixing the sample, it was transferred to a 300 μL microvial that was then placed in the autosampler. Using ChemStation, the software that operates the HPLC, the analysis parameters such as sample flowrate, column temperature, mobile phase flowrate, mobile phase composition, etc. can be altered. In one exemplary, but non-limiting analysis the parameters were: sample flow rate of 1 mL/min, column temperature of 80° C., column pressure of 60-70 bar, mobile phase composition of 97.9% water/1.9% acetonitrile with 0.2% trifluoroacetic acid; UV wavelength for analysis of 214.4 nm, injection volume of 10 μL, and sample run time of 10 minutes.

**[0145]** Under these conditions, the truncated jellyfish collation of SEQ ID NO: 91 has an elution time of about 5.4 minutes. ChemStation quantifies the peak area of the elution peak and calculates the protein concentration using a calibration curve that directly relates peak area to protein concentration. The calibration curve is generated using a known collagen solution that is serially diluted to contain collagen concentration ranges of 0.06 mg/mL to 1.00 mg/mL.

### Truncated Collagen without His Tag-Linker-Thrombin Cleavage Site

**[0146]** A truncated jellyfish collagen without a His tag, linker, and thrombin cleavage site is disclosed below. The codon-optimized nucleotide sequence encoding this collagen is provided in SEQ ID NO: 11. The amino acid sequence is disclosed in SEQ ID NO: 12. The DsbA secretion tag is encoded by nucleotides 1-72 and encodes amino acids 1-24. The truncated collagen sequence is encoded by nucleotides 73-639 and encodes amino acids 25-213.

(SEQ ID NO: 11)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGCA

TCGGCGGCGCAGTATGAAGATGGTCCGCAGGGTGTTGTTGGTGCAGATGGT

AAAGACGGTACCCCGGGTAATGCAGGTCAGAAAGGTCCGTCAGGTGAACCT

GGCAGCCCTGGTAAAGCAGGTAGTGCCGGTGAGCAGGGTCCGCCGGGCAAA

GATGGTAGTAATGGTGAGCCGGGTAGCCCTGGCAAAGAAGGTGAACGTGGT

CTGGCAGGACCGCCGGGTCCTGATGGTCGCCGCGGTGAAACGGGTTCACCG

GGTATTGCCGGTGCCCTGGGTAAACCAGGTCTGGAAGGTCCGAAAGGTTAT

CCTGGTCTGCGCGGTCGTGATGGTACCAATGGCAAACGTGGCGAACAGGGC

GAAACCGGTCCAGATGGTGTTCGTGGTATTCCGGGTAACGATGGTCAGAGC

GGTAAACCGGGCATTGATGGTATTGATGGCACCAATGGTCAGCCTGGCGAA

GCAGGTTATCAGGGTGGTCGCGGTACCCGTGGTCGCTGGGTGAAACAGGTG

ATGTTGGTCAGAATGGTGATCGCGGCGCACCGGGTCCGGATGGTAGCAAAG

GTAGCGCCGGTCGTCCGGGTTTACGTtaa

(SEQ ID NO: 12)
MKKIWLALAGLVLAFSASAAQYEDGPQGVVGADGKDGTPGNAGQKGPSGEP

GSPGKAGSAGEQGPPGKDGSNGEPGSPGKEGERGLAGPPGPDGRRGETGSP

GIAGALGKPGLEGPKGYPGLRGRDGTNGKRGEQGETGPDGVRGIPGNDGQS

GKPGIDGIDGTNGQPGEAGYQGGRGTRGQLGETGDVGQNGDRGAPGPDGSK

GSAGRPGLR

**[0147]** A polynucleotide encoding a truncated jellyfish collagen without a His tag, linker and thrombin cleavage site disclosed in SEQ ID NO: 90

(SEQ ID NO: 90)
GGTCCGCAGGGTGTTGTTGGTGCAGATGGTAAAGACGGTACCCCGGGTAAT

GCAGGTCAGAAAGGTCCGTCAGGTGAACCTGGCAGCCCTGGTAAAGCAGGT

AGTGCCGGTGAGCAGGGTCCGCCGGGCAAAGATGGTAGTAATGGTGAGCCG

GGTAGCCCTGGCAAAGAAGGTGAACGTGGTCTGGCAGGACCGCCGGGTCCT

GATGGTCGCCGCGGTGAAACGGGTTCACCGGGTATTGCCGGTGCCCTGGGT

AAACCAGGTCTGGAAGGTCCGAAAGGTTATCCTGGTCTGCGCGGTCGTGAT

GGTACCAATGGCAAACGTGGCGAACAGGGCGAAACCGGTCCAGATGGTGTT

CGTGGTATTCCGGGTAACGATGGTCAGAGCGGTAAACCGGGCATTGATGGT

ATTGATGGCACCAATGGTCAGCCTGGCGAAGCAGGTTATCAGGGTGGTCGC

GGTACCCGTGGTCAGCTGGGTGAAACAGGTGATGTTGGTCAGAATGGTGAT

CGCGGCGCACCGGGTCCGGATGGTAGCAAAGGTAGCGCCGGTCGTCCGGGT

TTACGTtaa

**[0148]** A truncated jellyfish collagen without a His tag, linker and thrombin cleavage site disclosed in SEQ ID NO: 91

(SEQ ID NO: 91)
GPQGVVGADGKDGTPGNAGQKGPSGEPGSPGKAGSAGEQGPPGKDGSNGEP

GSPGKEGERGLAGPPGPDGRRGETGSPGIAGALGKPGLEGPKGYPGLRGRD

GTNGKRGEQGETGPDGVRGIPGNDGQSGKPGIDGIDGTNGQPGEAGYQGGR

GTRGQLGETGDVGQNGDRGAPGPDGSKGSAGRPGLR

**[0149]** Truncated Collagen with GEK Repeats

**[0150]** A jellyfish collagen with GEK repeats is disclosed below. The codon-optimized nucleotide sequence encoding this collagen is provided in SEQ ID NO: 13. The amino acid sequence is disclosed in SEQ ID NO: 14. The DsbA secretion tag is encoded by nucleotides 1-72 and encodes amino acids 1-24. The GEK repeat is encoded by nucleotides 73-126 and encodes the GEK repeats of amino acids 25-42. The truncated collagen sequence is encoded by nucleotides 127-693 and encodes amino acids 43-231.

(SEQ ID NO: 13)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGCA

TCGGCGGCGCAGTATGAAGATGGTGAAAAAGGTGAaAAGGGCGAGAAAGGT

GAGAAAGGCGAAAAGGGTGAAAAAGGTCCGCAGGGTGTTGTTGGTGCAGAT

GGTAAAGACGGTACCCCGGGTAATGCAGGTCAGAAAGGTCCGTCAGGTGAA

CCTGGCAGCCCTGGTAAAGCAGGTAGTGCCGGTGAGCAGGGTCCGCCGGGC

AAAGATGGTAGTAATGGTGAGCCGGGTAGCCCTGGCAAAGAAGGTGAACGT

GGTCTGGCAGGACCGCCGGGTCCTGATGGTCGCCGCGGTGAAACGGGTTCA

CCGGGTATTGCCGGTGCCCTGGGTAAACCAGGTCTGGAAGGTCCGAAAGGT

TATCCTGGTCTGCGCGGTCGTGATGGTACCAATGGCAAACGTGGCGAACAG

GGCGAAACCGGTCCAGATGGTGTTCGTGGTATTCCGGGTAACGATGGTCAG

AGCGGTAAACCGGGCATTGATGGTATTGATGGCACCAATGGTCAGCCTGGC

GAAGCAGGTTATCAGGGTGGTCGCGGTACCCGTGGTCAGCTGGGTGAAACA

GGTGATGTTGGTCAGAATGGTGATCGCGGCGCACCGGGTCCGGATGGTAGC

AAAGGTAGCGCCGGTCGTCCGGGTTTACGTtaa

(SEQ ID NO: 14)
MKKIWLALAGLVLAFSASAAQYEDGEKGEKGEKGEKGEKGEKGPQGVVGAD

GKDGTPGNAGQKGPSGEPGSPGKAGSAGEQGPPGKDGSNGEPGSPGKEGER

GLAGPPGPDGRRGETGSPGIAGALGKPGLEGPKGYPGLRGRDGTNGKRGEQ

GETGPDGVRGIPGNDGQSGKPGIDGIDGTNGQPGEAGYQGGRGTRGQLGET

GDVGQNGDRGAPGPDGSKGSAGRPGLR

**[0151]** The polynucleotides of SEQ ID NO: 13 was codon optimized and synthesized by Gen9 DNA, now Ginkgo Bioworks internal synthesis. Overlaps between the pET28 vector and SEQ ID NO: 13 was designed to be between 30 and 40 bp long and added using PCR with the enzyme PrimeStar GXL polymerase (http://www.clontech.com/US/Products/PCR/GC_Rich/PrimeSTAR_GXL_DNA_Polymerase?sitex=10020:22372:US). The opened pET28a vector and insert DNA (SEQ ID NO: 13) was then assembled together into the final plasmid using SGI Gibson assembly (https://us.vwr.com/store/product/17613857/gibson-assembly-hifi-1-step-kit-synthetic-genomics-inc). Sequence of plasmid was then verified through Sanger sequencing through Eurofins Genomics (www.eurofinsgenomics.com).

**[0152]** The transformed cells were cultivated in minimal media and frozen in 1.5 aliquots with glycerol at a ratio of 50:50 of cells to glycerol. One vial of this frozen culture was revived in 50 ml of minimal media overnight at 37° C., 200 rpm. Cells were transferred into 300 ml of minimal media and grown for 6-9 hours to reach an OD600 of 5-10.

**[0153]** A bioreactor was prepared with 2.7 L of minimal media+glucose and 300 ml of OD600 of 5-10 culture was added to bring the starting volume to 3 L. Cells were grown at 28° C., pH7 with Dissolved Oxygen maintained at 20% saturation using a cascade containing agitation, air and oxygen. pH was controlled using 28% w/w Ammonium hydroxide solution. Fermentation was run in a fed-batch mode using a DO-stat based feeding algorithm once the initial bolus of 40 g/L was depleted around 13 hours. After 24-26 hours of initial growth, the OD600 reached above 100. At this point, 300 mL of 500 g/L sucrose was added and temperature was reduced to 25 C. High density culture was induced for protein production using 1 mM IPTG. Fermentation was continued for another 20-24 hours and cells were harvested using a bench top centrifuge at 9000 rcf, 15 C for 60 minutes. Cell pellet recovered from centrifugation was resuspended in a buffer containing 0.5M NaCl and 0.1M KH2PO4 at pH8 in a weight by weight ratio of 2× buffer to 1× cells.

**[0154]** The harvested cells were disrupted in a homogenizer at 14,000 psi pressure in 2 passes. Resulting slurry contained the collagen protein along with other proteins.

**[0155]** The collagen was purified by acid treatment whole cells recovered from bioreactor after centrifugation and resuspension in a buffer as described above. The pH of either the homogenized slurry or the resuspended suspension was decreased to 3 using 6M Hydrochloric acid. Acidified cell slurry was incubated overnight at 4° C. with mixing, followed by centrifugation. Supernatant of the acidified slurry was tested on a polyacrylamide gel and found to contain collagen in relatively high abundance compared to starting pellet. The collagen slurry thus obtained was high in salts. To obtain volume and salt reduction, concentration and diafiltration steps were performed using an EMD Millipore Tangential Flow Filtration system with ultrafiltration cassettes of 0.1 $m^2$ each. Total area of filtration was 0.2 $m^2$ using 2 cassettes in parallel. A volume reduction of 5× and a salt reduction of 19× was achieved in the TFF stage. Final collagen slurry was run on an SDS-PAGE gel to confirm presence of the collagen. This slurry was dried using a multi-tray lyophilizer over 3 days to obtain a white, fluffy collagen powder.

**[0156]** The purified collagen was analyzed on an SDS-PAGE gel and was observed to run at an apparent molecular weight of 35 kilodaltons. The 35 kilodalton band does not correspond to the expected size of 22 kilodaltons. The upshift between the expected size and the apparent size is thought to be due to the GEK repeats interacting with the gel matrix. The 35 kDa band was confirmed by mass spectrometry to be the correct collagen with the GEK repeats.

Truncated Collagen with GDK Repeats

**[0157]** A jellyfish collagen with GDK repeats is disclosed below. The codon-optimized nucleotide sequence encoding this collagen is provided in SEQ ID NO: 15. The amino acid sequence is disclosed in SEQ ID NO: 16. The DsbA secretion tag is encoded by nucleotides 1-72 and encodes amino acids 1-24. The GDK repeat is encoded by nucleotides 73-126 and encodes the GDK repeats of amino acids 25-42. The truncated collagen sequence is encoded by nucleotides 127-693 and encodes amino acids 43-231.

(SEQ ID NO: 15)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCG

CATCGGCGGCGCAGTATGAAGATGGTGATAAAGGTGATAAGGGCGACAA

AGGTGACAAAGGCGATAAGGGTGATAAAGGTCCGCAGGGTGTTGTTGGT

GCAGATGGTAAAGACGGTACCCCGGGTAATGCAGGTCAGAAAGGTCCGT

CAGGTGAACCTGGCAGCCCTGGTAAAGCAGGTAGTGCCGGTGAGCAGGG

TCCGCCGGGCAAAGATGGTAGTAATGGTGAGCCGGGTAGCCCTGGCAAA

GAAGGTGAACGTGGTCTGGCAGGACCGCCGGGTCCTGATGGTCGCCGCG

GTGAAACGGGTTCACCGGGTATTGCCGGTGCCCTGGGTAAACCAGGTCT

GGAAGGTCCGAAAGGTTATCCTGGTCTGCGCGGTCGTGATGGTACCAAT

GGCAAACGTGGCGAACAGGGCGAAACCGGTCCAGATGGTGTTCGTGGTA

TTCCGGGTAACGATGGTCAGAGCGGTAAACCGGGCATTGATGGTATTGA

TGGCACCAATGGTCAGCCTGGCGAAGCAGGTTATCAGGGTGGTCGCGGT

ACCCGTGGTCAGCTGGGTGAAACAGGTGATGTTGGTCAGAATGGTGATC

GCGGCGCACCGGGTCCGGATGGTAGCAAAGGTAGCGCCGGTCGTCCGGG

TTTACGTtaa

(SEQ ID NO: 16)
MKKIWLALAGLVLAFSASAAQYEDGDKGDKGDKGDKGDKGDKGPQGVVG

ADGKDGTPGNAGQKGPSGEPGSPGKAGSAGEQGPPGKDGSNGEPGSPGK

EGERGLAGPPGPDGRRGETGSPGIAGALGKPGLEGPKGYPGLRGRDGTN

GKRGEQGETGPDGVRGIPGNDGQSGKPGIDGIDGTNGQPGEAGYQGGRG

TRGQLGETGDVGQNGDRGAPGPDGSKGSAGRPGLR

**[0158]** The polynucleotides of SEQ ID NO: 15 was codon optimized and synthesized by Gen9 DNA, now Ginkgo Bioworks internal synthesis. Overlaps between the pET28 vector and SEQ ID NO: 15 was designed to be between 30 and 40 bp long and added using PCR with the enzyme PrimeStar GXL polymerase (http://www.clontech.com/US/Products/PCR/GC_Rich/PrimeSTAR_GXL_DNA_Polymerase?sitex=10020:22372:US). The opened pET28a vector and insert DNA (SEQ ID NO: 15) was then assembled together into the final plasmid using SGI Gibson assembly (https://us.vwr.com/store/product/17613857/gibson-assembly-hifi-1-step-kit-synthetic-genomics-inc). Sequence of plasmid was then verified through sanger sequencing through Eurofins Genomics (www.eurofinsgenomics.com).

**[0159]** The transformed cells were cultivated in minimal media and frozen in 1.5 aliquots with glycerol at a ratio of 50:50 of cells to glycerol. One vial of this frozen culture was revived in 50 ml of minimal media overnight at 37° C., 200 rpm. Cells were transferred into 300 ml of minimal media and grown for 6-9 hours to reach an OD600 of 5-10.

**[0160]** A bioreactor was prepared with 2.7 L of minimal media+glucose and 300 ml of OD600 of 5-10 culture was added to bring the starting volume to 3 L. Cells were grown at 28° C., pH7 with Dissolved Oxygen maintained at 20% saturation using a cascade containing agitation, air and oxygen. pH was controlled using 28% w/w Ammonium hydroxide solution. Fermentation was run in a fed-batch mode using a DO-stat based feeding algorithm once the initial bolus of 40 g/L was depleted around 13 hours. After 24-26 hours of initial growth, the OD600 reached above 100. At this point, 300 mL of 500 g/L sucrose was added and temperature was reduced to 25 C. High density culture was induced for protein production using 1 mM IPTG. Fermentation was continued for another 20-24 hours and cells were harvested using a bench top centrifuge at 9000 rcf, 15 C for 60 minutes. Cell pellet recovered from centrifugation was resuspended in a buffer containing 0.5M NaCl and 0.1M KH2PO4 at pH8 in a weight by weight ratio of 2× buffer to 1× cells.

**[0161]** The harvested cells were disrupted in a homogenizer at 14,000 psi pressure in 2 passes. Resulting slurry contained the collagen protein along with other proteins.

**[0162]** The collagen was purified by acid treatment of whole cells recovered from bioreactor after centrifugation and resuspension in a buffer as described above. The pH of either the homogenized slurry was decreased to 3 using 6M Hydrochloric acid. Acidified cell slurry was incubated overnight at 4° C. with mixing, followed by centrifugation. Supernatant of the acidified slurry was tested on a polyacrylamide gel and found to contain collagen in relatively high abundance compared to starting pellet. The collagen slurry thus obtained was high in salts. To obtain volume and salt reduction, concentration and diafiltration steps were performed using an EMD Millipore Tangential Flow Filtration system with ultrafiltration cassettes of 0.1 $m^2$ each. Total area of filtration was 0.2 $m^2$ using 2 cassettes in parallel. A volume reduction of 5× and a salt reduction of 19× was achieved in the TFF stage. Final collagen slurry was run on an SDS-PAGE gel to confirm presence of the collagen. This slurry was dried using a multi-tray lyophilizer over 3 days to obtain a white, fluffy collagen powder.

**[0163]** The purified collagen was analyzed on an SDS-PAGE gel and was observed to run at an apparent molecular weight of 35 kilodaltons. The 35 kilodalton band does not correspond to the expected size of 22 kilodaltons. The upshift between the expected size and the apparent size is thought to be due to the GDK repeats interacting with the gel matrix. The 35 kDa band was confirmed by mass spectrometry to be the correct collagen with the GDK repeats.

Truncated Collagen with DsbA Secretion Tag-His Tag-Linker-Thrombin Cleavage Site and GFP Beta-Lactamase Fusion (Version 1):

**[0164]** A jellyfish collagen with DsbA secretion tag-His tag-Linker-Thrombin cleavage site and GFP Beta-lactamase fusion is disclosed below. The codon-optimized nucleotide sequence encoding this collagen is provided in SEQ ID NO: 17. The amino acid sequence is disclosed in SEQ ID NO: 18. The DsbA secretion tag is encoded by nucleotides 1-72 and encodes amino acids 1-24. The His tag is encoded by nucleotides 73-99 and encodes a 9 histidine tag (SEQ ID NO: 129) of amino acids 25-33. The linker is encoded by nucleotides 100-111 and encodes amino acids 34-37. The thrombin cleavage side is encoded by nucleotides 112-135 and encodes amino acids 38-45. The green fluorescent protein (GFP) with linker is encoded by nucleotides 136-873 and encodes amino acids 46-291. The truncated collagen sequence is encoded by nucleotides 874-1440 and encodes amino acids 292-480. The Beta-lactamase with linker is encoded by nucleotides 1441-2232 and encodes amino acids

481-744. The Beta-lactamase was properly targeted to the periplasmic space even though the polypeptide did not have an independent secretion tag. The DsbA secretion tag directed the entire transcript (Truncated Collagen with DsbA secretion tag-His tag-Linker-Thrombin cleavage site and GFP Beta-lactamase fusion protein) to the periplasmic space and the Beta-lactamase functioned properly.

(SEQ ID NO: 17)

ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCG

CATCGGCGGCGCAGTATGAAGATCACCATCACCACCACCACCATCACCA

CTCTGGCTCGAGCCTGGTGCCGCGCGGCAGCCATATGTCTGGCTCGAGC

AGTAAAGGTGAAGAACTGTTCACCGGTGTTGTTCCGATCCTGGTTGAAC

TGGATGGTGATGTTAACGGCCACAAATTCTCTGTTCGTGGTGAAGGTGA

AGGTGATGCAACCAACGGTAAACTGACCCTGAAATTCATCTGCACTACC

GGTAAACTGCCGGTTCCATGGCCGACTCTGGTGACTACCCTGACCTATG

GTGTTCAGTGTTTTTCTCGTTACCCGGATCACATGAAGCAGCATGATTT

CTTCAAATCTGCAATGCCGGAAGGTTATGTACAGGAGCGCACCATTTCT

TTCAAAGACGATGGCACCTACAAAACCCGTGCAGAGGTTAAATTTGAAG

GTGATACTCTGGTGAACCGTATTGAACTGAAAGGCATTGATTTCAAAGA

GGACGGCAACATCCTGGGCCACAAACTGGAATATAACTTCAACTCCCAT

AACGTTTACATCACCGCAGACAAACAGAAGAACGGTATCAAAGCTAACT

TCAAAATTCGCCATAACGTTGAAGACGGTAGCGTACAGCTGGCGGACCA

CTACCAGCAGAACACTCCGATCGGTGATGGTCCGGTTCTGCTGCCGGAT

AACCACTACCTGTCCACCCAGTCTaaaCTGTCCAAAGACCCGAACGAAA

AGCGCGACCACATGGTGCTGCTGGAGTTCGTTACTGCAGCAGGTATCAC

GCACGGCATGGATGAACTCTACAAATCTGGCGCGCCGGGCGGTCCGCAG

GGTGTTGTTGGTGCAGATGGTAAAGACGGTACCCCGGGTAATGCAGGTC

AGAAAGGTCCGTCAGGTGAACCTGGCAGCCCTGGTAAAGCAGGTAGTGC

CGGTGAGCAGGGTCCGCCGGGCAAAGATGGTAGTAATGGTGAGCCGGGT

AGCCCTGGCAAAGAAGGTGAACGTGGTCTGGCAGGACCGCCGGGTCCTG

ATGGTCGCCGCGGTGAAACGGGTTCACCGGGTATTGCCGGTGCCCTGGG

TAAACCAGGTCTGGAAGGTCCGAAAGGTTATCCTGGTCTGCGCGGTCGT

GATGGTACCAATGGCAAACGTGGCGAACAGGGCGAAACCGGTCCAGATG

GTGTTCGTGGTATTCCGGGTAACGATGGTCAGAGCGGTAAACCGGGCAT

TGATGGTATTGATGGCACCAATGGTCAGCCTGGCGAAGCAGGTTATCAG

GGTGGTCGCGGTACCCGTGGTCAGCTGGGTGAAACAGGTGATGTTGGTC

AGAATGGTGATCGCGGCGCACCGGGTCCGGATGGTAGCAAAGGTAGCGC

CGGTCGTCCGGGTTTACGTcacccagaaacgctggtgaaagtaaaagat

gctgaagatcagttgggtgcacgagtgggttacatcgaactggatctca

acagcggtaagatccttgagagttttcgccccgaagaacgttttccaat

gatgagcacttttaaagttctgctatgtggcgcggtattatcccgtatt

gacgccgggcaagagcaactcggtcgccgcatacactattctcagaatg

-continued

acttggttgagtactcaccagtcacagaaaagcatcttacggatggcat

gacagtaagagaattatgcagtgctgccataaccatgagtgataacact

gcggccaacttacttctgacaacgatcggaggaccgaaggagctaaccg

ctatagcacaacatgggggatcatgtaactcgccttgatcgttgggaac

cggagctgaatgaagccataccaaacgacgagcgtgacaccacgatgcc

tgtagcaatggcaacaacgttgcgcaaactattaactggcgaactactt

actctagcttcccggcaacaattaatagactggatggaggcggataaag

ttgcaggaccacttctgcgctcggcccttccggctggctggtttattgc

tgataaatctggagccggtgagcgtgggtctcgcggtatcattgcagca

ctggggccagatggtaagccctcccgtatcgtagttatctacacgacgg

ggagtcaggcaactatggatgaacgaaatagacagatcgctgagatagg

tgcctcactgattaagcattggtaa

(SEQ ID NO: 18)

MKKIWLALAGLVLAFSASAAQYEDHHHHHHHHHSGSSLVPRGSHMSGSS

SKGEELFTGVVPILVELDGDVNGHKFSVRGEGEGDATNGKLTLKFICTT

GKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIS

FKDDGTYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFNSH

NVYITADKQKNGIKANFKIRHNVEDGSVQLADHYQQNTPIGDGPVLLPD

NHYLSTQSKLSKDPNEKRDHMVLLEFVTAAGITHGMDELYKSGAPGGPQ

GVVGADGKDGTPGNAGQKGPSGEPGSPGKAGSAGEQGPPGKDGSNGEPG

SPGKEGERGLAGPPGPDGRRGETGSPGIAGALGKPGLEGPKGYPGLRGR

DGTNGKRGEQGETGPDGVRGIPGNDGQSGKPGIDGIDGTNGQPGEAGYQ

GGRGTRGQLGETGDVGQNGDRGAPGPDGSKGSAGRPGLRHPETLVKVKD

AEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRI

DAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNT

AANLLLTTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTM

PVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSALPAGWFI

ADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDER

NRQIAEIGASLIKHW

**[0165]** The polynucleotides of SEQ ID NO: 17 was constructed by assembling several DNA fragments. The collagen containing sequence was codon optimized and synthesized by Gen9 DNA, now Ginkgo Bioworks internal synthesis. The GFP was also synthesized by Gen9. The Beta-lactamase was cloned out of the plasmid pKD46 (http://cgsc2.biology.yale.edu/Strain.php?ID=68099) using PCR with the enzyme PrimeStar GXL polymerase (http://www.clontech.com/US/Products/PCR/GC_Rich/PrimeSTAR_GXL_DNA_Polymerase?sitex=10020:22372:US). Overlaps between the pET28 vector, GFP, Collagen, and Beta-lactamase was designed to be between 30 and 40 bp long and added using PCR with the enzyme PrimeStar GXL polymerase. The opened pET28a vector and inserts were then assembled together into the final plasmid using SGI Gibson assembly (https://us.vwr.com/store/product/17613857/gibson-assembly-hifi-1-step-kit-synthetic-genomics-inc). Sequence of plasmid was then verified through sanger sequencing through Eurofins Genomics (www.eurofinsgenomics.com).

**[0166]** The transformed cells were cultivated in minimal media and frozen in 1.5 aliquots with glycerol at a ratio of 50:50 of cells to glycerol. One vial of this frozen culture was revived in 50 ml of minimal media overnight at 37° C., 200 rpm. Cells were transferred into 300 ml of minimal media and grown for 6-9 hours to reach an OD600 of 5-10.

**[0167]** A bioreactor was prepared with 2.7 L of minimal media+glucose and 300 ml of OD600 of 5-10 culture was added to bring the starting volume to 3 L. Cells were grown at 28° C., pH7 with Dissolved Oxygen maintained at 20% saturation using a cascade containing agitation, air and oxygen. pH was controlled using 28% w/w Ammonium hydroxide solution. Fermentation was run in a fed-batch mode using a DO-stat based feeding algorithm once the initial bolus of 40 g/L was depleted around 13 hours. After 24-26 hours of initial growth, the OD600 reached above 100. At this point, 300 mL of 500 g/L sucrose was added and temperature was reduced to 25 C. High density culture was induced for protein production using 1 mM IPTG. Fermentation was continued for another 20-24 hours and cells were harvested using a bench top centrifuge at 9000 rcf, 15 C for 60 minutes. Cell pellet recovered from centrifugation was resuspended in a buffer containing 0.5M NaCl and 0.1M KH2PO4 at pH8 in a weight by weight ratio of 2× buffer to 1× cells.

**[0168]** The harvested cells were disrupted in a homogenizer at 14,000 psi pressure in 2 passes. Resulting slurry contained the collagen protein along with other proteins.

**[0169]** The collagen was purified by acid treatment of non-homogenized whole cells recovered from the bioreactor after centrifugation and resuspension in the buffer described above. The pH of the resuspended suspension-was decreased to 3 using 6M Hydrochloric acid. Acidified cell slurry was incubated overnight at 4° C. with mixing, followed by centrifugation. The pH was then raised to 9 using 10N NaOH and the supernatant of the slurry was tested on a polyacrylamide gel and found to contain collagen in relatively high abundance compared to starting pellet. The collagen slurry thus obtained was high in salts. To obtain volume and salt reduction, concentration and diafiltration steps were performed using an EMD Millipore Tangential Flow Filtration system with ultrafiltration cassettes of 0.1 m2 each. Total area of filtration was 0.2 m2 using 2 cassettes in parallel. A volume reduction of 5× and a salt reduction of 19× was achieved in the TFF stage. Final collagen slurry was run on an SDS-PAGE gel to confirm presence of the collagen. This slurry was dried using a multi-tray lyophilizer over 3 days to obtain a white, fluffy collagen powder.

**[0170]** The purified collagen-GFP-Beta-lactamase fusion protein was analyzed on an SDS-PAGE gel and was observed to run at an apparent molecular weight of 90 kilodaltons. The expected size of the fusion protein is 85 kd. The 90 kDa band was confirmed by mass spectrometry to be the correct collagen fusion protein.

### Truncated Collagen with DsbA Secretion Tag-His Tag-Linker-Thrombin Cleavage Site and GFP Beta-Lactamase Fusion (Version 2):

**[0171]** A jellyfish collagen with DsbA secretion tag-His tag-Linker-Thrombin cleavage site and GFP Beta-lactamase fusion is disclosed below. The codon-optimized nucleotide sequence encoding this collagen is provided in SEQ ID NO: 19. The amino acid sequence is disclosed in SEQ ID NO: 20. The DsbA secretion tag is encoded by nucleotides 1-72 and encodes amino acids 1-24. The His tag is encoded by nucleotides 73-99 and encodes a 9 histidine tag (SEQ ID NO: 129) of amino acids 25-33. The linker is encoded by nucleotides 100-111 and encodes amino acids 34-37. The thrombin cleavage side is encoded by nucleotides 112-135 and encodes amino acids 38-45. The green fluorescent protein (GFP) with linker is encoded by nucleotides 136-873 and encodes amino acids 46-291 The truncated collagen sequence is encoded by nucleotides 874-1440 and encodes amino acids 292-480. The Beta-lactamase with linker is encoded by nucleotides 1441-2232 and encodes amino acids 481-744.

(SEQ ID NO: 19)

ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCG

CATCGGCGGCGCAGTATGAAGATCACCATCACCACCACCACCATCACCA

CTCTGGCTCGAGCCTGGTGCCGCGCGGCAGCCATATGTCTGGCTCGAGC

AGTAAAGGTGAAGAACTGTTCACCGGTGTTGTTCCGATCCTGGTTGAAC

TGGATGGTGATGTTAACGGCCACAAATTCTCTGTTCGTGGTGAAGGTGA

AGGTGATGCAACCAACGGTAAACTGACCCTGAAATTCATCTGCACTACC

GGTAAACTGCCGGTTCCATGGCCGACTCTGGTGACTACCCTGACCTATG

GTGTTCAGTGTTTTTCTCGTTACCCGGATCACATGAAGCAGCATGATTT

CTTCAAATCTGCAATGCCGGAAGGTTATGTACAGGAGCGCACCATTTCT

TTCAAAGACGATGGCACCTACAAAACCCGTGCAGAGGTTAAATTTGAAG

GTGATACTCTGGTGAACCGTATTGAACTGAAAGGCATTGATTTCAAAGA

GGACGGCAACATCCTGGGCCACAAACTGGAATATAACTTCAACTCCCAT

AACGTTTACATCACCGCAGACAAACAGAAGAACGGTATCAAAGCTAACT

TCAAAATTCGCCATAACGTTGAAGACGGTAGCGTACAGCTGGCGGACCA

CTACCAGCAGAACACTCCGATCGGTGATGGTCCGGTTCTGCTGCCGGAT

AACCACTACCTGTCCACCCAGTCTaaaCTGTCCAAAGACCCGAACGAAA

AGCGCGACCACATGGTGCTGCTGGAGTTCGTTACTGCAGCAGGTATCAC

GCACGGCATGGATGAACTCTACAAATCTGGCGCGCCGGGCGGTCCGCAG

GGTGTTGTTGGTGCAGATGGTAAAGACGGTACCCCGGGTAATGCAGGTC

AGAAAGGTCCGTCAGGTGAACCTGGCAGCCCTGGTAAAGCAGGTAGTGC

CGGTGAGCAGGGTCCGCCGGGCAAAGATGGTAGTAATGGTGAGCCGGGT

AGCCCTGGCAAAGAAGGTGAACGTGGTCTGGCAGGACCGCCGGGTCCTG

ATGGTCGCCGCGGTGAAACGGGTTCACCGGGTATTGCCGGTGCCCTGGG

TAAACCAGGTCTGGAAGGTCCGAAAGGTTATCCTGGTCTGCGCGGTCGT

GATGGTACCAATGGCAAACGTGGCGAACAGGGCGAAACCGGTCCAGATG

GTGTTCGTGGTATTCCGGGTAACGATGGTCAGAGCGGTAAACCGGGCAT

TGATGGTATTGATGGCACCAATGGTCAGCCTGGCGAAGCAGGTTATCAG

GGTGGTCGCGGTACCCGTGGTCAGCTGGGTGAAACAGGTGATGTTGGTC

AGAATGGTGATCGCGGCGCACCGGGTCCGGATGGTAGCAAAGGTAGCGC

-continued

CGGTCGTCCGGGTTTACGTcacccagaaacgctggtgaaagtaaaagat

gctgaagatcagttgggtgcacgagtgggttacatcgaactggatctca

acagcggtaagatccttgagagttttcgccccgaagaacgttttccaat

gatgagcacttttaaagttctgctatgtggcgcggtattatcccgtatt

gacgccgggcaagagcaactcggtcgccgcatacactattctcagaatg

acttggttgagtactcaccagtcacagaaaagcatcttacggatggcat

gacagtaagagaattatgcagtgctgccataaccatgagtgataacact

gcggccaacttacttctgacaacgatcggaggaccgaaggagctaaccg

ctttttgcacaacatgggggatcatgtaactcgccttgatcgttggga

accggagctgaatgaagccataccaaacgacgagcgtgacaccacgatg

cctgtagcaatggcaacaacgttgcgcaaactattaactggcgaactac

ttactctagcttcccggcaacaattaatagactggatggaggcggataa

agttgcaggaccacttctgcgctcggcccttccggctggctggtttatt

gctgataaatctggagccggtgagcgtgggtctcgcggtatcattgcag

cactggggccagatggtaagccctcccgtatcgtagttatctacacgac

ggggagtcaggcaactatggatgaacgaaatagacagatcgctgagata

ggtgcctcactgattaagcattggtaa

(SEQ ID NO: 20)

MKKIWLALAGLVLAFSASAAQYEDHHHHHHHHHSGSSLVPRGSHMSGSS

SKGEELFTGVVPILVELDGDVNGHKFSVRGEGEGDATNGKLTLKFICTT

GKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIS

FKDDGTYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFNSH

NVYITADKQKNGIKANFKIRHNVEDGSVQLADHYQQNTPIGDGPVLLPD

NHYLSTQSKLSKDPNEKRDHMVLLEFVTAAGITHGMDELYKSGAPGGP

QGVVGADGKDGTPGNAGQKGPSGEPGSPGKAGSAGEQGPPGKDGSNGEP

GSPGKEGERGLAGPPGPDGRRGETGSPGIAGALGKPGLEGPKGYPGLRG

RDGTNGKRGEQGETGPDGVRGIPGNDGQSGKPGIDGIDGTNGQPGEAGY

QGGRGTRGQLGETGDVGQNGDRGAPGPDGSKGSAGRPGLRHPETLVKVK

DAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSR

IDAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDN

TAANLLLTTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTT

MPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSALPAGWF

IADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIAE

IGASLIKHW

## Example 4: Production of Full-Length Elastin

**[0172]** Full length human elastin were expressed as described below. The wild-type, full length amino acid sequence of human elastin is provided below.

(SEQ ID NO: 21)

MAGLTAAAPRPGVLLLLLSILHPSRPGGVPGAIPGGVPGGVFYPGAGLG

ALGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVTFPGALVPGGVAD

AAAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGLP

GVYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFG

GPQPGVPLGYPIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYP

TGTGVGPQAAAAAAAKAAAKFGAGAAGVLPGVGGAGVPGVPGAIPGIGG

IAGVGTPAAAAAAAAAAKAAKYGAAAGLVPGGPGFGPGVVGVPGAGVPG

VGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAAKYGARPGVGVG

GIPTYGVGAGGFPGFGVGVGGIPGVAGVPGVGGVPGVGGVPGVGISPEA

QAAAAAKAAKYGAAGAGVLGGLVPGPQAAVPGVPGTGGVPGVGTPAAAA

AKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVA

PGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGV

PGLGVGAGVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLP

STPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPA

AAAAAAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAK

AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRK

RK

http://www.uniprot.org/uniprot/P15502

**[0173]** The non-codon optimized polynucleotide sequence encoding the full length elastin is disclosed below. In SEQ ID NO: 22, nucleotides 1-78 encode the DsbA secretion tag and nucleotides 79-2358 encode the full length human elastin.

(SEQ ID NO: 22)

ATGGCGGGTCTGACGGCGGCGGCCCCGCGGCCCGGAGTCCTCCTGCTCC

TGCTGTCCATCCTCCACCCCTCTCGGCCTGGAGGGGTCCCTGGGGCCAT

TCCTGGTGGAGTTCCTGGAGGAGTCTTTTATCCAGGGGCTGGTCTCGGA

GCCCTTGGAGGAGGAGCGCTGGGGCCTGGAGGCAAACCTCTTAAGCCAG

TTCCCGGAGGGCTTGCGGGTGCTGGCCTTGGGGCAGGGCTCGGCGCCTT

CCCCGCAGTTACCTTTCCGGGGGCTCTGGTGCCTGGTGGAGTGGCTGAC

GCTGCTGCAGCCTATAAAGCTGCTAAGGCTGGCGCTGGGCTTGGTGGTG

TCCCAGGAGTTGGTGGCTTAGGAGTGTCTGCAGGTGCGGTGGTTCCTCA

GCCTGGAGCCGGAGTGAAGCCTGGGAAAGTGCCGGGTGTGGGGCTGCCA

GGTGTATACCCAGGTGGCGTGCTCCCAGGAGCTCGGTTCCCCGGTGTGG

GGGTGCTCCCTGGAGTTCCCACTGGAGCAGGAGTTAAGCCCAAGGCTCC

AGGTGTAGGTGGAGCTTTTGCTGGAATCCCAGGAGTTGGACCCTTTGGG

GGACCGCAACCTGGAGTCCCACTGGGGTATCCCATCAAGGCCCCCAAGC

TGCCTGGTGGCTATGGACTGCCCTACACCACAGGGAAACTGCCCTATGG

CTATGGGCCCGGAGGAGTGGCTGGTGCAGCGGGCAAGGCTGGTTACCCA

ACAGGGACAGGGGTTGGCCCCCAGGCAGCAGCAGCAGCGGCAGCTAAAG

CAGCAGCAAAGTTCGGTGCTGGAGCAGCCGGAGTCCTCCCTGGTGTTGG

-continued

AGGGGCTGGTGTTCCTGGCGTGCCTGGGGCAATTCCTGGAATTGGAGGC

ATCGCAGGCGTTGGGACTCCAGCTGCAGCTGCAGCTGCAGCAGCAGCCG

CTAAGGCAGCCAAGTATGGAGCTGCTGCAGGCTTAGTGCCTGGTGGGCC

AGGCTTTGGCCCGGGAGTAGTTGGTGTCCCAGGAGCTGGCGTTCCAGGT

GTTGGTGTCCCAGGAGCTGGGATTCCAGTTGTCCCAGGTGCTGGGATCC

CAGGTGCTGCGGTTCCAGGGGTTGTGTCACCAGAAGCAGCTGCTAAGGC

AGCTGCAAAGGCAGCCAAATACGGGGCCAGGCCCGGAGTCGGAGTTGGA

GGCATTCCTACTTACGGGGTTGGAGCTGGGGGCTTTCCCGGCTTTGGTG

TCGGAGTCGGAGGTATCCCTGGAGTCGCAGGTGTCCCTGGTGTCGGAGG

TGTTCCCGGAGTCGGAGGTGTCCCGGGAGTTGGCATTTCCCCCGAAGCT

CAGGCAGCAGCTGCCGCCAAGGCTGCCAAGTACGGTGCTGCAGGAGCAG

GAGTGCTGGGTGGGCTAGTGCCAGGTCCCCAGGCGGCAGTCCCAGGTGT

GCCGGGCACGGGAGGAGTGCCAGGAGTGGGGACCCCAGCAGCTGCAGCT

GCTAAAGCAGCCGCCAAAGCCGCCCAGTTTGGGTTAGTTCCTGGTGTCG

GCGTGGCTCCTGGAGTTGGCGTGGCTCCTGGTGTCGGTGTGGCTCCTGG

AGTTGGCTTGGCTCCTGGAGTTGGCGTGGCTCCTGGAGTTGGTGTGGCT

CCTGGCGTTGGCGTGGCTCCCGGCATTGGCCCTGGTGGAGTTGCAGCTG

CAGCAAAATCCGCTGCCAAGGTGGCTGCCAAAGCCCAGCTCCGAGCTGC

AGCTGGGCTTGGTGCTGGCATCCCTGGACTTGGAGTTGGTGTCGGCGTC

CCTGGACTTGGAGTTGGTGCTGGTGTTCCTGGACTTGGAGTTGGTGCTG

GTGTTCCTGGCTTCGGGGCAGGTGCAGATGAGGGAGTTAGGCGGAGCCT

GTCCCCTGAGCTCAGGGAAGGAGATCCCTCCTCCTCTCAGCACCTCCCC

AGCACCCCCTCATCACCCAGGGTACCTGGAGCCCTGGCTGCCGCTAAAG

CAGCCAAATATGGAGCAGCAGTGCCTGGGGTCCTTGGAGGGCTCGGGGC

TCTCGGTGGAGTAGGCATCCCAGGCGGTGTGGTGGGAGCCGGACCCGCC

GCCGCCGCTGCCGCAGCCAAAGCTGCTGCCAAAGCCGCCCAGTTTGGCC

TAGTGGGAGCCGCTGGGCTCGGAGGACTCGGAGTCGGAGGGCTTGGAGT

TCCAGGTGTTGGGGGCCTTGGAGGTATACCTCCAGCTGCAGCCGCTAAA

GCAGCTAAATACGGTGCTGCTGGCCTTGGAGGTGTCCTAGGGGGTGCCG

GGCAGTTCCCACTTGGAGGAGTGGCAGCAAGACCTGGCTTCGGATTGTC

TCCCATTTTCCCAGGTGGGGCCTGCCTGGGGAAAGCTTGTGGCCGGAAG

AGAAAATGA

Codon Optimized Elastin with DsbA Secretion Tag-His Tag-Linker-Thrombin Cleavage Site

**[0174]** The codon optimized polynucleotide sequence encoding the full length human elastin with DsbA secretion tag-His tag-Linker-Thrombin cleavage site is disclosed below. In SEQ ID NO: 23: nucleotides 1-72 encode the DsbA secretion tag encoding amino acids 1-24 of SEQ ID NO: 24; nucleotides 73-99 encode the 9 His tag (SEQ ID NO: 129) encoding amino acids 25-33 of SEQ ID NO: 24; nucleotides 100-111 encode the linker encoding amino acids 34-37 of SEQ ID NO: 24; nucleotides 112-135 encode the thrombin cleavage tag encoding amino acids 38-45 of SEQ ID NO: 24; nucleotides 136-2415 encode the amino acids 46-805 of the full length human elastin of SEQ ID NO: 24.

(SEQ ID NO: 23)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCG

CATCGGCGGCGCAGTATGAAGATCACCATCACCACCACCACCATCACCA

CTCTGGCTCGAGCCTGGTGCCGCGCGGCAGCCATATGGGTGGCGTACCA

GGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTTTATCCGGGCGCCG

GTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCGGGCGGCAAACCGCT

GAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGCTTAGGCGCAGGTCTG

GGAGCATTTCCGGCAGTTACCTTTCCAGGGGCACTGGTTCCTGGAGGTG

TGGCCGATGCAGCCGCGGCATATAAAGCCGCTAAAGCCGGTGCGGGTTT

AGGAGGCGTCCCAGGTGTCGGTGGCCTGGGTGTTAGCGCCGGTGCAGTT

GTTCCGCAGCCGGGAGCAGGGGTTAAACCTGGTAAAGTGCCGGGAGTAG

GTCTGCCAGGCGTTTATCCTGGTGGTGTTTTGCCGGGTGCCCGTTTTCC

GGGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGAGCCGGTGTTAAACCG

AAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCCCGGGAGTTGGCC

CGTTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTATCCGATTAAAGC

ACCGAAACTGCCCGGCGGTTATGGTCTGCCGTACACAACCGGTAAACTG

CCGTATGGTTATGGCCCGGGTGGAGTTGCGGGTGCAGCAGGTAAAGCGG

GTTATCCTACCGGAACCGGTGTAGGTCCGCAGGCCGCTGCTGCCGCCGC

CGCAAAAGCAGCGGCTAAATTTGGCGCCGGAGCAGCGGGTGTTCTGCCT

GGAGTTGGTGGTGCGGGCGTGCCAGGGGTACCTGGTGCAATTCCGGGTA

TTGGTGGTATTGCCGGTGTCGGCACCCCGGCCGCGGCAGCTGCGGCAGC

GGCGGCTGCCAAAGCTGCTAAATACGGTGCCGCGGCGGGTCTGGTGCCA

GGAGGTCCGGGTTTTGGTCCGGGAGTGGTTGGCGTGCCTGGCGCAGGCG

TTCCTGGTGTGGGCGTTCCAGGTGCAGGGATTCCTGTTGTGCCTGGTGC

CGGTATTCCCGGCGCGGCCGTTCCGGGGGTGGTTAGCCCGGAAGCCGCA

GCGAAGGCTGCGGCAAAGGCAGCAAAGTATGGCGCACGCCCAGGAGTCG

GCGTGGGTGGTATCCCGACCTATGGGGTGGGCGCAGGGGGTTTTCCTGG

TTTCGGCGTAGGTGTAGGAGGTATACCGGGCGTGGCCGGTGTACCAGGG

GTTGGTGGCGTCCCTGGTGTTGGCGGTGTGCCAGGTGTTGGTATTTCAC

CGGAAGCACAGGCAGCAGCCGCAGCTAAGGCAGCGAAATATGGTGCCGC

CGGCGCAGGAGTTTTAGGTGGGCTGGTTCCGGGCCCGCAGGCAGCTGTG

CCGGGGGTTCCAGGCACCGGTGGTGTCCCTGGAGTCGGTACGCCGGCTG

CAGCGGCAGCCAAAGCGGCTGCGAAAGCAGCACAGTTTGGCTTAGTACC

GGGTGTGGGAGTTGCCCCCGGCGTTGGCGTTGCTCCAGGGGTGGGTGTT

GCTCCTGGCGTCGGTCTGGCTCCTGGAGTGGGCGTAGCACCCGGTGTGG

GGGTGGCCCCGGGTGTTGGGGTTGCACCGGGTATCGGTCCGGGCGGTGT

CGCAGCAGCAGCTAAAAGCGCGGCGAAAGTTGCGGCCAAAGCCCAACTG

CGCGCCGCCGCGGGCCTCGGTGCAGGTATTCCGGGGCTGGGTGTCGGAG

-continued

TTGGAGTCCCGGGTTTGGGCGTGGGCGCGGGAGTTCCGGGACTGGGAGT

GGGTGCCGGAGTTCCTGGCTTTGGTGCAGGCGCAGATGAAGGTGTTCGT

CGTAGCCTGAGTCCGGAACTGCGTGAAGGTGATCCGAGTAGCAGCCAGC

ATCTGCCGAGCACCCCGAGCAGCCCGCGTGTTCCGGGTGCATTAGCTGC

AGCAAAAGCCGCCAAGTATGGTGCAGCCGTGCCGGGCGTCTTAGGTGGT

CTGGGCGCCCTGGGTGGTGTAGGCATTCCGGGAGGTGTTGTGGGTGCAG

GACCGGCCGCCGCAGCTGCGGCCGCCAAAGCAGCTGCAAAAGCGGCCCA

GTTTGGTTTAGTGGGCGCCGCAGGTTTAGGCGGTTTAGGTGTGGGTGGA

CTGGGTGTACCTGGCGTAGGCGGTCTGGGTGGAATTCCGCCCGCAGCGG

CCGCGAAAGCGGCAAAATATGGCGCGGCAGGCCTGGGCGGCGTGCTGGG

TGGGGCAGGTCAGTTTCCGCTGGGCGGGGTTGCCGCACGTCCGGGATTT

GGTCTGAGCCCGATTTTCCCTGGCGGCGCATGTCTGGGTAAAGCATGTG

GTCGTAAACGTAAAtaa

(SEQ ID NO: 24)

MKKIWLALAGLVLAFSASAAQYEDHHHHHHHHHSGSSLVPRGSHMGGVP

GAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAGL

GAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAV

VPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGAGVKP

KAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKL

PYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKFGAGAAGVLP

GVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLVP

GGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAA

AKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPG

VGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAGVLGGLVPGPQAAV

PGVPGTGGVPGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGV

APGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQL

RAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVR

RSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGG

LGALGGVGIPGGVVGAGPAAAAAAAKAAAKAAQFGLVGAAGLGGLGVGG

LGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGF

GLSPIFPGGACLGKACGRKRK

**[0175]** The polynucleotide encoding the full length human elastin without the native sequence tag is disclosed in SEQ ID NO: 87.

(SEQ ID NO: 87)

GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTTT

ATCCGGGCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCGGG

CGGCAAACCGCTGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGCTTA

GGCGCAGGTCTGGGAGCATTTCCGGCAGTTACCTTTCCAGGGGCACTGG

TTCCTGGAGGTGTGGCCGATGCAGCCGCGGCATATAAAGCCGCTAAAGC

-continued

CGGTGCGGGTTTAGGAGGCGTCCCAGGTGTCGGTGGCCTGGGTGTTAGC

GCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGGGTTAAACCTGGTAAAG

TGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTGTTTTGCCGGG

TGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGAGCC

GGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCC

CGGGAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTA

TCCGATTAAAGCACCGAAACTGCCCGGCGGTTATGGTCTGCCGTACACA

ACCGGTAAACTGCCGTATGGTTATGGCCCGGGTGGAGTTGCGGGTGCAG

CAGGTAAAGCGGGTTATCCTACCGGAACCGGTGTAGGTCCGCAGGCCGC

TGCTGCCGCCGCCGCAAAAGCAGCGGCTAAATTTGGCGCCGGAGCAGCG

GGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGTGCCAGGGGTACCTGGTG

CAATTCCGGGTATTGGTGGTATTGCCGGTGTCGGCACCCCGGCCGCGGC

AGCTGCGGCAGCGGCGGCTGCCAAAGCTGCTAAATACGGTGCCGCGGCG

GGTCTGGTGCCAGGAGGTCCGGGTTTTGGTCCGGGAGTGGTTGGCGTGC

CTGGCGCAGGCGTTCCTGGTGTGGGCGTTCCAGGTGCAGGGATTCCTGT

TGTGCCTGGTGCCGGTATTCCCGGCGCGGCCGTTCCGGGGGTGGTTAGC

CCGGAAGCCGCAGCGAAGGCTGCGGCAAAGGCAGCAAAGTATGGCGCAC

GCCCAGGAGTCGGCGTGGGTGGTATCCCGACCTATGGGGTGGGCGCAGG

GGGTTTTCCTGGTTTCGGCGTAGGTGTAGGAGGTATACCGGGCGTGGCC

GGTGTACCAGGGGTTGGTGGCGTCCCTGGTGTTGGCGGTGTGCCAGGTG

TTGGTATTTCACCGGAAGCACAGGCAGCAGCCGCAGCTAAGGCAGCGAA

ATATGGTGCCGCCGGCGCAGGAGTTTTAGGTGGGCTGGTTCCGGGCCCG

CAGGCAGCTGTGCCGGGGGTTCCAGGCACCGGTGGTGTCCCTGGAGTCG

GTACGCCGGCTGCAGCGGCAGCCAAAGCGGCTGCGAAAGCAGCACAGTT

TGGCTTAGTACCGGGTGTGGGAGTTGCCCCCGGCGTTGGCGTTGCTCCA

GGGGTGGGTGTTGCTCCTGGCGTCGGTCTGGCTCCTGGAGTGGGCGTAG

CACCCGGTGTGGGGGTGGCCCCGGGTGTTGGGGTTGCACCGGGTATCGG

TCCGGGCGGTGTCGCAGCAGCAGCTAAAAGCGCGGCGAAAGTTGCGGCC

AAAGCCCAACTGCGCGCCGCCGCGGGCCTCGGTGCAGGTATTCCGGGGC

TGGGTGTCGGAGTTGGAGTCCCGGGTTTGGGCGTGGGCGCGGGAGTTCC

GGGACTGGGAGTGGGTGCCGGAGTTCCTGGCTTTGGTGCAGGCGCAGAT

GAAGGTGTTCGTCGTAGCCTGAGTCCGGAACTGCGTGAAGGTGATCCGA

GTAGCAGCCAGCATCTGCCGAGCACCCCGAGCAGCCCGCGTGTTCCGGG

TGCATTAGCTGCAGCAAAAGCCGCCAAGTATGGTGCAGCCGTGCCGGGC

GTCTTAGGTGGTCTGGGCGCCCTGGGTGGTGTAGGCATTCCGGGAGGTG

TTGTGGGTGCAGGACCGGCCGCCGCAGCTGCGGCCGCCAAAGCAGCTGC

AAAAGCGGCCCAGTTTGGTTTAGTGGGCGCCGCAGGTTTAGGCGGTTTA

GGTGTGGGTGGACTGGGTGTACCTGGCGTAGGCGGTCTGGGTGGAATTC

CGCCCGCAGCGGCCGCGAAAGCGGCAAAATATGGCGCGGCAGGCCTGGG

-continued

CGGCGTGCTGGGTGGGGCAGGTCAGTTTCCGCTGGGCGGGGTTGCCGCA

CGTCCGGGATTTGGTCTGAGCCCGATTTTCCCTGGCGGCGCATGTCTGG

GTAAAGCATGTGGTCGTAAACGTAAAtaa

**[0176]** The full length human elastin sequence without the native sequence tag is disclosed in SEQ ID NO: 88.

(SEQ ID NO: 88)

GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGL

GAGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVS

AGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGA

GVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYT

TGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKFGAGAA

GVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAA

GLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVS

PEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVA

GVPGVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAGVLGGLVPGP

QAAVPGVPGTGGVPGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAP

GVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAA

KAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGAD

EGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPG

VLGGLGALGGVGIPGGVVGAGPAAAAAAAKAAAKAAQFGLVGAAGLGGL

GVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAA

RPGFGLSPIFPGGACLGKACGRKRK

Codon Optimized Elastin with DsbA Secretion Tag

**[0177]** The codon optimized polynucleotide sequence encoding the full length human elastin with a DsbA secretion tag is disclosed in SEQ ID NO: 25. In SEQ ID NO: 25: nucleotides 1-72 encode the DsbA secretion tag encoding amino acids 1-24 of SEQ ID NO: 26; nucleotides 73-2355 encode the amino acids 25-785 of the full length human elastin of SEQ ID NO: 26.

(SEQ ID NO: 25)

ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGC

GCATCGGCGGCGCAGTATGAAGATATGGGTGGCGTACCAGGCGCAATT

CCTGGGGGTGTCCCAGGCGGTGTTTTTATCCGGGCGCCGGTCTTGGC

GCACTGGGTGGCGGTGCACTGGGCCCGGGCGGCAAACCGCTGAAACCG

GTACCAGGTGGTTTAGCAGGCGCCGGCTTAGGCGCAGGTCTGGGAGCA

TTTCCGGCAGTTACCTTTCCAGGGGCACTGGTTCCTGGAGGTGTGGCC

GATGCAGCCGCGGCATATAAAGCCGCTAAAGCCGGTGCGGGTTTAGGA

GGCGTCCCAGGTGTCGGTGGCCTGGGTGTTAGCGCCGGTGCAGTTGTT

CCGCAGCCGGGAGCAGGGGTTAAACCTGGTAAAGTGCCGGGAGTAGGT

CTGCCAGGCGTTTATCCTGGTGGTGTTTTGCCGGGTGCCCGTTTTCCG

-continued

GGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGAGCCGGTGTTAAACCG

AAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCCCGGGAGTTGGC

CCGTTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTATCCGATTAAA

GCACCGAAACTGCCCGGCGGTTATGGTCTGCCGTACACAACCGGTAAA

CTGCCGTATGGTTATGGCCCGGGTGGAGTTGCGGGTGCAGCAGGTAAA

GCGGGTTATCCTACCGGAACCGGTGTAGGTCCGCAGGCCGCTGCTGCC

GCCGCCGCAAAAGCAGCGGCTAAATTTGGCGCCGGAGCAGCGGGTGTT

CTGCCTGGAGTTGGTGGTGCGGGCGTGCCAGGGGTACCTGGTGCAATT

CCGGGTATTGGTGGTATTGCCGGTGTCGGCACCCCGGCCGCGGCAGCT

GCGGCAGCGGCGGCTGCCAAAGCTGCTAAATACGGTGCCGCGGCGGGT

CTGGTGCCAGGAGGTCCGGGTTTTGGTCCGGGAGTGGTTGGCGTGCCT

GGCGCAGGCGTTCCTGGTGTGGGCGTTCCAGGTGCAGGGATTCCTGTT

GTGCCTGGTGCCGGTATTCCCGGCGCGGCCGTTCCGGGGGTGGTTAGC

CCGGAAGCCGCAGCGAAGGCTGCGGCAAAGGCAGCAAAGTATGGCGCA

CGCCCAGGAGTCGGCGTGGGTGGTATCCCGACCTATGGGGTGGGCGCA

GGGGGTTTTCCTGGTTTCGGCGTAGGTGTAGGAGGTATACCGGGCGTG

GCCGGTGTACCAGGGGTTGGTGGCGTCCCTGGTGTTGGCGGTGTGCCA

GGTGTTGGTATTTCACCGGAAGCACAGGCAGCAGCCGCAGCTAAGGCA

GCGAAATATGGTGCCGCCGGCGCAGGAGTTTTAGGTGGGCTGGTTCCG

GGCCCGCAGGCAGCTGTGCCGGGGGTTCCAGGCACCGGTGGTGTCCCT

GGAGTCGGTACGCCGGCTGCAGCGGCAGCCAAAGCGGCTGCGAAAGCA

GCACAGTTTGGCTTAGTACCGGGTGTGGGAGTTGCCCCCGGCGTTGGC

GTTGCTCCAGGGGTGGGTGTTGCTCCTGGCGTCGGTCTGGCTCCTGGA

GTGGGCGTAGCACCCGGTGTGGGGGTGGCCCCGGGTGTTGGGGTTGCA

CCGGGTATCGGTCCGGGCGGTGTCGCAGCAGCAGCTAAAAGCGCGGCG

AAAGTTGCGGCCAAAGCCCAACTGCGCGCCGCCGCGGGCCTCGGTGCA

GGTATTCCGGGGCTGGGTGTCGGAGTTGGAGTCCCGGGTTTGGGCGTG

GGCGCGGGAGTTCCGGGACTGGGAGTGGGTGCCGGAGTTCCTGGCTTT

GGTGCAGGCGCAGATGAAGGTGTTCGTCGTAGCCTGAGTCCGGAACTG

CGTGAAGGTGATCCGAGTAGCAGCCAGCATCTGCCGAGCACCCCGAGC

AGCCCGCGTGTTCCGGGTGCATTAGCTGCAGCAAAAGCCGCCAAGTAT

GGTGCAGCCGTGCCGGGCGTCTTAGGTGGTCTGGGCGCCCTGGGTGGT

GTAGGCATTCCGGGAGGTGTTGTGGGTGCAGGACCGGCCGCCGCAGCT

GCGGCCGCCAAAGCAGCTGCAAAAGCGGCCCAGTTTGGTTTAGTGGGC

GCCGCAGGTTTAGGCGGTTTAGGTGTGGGTGGACTGGGTGTACCTGGC

GTAGGCGGTCTGGGTGGAATTCCGCCCGCAGCGGCCGCGAAAGCGGCA

AAATATGGCGCGGCAGGCCTGGGCGGCGTGCTGGGTGGGGCAGGTCAG

TTTCCGCTGGGCGGGGTTGCCGCACGTCCGGGATTTGGTCTGAGCCCG

-continued

ATTTTCCCTGGCGGCGCATGTCTGGGTAAAGCATGTGGTCGTAAACGT

AAAtaa

(SEQ ID NO: 26)

MKKIWLALAGLVLAFSASAAQYEDMGGVPGAIPGGVPGGVFYPGAGLGA

LGGGALGPGGKPLKPVPGGLAGAGLGAGLGAFPAVTFPGALVPGGVADA

AAAYKAAKAGAGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGLPG

VYPGGVLPGARFPGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGG

PQPGVPLGYPIKAPKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPT

GTGVGPQAAAAAAAKAAAKFGAGAAGVLPGVGGAGVPGVPGAIPGIGGI

AGVGTPAAAAAAAAAAKAAKYGAAAGLVPGGPGFGPGVVGVPGAGVPGV

GVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAAKYGARPGVGVGG

IPTYGVGAGGFPGFGVGVGGIPGVAGVPGVGGVPGVGGVPGVGISPEAQ

AAAAAKAAKYGAAGAGVLGGLVPGPQAAVPGVPGTGGVPGVGTPAAAAA

KAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAP

GVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVP

GLGVGAGVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPS

TPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAA

AAAAAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKA

AKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKR

K

**[0178]** The polynucleotides of SEQ ID NO: 22 was codon optimized and synthesized by Gen9 DNA, now Ginkgo Bioworks internal synthesis. Overlaps between the pET28 vector and SEQ ID NO: 22 was designed to be between 30 and 40 bp long and added using PCR with the enzyme PrimeStar GXL polymerase (http://www.clontech.com/US/Products/PCR/GC_Rich/PrimeSTAR_GXL_DNA_Polymerase?sitex=10020:22372:US). The opened pET28a vector and insert DNA (SEQ ID NO: 22) was then assembled together into the final plasmid using SGI Gibson assembly (https://us.vwr.com/store/product/17613857/gibson-assembly-hifi-1-step-kit-synthetic-genomics-inc). Sequence of plasmid was then verified through sanger sequencing through Eurofins Genomics (www.eurofinsgenomics.com).

**[0179]** The transformed cells were cultivated in minimal media and frozen in 1.5 aliquots with glycerol at a ratio of 50:50 of cells to glycerol. One vial of this frozen culture was revived in 50 ml of minimal media overnight at 37° C., 200 rpm. Cells were transferred into 300 ml of minimal media and grown for 6-9 hours to reach an OD600 of 5-10.

**[0180]** A bioreactor was prepared with 2.7 L of minimal media+glucose and 300 ml of OD600 of 5-10 culture was added to bring the starting volume to 3 L. Cells were grown at 28° C., pH7 with Dissolved Oxygen maintained at 20% saturation using a cascade containing agitation, air and oxygen. pH was controlled using 28% w/w Ammonium hydroxide solution. Fermentation was run in a fed-batch mode using a DO-stat based feeding algorithm once the initial bolus of 40 g/L was depleted around 13 hours. After 24-26 hours of initial growth, the OD600 reached above 100. At this point, 300 mL of 500 g/L sucrose was added and temperature was reduced to 25 C. High density culture was induced for protein production using 1 mM IPTG. Fermentation was continued for another 20-24 hours and cells were harvested using a bench top centrifuge at 9000 rcf, 15 C for 60 minutes. Cell pellet recovered from centrifugation was resuspended in a buffer containing 0.5M NaCl and 0.1M KH2PO4 at pH8 in a weight by weight ratio of 2× buffer to 1× cells.

**[0181]** The fermentations were performed at various temperature ranging from 25° to 28° C. For some fermentations, the temperature of the fermentation was maintained at a constant temperature and immediately upon completion of fermentation (OD600 of 5-10) the elastin was purified. For other fermentations, the temperature of the fermentations is maintained for a desired period of time and when cell densities of OD600 of 5-10 are reached, the temperature is reduced to induce protein production. Typically, the temperature is reduced from 28° C. to 25° C. After the fermentation at 25° C. is continued for 40-60 hours, the elastin is isolated.

**[0182]** The harvested cells were disrupted in a homogenizer at 14,000 psi pressure in 2 passes. Resulting slurry contained the collagen protein along with other proteins.

**[0183]** The supernatant from the homogenized cells was analyzed on an SDS-PAGE gel and a clear band was observed at around 70 kilodaltons corresponding to the expected size of 68 kilodaltons. The purified elastin is analyzed by mass spectrometry.

Full Length Elastin with DsbA Secretion Tag-His Tag-Linker-Thrombin Cleavage Site and GFP Beta-Lactamase Fusion

**[0184]** A human elastin with DsbA secretion tag-His tag-Linker-Thrombin cleavage site and GFP Beta-lactamase fusion is disclosed below. The codon-optimized nucleotide sequence encoding this elastin is provided in SEQ ID NO: 27. The amino acid sequence is disclosed in SEQ ID NO: 28. The DsbA secretion tag is encoded by nucleotides 1-72 and encodes amino acids 1-24. The His tag is encoded by nucleotides 73-99 and encodes a 9 histidine tag (SEQ ID NO: 129) of amino acids 25-33. The linker is encoded by nucleotides 100-111 and encodes amino acids 34-37. The thrombin cleavage side is encoded by nucleotides 112-135 and encodes amino acids 38-45. The green fluorescent protein (GFP) with linker is encoded by nucleotides 136-873 and encodes amino acids 46-291. The full-length elastin sequence is encoded by nucleotides 874-3153 and encodes amino acids 292-1051. The Beta-lactamase with linker is encoded by nucleotides 3154-3945 and encodes amino acids 1052-1315.

(SEQ ID NO: 27)

ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCG

CATCGGCGGCGCAGTATGAAGATCACCATCACCACCACCACCATCACCA

CTCTGGCTCGAGCCTGGTGCCGCGCGGCAGCCATATGTCTGGCTCGAGC

AGTAAAGGTGAAGAACTGTTCACCGGTGTTGTTCCGATCCTGGTTGAAC

TGGATGGTGATGTTAACGGCCACAAATTCTCTGTTCGTGGTGAAGGTGA

AGGTGATGCAACCAACGGTAAACTGACCCTGAAATTCATCTGCACTACC

GGTAAACTGCCGGTTCCATGGCCGACTCTGGTGACTACCCTGACCTATG

-continued

GTGTTCAGTGTTTTTCTCGTTACCCGGATCACATGAAGCAGCATGATTT

CTTCAAATCTGCAATGCCGGAAGGTTATGTACAGGAGCGCACCATTTCT

TTCAAAGACGATGGCACCTACAAAACCCGTGCAGAGGTTAAATTTGAAG

GTGATACTCTGGTGAACCGTATTGAACTGAAAGGCATTGATTTCAAAGA

GGACGGCAACATCCTGGGCCACAAACTGGAATATAACTTCAACTCCCAT

AACGTTTACATCACCGCAGACAAACAGAAGAACGGTATCAAAGCTAACT

TCAAAATTCGCCATAACGTTGAAGACGGTAGCGTACAGCTGGCGGACCA

CTACCAGCAGAACACTCCGATCGGTGATGGTCCGGTTCTGCTGCCGGAT

AACCACTACCTGTCCACCCAGTCTaaaCTGTCCAAAGACCCGAACGAAA

AGCGCGACCACATGGTGCTGCTGGAGTTCGTTACTGCAGCAGGTATCAC

GCACGGCATGGATGAACTCTACAAATCTGGCGCGCCGGGCGGTGGCGTA

CCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTTTATCCGGGCG

CCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCGGGCGGCAAACC

GCTGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGCTTAGGCGCAGGT

CTGGGAGCATTTCCGGCAGTTACCTTTCCAGGGGCACTGGTTCCTGGAG

GTGTGGCCGATGCAGCCGCGGCATATAAAGCCGCTAAAGCCGGTGCGGG

TTTAGGAGGCGTCCCAGGTGTCGGTGGCCTGGGTGTTAGCGCCGGTGCA

GTTGTTCCGCAGCCGGGAGCAGGGGTTAAACCTGGTAAAGTGCCGGGAG

TAGGTCTGCCAGGCGTTTATCCTGGTGGTGTTTTGCCGGGTGCCCGTTT

TCCGGGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGAGCCGGTGTTAAA

CCGAAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCCCGGGAGTTG

GCCCGTTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTATCCGATTAA

AGCACCGAAACTGCCCGGCGGTTATGGTCTGCCGTACACAACCGGTAAA

CTGCCGTATGGTTATGGCCCGGGTGGAGTTGCGGGTGCAGCAGGTAAAG

CGGGTTATCCTACCGGAACCGGTGTAGGTCCGCAGGCCGCTGCTGCCGC

CGCCGCAAAAGCAGCGGCTAAATTTGGCGCCGGAGCAGCGGGTGTTCTG

CCTGGAGTTGGTGGTGCGGGCGTGCCAGGGGTACCTGGTGCAATTCCGG

GTATTGGTGGTATTGCCGGTGTCGGCACCCCGGCCGCGGCAGCTGCGGC

AGCGGCGGCTGCCAAAGCTGCTAAATACGGTGCCGCGGCGGGTCTGGTG

CCAGGAGGTCCGGGTTTTGGTCCGGGAGTGGTTGGCGTGCCTGGCGCAG

GCGTTCCTGGTGTGGGCGTTCCAGGTGCAGGGATTCCTGTTGTGCCTGG

TGCCGGTATTCCCGGCGCGGCCGTTCCGGGGGTGGTTAGCCCGGAAGCC

GCAGCGAAGGCTGCGGCAAAGGCAGCAAAGTATGGCGCACGCCCAGGAG

TCGGCGTGGGTGGTATCCCGACCTATGGGGTGGGCGCAGGGGGTTTTCC

TGGTTTCGGCGTAGGTGTAGGAGGTATACCGGGCGTGGCCGGTGTACCA

GGGGTTGGTGGCGTCCCTGGTGTTGGCGGTGTGCCAGGTGTTGGTATTT

CACCGGAAGCACAGGCAGCAGCCGCAGCTAAGGCAGCGAAATATGGTGC

CGCCGGCGCAGGAGTTTTAGGTGGGCTGGTTCCGGGCCCGCAGGCAGCT

GTGCCGGGGGTTCCAGGCACCGGTGGTGTCCCTGGAGTCGGTACGCCGG

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CTGCAGCGGCAGCCAAAGCGGCTGCGAAAGCAGCACAGTTTGGCTTAGT

ACCGGGTGTGGGAGTTGCCCCCGGCGTTGGCGTTGCTCCAGGGGTGGGT

GTTGCTCCTGGCGTCGGTCTGGCTCCTGGAGTGGGCGTAGCACCCGGTG

TGGGGGTGGCCCCGGGTGTTGGGGTTGCACCGGGTATCGGTCCGGGCGG

TGTCGCAGCAGCAGCTAAAAGCGCGGCGAAAGTTGCGGCCAAAGCCCAA

CTGCGCGCCGCCGCGGGCCTCGGTGCAGGTATTCCGGGGCTGGGTGTCG

GAGTTGGAGTCCCGGGTTTGGGCGTGGGCGCGGGAGTTCCGGGACTGGG

AGTGGGTGCCGGAGTTCCTGGCTTTGGTGCAGGCGCAGATGAAGGTGTT

CGTCGTAGCCTGAGTCCGGAACTGCGTGAAGGTGATCCGAGTAGCAGCC

AGCATCTGCCGAGCACCCCGAGCAGCCCGCGTGTTCCGGGTGCATTAGC

TGCAGCAAAAGCCGCCAAGTATGGTGCAGCCGTGCCGGGCGTCTTAGGT

GGTCTGGGCGCCCTGGGTGGTGTAGGCATTCCGGGAGGTGTTGTGGGTG

CAGGACCGGCCGCCGCAGCTGCGGCCGCCAAAGCAGCTGCAAAAGCGGC

CCAGTTTGGTTTAGTGGGCGCCGCAGGTTTAGGCGGTTTAGGTGTGGGT

GGACTGGGTGTACCTGGCGTAGGCGGTCTGGGTGGAATTCCGCCCGCAG

CGGCCGCGAAAGCGGCAAAATATGGCGCGGCAGGCCTGGGCGGCGTGCT

GGGTGGGGCAGGTCAGTTTCCGCTGGGCGGGGTTGCCGCACGTCCGGGA

TTTGGTCTGAGCCCGATTTTCCCTGGCGGCGCATGTCTGGGTAAAGCAT

GTGGTCGTAAACGTAAAcacccagaaacgctggtgaaagtaaaagatgc

tgaagatcagttgggtgcacgagtgggttacatcgaactggatctcaac

agcggtaagatccttgagagttttcgccccgaagaacgttttccaatga

tgagcacttttaaagttctgctatgtggcgcggtattatcccgtattga

cgccgggcaagagcaactcggtcgccgcatacactattctcagaatgac

ttggttgagtactcaccagtcacagaaaagcatcttacggatggcatga

cagtaagagaattatgcagtgctgccataaccatgagtgataacactgc

ggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgct

tttttgcacaacatgggggatcatgtaactcgccttgatcgttgggaac

cggagctgaatgaagccataccaaacgacgagcgtgacaccacgatgcc

tgtagcaatggcaacaacgttgcgcaaactattaactggcgaactactt

actctagcttcccggcaacaattaatagactggatggaggcggataaag

ttgcaggaccacttctgcgctcggcccttccggctggctggtttattgc

tgataaatctggagccggtgagcgtgggtctcgcggtatcattgcagca

ctggggccagatggtaagccctcccgtatcgtagttatctacacgacgg

ggagtcaggcaactatggatgaacgaaatagacagatcgctgagatagg

tgcctcactgattaagcattggtaa

(SEQ ID NO: 28)

MKKIWLALAGLVLAFSASAAQYEDHHHHHHHHHSGSSLVPRGSHMSGSS

SKGEELFTGVVPILVELDGDVNGHKFSVRGEGEGDATNGKLTLKFICTT

GKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIS

FKDDGTYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFNSH

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NVYITADKQKNGIKANFKIRHNVEDGSVQLADHYQQNTPIGDGPVLLPD

NHYLSTQSKLSKDPNEKRDHMVLLEFVTAAGITHGMDELYKSGAPGGGV

PGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGAG

LGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGA

VVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGAGVK

PKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGK

LPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKFGAGAAGVL

PGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLV

PGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEA

AAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVP

GVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAGVLGGLVPGPQAA

VPGVPGTGGVPGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVG

VAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQ

LRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGV

RRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLG

GLGALGGVGIPGGVVGAGPAAAAAAAKAAAKAAQFGLVGAAGLGGLGVG

GLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPG

FGLSPIFPGGACLGKACGRKRKHPETLVKVKDAEDQLGARVGYIELDLN

SGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQND

LVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTA

FLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELL

TLASRQQLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAA

LGPDGKPSRIVVIYTTGSQATMDERNRQIAEIGASLIKHW

## Example 5: Production of Truncated Elastin

**[0185]** Truncated human elastin is produced using the expression system as described in Example 4. The full length amino acid sequence lacking the native secretion tag is disclosed in SEQ ID NO: 29.

(SEQ ID NO: 29)

GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGL

GAGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVS

AGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGA

GVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYT

TGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKFGAGAA

GVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAA

GLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVS

PEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVA

GVPGVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAGVLGGLVPGP

QAAVPGVPGTGGVPGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAP

-continued

GVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAA

KAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGAD

EGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPG

VLGGLGALGGVGIPGGVVGAGPAAAAAAAKAAAKAAQFGLVGAAGLGGL

GVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAA

RPGFGLSPIFPGGACLGKACGRKRK

**[0186]** The codon optimized polynucleotide sequence encoding the full length human elastin lacking the native secretion tag is disclosed in SEQ ID NO: 30.

(SEQ ID NO: 30)

GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTTT

ATCCGGGCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCGGG

CGGCAAACCGCTGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGCTTA

GGCGCAGGTCTGGGAGCATTTCCGGCAGTTACCTTTCCAGGGGCACTGG

TTCCTGGAGGTGTGGCCGATGCAGCCGCGGCATATAAAGCCGCTAAAGC

CGGTGCGGGTTTAGGAGGCGTCCCAGGTGTCGGTGGCCTGGGTGTTAGC

GCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGGGTTAAACCTGGTAAAG

TGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTGTTTTGCCGGG

TGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGAGCC

GGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCC

CGGGAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTA

TCCGATTAAAGCACCGAAACTGCCCGGCGGTTATGGTCTGCCGTACACA

ACCGGTAAACTGCCGTATGGTTATGGCCCGGGTGGAGTTGCGGGTGCAG

CAGGTAAAGCGGGTTATCCTACCGGAACCGGTGTAGGTCCGCAGGCCGC

TGCTGCCGCCGCCGCAAAAGCAGCGGCTAAATTTGGCGCCGGAGCAGCG

GGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGTGCCAGGGGTACCTGGTG

CAATTCCGGGTATTGGTGGTATTGCCGGTGTCGGCACCCCGGCCGCGGC

AGCTGCGGCAGCGGCGGCTGCCAAAGCTGCTAAATACGGTGCCGCGGCG

GGTCTGGTGCCAGGAGGTCCGGGTTTTGGTCCGGGAGTGGTTGGCGTGC

CTGGCGCAGGCGTTCCTGGTGTGGGCGTTCCAGGTGCAGGGATTCCTGT

TGTGCCTGGTGCCGGTATTCCCGGCGCGGCCGTTCCGGGGGTGGTTAGC

CCGGAAGCCGCAGCGAAGGCTGCGGCAAAGGCAGCAAAGTATGGCGCAC

GCCCAGGAGTCGGCGTGGGTGGTATCCCGACCTATGGGGTGGGCGCAGG

GGGTTTTCCTGGTTTCGGCGTAGGTGTAGGAGGTATACCGGGCGTGGCC

GGTGTACCAGGGGTTGGTGGCGTCCCTGGTGTTGGCGGTGTGCCAGGTG

TTGGTATTTCACCGGAAGCACAGGCAGCAGCCGCAGCTAAGGCAGCGAA

ATATGGTGCCGCCGGCGCAGGAGTTTTAGGTGGGCTGGTTCCGGGCCCG

CAGGCAGCTGTGCCGGGGGTTCCAGGCACCGGTGGTGTCCCTGGAGTCG

GTACGCCGGCTGCAGCGGCAGCCAAAGCGGCTGCGAAAGCAGCACAGTT

-continued

TGGCTTAGTACCGGGTGTGGGAGTTGCCCCCGGCGTTGGCGTTGCTCCA

GGGGTGGGTGTTGCTCCTGGCGTCGGTCTGGCTCCTGGAGTGGGCGTAG

CACCCGGTGTGGGGGTGGCCCCGGGTGTTGGGGTTGCACCGGGTATCGG

TCCGGGCGGTGTCGCAGCAGCAGCTAAAAGCGCGGCGAAAGTTGCGGCC

AAAGCCCAACTGCGCGCCGCCGCGGGCCTCGGTGCAGGTATTCCGGGGC

TGGGTGTCGGAGTTGGAGTCCCGGGTTTGGGCGTGGGCGCGGGAGTTCC

GGGACTGGGAGTGGGTGCCGGAGTTCCTGGCTTTGGTGCAGGCGCAGAT

GAAGGTGTTCGTCGTAGCCTGAGTCCGGAACTGCGTGAAGGTGATCCGA

GTAGCAGCCAGCATCTGCCGAGCACCCCGAGCAGCCCGCGTGTTCCGGG

TGCATTAGCTGCAGCAAAAGCCGCCAAGTATGGTGCAGCCGTGCCGGGC

GTCTTAGGTGGTCTGGGCGCCCTGGGTGGTGTAGGCATTCCGGGAGGTG

TTGTGGGTGCAGGACCGGCCGCCGCAGCTGCGGCCGCCAAAGCAGCTGC

AAAAGCGGCCCAGTTTGGTTTAGTGGGCGCCGCAGGTTTAGGCGGTTTA

GGTGTGGGTGGACTGGGTGTACCTGGCGTAGGCGGTCTGGGTGGAATTC

CGCCCtaa

**[0187]** The amino acid sequence of a 60.7 kDa human elastin truncated at the C-terminal is disclosed in SEQ ID NO: 31. The 60.7 kDa truncated elastin has amino acids 706-761 deleted from the full length elastin.

(SEQ ID NO: 31)
GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGL

GAGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVS

AGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGA

GVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYT

TGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKFGAGAA

GVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAA

GLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVS

PEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVA

GVPGVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAGVLGGLVPGP

QAAVPGVPGTGGVPGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAP

GVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAAAKSAAKVAA

KAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGAD

EGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPG

VLGGLGALGGVGIPGGVVGAGPAAAAAAAKAAAKAAQFGLVGAAGLGGL

GVGGLGVPGVGGLGGIPP

**[0188]** The codon optimized polynucleotide sequence encoding the truncated 60.7 kDa human elastin is disclosed in SEQ ID NO: 32.

(SEQ ID NO: 32)
GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTTT

ATCCGGGCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCGGG

CGGCAAACCGCTGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGCTTA

GGCGCAGGTCTGGGAGCATTTCCGGCAGTTACCTTTCCAGGGGCACTGG

TTCCTGGAGGTGTGGCCGATGCAGCCGCGGCATATAAAGCCGCTAAAGC

CGGTGCGGGTTTAGGAGGCGTCCCAGGTGTCGGTGGCCTGGGTGTTAGC

GCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGGGTTAAACCTGGTAAAG

TGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTGTTTTGCCGGG

TGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGAGCC

GGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCC

CGGGAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTA

TCCGATTAAAGCACCGAAACTGCCCGGCGGTTATGGTCTGCCGTACACA

ACCGGTAAACTGCCGTATGGTTATGGCCCGGGTGGAGTTGCGGGTGCAG

CAGGTAAAGCGGGTTATCCTACCGGAACCGGTGTAGGTCCGCAGGCCGC

TGCTGCCGCCGCCGCAAAAGCAGCGGCTAAATTTGGCGCCGGAGCAGCG

GGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGTGCCAGGGGTACCTGGTG

CAATTCCGGGTATTGGTGGTATTGCCGGTGTCGGCACCCCGGCCGCGGC

AGCTGCGGCAGCGGCGGCTGCCAAAGCTGCTAAATACGGTGCCGCGGCG

GGTCTGGTGCCAGGAGGTCCGGGTTTTGGTCCGGGAGTGGTTGGCGTGC

CTGGCGCAGGCGTTCCTGGTGTGGGCGTTCCAGGTGCAGGGATTCCTGT

TGTGCCTGGTGCCGGTATTCCCGGCGCGGCCGTTCCGGGGGTGGTTAGC

CCGGAAGCCGCAGCGAAGGCTGCGGCAAAGGCAGCAAAGTATGGCGCAC

GCCCAGGAGTCGGCGTGGGTGGTATCCCGACCTATGGGGTGGGCGCAGG

GGGTTTTCCTGGTTTCGGCGTAGGTGTAGGAGGTATACCGGGCGTGGCC

GGTGTACCAGGGGTTGGTGGCGTCCCTGGTGTTGGCGGTGTGCCAGGTG

TTGGTATTTCACCGGAAGCACAGGCAGCAGCCGCAGCTAAGGCAGCGAA

ATATGGTGCCGCCGGCGCAGGAGTTTTAGGTGGGCTGGTTCCGGGCCCG

CAGGCAGCTGTGCCGGGGGTTCCAGGCACCGGTGGTGTCCCTGGAGTCG

GTACGCCGGCTGCAGCGGCAGCCAAAGCGGCTGCGAAAGCAGCACAGTT

TGGCTTAGTACCGGGTGTGGGAGTTGCCCCCGGCGTTGGCGTTGCTCCA

GGGGTGGGTGTTGCTCCTGGCGTCGGTCTGGCTCCTGGAGTGGGCGTAG

CACCCGGTGTGGGGGTGGCCCCGGGTGTTGGGGTTGCACCGGGTATCGG

TCCGGGCGGTGTCGCAGCAGCAGCTAAAAGCGCGGCGAAAGTTGCGGCC

AAAGCCCAACTGCGCGCCGCCGCGGGCCTCGGTGCAGGTATTCCGGGGC

TGGGTGTCGGAGTTGGAGTCCCGGGTTTGGGCGTGGGCGCGGGAGTTCC

GGGACTGGGAGTGGGTGCCGGAGTTCCTGGCTTTGGTGCAGGCGCAGAT

GAAGGTGTTCGTCGTAGCCTGAGTCCGGAACTGCGTGAAGGTGATCCGA

GTAGCAGCCAGCATCTGCCGAGCACCCCGAGCAGCCCGCGTGTTCCGGG

TGCATTAGCTGCAGCAAAAGCCGCCAAGTATGGTGCAGCCGTGCCGGGC

-continued

GTCTTAGGTGGTCTGGGCGCCCTGGGTGGTGTAGGCATTCCGGGAGGTG

TTGTGGGTGCAGGACCGGCCGCCGCAGCTGCGGCCGCCAAAGCAGCTGC

AAAAGCGGCCCAGTTTGGTTTAGTGGGCGCCGCAGGTTTAGGCGGTTTA

GGTGTGGGTGGACTGGGTGTACCTGGCGTAGGCGGTCTGGGTGGAATTC

CGCCCtaa

**[0189]** The amino acid sequence of a 58.8 kDa human elastin truncated at the N-terminal is disclosed in SEQ ID NO: 33. The 58.8 kDa truncated elastin has amino acids 2-85 deleted from the full length elastin.

(SEQ ID NO: 33)
GLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARF

PGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKA

PKLPGGYGLPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAA

KAAAKFGAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAA

AKAAKYGAAAGLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIP

GAAVPGVVSPEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVG

VGGIPGVAGVPGVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAGVL

GGLVPGPQAAVPGVPGTGGVPGVGTPAAAAAKAAAKAAQFGLVPGVGVAP

GVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAAAKSA

AKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFG

AGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAA

VPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAKAAAKAAQFGLVGAAGLG

GLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVA

ARPGFGLSPIFPGGACLGKACGRKRK

**[0190]** The codon optimized polynucleotide sequence encoding the 58.8 kDa truncated human elastin is disclosed in SEQ ID NO: 34.

(SEQ ID NO: 34)
GGTTTAGGAGGCGTCCCAGGTGTCGGTGGCCTGGGTGTTAGCGCCGGT

GCAGTTGTTCCGCAGCCGGGAGCAGGGGTTAAACCTGGTAAAGTGCCG

GGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTGTTTTGCCGGGTGCC

CGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGAGCCGGT

GTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCCCG

GGAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTAT

CCGATTAAAGCACCGAAACTGCCCGGCGGTTATGGTCTGCCGTACACA

ACCGGTAAACTGCCGTATGGTTATGGCCCGGGTGGAGTTGCGGGTGCA

GCAGGTAAAGCGGGTTATCCTACCGGAACCGGTGTAGGTCCGCAGGCC

GCTGCTGCCGCCGCCGCAAAAGCAGCGGCTAAATTTGGCGCCGGAGCA

GCGGGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGTGCCAGGGGTACCT

GGTGCAATTCCGGGTATTGGTGGTATTGCCGGTGTCGGCACCCCGGCC

-continued

GCGGCAGCTGCGGCAGCGGCGGCTGCCAAAGCTGCTAAATACGGTGCC

GCGGCGGGTCTGGTGCCAGGAGGTCCGGGTTTTGGTCCGGGAGTGGTT

GGCGTGCCTGGCGCAGGCGTTCCTGGTGTGGGCGTTCCAGGTGCAGGG

ATTCCTGTTGTGCCTGGTGCCGGTATTCCCGGCGCGGCCGTTCCGGGG

GTGGTTAGCCCGGAAGCCGCAGCGAAGGCTGCGGCAAAGGCAGCAAAG

TATGGCGCACGCCCAGGAGTCGGCGTGGGTGGTATCCCGACCTATGGG

GTGGGCGCAGGGGGTTTTCCTGGTTTCGGCGTAGGTGTAGGAGGTATA

CCGGGCGTGGCCGGTGTACCAGGGGTTGGTGGCGTCCCTGGTGTTGGC

GGTGTGCCAGGTGTTGGTATTTCACCGGAAGCACAGGCAGCAGCCGCA

GCTAAGGCAGCGAAATATGGTGCCGCCGGCGCAGGAGTTTTAGGTGGG

CTGGTTCCGGGCCCGCAGGCAGCTGTGCCGGGGGTTCCAGGCACCGGT

GGTGTCCCTGGAGTCGGTACGCCGGCTGCAGCGGCAGCCAAAGCGGCT

GCGAAAGCAGCACAGTTTGGCTTAGTACCGGGTGTGGGAGTTGCCCCC

GGCGTTGGCGTTGCTCCAGGGGTGGGTGTTGCTCCTGGCGTCGGTCTG

GCTCCTGGAGTGGGCGTAGCACCCGGTGTGGGGGTGGCCCCGGGTGTT

GGGGTTGCACCGGGTATCGGTCCGGGCGGTGTCGCAGCAGCAGCTAAA

AGCGCGGCGAAAGTTGCGGCCAAAGCCCAACTGCGCGCCGCCGCGGGC

CTCGGTGCAGGTATTCCGGGGCTGGGTGTCGGAGTTGGAGTCCCGGGT

TTGGGCGTGGGCGCGGGAGTTCCGGGACTGGGAGTGGGTGCCGGAGTT

CCTGGCTTTGGTGCAGGCGCAGATGAAGGTGTTCGTCGTAGCCTGAGT

CCGGAACTGCGTGAAGGTGATCCGAGTAGCAGCCAGCATCTGCCGAGC

ACCCCGAGCAGCCCGCGTGTTCCGGGTGCATTAGCTGCAGCAAAAGCC

GCCAAGTATGGTGCAGCCGTGCCGGGCGTCTTAGGTGGTCTGGGCGCC

CTGGGTGGTGTAGGCATTCCGGGAGGTGTTGTGGGTGCAGGACCGGCC

GCCGCAGCTGCGGCCGCCAAAGCAGCTGCAAAAGCGGCCCAGTTTGGT

TTAGTGGGCGCCGCAGGTTTAGGCGGTTTAGGTGTGGGTGGACTGGGT

GTACCTGGCGTAGGCGGTCTGGGTGGAATTCCGCCCGCAGCGGCCGCG

AAAGCGGCAAAATATGGCGCGGCAGGCCTGGGCGGCGTGCTGGGTGGG

GCAGGTCAGTTTCCGCTGGGCGGGGTTGCCGCACGTCCGGGATTTGGT

CTGAGCCCGATTTTCCCTGGCGGCGCATGTCTGGGTAAAGCATGTGGT

CGTAAACGTAAAtaa

**[0191]** The amino acid sequence of a 57 kDa human elastin truncated at the C-terminal is disclosed in SEQ ID NO: 35. The 57 kDa truncated elastin has amino acids 661-761 deleted from the full length elastin.

(SEQ ID NO: 35)
GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAG

LGAGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLG

VSAGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVP

-continued

TGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYG

LPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKF

GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAA

KYGAAAGLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGA

AVPGVVSPEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVG

VGGIPGVAGVPGVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAG

VLGGLVPGPQAAVPGVPGTGGVPGVGTPAAAAAKAAAKAAQFGLVPGV

GVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVA

AAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGV

GAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALA

AAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGP

**[0192]** The codon optimized polynucleotide sequence encoding the 57 kDa truncated human elastin is disclosed in SEQ ID NO: 36

(SEQ ID NO: 36)
GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTT

TATCCGGGCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCG

GGCGGCAAACCGCTGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGC

TTAGGCGCAGGTCTGGGAGCATTTCCGGCAGTTACCTTTCCAGGGGCA

CTGGTTCCTGGAGGTGTGGCCGATGCAGCCGCGGCATATAAAGCCGCT

AAAGCCGGTGCGGGTTTAGGAGGCGTCCCAGGTGTCGGTGGCCTGGGT

GTTAGCGCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGGGTTAAACCT

GGTAAAGTGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTGTT

TTGCCGGGTGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCG

ACCGGAGCCGGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTT

GCAGGCATCCCGGGAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTT

CCGTTAGGTTATCCGATTAAAGCACCGAAACTGCCCGGCGGTTATGGT

CTGCCGTACACAACCGGTAAACTGCCGTATGGTTATGGCCCGGGTGGA

GTTGCGGGTGCAGCAGGTAAAGCGGGTTATCCTACCGGAACCGGTGTA

GGTCCGCAGGCCGCTGCTGCCGCCGCCGCAAAAGCAGCGGCTAAATTT

GGCGCCGGAGCAGCGGGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGTG

CCAGGGGTACCTGGTGCAATTCCGGGTATTGGTGGTATTGCCGGTGTC

GGCACCCCGGCCGCGGCAGCTGCGGCAGCGGCGGCTGCCAAAGCTGCT

AAATACGGTGCCGCGGCGGGTCTGGTGCCAGGAGGTCCGGGTTTTGGT

CCGGGAGTGGTTGGCGTGCCTGGCGCAGGCGTTCCTGGTGTGGGCGTT

CCAGGTGCAGGGATTCCTGTTGTGCCTGGTGCCGGTATTCCCGGCGCG

GCCGTTCCGGGGGTGGTTAGCCCGGAAGCCGCAGCGAAGGCTGCGGCA

AAGGCAGCAAAGTATGGCGCACGCCCAGGAGTCGGCGTGGGTGGTATC

CCGACCTATGGGGTGGGCGCAGGGGGTTTTCCTGGTTTCGGCGTAGGT

GTAGGAGGTATACCGGGCGTGGCCGGTGTACCAGGGGTTGGTGGCGTC

-continued

CCTGGTGTTGGCGGTGTGCCAGGTGTTGGTATTTCACCGGAAGCACAG

GCAGCAGCCGCAGCTAAGGCAGCGAAATATGGTGCCGCCGGCGCAGGA

GTTTTAGGTGGGCTGGTTCCGGGCCCGCAGGCAGCTGTGCCGGGGGTT

CCAGGCACCGGTGGTGTCCCTGGAGTCGGTACGCCGGCTGCAGCGGCA

GCCAAAGCGGCTGCGAAAGCAGCACAGTTTGGCTTAGTACCGGGTGTG

GGAGTTGCCCCCGGCGTTGGCGTTGCTCCAGGGGTGGGTGTTGCTCCT

GGCGTCGGTCTGGCTCCTGGAGTGGGCGTAGCACCCGGTGTGGGGGTG

GCCCCGGGTGTTGGGGTTGCACCGGGTATCGGTCCGGGCGGTGTCGCA

GCAGCAGCTAAAAGCGCGGCGAAAGTTGCGGCCAAAGCCCAACTGCGC

GCCGCCGCGGGCCTCGGTGCAGGTATTCCGGGGCTGGGTGTCGGAGTT

GGAGTCCCGGGTTTGGGCGTGGGCGCGGGAGTTCCGGGACTGGGAGTG

GGTGCCGGAGTTCCTGGCTTTGGTGCAGGCGCAGATGAAGGTGTTCGT

CGTAGCCTGAGTCCGGAACTGCGTGAAGGTGATCCGAGTAGCAGCCAG

CATCTGCCGAGCACCCCGAGCAGCCCGCGTGTTCCGGGTGCATTAGCT

GCAGCAAAAGCCGCCAAGTATGGTGCAGCCGTGCCGGGCGTCTTAGGT

GGTCTGGGCGCCCTGGGTGGTGTAGGCATTCCGGGAGGTGTTGTGGGT

GCAGGACCGtaa

**[0193]** The amino acid sequence of a 53.9 kDa human elastin truncated at the C-terminal is disclosed in SEQ ID NO: 37. The 53.9 kDa truncated elastin has amino acids 624-761 deleted from the full length elastin.

(SEQ ID NO: 37)
GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAG

LGAGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLG

VSAGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVP

TGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYG

LPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKF

GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAA

KYGAAAGLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGA

AVPGVVSPEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVG

VGGIPGVAGVPGVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAG

VLGGLVPGPQAAVPGVPGTGGVPGVGTPAAAAAKAAAKAAQFGLVPGV

GVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVA

AAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGV

GAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGA

**[0194]** The codon optimized polynucleotide sequence encoding the 53.9 kDa truncated human elastin is disclosed in SEQ ID NO: 38

(SEQ ID NO: 38)

GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTT

TATCCGGGCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCG

GGCGGCAAACCGCTGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGC

TTAGGCGCAGGTCTGGGAGCATTTCCGGCAGTTACCTTTCCAGGGGCA

CTGGTTCCTGGAGGTGTGGCCGATGCAGCCGCGGCATATAAAGCCGCT

AAAGCCGGTGCGGGTTTAGGAGGCGTCCCAGGTGTCGGTGGCCTGGGT

GTTAGCGCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGGGTTAAACCT

GGTAAAGTGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTGTT

TTGCCGGGTGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCG

ACCGGAGCCGGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTT

GCAGGCATCCCGGGAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTT

CCGTTAGGTTATCCGATTAAAGCACCGAAACTGCCCGGCGGTTATGGT

CTGCCGTACACAACCGGTAAACTGCCGTATGGTTATGGCCCGGGTGGA

GTTGCGGGTGCAGCAGGTAAAGCGGGTTATCCTACCGGAACCGGTGTA

GGTCCGCAGGCCGCTGCTGCCGCCGCCGCAAAAGCAGCGGCTAAATTT

GGCGCCGGAGCAGCGGGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGTG

CCAGGGGTACCTGGTGCAATTCCGGGTATTGGTGGTATTGCCGGTGTC

GGCACCCCGGCCGCGGCAGCTGCGGCAGCGGCGGCTGCCAAAGCTGCT

AAATACGGTGCCGCGGCGGGTCTGGTGCCAGGAGGTCCGGGTTTTGGT

CCGGGAGTGGTTGGCGTGCCTGGCGCAGGCGTTCCTGGTGTGGGCGTT

CCAGGTGCAGGGATTCCTGTTGTGCCTGGTGCCGGTATTCCCGGCGCG

GCCGTTCCGGGGGTGGTTAGCCCGGAAGCCGCAGCGAAGGCTGCGGCA

AAGGCAGCAAAGTATGGCGCACGCCCAGGAGTCGGCGTGGGTGGTATC

CCGACCTATGGGGTGGGCGCAGGGGGTTTTCCTGGTTTCGGCGTAGGT

GTAGGAGGTATACCGGGCGTGGCCGGTGTACCAGGGGTTGGTGGCGTC

CCTGGTGTTGGCGGTGTGCCAGGTGTTGGTATTTCACCGGAAGCACAG

GCAGCAGCCGCAGCTAAGGCAGCGAAATATGGTGCCGCCGGCGCAGGA

GTTTTAGGTGGGCTGGTTCCGGGCCCGCAGGCAGCTGTGCCGGGGGTT

CCAGGCACCGGTGGTGTCCCTGGAGTCGGTACGCCGGCTGCAGCGGCA

GCCAAAGCGGCTGCGAAAGCAGCACAGTTTGGCTTAGTACCGGGTGTG

GGAGTTGCCCCCGGCGTTGGCGTTGCTCCAGGGGTGGGTGTTGCTCCT

GGCGTCGGTCTGGCTCCTGGAGTGGGCGTAGCACCCGGTGTGGGGGTG

GCCCCGGGTGTTGGGGTTGCACCGGGTATCGGTCCGGGCGGTGTCGCA

GCAGCAGCTAAAAGCGCGGCGAAAGTTGCGGCCAAAGCCCAACTGCGC

GCCGCCGCGGGCCTCGGTGCAGGTATTCCGGGGCTGGGTGTCGGAGTT

GGAGTCCCGGGTTTGGGCGTGGGCGCGGGAGTTCCGGGACTGGGAGTG

GGTGCCGGAGTTCCTGGCTTTGGTGCAGGCGCAGATGAAGGTGTTCGT

CGTAGCCTGAGTCCGGAACTGCGTGAAGGTGATCCGAGTAGCAGCCAG

CATCTGCCGAGCACCCCGAGCAGCCCGCGTGTTCCGGGTGCAtaa

**[0195]** The amino acid sequence of a 45.3 kDa human elastin truncated at the C-terminal is disclosed in SEQ ID NO: 39. The 45.3 kDa truncated elastin has amino acids 529-761 deleted from the full length elastin.

(SEQ ID NO: 39)

GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAG

LGAGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLG

VSAGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVP

TGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYG

LPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKF

GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAKAA

KYGAAAGLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGA

AVPGVVSPEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVG

VGGIPGVAGVPGVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAG

VLGGLVPGPQAAVPGVPGTGGVPGVGTPAAAAAKAAAKAAQFGLVPGV

GVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGV

**[0196]** The codon optimized polynucleotide sequence encoding the 45.3 kDa truncated human elastin is disclosed in SEQ ID NO: 40

(SEQ ID NO: 40)

GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTT

TATCCGGGCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCG

GGCGGCAAACCGCTGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGC

TTAGGCGCAGGTCTGGGAGCATTTCCGGCAGTTACCTTTCCAGGGGCA

CTGGTTCCTGGAGGTGTGGCCGATGCAGCCGCGGCATATAAAGCCGCT

AAAGCCGGTGCGGGTTTAGGAGGCGTCCCAGGTGTCGGTGGCCTGGGT

GTTAGCGCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGGGTTAAACCT

GGTAAAGTGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTGTT

TTGCCGGGTGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCG

ACCGGAGCCGGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTT

GCAGGCATCCCGGGAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTT

CCGTTAGGTTATCCGATTAAAGCACCGAAACTGCCCGGCGGTTATGGT

CTGCCGTACACAACCGGTAAACTGCCGTATGGTTATGGCCCGGGTGGA

GTTGCGGGTGCAGCAGGTAAAGCGGGTTATCCTACCGGAACCGGTGTA

GGTCCGCAGGCCGCTGCTGCCGCCGCCGCAAAAGCAGCGGCTAAATTT

GGCGCCGGAGCAGCGGGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGTG

CCAGGGGTACCTGGTGCAATTCCGGGTATTGGTGGTATTGCCGGTGTC

GGCACCCCGGCCGCGGCAGCTGCGGCAGCGGCGGCTGCCAAAGCTGCT

AAATACGGTGCCGCGGCGGGTCTGGTGCCAGGAGGTCCGGGTTTTGGT

CCGGGAGTGGTTGGCGTGCCTGGCGCAGGCGTTCCTGGTGTGGGCGTT

CCAGGTGCAGGGATTCCTGTTGTGCCTGGTGCCGGTATTCCCGGCGCG

-continued

GCCGTTCCGGGGGTGGTTAGCCCGGAAGCCGCAGCGAAGGCTGCGGCA

AAGGCAGCAAAGTATGGCGCACGCCCAGGAGTCGGCGTGGGTGGTATC

CCGACCTATGGGGTGGGCGCAGGGGGTTTTCCTGGTTTCGGCGTAGGT

GTAGGAGGTATACCGGGCGTGGCCGGTGTACCAGGGGTTGGTGGCGTC

CCTGGTGTTGGCGGTGTGCCAGGTGTTGGTATTTCACCGGAAGCACAG

GCAGCAGCCGCAGCTAAGGCAGCGAAATATGGTGCCGCCGGCGCAGGA

GTTTTAGGTGGGCTGGTTCCGGGCCCGCAGGCAGCTGTGCCGGGGGTT

CCAGGCACCGGTGGTGTCCCTGGAGTCGGTACGCCGGCTGCAGCGGCA

GCCAAAGCGGCTGCGAAAGCAGCACAGTTTGGCTTAGTACCGGGTGTG

GGAGTTGCCCCCGGCGTTGGCGTTGCTCCAGGGGTGGGTGTTGCTCCT

GGCGTCGGTCTGGCTCCTGGAGTGGGCGTAGCACCCGGTGTGGGGGTG

GCCCCGGGTGTTGGGGTTGCACCGGGTATCGGTCCGGGCGGTGTCtaa

**[0197]** The amino acid sequence of a 44.4 kDa human elastin truncated at the N-terminal is disclosed in SEQ ID NO: 41. The 44.4 kDa truncated elastin has amino acids 2-246 deleted from the full length elastin.

(SEQ ID NO: 41)

GVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAA

AGLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGV

VSPEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIP

GVAGVPGVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAGVLGGL

VPGPQAAVPGVPGTGGVPGVGTPAAAAAKAAAKAAQFGLVPGVGVAPG

VGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAAAKS

AAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVP

GFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAA

KYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAKAAAKAAQFGL

VGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGA

GQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK

**[0198]** The codon optimized polynucleotide sequence encoding the 44.4 kDa truncated human elastin is disclosed in SEQ ID NO: 42

(SEQ ID NO: 42)

GGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGTGCCAGGGGTACCTGGT

GCAATTCCGGGTATTGGTGGTATTGCCGGTGTCGGCACCCCGGCCGCG

GCAGCTGCGGCAGCGGCGGCTGCCAAAGCTGCTAAATACGGTGCCGCG

GCGGGTCTGGTGCCAGGAGGTCCGGGTTTTGGTCCGGGAGTGGTTGGC

GTGCCTGGCGCAGGCGTTCCTGGTGTGGGCGTTCCAGGTGCAGGGATT

CCTGTTGTGCCTGGTGCCGGTATTCCCGGCGCGGCCGTTCCGGGGGTG

GTTAGCCCGGAAGCCGCAGCGAAGGCTGCGGCAAAGGCAGCAAAGTAT

GGCGCACGCCCAGGAGTCGGCGTGGGTGGTATCCCGACCTATGGGGTG

-continued

GGCGCAGGGGGTTTTCCTGGTTTCGGCGTAGGTGTAGGAGGTATACCG

GGCGTGGCCGGTGTACCAGGGGTTGGTGGCGTCCCTGGTGTTGGCGGT

GTGCCAGGTGTTGGTATTTCACCGGAAGCACAGGCAGCAGCCGCAGCT

AAGGCAGCGAAATATGGTGCCGCCGGCGCAGGAGTTTTAGGTGGGCTG

GTTCCGGGCCCGCAGGCAGCTGTGCCGGGGGTTCCAGGCACCGGTGGT

GTCCCTGGAGTCGGTACGCCGGCTGCAGCGGCAGCCAAAGCGGCTGCG

AAAGCAGCACAGTTTGGCTTAGTACCGGGTGTGGGAGTTGCCCCCGGC

GTTGGCGTTGCTCCAGGGGTGGGTGTTGCTCCTGGCGTCGGTCTGGCT

CCTGGAGTGGGCGTAGCACCCGGTGTGGGGGTGGCCCCGGGTGTTGGG

GTTGCACCGGGTATCGGTCCGGGCGGTGTCGCAGCAGCAGCTAAAAGC

GCGGCGAAAGTTGCGGCCAAAGCCCAACTGCGCGCCGCCGCGGGCCTC

GGTGCAGGTATTCCGGGGCTGGGTGTCGGAGTTGGAGTCCCGGGTTTG

GGCGTGGGCGCGGGAGTTCCGGGACTGGGAGTGGGTGCCGGAGTTCCT

GGCTTTGGTGCAGGCGCAGATGAAGGTGTTCGTCGTAGCCTGAGTCCG

GAACTGCGTGAAGGTGATCCGAGTAGCAGCCAGCATCTGCCGAGCACC

CCGAGCAGCCCGCGTGTTCCGGGTGCATTAGCTGCAGCAAAAGCCGCC

AAGTATGGTGCAGCCGTGCCGGGCGTCTTAGGTGGTCTGGGCGCCCTG

GGTGGTGTAGGCATTCCGGGAGGTGTTGTGGGTGCAGGACCGGCCGCC

GCAGCTGCGGCCGCCAAAGCAGCTGCAAAAGCGGCCCAGTTTGGTTTA

GTGGGCGCCGCAGGTTTAGGCGGTTTAGGTGTGGGTGGACTGGGTGTA

CCTGGCGTAGGCGGTCTGGGTGGAATTCCGCCCGCAGCGGCCGCGAAA

GCGGCAAAATATGGCGCGGCAGGCCTGGGCGGCGTGCTGGGTGGGGCA

GGTCAGTTTCCGCTGGGCGGGGTTGCCGCACGTCCGGGATTTGGTCTG

AGCCCGATTTTCCCTGGCGGCGCATGTCTGGGTAAAGCATGTGGTCGT

AAACGTAAAtaa

**[0199]** The amino acid sequence of a 40.4 kDa human elastin truncated at the N-terminal is disclosed in SEQ ID NO: 43. The 40.4 kDa truncated elastin has amino acids 2-295 deleted from the full length elastin.

(SEQ ID NO: 43)

GLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVV

SPEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPG

VAGVPGVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAGVLGGLV

PGPQAAVPGVPGTGGVPGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGV

GVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAAAAKSA

AKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPG

FGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAK

YGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAKAAAKAAQFGLV

GAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAG

QFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK

**[0200]** The codon optimized polynucleotide sequence encoding the 40.4 kDa truncated human elastin is disclosed in SEQ ID NO: 44

(SEQ ID NO: 44)
GGTCTGGTGCCAGGAGGTCCGGGTTTTGGTCCGGGAGTGGTTGGCGTG

CCTGGCGCAGGCGTTCCTGGTGTGGGCGTTCCAGGTGCAGGGATTCCT

GTTGTGCCTGGTGCCGGTATTCCCGGCGCGGCCGTTCCGGGGGTGGTT

AGCCCGGAAGCCGCAGCGAAGGCTGCGGCAAAGGCAGCAAAGTATGGC

GCACGCCCAGGAGTCGGCGTGGGTGGTATCCCGACCTATGGGGTGGGC

GCAGGGGGTTTTCCTGGTTTCGGCGTAGGTGTAGGAGGTATACCGGGC

GTGGCCGGTGTACCAGGGGTTGGTGGCGTCCCTGGTGTTGGCGGTGTG

CCAGGTGTTGGTATTTCACCGGAAGCACAGGCAGCAGCCGCAGCTAAG

GCAGCGAAATATGGTGCCGCCGGCGCAGGAGTTTTAGGTGGGCTGGTT

CCGGGCCCGCAGGCAGCTGTGCCGGGGGTTCCAGGCACCGGTGGTGTC

CCTGGAGTCGGTACGCCGGCTGCAGCGGCAGCCAAAGCGGCTGCGAAA

GCAGCACAGTTTGGCTTAGTACCGGGTGTGGGAGTTGCCCCCGGCGTT

GGCGTTGCTCCAGGGGTGGGTGTTGCTCCTGGCGTCGGTCTGGCTCCT

GGAGTGGGCGTAGCACCCGGTGTGGGGGTGGCCCCGGGTGTTGGGGTT

GCACCGGGTATCGGTCCGGGCGGTGTCGCAGCAGCAGCTAAAAGCGCG

GCGAAAGTTGCGGCCAAAGCCCAACTGCGCGCCGCCGCGGGCCTCGGT

GCAGGTATTCCGGGGCTGGGTGTCGGAGTTGGAGTCCCGGGTTTGGGC

GTGGGCGCGGGAGTTCCGGGACTGGGAGTGGGTGCCGGAGTTCCTGGC

TTTGGTGCAGGCGCAGATGAAGGTGTTCGTCGTAGCCTGAGTCCGGAA

CTGCGTGAAGGTGATCCGAGTAGCAGCCAGCATCTGCCGAGCACCCCG

AGCAGCCCGCGTGTTCCGGGTGCATTAGCTGCAGCAAAAGCCGCCAAG

TATGGTGCAGCCGTGCCGGGCGTCTTAGGTGGTCTGGGCGCCCTGGGT

GGTGTAGGCATTCCGGGAGGTGTTGTGGGTGCAGGACCGGCCGCCGCA

GCTGCGGCCGCCAAAGCAGCTGCAAAAGCGGCCCAGTTTGGTTTAGTG

GGCGCCGCAGGTTTAGGCGGTTTAGGTGTGGGTGGACTGGGTGTACCT

GGCGTAGGCGGTCTGGGTGGAATTCCGCCCGCAGCGGCCGCGAAAGCG

GCAAAATATGGCGCGGCAGGCCTGGGCGGCGTGCTGGGTGGGGCAGGT

CAGTTTCCGCTGGGCGGGGTTGCCGCACGTCCGGGATTTGGTCTGAGC

CCGATTTTCCCTGGCGGCGCATGTCTGGGTAAAGCATGTGGTCGTAAA

CGTAAAtaa

**[0201]** The amino acid sequence of a 39.8 kDa human elastin truncated at the C-terminal is disclosed in SEQ ID NO: 45. The 39.8 kDa truncated elastin has amino acids 462-761 deleted from the full length elastin.

(SEQ ID NO: 45)
GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAG

LGAGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLG

-continued
VSAGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVP

TGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYG

LPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKF

GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAKAA

KYGAAAGLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGA

AVPGVVSPEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVG

VGGIPGVAGVPGVGGVPGVGGVPGVGISPEAQAAAAAKAAKYGAAGAG

VLGGLVPGPQAAVPGVPGTGGVPGVGTP

**[0202]** The codon optimized polynucleotide sequence encoding the 39.8 kDa truncated human elastin is disclosed in SEQ ID NO: 46

(SEQ ID NO: 46)
GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTT

TATCCGGGCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCG

GGCGGCAAACCGCTGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGC

TTAGGCGCAGGTCTGGGAGCATTTCCGGCAGTTACCTTTCCAGGGGCA

CTGGTTCCTGGAGGTGTGGCCGATGCAGCCGCGGCATATAAAGCCGCT

AAAGCCGGTGCGGGTTTAGGAGGCGTCCCAGGTGTCGGTGGCCTGGGT

GTTAGCGCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGGGTTAAACCT

GGTAAAGTGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTGTT

TTGCCGGGTGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCG

ACCGGAGCCGGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTT

GCAGGCATCCCGGGAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTT

CCGTTAGGTTATCCGATTAAAGCACCGAAACTGCCCGGCGGTTATGGT

CTGCCGTACACAACCGGTAAACTGCCGTATGGTTATGGCCCGGGTGGA

GTTGCGGGTGCAGCAGGTAAAGCGGGTTATCCTACCGGAACCGGTGTA

GGTCCGCAGGCCGCTGCTGCCGCCGCCGCAAAAGCAGCGGCTAAATTT

GGCGCCGGAGCAGCGGGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGTG

CCAGGGGTACCTGGTGCAATTCCGGGTATTGGTGGTATTGCCGGTGTC

GGCACCCCGGCCGCGGCAGCTGCGGCAGCGGCGGCTGCCAAAGCTGCT

AAATACGGTGCCGCGGCGGGTCTGGTGCCAGGAGGTCCGGGTTTTGGT

CCGGGAGTGGTTGGCGTGCCTGGCGCAGGCGTTCCTGGTGTGGGCGTT

CCAGGTGCAGGGATTCCTGTTGTGCCTGGTGCCGGTATTCCCGGCGCG

GCCGTTCCGGGGGTGGTTAGCCCGGAAGCCGCAGCGAAGGCTGCGGCA

AAGGCAGCAAAGTATGGCGCACGCCCAGGAGTCGGCGTGGGTGGTATC

CCGACCTATGGGGTGGGCGCAGGGGGTTTTCCTGGTTTCGGCGTAGGT

GTAGGAGGTATACCGGGCGTGGCCGGTGTACCAGGGGTTGGTGGCGTC

CCTGGTGTTGGCGGTGTGCCAGGTGTTGGTATTTCACCGGAAGCACAG

GCAGCAGCCGCAGCTAAGGCAGCGAAATATGGTGCCGCCGGCGCAGGA

-continued

GTTTTAGGTGGGCTGGTTCCGGGCCCGCAGGCAGCTGTGCCGGGGGTT

CCAGGCACCGGTGGTGTCCCTGGAGTCGGTACGCCGtaa

**[0203]** The amino acid sequence of a 36.1 kDa human elastin truncated at the C-terminal is disclosed in SEQ ID NO: 47. The 36.1 kDa truncated elastin has amino acids 418-761 deleted from the full length elastin.

(SEQ ID NO: 47)
GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAG

LGAGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLG

VSAGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVP

TGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYG

LPYTTGKLPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKF

GAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAA

KYGAAAGLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGA

AVPGVVSPEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVG

VGGIPGVAGVPGVGGVPGVGGVPGVGISPEAQ

**[0204]** The codon optimized polynucleotide sequence encoding the 36.1 kDa truncated human elastin is disclosed in SEQ ID NO: 48

(SEQ ID NO: 48)
GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTT

TATCCGGGCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCG

GGCGGCAAACCGCTGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGC

TTAGGCGCAGGTCTGGGAGCATTTCCGGCAGTTACCTTTCCAGGGGCA

CTGGTTCCTGGAGGTGTGGCCGATGCAGCCGCGGCATATAAAGCCGCT

AAAGCCGGTGCGGGTTTAGGAGGCGTCCCAGGTGTCGGTGGCCTGGGT

GTTAGCGCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGGGTTAAACCT

GGTAAAGTGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTGTT

TTGCCGGGTGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCG

ACCGGAGCCGGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTT

GCAGGCATCCCGGGAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTT

CCGTTAGGTTATCCGATTAAAGCACCGAAACTGCCCGGCGGTTATGGT

CTGCCGTACACAACCGGTAAACTGCCGTATGGTTATGGCCCGGGTGGA

GTTGCGGGTGCAGCAGGTAAAGCGGGTTATCCTACCGGAACCGGTGTA

GGTCCGCAGGCCGCTGCTGCCGCCGCCGCAAAAGCAGCGGCTAAATTT

GGCGCCGGAGCAGCGGGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGTG

CCAGGGGTACCTGGTGCAATTCCGGGTATTGGTGGTATTGCCGGTGTC

GGCACCCCGGCCGCGGCAGCTGCGGCAGCGGCGGCTGCCAAAGCTGCT

AAATACGGTGCCGCGGCGGGTCTGGTGCCAGGAGGTCCGGGTTTTGGT

CCGGGAGTGGTTGGCGTGCCTGGCGCAGGCGTTCCTGGTGTGGGCGTT

-continued

CCAGGTGCAGGGATTCCTGTTGTGCCTGGTGCCGGTATTCCCGGCGCG

GCCGTTCCGGGGGTGGTTAGCCCGGAAGCCGCAGCGAAGGCTGCGGCA

AAGGCAGCAAAGTATGGCGCACGCCCAGGAGTCGGCGTGGGTGGTATC

CCGACCTATGGGGTGGGCGCAGGGGGTTTTCCTGGTTTCGGCGTAGGT

GTAGGAGGTATACCGGGCGTGGCCGGTGTACCAGGGGTTGGTGGCGTC

CCTGGTGTTGGCGGTGTGCCAGGTGTTGGTATTTCACCGGAAGCACAG

taa

**[0205]** The amino acid sequence of a 34.9 kDa human elastin truncated at the N-terminal is disclosed in SEQ ID NO: 49. The 34.9 kDa truncated elastin has amino acids 2-360 deleted from the full length elastin.

(SEQ ID NO: 49)
RPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPGVGGVPGVGGVPGV

GISPEAQAAAAAKAAKYGAAGAGVLGGLVPGPQAAVPGVPGTGGVPGVGT

PAAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPG

VGVAPGVGVAPGIGPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVG

VGVPGLGVGAGVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSSQH

LPSTPSSPRVPGALAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGP

AAAAAAAKAAAKAAQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAK

AAKYGAAGLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKR

K

**[0206]** The codon optimized polynucleotide sequence encoding the 34.9 kDa truncated human elastin is disclosed in SEQ ID NO: 50

(SEQ ID NO: 50)
CGCCCAGGAGTCGGCGTGGGTGGTATCCCGACCTATGGGGTGGGCGCAGG

GGGTTTTCCTGGTTTCGGCGTAGGTGTAGGAGGTATACCGGGCGTGGCCG

GTGTACCAGGGGTTGGTGGCGTCCCTGGTGTTGGCGGTGTGCCAGGTGTT

GGTATTTCACCGGAAGCACAGGCAGCAGCCGCAGCTAAGGCAGCGAAATA

TGGTGCCGCCGGCGCAGGAGTTTTAGGTGGGCTGGTTCCGGGCCCGCAGG

CAGCTGTGCCGGGGGTTCCAGGCACCGGTGGTGTCCCTGGAGTCGGTACG

CCGGCTGCAGCGGCAGCCAAAGCGGCTGCGAAAGCAGCACAGTTTGGCTT

AGTACCGGGTGTGGGAGTTGCCCCCGGCGTTGGCGTTGCTCCAGGGGTGG

GTGTTGCTCCTGGCGTCGGTCTGGCTCCTGGAGTGGGCGTAGCACCCGGT

GTGGGGGTGGCCCCGGGTGTTGGGGTTGCACCGGGTATCGGTCCGGGCGG

TGTCGCAGCAGCAGCTAAAAGCGCGGCGAAAGTTGCGGCCAAAGCCCAAC

TGCGCGCCGCCGCGGGCCTCGGTGCAGGTATTCCGGGGCTGGGTGTCGGA

GTTGGAGTCCCGGGTTTGGGCGTGGGCGCGGGAGTTCCGGGACTGGGAGT

GGGTGCCGGAGTTCCTGGCTTTGGTGCAGGCGCAGATGAAGGTGTTCGTC

GTAGCCTGAGTCCGGAACTGCGTGAAGGTGATCCGAGTAGCAGCCAGCAT

-continued

CTGCCGAGCACCCCGAGCAGCCCGCGTGTTCCGGGTGCATTAGCTGCAGC

AAAAGCCGCCAAGTATGGTGCAGCCGTGCCGGGCGTCTTAGGTGGTCTGG

GCGCCCTGGGTGGTGTAGGCATTCCGGGAGGTGTTGTGGGTGCAGGACCG

GCCGCCGCAGCTGCGGCCGCCAAAGCAGCTGCAAAAGCGGCCCAGTTTGG

TTTAGTGGGCGCCGCAGGTTTAGGCGGTTTAGGTGTGGGTGGACTGGGTG

TACCTGGCGTAGGCGGTCTGGGTGGAATTCCGCCCGCAGCGGCCGCGAAA

GCGGCAAAATATGGCGCGGCAGGCCTGGGCGGCGTGCTGGGTGGGGCAGG

TCAGTTTCCGCTGGGCGGGGTTGCCGCACGTCCGGGATTTGGTCTGAGCC

CGATTTTCCCTGGCGGCGCATGTCTGGGTAAAGCATGTGGTCGTAAACGT

AAAtaa

**[0207]** The amino acid sequence of a 32 kDa human elastin truncated at the C-terminal is disclosed in SEQ ID NO: 51. The 32 kDa truncated elastin has amino acids 373-761 deleted from the full length elastin.

(SEQ ID NO: 51)
GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGA

GLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAV

VPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKA

PGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKLPYGY

GPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKFGAGAAGVLPGVGGAG

VPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLVPGGPGFGPG

VVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKAAAKAAKY

GARPGVGVGGIPTY

**[0208]** The codon optimized polynucleotide sequence encoding the 32 kDa truncated human elastin is disclosed in SEQ ID NO: 52

(SEQ ID NO: 52)
GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTTATCCGG

GCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCGGGCGGCAAACCGC

TGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGCTTAGGCGCAGGTCTGGGAG

CATTTCCGGCAGTTACCTTTCCAGGGGCACTGGTTCCTGGAGGTGTGGCCGATGC

AGCCGCGGCATATAAAGCCGCTAAAGCCGGTGCGGGTTTAGGAGGCGTCCCAGG

TGTCGGTGGCCTGGGTGTTAGCGCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGG

GTTAAACCTGGTAAAGTGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTG

TTTTGCCGGGTGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGA

GCCGGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCCCGG

GAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTATCCGATTAA

AGCACCGAAACTGCCCGGCGGTTATGGTCTGCCGTACACAACCGGTAAACTGCCG

TATGGTTATGGCCCGGGTGGAGTTGCGGGTGCAGCAGGTAAAGCGGGTTATCCTA

CCGGAACCGGTGTAGGTCCGCAGGCCGCTGCTGCCGCCGCCGCAAAAGCAGCGG

CTAAATTTGGCGCCGGAGCAGCGGGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGT

GCCAGGGGTACCTGGTGCAATTCCGGGTATTGGTGGTATTGCCGGTGTCGGCACC

CCGGCCGCGGCAGCTGCGGCAGCGGCGGCTGCCAAAGCTGCTAAATACGGTGCC

GCGGCGGGTCTGGTGCCAGGAGGTCCGGGTTTTGGTCCGGGAGTGGTTGGCGTGC

CTGGCGCAGGCGTTCCTGGTGTGGGCGTTCCAGGTGCAGGGATTCCTGTTGTGCC

TGGTGCCGGTATTCCCGGCGCGGCCGTTCCGGGGGTGGTTAGCCCGGAAGCCGCA

GCGAAGGCTGCGGCAAAGGCAGCAAAGTATGGCGCACGCCCAGGAGTCGGCGTG

GGTGGTATCCCGACCTATtaa

**[0209]** The amino acid sequence of a 29.9 kDa human elastin truncated at the C-terminal is disclosed in SEQ ID NO: 53. The 60.7 kDa truncated elastin has amino acids 347-761 deleted from the full length elastin.

```
                                            (SEQ ID NO: 53)
GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLG

AGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAG

AVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGAGVK

PKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKL

PYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKFGAGAAGVLPG

VGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLVPGG

PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPE
```

**[0210]** The codon optimized polynucleotide sequence encoding the 29.9 kDa truncated human elastin is disclosed in SEQ ID NO: 54

```
                                                      (SEQ ID NO: 54)
GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTTTATCCGG

GCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCGGGCGGCAAACCGC

TGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGCTTAGGCGCAGGTCTGGGAG

CATTTCCGGCAGTTACCTTTCCAGGGGCACTGGTTCCTGGAGGTGTGGCCGATGC

AGCCGCGGCATATAAAGCCGCTAAAGCCGGTGCGGGTTTAGGAGGCGTCCCAGG

TGTCGGTGGCCTGGGTGTTAGCGCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGG

GTTAAACCTGGTAAAGTGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTG

TTTTGCCGGGTGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGA

GCCGGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCCCGG

GAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTATCCGATTAA

AGCACCGAAACTGCCCGGCGGTTATGGTCTGCCGTACACAACCGGTAAACTGCCG

TATGGTTATGGCCCGGGTGGAGTTGCGGGTGCAGCAGGTAAAGCGGGTTATCCTA

CCGGAACCGGTGTAGGTCCGCAGGCCGCTGCTGCCGCCGCCGCAAAAGCAGCGG

CTAAATTTGGCGCCGGAGCAGCGGGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGT

GCCAGGGGTACCTGGTGCAATTCCGGGTATTGGTGGTATTGCCGGTGTCGGCACC

CCGGCCGCGGCAGCTGCGGCAGCGGCGGCTGCCAAAGCTGCTAAATACGGTGCC

GCGGCGGGTCTGGTGCCAGGAGGTCCGGGTTTTGGTCCGGGAGTGGTTGGCGTGC

CTGGCGCAGGCGTTCCTGGTGTGGGCGTTCCAGGTGCAGGGATTCCTGTTGTGCC

TGGTGCCGGTATTCCCGGCGCGGCCGTTCCGGGGGTGGTTAGCCCGGAAtaa
```

**[0211]** The amino acid sequence of a 29.4 kDa human elastin truncated at the N-terminal is disclosed in SEQ ID NO: 55. The 29.4 kDa truncated elastin has amino acids 2-425 deleted from the full length elastin.

```
                                            (SEQ ID NO: 55)
KYGAAGAGVLGGLVPGPQAAVPGVPGTGGVPGVGTPAAAAAKAAAKAAQF

GLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGP

GGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGL

GVGAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALA

AAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAKAAAKAAQ

FGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGG

AGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK
```

**[0212]** The codon optimized polynucleotide sequence encoding the 29.4 kDa truncated human elastin is disclosed in SEQ ID NO: 56

(SEQ ID NO: 56)
AAATATGGTGCCGCCGGCGCAGGAGTTTTAGGTGGGCTGGTTCCGGGCCCGCAG

GCAGCTGTGCCGGGGGTTCCAGGCACCGGTGGTGTCCCTGGAGTCGGTACGCCGG

CTGCAGCGGCAGCCAAAGCGGCTGCGAAAGCAGCACAGTTTGGCTTAGTACCGG

GTGTGGGAGTTGCCCCCGGCGTTGGCGTTGCTCCAGGGGTGGGTGTTGCTCCTGG

CGTCGGTCTGGCTCCTGGAGTGGGCGTAGCACCCGGTGTGGGGGTGGCCCCGGGT

GTTGGGGTTGCACCGGGTATCGGTCCGGGCGGTGTCGCAGCAGCAGCTAAAAGC

GCGGCGAAAGTTGCGGCCAAAGCCCAACTGCGCGCCGCCGCGGGCCTCGGTGCA

GGTATTCCGGGGCTGGGTGTCGGAGTTGGAGTCCCGGGTTTGGGCGTGGGCGCGG

GAGTTCCGGGACTGGGAGTGGGTGCCGGAGTTCCTGGCTTTGGTGCAGGCGCAG

ATGAAGGTGTTCGTCGTAGCCTGAGTCCGGAACTGCGTGAAGGTGATCCGAGTAG

CAGCCAGCATCTGCCGAGCACCCCGAGCAGCCCGCGTGTTCCGGGTGCATTAGCT

GCAGCAAAAGCCGCCAAGTATGGTGCAGCCGTGCCGGGCGTCTTAGGTGGTCTG

GGCGCCCTGGGTGGTGTAGGCATTCCGGGAGGTGTTGTGGGTGCAGGACCGGCC

GCCGCAGCTGCGGCCGCCAAAGCAGCTGCAAAAGCGGCCCAGTTTGGTTTAGTG

GGCGCCGCAGGTTTAGGCGGTTTAGGTGTGGGTGGACTGGGTGTACCTGGCGTAG

GCGGTCTGGGTGGAATTCCGCCCGCAGCGGCCGCGAAAGCGGCAAAATATGGCG

CGGCAGGCCTGGGCGGCGTGCTGGGTGGGGCAGGTCAGTTTCCGCTGGGCGGGG

TTGCCGCACGTCCGGGATTTGGTCTGAGCCCGATTTTCCCTGGCGGCGCATGTCTG

GGTAAAGCATGTGGTCGTAAACGTAAAtaa

**[0213]** The amino acid sequence of a 25.3 kDa human elastin truncated at the N-terminal is disclosed in SEQ ID NO: 57. The 25.3 kDa truncated elastin has amino acids 2-473 deleted from the full length elastin.

(SEQ ID NO: 57)
QFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGI

GPGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVP

-continued
GLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGA

LAAAKAAKYGAAVPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAKAAAKA

AQFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVL

GGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK

**[0214]** The codon optimized polynucleotide sequence encoding the 25.3 kDa truncated human elastin is disclosed in SEQ ID NO: 58

(SEQ ID NO: 58)
CAGTTTGGCTTAGTACCGGGTGTGGGAGTTGCCCCCGGCGTTGGCGTTGCTCCAG

GGGTGGGTGTTGCTCCTGGCGTCGGTCTGGCTCCTGGAGTGGGCGTAGCACCCGG

TGTGGGGGTGGCCCCGGGTGTTGGGGTTGCACCGGGTATCGGTCCGGGCGGTGTC

GCAGCAGCAGCTAAAAGCGCGGCGAAAGTTGCGGCCAAAGCCCAACTGCGCGCC

GCCGCGGGCCTCGGTGCAGGTATTCCGGGGCTGGGTGTCGGAGTTGGAGTCCCGG

GTTTGGGCGTGGGCGCGGGAGTTCCGGGACTGGGAGTGGGTGCCGGAGTTCCTG

GCTTTGGTGCAGGCGCAGATGAAGGTGTTCGTCGTAGCCTGAGTCCGGAACTGCG

TGAAGGTGATCCGAGTAGCAGCCAGCATCTGCCGAGCACCCCGAGCAGCCCGCG

TGTTCCGGGTGCATTAGCTGCAGCAAAAGCCGCCAAGTATGGTGCAGCCGTGCCG

GGCGTCTTAGGTGGTCTGGGCGCCCTGGGTGGTGTAGGCATTCCGGGAGGTGTTG

TGGGTGCAGGACCGGCCGCCGCAGCTGCGGCCGCCAAAGCAGCTGCAAAAGCGG

-continued

CCCAGTTTGGTTTAGTGGGCGCCGCAGGTTTAGGCGGTTTAGGTGTGGGTGGACT

GGGTGTACCTGGCGTAGGCGGTCTGGGTGGAATTCCGCCCGCAGCGGCCGCGAA

AGCGGCAAAATATGGCGCGGCAGGCCTGGGCGGCGTGCTGGGTGGGGCAGGTCA

GTTTCCGCTGGGCGGGGTTGCCGCACGTCCGGGATTTGGTCTGAGCCCGATTTTC

CCTGGCGGCGCATGTCTGGGTAAAGCATGTGGTCGTAAACGTAAAtaa

**[0215]** The amino acid sequence of a 24.1 kDa human elastin truncated at the C-terminal is disclosed in SEQ ID NO: 59. The 24.1 kDa truncated elastin has amino acids 277-761 deleted from the full length elastin.

(SEQ ID NO: 59)

GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLG

AGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAG

AVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGAGVK

PKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKL

PYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAKAAAKFGAGAAGVLPG

VGGAGVPGVPGAIPGIGGIAGVGTP

**[0216]** The codon optimized polynucleotide sequence encoding the 24.1 kDa truncated human elastin is disclosed in SEQ ID NO: 60

**[0217]** The amino acid sequence of a 20.3 kDa human elastin truncated at the C-terminal is disclosed in SEQ ID NO: 61. The 20.3 kDa truncated elastin has amino acids 229-761 deleted from the full length elastin.

(SEQ ID NO: 61)

GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGA

GLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAGAV

VPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGAGVKPKA

PGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKLPYGY

GPGGVAGAAGKAGYPTGTGVGPQ

**[0218]** The codon optimized polynucleotide sequence encoding the 20.3 kDa truncated human elastin is disclosed in SEQ ID NO: 62

(SEQ ID NO: 60)

GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTTTATCCGG

GCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCGGGCGGCAAACCGC

TGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGCTTAGGCGCAGGTCTGGGAG

CATTTCCGGCAGTTACCTTTCCAGGGGCACTGGTTCCTGGAGGTGTGGCCGATGC

AGCCGCGGCATATAAAGCCGCTAAAGCCGGTGCGGGTTTAGGAGGCGTCCCAGG

TGTCGGTGGCCTGGGTGTTAGCGCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGG

GTTAAACCTGGTAAAGTGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTG

TTTTGCCGGGTGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGA

GCCGGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCCCGG

GAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTATCCGATTAA

AGCACCGAAACTGCCCGGCGGTTATGGTCTGCCGTACACAACCGGTAAACTGCCG

TATGGTTATGGCCCGGGTGGAGTTGCGGGTGCAGCAGGTAAAGCGGGTTATCCTA

CCGGAACCGGTGTAGGTCCGCAGGCCGCTGCTGCCGCCGCCGCAAAAGCAGCGG

CTAAATTTGGCGCCGGAGCAGCGGGTGTTCTGCCTGGAGTTGGTGGTGCGGGCGT

GCCAGGGGTACCTGGTGCAATTCCGGGTATTGGTGGTATTGCCGGTGTCGGCACC

CCGtaa

(SEQ ID NO: 62)
GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTTATCCGG

GCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCGGGCGGCAAACCGC

TGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGCTTAGGCGCAGGTCTGGGAG

CATTTCCGGCAGTTACCTTTCCAGGGGCACTGGTTCCTGGAGGTGTGGCCGATGC

AGCCGCGGCATATAAAGCCGCTAAAGCCGGTGCGGGTTTAGGAGGCGTCCCAGG

TGTCGGTGGCCTGGGTGTTAGCGCCGGTGCAGTTGTTCCGCAGCCGGGAGCAGGG

GTTAAACCTGGTAAAGTGCCGGGAGTAGGTCTGCCAGGCGTTTATCCTGGTGGTG

TTTTGCCGGGTGCCCGTTTTCCGGGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGA

GCCGGTGTTAAACCGAAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCCCGG

GAGTTGGCCCGTTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTATCCGATTAA

AGCACCGAAACTGCCCGGCGGTTATGGTCTGCCGTACACAACCGGTAAACTGCCG

TATGGTTATGGCCCGGGTGGAGTTGCGGGTGCAGCAGGTAAAGCGGGTTATCCTA

CCGGAACCGGTGTAGGTCCGCAGtaa

**[0219]** The amino acid sequence of a 19.6 kDa human elastin truncated at the N-terminal is disclosed in SEQ ID NO: 63. The 19.6 kDa truncated elastin has amino acids 2-542 deleted from the full length elastin.

(SEQ ID NO: 63)
QLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAGVPGFGAGADEGV

RRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAAKYGAAVPGVLGG

LGALGGVGIPGGVVGAGPAAAAAAAKAAAKAAQFGLVGAAGLGGLGVGGL

GVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAARPGFGL

SPIFPGGACLGKACGRKRK

**[0220]** The codon optimized polynucleotide sequence encoding the 19.6 kDa truncated human elastin is disclosed in SEQ ID NO: 64

(SEQ ID NO: 64)
CAACTGCGCGCCGCCGCGGGCCTCGGTGCAGGTATTCCGGGGCTGGGTGTC

GGAGTTGGAGTCCCGGGTTTGGGCGTGGGCGCGGGAGTTCCGGGACTGGGA

GTGGGTGCCGGAGTTCCTGGCTTTGGTGCAGGCGCAGATGAAGGTGTTCGT

CGTAGCCTGAGTCCGGAACTGCGTGAAGGTGATCCGAGTAGCAGCCAGCAT

CTGCCGAGCACCCCGAGCAGCCCGCGTGTTCCGGGTGCATTAGCTGCAGCA

AAAGCCGCCAAGTATGGTGCAGCCGTGCCGGGCGTCTTAGGTGGTCTGGGC

GCCCTGGGTGGTGTAGGCATTCCGGGAGGTGTTGTGGGTGCAGGACCGGCC

GCCGCAGCTGCGGCCGCCAAAGCAGCTGCAAAAGCGGCCCAGTTTGGTTTA

GTGGGCGCCGCAGGTTTAGGCGGTTTAGGTGTGGGTGGACTGGGTGTACCT

GGCGTAGGCGGTCTGGGTGGAATTCCGCCCGCAGCGGCCGCGAAAGCGGCA

AAATATGGCGCGGCAGGCCTGGGCGGCGTGCTGGGTGGGGCAGGTCAGTTT

-continued

CCGCTGGGCGGGGTTGCCGCACGTCCGGGATTTGGTCTGAGCCCGATTTTC

CCTGGCGGCGCATGTCTGGGTAAAGCATGTGGTCGTAAACGTAAAtaa

**[0221]** The amino acid sequence of a 11 kDa human elastin truncated at the N-terminal is disclosed in SEQ ID NO: 65. The 11 kDa truncated elastin has amino acids 2-635 deleted from the full length elastin.

(SEQ ID NO: 65)
VPGVLGGLGALGGVGIPGGVVGAGPAAAAAAAKAAAKAAQFGLVGAAGLGG

LGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFPLGGVAAR

PGFGLSPIFPGGACLGKACGRKRK

**[0222]** The codon optimized polynucleotide sequence encoding the 11 kDa truncated human elastin is disclosed in SEQ ID NO: 66

(SEQ ID NO: 66)
GTGCCGGGCGTCTTAGGTGGTCTGGGCGCCCTGGGTGGTGTAGGCATTCCG

GGAGGTGTTGTGGGTGCAGGACCGGCCGCCGCAGCTGCGGCCGCCAAAGCA

GCTGCAAAAGCGGCCCAGTTTGGTTTAGTGGGCGCCGCAGGTTTAGGCGGT

TTAGGTGTGGGTGGACTGGGTGTACCTGGCGTAGGCGGTCTGGGTGGAATT

CCGCCCGCAGCGGCCGCGAAAGCGGCAAAATATGGCGCGGCAGGCCTGGGC

GGCGTGCTGGGTGGGGCAGGTCAGTTTCCGCTGGGCGGGGTTGCCGCACGT

CCGGGATTTGGTCTGAGCCCGATTTTCCCTGGCGGCGCATGTCTGGGTAAA

GCATGTGGTCGTAAACGTAAAtaa

**[0223]** The amino acid sequence of a 7.9 kDa human elastin truncated at the N-terminal is disclosed in SEQ ID NO: 67. The 7.9 kDa truncated elastin has amino acids 2-674 deleted from the full length elastin.

(SEQ ID NO: 67)
QFGLVGAAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGG

AGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK

**[0224]** The codon optimized polynucleotide sequence encoding the 7.9 kDa truncated human elastin is disclosed in SEQ ID NO: 68

(SEQ ID NO: 68)
CAGTTTGGTTTAGTGGGCGCCGCAGGTTTAGGCGGTTTAGGTGTGGGTGGA

CTGGGTGTACCTGGCGTAGGCGGTCTGGGTGGAATTCCGCCCGCAGCGGCC

GCGAAAGCGGCAAAATATGGCGCGGCAGGCCTGGGCGGCGTGCTGGGTGGG

GCAGGTCAGTTTCCGCTGGGCGGGGTTGCCGCACGTCCGGGATTTGGTCTG

AGCCCGATTTTCCCTGGCGGCGCATGTCTGGGTAAAGCATGTGGTCGTAAA

CGTAAAtaa

**[0225]** The amino acid sequence of a 6.3 kDa human elastin truncated at the C-terminal is disclosed in SEQ ID NO: 69. The 6.3 kDa truncated elastin has amino acids 74-761 deleted from the full length elastin.

(SEQ ID NO: 69)
GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLGA

GLGAFPAVTFPGALVPGGVAD

**[0226]** The codon optimized polynucleotide sequence encoding the 6.3 kDa truncated human elastin is disclosed in SEQ ID NO: 70:

(SEQ ID NO: 70)
GGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTTTTTTAT

CCGGGCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCGGGCGGC

AAACCGCTGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGCTTAGGCGCA

GGTCTGGGAGCATTTCCGGCAGTTACCTTTCCAGGGGCACTGGTTCCTGGA

GGTGTGGCCGATtaa

**[0227]** The amino acid sequence of a 4.3 kDa human elastin truncated at the N-terminal is disclosed in SEQ ID NO: 71. The 4.3 kDa truncated elastin has amino acids 2-717 deleted from the full length elastin.

(SEQ ID NO: 71)
GLGGVLGGAGQFPLGGVAARPGFGLSPIFPGGACLGKACGRKRK

**[0228]** The codon optimized polynucleotide sequence encoding the 4.3 kDa truncated human elastin is disclosed in SEQ ID NO: 72

(SEQ ID NO: 72)
GGCCTGGGCGGCGTGCTGGGTGGGGCAGGTCAGTTTCCGCTGGGCGGGGTT

GCCGCACGTCCGGGATTTGGTCTGAGCCCGATTTTCCCTGGCGGCGCATGT

CTGGGTAAAGCATGTGGTCGTAAACGTAAAtaa

Truncated Human Elastin 1 with DsbA Secretion and FLAG Tag

**[0229]** The amino acid sequence of truncated human elastin 1 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 98. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 99 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 98. The elastin nucleotide sequences are nucleotides 58-657 of SEQ ID NO: 99 and the amino acid sequences are amino acids 20-219 of SEQ ID NO: 98. The FLAG nucleotide sequences are nucleotides 658-684 of SEQ ID NO: 99 and the amino acid sequences are amino acids 220-228 of SEQ ID NO: 98.

(SEQ ID NO: 98)
MKKIWLALAGLVLAFSASAGGVPGAIPGGVPGGVFYPGAGLGALGGGALGP

GGKPLKPVPGGLAGAGLGAGLGAFPAVTFPGALVPGGVADAAAAYKAAKAG

AGLGGVPGVGGLGVSAGAVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARF

PGVGVLPGVPTGAGVKPKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAP

KLPGGYGLPYTTGKLGDYKDDDDK

**[0230]** The nucleic acid sequence of truncated human elastin 1 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 99.

(SEQ ID NO: 99)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGCA

TCGGCGGGTGGCGTACCAGGCGCAATTCCTGGGGGTGTCCCAGGCGGTGTT

TTTTATCCGGGCGCCGGTCTTGGCGCACTGGGTGGCGGTGCACTGGGCCCG

GGCGGCAAACCGCTGAAACCGGTACCAGGTGGTTTAGCAGGCGCCGGCTTA

GGCGCAGGTCTGGGAGCATTTCCGGCAGTTACCTTTCCAGGGGCACTGGTT

CCTGGAGGTGTGGCCGATGCAGCCGCGGCATATAAAGCCGCTAAAGCCGGT

GCGGGTTTAGGAGGCGTCCCAGGTGTCGGTGGCCTGGGTGTTAGCGCCGGT

GCAGTTGTTCCGCAGCCGGGAGCAGGGGTTAAACCTGGTAAAGTGCCGGGA

GTAGGTCTGCCAGGCGTTTATCCTGGTGGTGTTTTGCCGGGTGCCCGTTTT

CCGGGCGTTGGTGTTCTTCCAGGCGTGCCGACCGGAGCCGGTGTTAAACCG

AAAGCCCCCGGTGTTGGAGGTGCATTTGCAGGCATCCCGGGAGTTGGCCCG

TTTGGTGGTCCGCAACCTGGGGTTCCGTTAGGTTATCCGATTAAAGCACCG

AAACTGCCCGGCGGTTATGGTCTGCCGTACACAACCGGTAAACTGGGTGAC

TACAAAGACGACGACGACAAAtaa

**[0231]** The polynucleotide of SEQ ID NO: 99 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated elastin was purified as described herein. The purified elastin produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 25 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

Truncated Human Elastin 2 with DsbA Secretion and FLAG Tag

**[0232]** The amino acid sequence of truncated human elastin type 2 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 100. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 101 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 100. The elastin nucleotide sequences are nucleotides 58-657 of SEQ ID NO: 101 and the amino acid sequences are amino acids 20-219 of SEQ ID NO: 100. The FLAG nucleotide sequences are nucleotides 658-684 of SEQ ID NO: 101 and the amino acid sequences are amino acids 220-228 of SEQ ID NO: 100.

(SEQ ID NO: 100)
MKKIWLALAGLVLAFSASAPYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAA

AAKAAAKFGAGAAGVLPGVGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAA

AAKAAKYGAAAGLVPGGPGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIP

GAAVPGVVSPEAAAKAAAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGV

GGIPGVAGVPGVGGVGDYKDDDDK

**[0233]** The nucleic acid sequence of truncated human elastin 2 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 101.

(SEQ ID NO: 101)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGCA

TCGGCGCCGTATGGTTATGGCCCGGGTGGAGTTGCGGGTGCAGCAGGTAAA

GCGGGTTATCCTACCGGAACCGGTGTAGGTCCGCAGGCCGCTGCTGCCGCC

GCCGCAAAAGCAGCGGCTAAATTTGGCGCCGGAGCAGCGGGTGTTCTGCCT

GGAGTTGGTGGTGCGGGCGTGCCAGGGGTACCTGGTGCAATTCCGGGTATT

GGTGGTATTGCCGGTGTCGGCACCCCGGCCGCGGCAGCTGCGGCAGCGGCG

GCTGCCAAAGCTGCTAAATACGGTGCCGCGGCGGGTCTGGTGCCAGGAGGT

CCGGGTTTTGGTCCGGGAGTGGTTGGCGTGCCTGGCGCAGGCGTTCCTGGT

GTGGGCGTTCCAGGTGCAGGGATTCCTGTTGTGCCTGGTGCCGGTATTCCC

GGCGCGGCCGTTCCGGGGGTGGTTAGCCCGGAAGCCGCAGCGAAGGCTGCG

GCAAAGGCAGCAAAGTATGGCGCACGCCCAGGAGTCGGCGTGGGTGGTATC

CCGACCTATGGGGTGGGCGCAGGGGGTTTTCCTGGTTTCGGCGTAGGTGTA

GGAGGTATACCGGGCGTGGCCGGTGTACCAGGGGTTGGTGGCGTCGGTGAC

TACAAAGACGACGACGACAAAtaa

**[0234]** The polynucleotide of SEQ ID NO: 101 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated elastin was purified as described herein. The purified elastin produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 25 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

### Example 6: Effect of Truncated Collagen on Fibroblast Cell Viability, Procollagen Synthesis, and Elastin Synthesis

**[0235]** A human fibroblast cell culture was used to assess the ability of the truncated jellyfish collagen molecule of Example 2 to determine its effect on procollagen, and elastin synthesis. The human fibroblast cell culture was also used to determine the increased viability of the human fibroblast cells after exposure to the truncated jellyfish collagen.

**[0236]** A stock solution of 2% w/w truncated collagen was prepared from the histidine tagged truncated collagen of example 3. Aliquots from the 2% stock truncated collagen solution were then used in the experiments described below.

Preparation of Fibroblasts

**[0237]** Fibroblasts were seeded into the individual wells of a 24-well plate in 0.5 ml of Fibroblast Growth Media (FGM) and incubated overnight at 37±2° C. and 5±1% $CO_2$. On the following day the media was removed via aspiration to eliminate any non-adherent cells and replaced with 0.5 ml of fresh FGM. The cells were grown until confluent, with a media change every 48 to 72 hours. Upon reaching confluency the cells were treated for 24 hours with DMEM supplemented with 1.5% FBS to wash out any effects from the growth factors included in the normal culture media. After the 24-hour wash out period the cells were treated with the truncated jellyfish collagen at specified concentrations dissolved in FGM with 1.5% FBS. Transforming Growth Factor Beta (TGF-β) (20 ng/ml) was used as a positive control for collagen and elastin synthesis. Untreated cells (negative controls) just received DMEM with 1.5% FBS. The cells were incubated for 48 hours and at the end of the incubation period cell culture medium was collected and either stored frozen (−75° C.) or assayed immediately. Materials were tested in triplicate.

MTT Assay

**[0238]** The MTT (3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide, a tetrazole) assay is a colorimetric assay used to determine the metabolic activity of cells. Changes in cell number were assessed via an MTT assay. When cells are exposed to MTT, reduction of MTT by mitochondria in viable cells results in the formation of insoluble purple formazin crystals that are extracted from the cells with isopropanol and quantified spectrophotometrically. Non-living cells cannot reduce MTT and therefore cannot produce the purple formazin crystals. The intensity of the purple color is directly proportional to the number of living cells (metabolically active cells). The intensity of the purple color is directly proportional to the metabolic activity of the cells and is inversely proportional to the toxicity of the test material.

**[0239]** After the 2-day incubation discussed above, the cell culture medium was removed (see above) and the fibroblasts were washed twice with PBS to remove any remaining jellyfish glycogen molecules. After the final wash, 500 μl of DMEM supplemented with 0.5 mg/ml MTT was added to each well and the cells were incubated for 1 hour at 37±2° C. and 5±1% $CO_2$. After the incubation, the DMEM/MTT solution was removed and the cells were washed again once with PBS and then 0.5 ml of isopropyl alcohol was added to the well to extract the purple formazin crystals. Two hundred microliters of the isopropyl extracts was transferred to a 96-well plate and the plate was read at 540 nm using isopropyl alcohol as a blank.

**[0240]** The mean MTT absorbance value for the negative control cells was calculated and used to represent 100% cell viability. The individual MTT absorbance values from the cells undergoing the various treatments were then divided by the mean value for the negative control cells and expressed as a percent to determine the change in cell viability caused by each treatment.

**[0241]** In Tables 1, 2 and 3 of this example, the experiments were performed by using the designated aliquots of the 2% stock truncated collagen solution in the assays. For example, in the samples that tested the "10% Collagen Solution," an aliquot of the 2% truncated collagens in an amount sufficient to provide 10% of the assay volume was used. For a total assay volume of 1.0 ml, 100 μl of the 2% stock truncated collagen solution was used. In Tables 1, 2 and 3, "10% Collagen Solution" is 0.2% collagen, "5% Collagen Solution" is 0.1% collagen, "1% Collagen Solution" is 0.02% collagen, "0.5% Collagen Solution" is 0.01% collagen, "0.1% Collagen Solution" is 0.002% collagen, "0.05% Collagen Solution" is 0.001% collagen, "0.01% Collagen Solution" is 0.0002% collagen, "0.005% Collagen Solution" is 0.0001% collagen, f

**[0242]** The results for the MTT assay are presented in Table 3. The values are presented as the mean percent viability±the deviation from the mean.

TABLE 3

| MTT Assay | |
|---|---|
| Untreated | 100 ± 6.1 |
| 20 ng/ml TGF-B | 110 ± 2.9 |
| 10% Collagen Solution | 131 ± 7.8* |
| 5% Collagen Solution | 140 ± 8.3* |
| 1% Collagen Solution | 116 ± 0.9 |
| 0.5% Collagen Solution | 105 ± 4.8 |
| 0.1% Collagen Solution | 102 ± 1.1 |
| 0.05% Collagen Solution | 106 ± 3.4 |
| 0.01% Collagen Solution | 112 ± 1.9 |
| 0.005% Collagen Solution | 103 ± 3.9 |

*Denotes values that are significantly different from the Untreated group ($p < 0.05$).

**[0243]** The histidine tagged truncated jellyfish collagen showed protective effect by increasing the cell viability of human fibroblast cells. As can be seen in Table 3, the highest value in the MTT assay was observed when the fibroblast cells were exposed to 0.02% to 0.2% truncated jellyfish collagen.

Procollagen Synthesis

**[0244]** Fibroblasts are the main source of the extracellular matrix peptides, including the structural proteins collagen and elastin. Procollagen is a large peptide synthesized by fibroblasts in the dermal layer of the skin and is the precursor for collagen. As the peptide is processed to form a mature collagen protein, the propeptide portion is cleaved off (type I C-peptide). Both the mature collagen protein and the type I C-peptide fragment are then released into the extracellular environment. As collagen is synthesized the type I C-peptide fragment accumulates into the tissue culture medium. Since there is a 1:1 stoichiometric ratio between the two parts of the procollagen peptide, assaying for type I C-peptide will reflect the amount of collagen synthesized. Type 1 C-peptide can be assayed via an ELISA based method.

**[0245]** A series of type I C-peptide standards was prepared ranging from 0 ng/ml to 640 ng/ml. Next, an ELISA microplate was prepared by removing any unneeded strips from the plate frame followed by the addition of 100 μl of peroxidase-labeled anti procollagen type I-C peptide antibody to each well used in the assay. Twenty (20) μl of either sample (collected tissue culture media) or standard was then added to appropriate wells and the microplate was covered and allowed to incubate for 3±0.25 hours at 37° C. After the incubation the wells were aspirated and washed three times with 400 μl of wash buffer. After the last wash was removed 100 μl of peroxidase substrate solution (hydrogen peroxide+tetramethylbenzidine as a chromagen) was added to each well and the plate was incubated for 15±5 minutes at room temperature. After the incubation 100 μl of stop solution (1 N sulfuric acid) was added to each well and the plate was read using a microplate reader at 450 nm.

**[0246]** To quantify the amount of each substance present, a standard curve was generated using known concentrations of each substance. A regression analysis was performed to establish the line that best fits these data points. Absorbance values for the test materials and untreated samples were used to estimate the amount of each substance present in each sample.

**[0247]** The results for the ELISA assays are presented in Table 4.

TABLE 4

Type I Collagen Assay.
The values presented are mean concentration (ng/ml) ± the deviation from the mean.

| Treatment | Type I C-Peptide (ng/ml) |
|---|---|
| Untreated | 1718 ± 94 |
| 20 ng/ml TGF-B | 3028 ± 332* |
| 10% Collagen Solution | 1940 ± 100 |
| 5% Collagen Solution | 2394 ± 125* |
| 1% Collagen Solution | 1773 ± 183 |
| 0.5% Collagen Solution | 1127 ± 19* |
| 0.1% Collagen Solution | 1158 ± 10* |
| 0.05% Collagen Solution | 1416 ± 64 |
| 0.01% Collagen Solution | 1835 ± 404 |
| 0.005% Collagen Solution | 1551 ± 149 |

*Denotes values that are significantly different from the Untreated group ($p < 0.05$).

**[0248]** The truncated histidine tagged jellyfish collagen was observed to have a biphasic effect on collagen synthesis. At the 1%, 5% and the 10% levels, collagen synthesis increased. At the 5% concentration truncated jellyfish collagen significantly increased collagen synthesis with a p-value of less than 0.05.

Elastin Synthesis

**[0249]** Elastin is the main component of a network of elastic fibers that give tissues their ability to recoil after a transient stretch. This protein is released by fibroblasts (soluble elastin) into the extracellular space where it is then cross-linked to other elastin proteins to form an extensive network of fibers and sheets (insoluble elastin). Soluble elastin can be readily measured from cell culture medium via an ELISA based method.

**[0250]** Soluble α-elastin was dissolved in 0.1 M sodium carbonate (pH 9.0) at a concentration of 1.25 μg/ml. 150 μl of this solution was then applied to the wells of a 96-well maxisorp Nunc plate and the plate was incubated overnight at 4° C. On the following day the wells were saturated with PBS containing 0.25% BSA and 0.05% Tween 20. The plate was then incubated with this blocking solution for 1 hour at 37° C. and then washed two times with PBS containing 0.05% Tween 20.

**[0251]** A set of α-elastin standards was generated ranging from 0 to 100 ng/ml. 180 μl of either standard or truncated jellyfish collagen was then transferred to a 650 μl microcentrifuge tube. An anti-elastin antibody solution was prepared (the antibody was diluted 1:100 in PBS containing 0.25% BSA and 0.05% Tween 20) and 20 μl of the solution was added to the tube. The tubes were then incubated overnight at 4±2° C. On the following day, 150 μl was transferred from each tube to the 96-well elastin ELISA plate, and the plate was incubated for 1 hour at room temperature. The plate was then washed 3 times with PBS containing 0.05% Tween 20. After washing, 200 μl of a solution containing a peroxidase linked secondary antibody diluted in PBS containing 0.25% BSA and 0.05% Tween 20 was added, and the plate was incubated for 1 hour at room temperature. After washing the plate three times, 200 μl of a substrate solution was added and the plate was incubated for 10 to 30 minutes in the dark at room temperature. After this final incubation the plate was read at 460 nm using a plate reader.

TABLE 5

The values are also presented as mean concentration (ng/ml) ± deviation from the mean.

| Treatment | Elastin (ng/ml) |
|---|---|
| Untreated | 79 ± 19 |
| 20 ng/ml TGFB1 | 243 ± 35* |
| 10% Collagen Solution | 68 ± 18 |
| 5% Collagen Solution | 99 ± 13 |
| 1% Collagen Solution | 126 ± 21 |
| 0.5% Collagen Solution | 145 ± 21* |
| 0.1% Collagen Solution | 76 ± 14 |
| 0.05% Collagen Solution | 58 ± 6 |
| 0.01% Collagen Solution | 53 ± 5 |
| 0.005% Collagen Solution | 56 ± 24 |

*Denotes values that are significantly different from the Untreated group ($p < 0.05$).

**[0252]** Truncated his-tagged jellyfish collagen significantly increased elastin production when it was used at the 0.5% concentration as shown in Table 5.

### Example 7: Effect of Truncated Collagen on Keratinocyte Proliferation and UVB Protection

**[0253]** A human keratinocyte cell culture model was used to assess the ability of the test materials to exert an effect on cell proliferation. In addition, the impact of the test materials on the cell viability after an exposure to UVB was also assessed.

**[0254]** A stock solution of 2% w/w truncated collagen was prepared from the truncated collagen of example 1. Aliquots from the 2% stock truncated collagen solution was then used in the experiments described below.

**[0255]** This study was conducted in two parts. In the first part cultured keratinocytes were incubated with the test materials for 48 hours, after which changes in the number of viable cells were assessed using an MTT assay. In the second part of the study cultured keratinocytes were irradiated with UVB and then treated with the test materials for 48 hours. At the end of the 48 hour period the number of viable cells was again assessed via an MTT assay.

**[0256]** Changes in cell number of viable cells can be determined using an MTT (3-(4,5-Dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide, a tetrazole) assay. The MTT assay is a colorimetric analysis of the metabolic activity of the cell, which is a reflection of the number of viable cells. Reduction of MTT by mitochondria in viable cells results in the formation of insoluble purple formazin crystals that are extracted from the cells with isopropanol and quantified spectrophotometrically. The intensity of the purple color is directly proportional to the number of metabolically active cells.

Proliferation Assay

**[0257]** For the proliferation assay the keratinocytes were seeded into 96-well plates using without growth factors and incubated for 24 hours at 37±2° C. and 5±1% $CO_2$. After this initial incubation the media was replaced with media supplemented with the test materials. Normal media (with growth factors) was used as a positive control. After the addition of the test materials the cells were cultured for 48 hours as described above. At the end of the incubation period changes in the number of viable cells was determined using an MTT assay.

UVB Protection Assay

**[0258]** For the UVB protection assay the keratinocytes were seeded into 96-well plates using normal media and incubated for 24 hours at 37±2° C. and 5±1% $CO_2$. After this initial incubation the media was replaced with 100 μl of phosphate buffered saline (PBS) and the cells were exposed to UVB (40 mJ/cm2). After the UVB exposure, the PBS was replaced with fresh media supplemented with the test materials (ascorbic acid at 100 μg/ml served as the positive control) and the cells were cultured for 48 hours at 37±2° C. and 5±1% $CO_2$. At the end of the 48 hour incubation cell viability was determined using an MTT assay.

MTT Assay

**[0259]** After the 48-hour incubation the cell culture medium was removed and replaced with 200 μl of culture media supplemented with 0.5 mg/ml MTT. The well plates were incubated for 1 hour at 37±2° C. and 5±1% $CO_2$. After the incubation, the MTT solution was removed and the cells were washed once with phosphate buffered saline and then 200 μl of isopropyl alcohol was added to the well to extract the purple formazin crystals. The 96-well plate was read at 540 nm using isopropyl alcohol as a blank.

**[0260]** The mean absorbance value for the cells not treated with test materials (proliferation assay: Untreated Group) or not exposed to UVB (UVB protection assay: Non-UVB Exposed Group) was calculated and used to represent 100% cell viability. The individual absorbance values from the cells undergoing the various treatments were then divided by the mean absorbance value representing 100% cell viability and expressed as a percent to determine the change in cell viability caused by each treatment.

**[0261]** The results for the Proliferation assay using the his-tagged truncated jellyfish collagen are presented in Table 6. The results for the UVB Protection assay using the his-tagged truncated jellyfish collagen are presented in Table 7. The values for both assays are presented as mean viability±standard deviation.

TABLE 6

| Proliferation Assay | |
|---|---|
| Untreated | 100 ± 3.4 |
| Positive Control (Growth Factors) | 139 ± 3.8* |
| 10% Collagen Solution | 103 ± 9.4 |
| 5% Collagen Solution | 97 ± 7.3 |
| 1% Collagen Solution | 94 ± 5.0 |

TABLE 6-continued

| Proliferation Assay | |
|---|---|
| 0.5% Collagen Solution | 93 ± 7.0 |
| 0.1% Collagen Solution | 95 ± 2.5 |
| 0.05% Collagen Solution | 99 ± 6.0 |
| 0.01% Collagen Solution | 96 ± 6.4 |
| 0.005% Collagen Solution | 96 ± 2.8 |

*Denotes values which are significantly different from the Untreated Group ($p < 0.05$)

TABLE7

| UVB Protection Assay | |
|---|---|
| Non-UVB Exposed | 100 ± 1.7* |
| Untreated | 77 ± 1.8 |
| 100 ug/ml Trolox | 92 ± 2.0* |
| 10% Collagen Solution | 76 ± 8.6 |
| 5% Collagen Solution | 92 ± 3.9* |
| 1% Collagen Solution | 91 ± 2.9* |
| 0.5% Collagen Solution | 100 ± 4.5* |
| 0.1% Collagen Solution | 86 ± 4.8 |
| 0.05% Collagen Solution | 91 ± 1.6* |
| 0.01% Collagen Solution | 83 ± 7.5 |
| 0.005% Collagen Solution | 82 ± 4.7 |

*Denotes values which are significantly different from the Untreated Group ($p < 0.05$)

**[0262]** For the proliferation assay the Untreated group was used to represent 100% cell viability. Values above 100% reflect an increase in the number of viable cells and hence are indicative of cell proliferation. In this study, the test material was not observed to promote cell proliferation.

**[0263]** In addition, the keratinocyte proliferation assay was performed using the truncated collagen of SEQ ID NO: 91. A 1% and 0.5% collagen solution of a 5% stock solution was prepared according to Example 8 and tested. The truncated collagen of SEQ ID NO: 91 had keratinocyte cell viability assay values of 102±2.9 and 102±2.0, respectively. The observed values were statistically significant ($p<0.05$).

**[0264]** In addition to its effects on cell proliferation, the test material was also screened to determine if it had an impact on cell recovery after UVB exposure. In this study, exposure to UVB was observed to result in a significant reduction in the number of viable cells 48 hours post exposure. However, treatment with the test material prevented this decrease in cell viability. The effect was evident within a concentration range between 0.05% and 5% of the test material, with an optimal effect at a concentration of 0.05%. Within this range of concentrations cell viability was significantly greater than the untreated group (with the lone exception of the 0.01% concentration), demonstrating that the material has UVB protective effect. Since this material was added after the UVB exposure it could be acting to reduce the damaging effects of the UVB irradiation, or it could be helping the damaged cells to recover at a faster rate. With respect to the latter, then truncated collagen is beneficial when applied topically to the skin and has a regenerative effect on skin cells damaged by UVB.

**[0265]** In addition, the UVB protection assay was performed using the truncated collagen of SEQ ID NO: 91. A 1% and 0.5% collagen solution of SEQ ID NO: 91 had keratinocyte cell viability assay values of 80±4.6 and 78±2.5, respectively. The observed values were statistically significant ($p<0.05$).

## Example 8: Effect of Truncated Collagen on Thymine Dimer Formation

**[0266]** Upon exposure to ultraviolet radiation the thymine dimer (TT dimer) content in DNA present in cells increases. Increases in TT dimer formation are correlated with skin damage and certain types of cell proliferative diseases including skin cancer.

**[0267]** The polynucleotide of SEQ ID NO: 11 was expressed in the expression system of Example 1 and purified as described in this example. The encoded polypeptide includes the DsbA secretion tag. As the polypeptide is processed through the secretion pathway, the DsbA tag, amino acids 1-24 of SEQ ID NO: 12 is cleaved by the host cell. The truncated collagen without the DsbA secretion tag is provided in SEQ ID NO: 91.

**[0268]** The truncated collagen of SEQ ID NO: 91 was tested to determine if it could reduce TT dimer formation is human epidermal keratinocytes. For this study, the cells were exposed to UVB (25 mJ/cm2). Following the exposures cells were treated with the test materials or Trolox (100 ug/ml) and incubated overnight. On the following day cellular DNA was extracted and assayed for thymine dimer content using an ELISA based method.

**[0269]** Human keratinocytes were seeded into 12-well plates using normal media and incubated for 24 hours at 37±2° C. and 5±1% $CO_2$. After this initial incubation the media was replaced with 100 μl of phosphate buffered saline (PBS) and the cells were exposed to UVB (25 mJ/cm2). After the UVB exposure, the PBS was replaced with fresh media supplemented with the test materials or Trolox (100 μg/ml, this served as the positive control) and the cells were cultured overnight at 37±2° C. and 5±1% $CO_2$. At the end of the incubation cellular DNA was extracted.

**[0270]** After the overnight incubation the cell culture media was removed from the wells and replaced with 200 μl of PBS and 20 μl of Proteinase K. After swirling the plate to mix the PBS and Proteinase K, 200 μl of buffer AL was added to each well. After again swirling the plate to mix the reagents, the plates were incubated for 10 minutes at 55±2° C. After cooling the plate to room temperature, the DNA was precipitated by the addition of 200 μl of 100% ethanol. The precipitated DNA mixtures were then transferred to DNEasy Spin Columns in 2 ml collection tubes and centrifuged at 8,000 RPM for 1 minute. The flow through and collection tubes were discarded, and 500 μl of Wash Buffer One was added to the spin column and the column was placed into a new collection tube and centrifuged at 8,000 RPM for 1 minute. The flow through and collection tube were again discarded, and 500 μl of Wash Buffer Two was added to the spin column and the column was placed into a new collection tube and centrifuged at 14,000 RPM for 3 minutes. The spin column was then placed into a new 1.5 ml centrifuge tube and 110 μl of ultrapure water was added to the column. The column was incubated for 1 minute at room temperature and then centrifuged at 8,000 RPM for 1 minute.

**[0271]** Extracted DNA was quantified via a fluorometric assay. A 2 μl aliquot of the DNA sample was mixed with 100 μl TE buffer in a 96-well plate. A series of DNA standards was also transferred to wells in a 96-well plate (in duplicate). Finally, 100 μl of dilute Cyquant Green dye was added to each well and the fluorescence intensity of each well was determined using an excitation wavelength of 480 nm and an emission wavelength of 520 nm.

**[0272]** Thymine Dimer Detection was determined using an OxiSelect™ UV-Induced DNA Damage ELISA Kit)

**[0273]** Aliquots of genomic DNA samples or standards were converted to single stranded DNA by incubating the samples at 95° C. for 10 minutes and then chilled on ice. 100 µl or each sample or standard was transferred to a DNA binding ELISA plate and incubated overnight at 4° C. On the following day the wells were rinsed once with 100 µl of PBS and then blocked with 150 µl of Assay Diluent for one hour at room temperature. After removing the Assay Diluent, 100 µl of anti-CPD antibody was added to each well and the plate was incubated for one hour at room temperature. After this incubation, the plate was washed three times with 250 µl of wash buffer per well, and then 150 µl of Blocking Reagent was added to the plate. The plate will be blocked again for one hour at room temperature, and then washed three times as described before. 100 µl of Secondary Antibody was then added to each well and the plate was incubated for 1 hour at room temperature. After washing the plate again, 100 µl of substrate was added to each well and the plate was incubated for 5-20 minutes to allow for color generation in the plate. The color generation reaction was stopped by the addition of 100 µl of stop solution and the plate was read at 460 nm using a plate reader.

**[0274]** To quantify the amount of DNA present, a standard curve was generated using known concentrations of DNA and their respective fluorescence intensity (measured in RFUs or relative fluorescence units). A regression analysis was performed to establish the line that best fits these data points. The Relative Fluorescence Units (RFU) for each unknown sample was then used to estimate the amount of DNA.

**[0275]** A series of DNA standards with known amounts of thymine dimer content were used to generate a standard curve. This standard curve was used to determine the amount of DNA damage in the sample DNA. Means for each treatment group were calculated and compared using an ANOVA. In table 8 and FIG. **5**, a standard 5% collagen solution (5 g truncated collagen in 95 ml deionized water was further diluted with phosphate buffered saline (PBS) to the indicated percent solution.

TABLE 8

Thymine Dimer Assay

| Treatment | Thymine Dimer, ng/ml |
|---|---|
| Non-UVB Exposed | 0.1 ± 0.2* |
| Untreated | 10.7 ± 1.4* |
| 100 µg/ml Trolox | 1.6 ± 0.3* |
| 5% Truncated Collagen | 3.5 ± 0.3* |
| 1% Truncated Collagen | 5.5 ± 1.0* |
| 0.5% Truncated Collagen | 8.9 ± 0.8 |
| 0.1% Truncated Collagen | 9.2 ± 0.9 |
| 0.05% Truncated Collagen | 9.2 ± 0.3 |

*Denotes values which are statistically significantly different from untreated with P < 0.05

**[0276]** Table 8 shows that the 5% and the 1% truncated collagen solution reduced TT dimer formation with statistical significance ($p<0.05$). The data is presented graphically in FIG. **5**.

**[0277]** The experiment was repeated with a different lot of truncated collagen (SEQ ID NO: 91). The amount of TT dimer in ng/ml in non-UVB exposed cells was 1.3±1.2, untreated cells was 18.1±0.4, 100 µg/ml Trolox treated cells was 7.9±0.3, 5% collagen was 13.1±0.2, and 1% collagen was 17.4±0.7. The reduction in TT dimer formation for non-UVB exposed cells, Trolox treated cells, 5% collagen treated cells and 1% collagen treated cells was statistically significant compared to untreated cells ($p<0.05$).

## Example 9: Human Collagens

### Truncated Human Collagen Type 21 Alpha 1

**[0278]** A truncated human collagen type 21 alpha 1 without a His tag, linker, and thrombin cleavage site is disclosed below. The codon-optimized nucleotide sequence encoding this collagen and the amino acid sequence are disclosed below. In SEQ ID NOs: 73 and 74, the DsbA secretion tag is encoded by nucleotides 1-72 and encodes amino acids 1-24. In SEQ ID NOs: 73 and 74, the truncated collagen sequence is encoded by nucleotides 73-633 and encodes amino acids 25-211.

**[0279]** The codon-optimized nucleotide sequence encoding this collagen is provided in SEQ ID NO: 73.

(SEQ ID NO: 73)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGCA

TCGGCGGCGCAGTATGAAGATGCAGGTTTTCCGGGTCTGCCTGGTCCGGCA

GGCGAACCGGGTCGTCATGGTAAAGATGGTCTGATGGGTAGTCCGGGTTTT

AAAGGTGAAGCAGGTTCACCGGGTGCACCTGGTCAGGATGGCACCCGTGGT

GAACCGGGTATTCCGGGATTTCCGGGTAATCGTGGCCTGATGGGTCAGAAA

GGTGAAATTGGTCCGCCTGGTCAGCAGGGTAAAAAAGGCGCACCGGGTATG

CCAGGACTGATGGGTTCAAATGGCAGTCCGGGTCAGCCAGGCACACCGGGT

TCAAAAGGTAGCAAAGGCGAACCTGGTATTCAGGGTATGCCTGGTGCAAGC

GGTCTGAAAGGCGAGCCAGGTGCCACCGGTTCTCCGGGTGAACCAGGTTAT

ATGGGTCTGCCAGGTATCCAAGGCAAAAAAGGTGATAAAGGTAATCAGGGC

GAAAAAGGCATTCAGGGCCAGAAAGGCGAAAATGGCCGTCAGGGTATTCCA

GGCCAGCAGGGCATCCAGGGTCATCATGGTGCAAAAGGTGAACGTGGTGAA

AAGGGCGAACCAGGTGTTCGTtaa

**[0280]** The amino acid sequence is disclosed in SEQ ID NO: 74.

(SEQ ID NO: 74)
MKKIWLALAGLVLAFSASAAQYEDAGFPGLPGPAGEPGRHGKDGLMGSPGF

KGEAGSPGAPGQDGTRGEPGIPGFPGNRGLMGQKGEIGPPGQQGKKGAPGM

PGLMGSNGSPGQPGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGY

MGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGIPGQQGIQGHHGAKGERGE

KGEPGVR

**[0281]** The codon-optimized nucleotide sequence encoding the truncated human collagen type 21 alpha 1 without the DsbA secretion tag collagen is provided in SEQ ID NO: 75.

(SEQ ID NO: 75)
TGCAGGTTTTCCGGGTCTGCCTGGTCCGGCAGGCGAACCGGGTCGTCATG

GTAAAGATGGTCTGATGGGTAGTCCGGGTTTTAAAGGTGAAGCAGGTTCA

CCGGGTGCACCTGGTCAGGATGGCACCCGTGGTGAACCGGGTATTCCGGG

ATTTCCGGGTAATCGTGGCCTGATGGGTCAGAAAGGTGAAATTGGTCCGC

CTGGTCAGCAGGGTAAAAAAGGCGCACCGGGTATGCCAGGACTGATGGG

TTCAAATGGCAGTCCGGGTCAGCCAGGCACACCGGGTTCAAAAGGTAGCA

AAGGCGAACCTGGTATTCAGGGTATGCCTGGTGCAAGCGGTCTGAAAGGC

GAGCCAGGTGCCACCGGTTCTCCGGGTGAACCAGGTTATATGGGTCTGCC

AGGTATCCAAGGCAAAAAAGGTGATAAAGGTAATCAGGGCGAAAAAGGC

ATTCAGGGCCAGAAAGGCGAAAATGGCCGTCAGGGTATTCCAGGCCAGC

AGGGCATCCAGGGTCATCATGGTGCAAAAGGTGAACGTGGTGAAAAGGG

CGAACCAGGTGTTCGTtaa

**[0282]** The amino acid sequence of truncated human collagen type 21 alpha 1 without the DsbA secretion tag is disclosed in SEQ ID NO: 76.

(SEQ ID NO: 76)
AGFPGLPGPAGEPGRHGKDGLMGSPGFKGEAGSPGAPGQDGTRGEPGIPG

FPGNRGLMGQKGEIGPPGQQGKKGAPGMPGLMGSNGSPGQPGTPGSKGSK

GEPGIQGMPGASGLKGEPGATGSPGEPGYMGLPGIQGKKGDKGNQGEKGI

QGQKGENGRQGIPGQQGIQGHHGAKGERGEKGEPGVR

**[0283]** A truncated human collagen type 1 alpha 2 without a His tag, linker, and thrombin cleavage site is disclosed below. The codon-optimized nucleotide sequence and the amino acid sequences are disclosed below. In SEQ ID NOs: 78 and 79, The DsbA secretion tag is encoded by nucleotides 1-72 and encodes amino acids 1-24. The truncated collagen sequence is encoded by nucleotides 73-636 and encodes amino acids 25-212.

**[0284]** The codon-optimized nucleotide sequence encoding this collagen is provided in SEQ ID NO: 77.

(SEQ ID NO: 77)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGC

ATCGGCGGCGCAGTATGAAGATATGGGTCCGCCTGGTAGCCGTGGTGCAA

GTGGTCCGGCAGGCGTTCGTGGTCCGAATGGTGATGCAGGTCGTCCGGGT

GAACCGGGTCTGATGGGTCCTCGTGGTCTGCCTGGTTCACCGGGTAATAT

TGGTCCTGCAGGTAAAGAAGGTCCGGTTGGTCTGCCAGGTATTGATGGCC

GTCCGGGTCCGATTGGTCCAGCCGGTGCACGTGGTGAACCTGGCAATATT

GGTTTTCCGGGTCCTAAAGGTCCGACCGGTGATCCGGGTAAAAATGGTGA

TAAAGGTCATGCAGGTCTGGCAGGCGCACGCGGTGCACCTGGTCCGGATG

GTAATAATGGTGCACAGGGTCCACCGGGTCCGCAGGGTGTTCAAGGTGGT

AAAGGCGAACAGGGTCCTGCCGGTCCTCCGGGTTTTCAGGGACTGCCTGG

TCCGAGCGGTCCTGCGGGTGAAGTTGGTAAACCTGGTGAACGCGGTCTGC

-continued
ATGGTGAATTTGGCCTGCCTGGGCCTGCAGGTCCGCGTGGCGAACGTGGT

CCGCCAGGTGAAAGCGGTGCAGCAGGTCCGACAGGTtaa

**[0285]** The amino acid sequence is disclosed in SEQ ID NO: 78.

(SEQ ID NO: 78)
MKKIWLALAGLVLAFSASAAQYEDMGPPGSRGASGPAGVRGPNGDAGRPG

EPGLMGPRGLPGSPGNIGPAGKEGPVGLPGIDGRPGPIGPAGARGEPGNI

GFPGPKGPTGDPGKNGDKGHAGLAGARGAPGPDGNNGAQGPPGPQGVQGG

KGEQGPAGPPGFQGLPGPSGPAGEVGKPGERGLHGEFGLPGPAGPRGERG

PPGESGAAGPTG

**[0286]** The nucleic acid sequence of truncated human collagen type 1 alpha 2(1) without the DsbA secretion tag is disclosed in SEQ ID NO: 79.

(SEQ ID NO: 79)
ATGGGTCCGCCTGGTAGCCGTGGTGCAAGTGGTCCGGCAGGCGTTCGTGG

TCCGAATGGTGATGCAGGTCGTCCGGGTGAACCGGGTCTGATGGGTCCTC

GTGGTCTGCCTGGTTCACCGGGTAATATTGGTCCTGCAGGTAAAGAAGGT

CCGGTTGGTCTGCCAGGTATTGATGGCCGTCCGGGTCCGATTGGTCCAGC

CGGTGCACGTGGTGAACCTGGCAATATTGGTTTTCCGGGTCCTAAAGGTC

CGACCGGTGATCCGGGTAAAAATGGTGATAAAGGTCATGCAGGTCTGGCA

GGCGCACGCGGTGCACCTGGTCCGGATGGTAATAATGGTGCACAGGGTCC

ACCGGGTCCGCAGGGTGTTCAAGGTGGTAAAGGCGAACAGGGTCCTGCCG

GTCCTCCGGGTTTTCAGGGACTGCCTGGTCCGAGCGGTCCTGCGGGTGAA

GTTGGTAAACCTGGTGAACGCGGTCTGCATGGTGAATTTGGCCTGCCTGG

GCCTGCAGGTCCGCGTGGCGAACGTGGTCCGCCAGGTGAAAGCGGTGCAG

CAGGTCCGACAGGTtaa

**[0287]** The amino acid sequence of truncated human collagen type 1 alpha 2(1) without the DsbA secretion tag is disclosed in SEQ ID NO: 80.

(SEQ ID NO: 80)
MGPPGSRGASGPAGVRGPNGDAGRPGEPGLMGPRGLPGSPGNIGPAGKEG

PVGLPGIDGRPGPIGPAGARGEPGNIGFPGPKGPTGDPGKNGDKGHAGLA

GARGAPGPDGNNGAQGPPGPQGVQGGKGEQGPAGPPGFQGLPGPSGPAGE

VGKPGERGLHGEFGLPGPAGPRGERGPPGESGAAGPTG

## Truncated Human Collagen Type 1 Alpha 2 (2)

**[0288]** A truncated human collagen type 1 alpha 2 without a His tag, linker, and thrombin cleavage site is disclosed below. The codon-optimized nucleotide sequence and the amino acid sequences are disclosed below. in SEQ ID NO: 82 and 83, the DsbA secretion tag is encoded by nucleotides 1-72 and encodes amino acids 1-24. The truncated collagen sequence is encoded by nucleotides 73-609 and encodes amino acids 25-203.

**[0289]** The codon-optimized nucleotide sequence encoding this collagen is provided in SEQ ID NO: 81.

(SEQ ID NO: 81)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGC

ATCGGCGGCGCAGTATGAAGATGGTTTTCAGGGTCCTGCCGGTGAACCGG

GTGAACCTGGTCAGACAGGTCCGGCAGGCGCACGTGGTCCTGCAGGTCCT

CCTGGTAAAGCCGGTGAAGATGGTCATCCGGGTAAACCGGGTCGTCCTGG

TGAACGTGGTGTTGTTGGTCCGCAGGGTGCCCGTGGTTTTCCGGGTACTC

CGGGTCTGCCAGGTTTTAAAGGTATTCGTGGTCATAATGGTCTGGATGGT

CTGAAAGGTCAGCCTGGTGCACCGGGTGTTAAAGGTGAACCAGGTGCTCC

GGGTGAAAATGGCACACCGGGTCAGACCGGTGCGCGTGGTCTGCCTGGCG

AACGCGGTCGTGTTGGTGCACCTGGTCCAGCCGGTGCACGCGGTAGTGAT

GGTAGCGTTGGTCCGGTTGGTCCAGCGGGTCCGATTGGTAGCGCAGGTCC

ACCGGGTTTTCCAGGCGCACCGGGTCCGAAAGGTGAAATTGGTGCAGTTG

GTAATGCAGGCCCTGCCGGTCCAGCAGGACCGCGTGGTGAAGTTGGCCTG

CCTGGTCTGtaa

**[0290]** The amino acid sequence is disclosed in SEQ ID NO: 82.

(SEQ ID NO: 82)
MKKIWLALAGLVLAFSASAAQYEDGFQGPAGEPGEPGQTGPAGARGPAGP

PGKAGEDGHPGKPGRPGERGVVGPQGARGFPGTPGLPGFKGIRGHNGLDG

LKGQPGAPGVKGEPGAPGENGTPGQTGARGLPGERGRVGAPGPAGARGSD

GSVGPVGPAGPIGSAGPPGFPGAPGPKGEIGAVGNAGPAGPAGPRGEVGL

PGL

**[0291]** The nucleic acid sequence of truncated human collagen type 1 alpha 2(2) without the DsbA secretion tag is disclosed in SEQ ID NO: 83.

(SEQ ID NO: 83)
GGTTTTCAGGGTCCTGCCGGTGAACCGGGTGAACCTGGTCAGACAGGTCC

GGCAGGCGCACGTGGTCCTGCAGGTCCTCCTGGTAAAGCCGGTGAAGATG

GTCATCCGGGTAAACCGGGTCGTCCTGGTGAACGTGGTGTTGTTGGTCCG

CAGGGTGCCCGTGGTTTTCCGGGTACTCCGGGTCTGCCAGGTTTTAAAGG

TATTCGTGGTCATAATGGTCTGGATGGTCTGAAAGGTCAGCCTGGTGCAC

CGGGTGTTAAAGGTGAACCAGGTGCTCCGGGTGAAAATGGCACACCGGGT

CAGACCGGTGCGCGTGGTCTGCCTGGCGAACGCGGTCGTGTTGGTGCACC

TGGTCCAGCCGGTGCACGCGGTAGTGATGGTAGCGTTGGTCCGGTTGGTC

CAGCGGGTCCGATTGGTAGCGCAGGTCCACCGGGTTTTCCAGGCGCACCG

GGTCCGAAAGGTGAAATTGGTGCAGTTGGTAATGCAGGCCCTGCCGGTCC

AGCAGGACCGCGTGGTGAAGTTGGCCTGCCTGGTCTGtaa

**[0292]** The amino acid sequence of truncated human collagen type 1 alpha 2(2) without the DsbA secretion tag is disclosed in SEQ ID NO: 84.

(SEQ ID NO: 84)
GFQGPAGEPGEPGQTGPAGARGPAGPPGKAGEDGHPGKPGRPGERGVVGP

QGARGFPGTPGLPGFKGIRGHNGLDGLKGQPGAPGVKGEPGAPGENGTPG

QTGARGLPGERGRVGAPGPAGARGSDGSVGPVGPAGPIGSAGPPGFPGAP

GPKGEIGAVGNAGPAGPAGPRGEVGLPGL

**[0293]** The polynucleotides of SEQ ID NO: 73, 77 or 81 were subcloned in vector pET28a as described herein to prepare a transformation vector. Host cells were transformed with the vector the polynucleotides were expressed as described in Example 2.

**[0294]** After the fermentation was completed, the truncated human collagen was purified from the fermentation broth using the procedures disclosed in Example 3. The purified truncated human collagens were analyzed using SDS-PAGE and HPLC as disclosed in Example 3.

**[0295]** All three truncated human collagens ran at the expected molecular weights in the SDS-PAGE analysis. In analyzing the truncated human collagens using HPLC, a standard curve using the jellyfish collagen of Example 3 was utilized. The retention times of the human collagens were slightly different than the jellyfish collagen. The retention time of SEQ ID NO: 76 was 5.645 minutes, the retention time of SEQ ID NO: 80 was 5.631 minutes, and SEQ ID NO: 84 ran at two peaks and the retention times were 5.531 and 5.7 minutes.

### Truncated Human Collagen Type 1 Alpha 2 Truncation 5 with DsbA Secretion and FLAG Tag

**[0296]** The amino acid sequence of truncated human collagen type 1 alpha 2 truncation 5 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 92. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 93 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 92. The collagen nucleotide sequences are nucleotides 58-657 of SEQ ID NO: 93 and the amino acid sequences are amino acids 20-219 of SEQ ID NO: 92. The FLAG nucleotide sequences are nucleotides 658-684 of SEQ ID NO: 93 and the amino acid sequences are amino acids 220-228.

(SEQ ID NO: 92)
MKKIWLALAGLVLAFSASAGDQGPVGRTGEVGAVGPPGFAGEKGPSGEAG

TAGPPGTPGPQGLLGAPGILGLPGSRGERGLPGVAGAVGEPGPLGIAGPP

GARGPPGAVGSPGVNGAPGEAGRDGNPGNDGPPGRDGQPGHKGERGYPGN

IGPVGAAGAPGPHGPVGPAGKHGNRGETGPSGPVGPAGAVGPRGPSGPQG

IRGDKGEPGEKGPRGLPGLGDYKDDDDK

**[0297]** The nucleic acid sequence of truncated human collagen type 1 alpha 2 truncation 5 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 93.

(SEQ ID NO: 93)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGC

ATCGGCGGGTGATCAGGGTCCGGTTGGTCGTACCGGTGAAGTTGGTGCAG

TCGGGCCGCCGGGTTTTGCGGGTGAAAAAGGCCCGTCAGGTGAAGCAGGC

ACCGCTGGCCCTCCTGGCACGCCTGGCCCACAGGGTTTACTGGGCGCACC

-continued

TGGAATTCTGGGACTGCCGGGCAGCCGTGGAGAACGCGGTTTACCAGGTG

TTGCCGGTGCCGTTGGTGAACCTGGTCCACTGGGCATTGCAGGGCCGCCT

GGCGCACGGGGACCGCCTGGTGCTGTTGGTAGTCCGGGTGTGAATGGTGC

TCCGGGTGAAGCCGGTCGTGACGGTAATCCGGGAAATGACGGCCCGCCAG

GCCGCGATGGTCAGCCGGGTCATAAAGGTGAGCGTGGTTACCCAGGTAAT

ATTGGTCCAGTCGGTGCCGCCGGTGCGCCGGGTCCTCATGGCCCTGTCGG

TCCAGCCGGTAAACATGGTAATCGCGGTGAGACAGGTCCGTCAGGACCAG

TGGGCCCTGCTGGCGCAGTCGGTCCGCGCGGGCCGAGTGGCCCTCAGGGT

ATTCGTGGCGATAAAGGGGAACCGGGCGAAAAAGGGCCGCGGGGTCTGCC

AGGCCTGGGTGACTACAAAGACGACGACGACAAAtaa

**[0298]** The polynucleotide of SEQ ID NO: 93 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated collagen was purified as described herein. The purified collagen produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 100 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

### Truncated Human Collagen Type 1 Alpha 2 Truncation 6 with DsbA Secretion and FLAG Tag

**[0299]** The amino acid sequence of truncated human collagen type 1 alpha 2 truncation 6 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 94. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 95 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 94. The collagen nucleotide sequences are nucleotides 58-657 of SEQ ID NO: 95 and the amino acid sequences are amino acids 20-219 of SEQ ID NO: 94. The FLAG nucleotide sequences are nucleotides 658-684 of SEQ ID NO: 95 and the amino acid sequences are amino acids 220-228 of SEQ ID NO: 94.

(SEQ ID NO: 94)
MKKIWLALAGLVLAFSASAKGHNGLQGLPGIAGHHGDQGAPGSVGPAGPR

GPAGPSGPAGKDGRTGHPGTVGPAGIRGPQGHQGPAGPPGPPGPPGPPGV

SGGGYDFGYDGDFYRADQPRSAPSLRPKDYEVDATLKSLNNQIETLLTPE

GSRKNPARTCRDLRLSHPEWSSGYYWIDPNQGCTMDAIKVYCDFSTGETC

IRAQPENIPAKNWYRSSKDGDYKDDDDK

**[0300]** The nucleic acid sequence of truncated human collagen type 1 alpha 2 truncation 6 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 95.

(SEQ ID NO: 95)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGCGC

ATCGGCGAAAGGTCACAATGGACTGCAAGGCCTGCCAGGTATTGCAGGTC

ATCATGGTGATCAAGGTGCCCCGGGAAGCGTTGGTCCGGCGGGGCCGAGA

GGCCCTGCGGGACCTTCAGGTCCGGCAGGCAAAGATGGTCGGACAGGCCA

TCCGGGCACCGTTGGCCCTGCAGGAATTCGTGGACCGCAGGGTCATCAGG

-continued
GACCTGCTGGTCCGCCAGGTCCCCCGGGCCCTCCGGGACCACCGGGTGTT

AGTGGTGGTGGTTATGATTTTGGCTATGATGGTGATTTTTATCGTGCAGA

TCAGCCGCGTAGCGCACCGAGCCTGCGTCCTAAAGATTATGAAGTTGATG

CAACCCTGAAAAGCCTGAATAATCAGATTGAAACACTGCTGACACCGGAA

GGTAGCCGTAAAAATCCGGCCCGTACCTGTCGTGATCTGCGTCTGAGCCA

CCCGGAATGGAGCAGCGGTTATTATTGGATTGATCCGAATCAAGGTTGTA

CCATGGATGCAATTAAAGTTTATTGTGATTTTAGCACAGGTGAAACATGT

ATCCGTGCACAGCCGGAAAATATTCCGGCCAAAAATTGGTATCGTAGTAG

CAAAGATGGTGACTACAAAGACGACGACGACAAAtaa

**[0301]** The polynucleotide of SEQ ID NO: 94 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated collagen was purified as described herein. The purified collagen produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 25 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

### Truncated Human Collagen Type 1 Alpha 2 Truncation 7 with DsbA Secretion and FLAG Tag

**[0302]** The amino acid sequence of truncated human collagen type 1 alpha 2 truncation 7 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 96. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 97 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 96. The collagen nucleotide sequences are nucleotides 58-759 of SEQ ID NO: 96 and the amino acid sequences are amino acids 20-253 of SEQ ID NO: 96. The FLAG nucleotide sequences are nucleotides 760-786 of SEQ ID NO: 97 and the amino acid sequences are amino acids 254-262 of SEQ ID NO: 96.

(SEQ ID NO: 96)
MKKIWLALAGLVLAFSASAYEVDATLKSLNNQIETLLTPEGSRKNPARTC

RDLRLSHPEWSSGYYWIDPNQGCTMDAIKVYCDFSTGETCIRAQPENIPA

KNWYRSSKDKKHVWLGETINAGSQFEYNVEGVTSKEMATQLAFMRLLANY

ASQNITYHCKNSIAYMDEETGNLKKAVILQGSNDVELVAEGNSRFTYTVL

VDGCSKKTNEWGKTIIEYKTNKPSRLPFLDIAPLDIGGADQEFFVDIGPV

CFKGDYKDDDDK

**[0303]** The nucleic acid sequence of truncated human collagen type 1 alpha 2 truncation 7 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 97.

(SEQ ID NO: 97)
TGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAGC

GCATCGGCGTATGAAGTTGATGCAACCCTGAAAAGCCTGAATAATCA

GATTGAAACACTGCTGACACCGGAAGGTAGCCGTAAAAATCCGGCCC

GTACCTGTCGTGATCTGCGTCTGAGCCACCCGGAATGGAGCAGCGGT

TATTATTGGATTGATCCGAATCAAGGTTGTACCATGGATGCAATTAA

AGTTTATTGTGATTTTAGCACAGGTGAAACATGTATCCGTGCACAGC

-continued

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CGGAAAATATTCCGGCCAAAAATTGGTATCGTAGTAGCAAAGATAAA

AAACATGTGTGGCTGGGTGAAACCATTAATGCAGGTAGCCAGTTTGA

ATACAATGTTGAAGGTGTTACCAGCAAAGAAATGGCAACACAGCTGG

CATTTATGCGTCTGCTGGCAAATTATGCAAGCCAGAATATTACATAT

CATTGTAAAAATAGCATTGCATATATGGATGAAGAAACCGGTAATCT

GAAAAAAGCAGTTATTCTGCAGGGTAGCAATGATGTTGAACTGGTTG

CCGAAGGTAATAGCCGTTTTACATATACCGTTCTGGTTGATGGTTGT

AGCAAAAAAACCAATGAATGGGGTAAAACCATCATTGAATATAAAAC

CAACAAACCGAGCCGTCTGCCGTTTCTGGATATCGCTCCGCTGGATA

TTGGTGGTGCCGATCAGGAATTTTTTGTCGATATCGGTCCTGTGTGT

TTTAAAGGTGACTACAAAGACGACGACGACAAAtaa
```

**[0304]** The polynucleotide of SEQ ID NO: 97 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated collagen was purified as described herein. The purified collagen produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 30 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

### Example 10: Protective Effect of Truncated Human Collagen on Fibroblasts

**[0305]** The effect of truncated human collagen on fibroblast cell viability, procollagen synthesis, and elastin Synthesis is determined according to the methods of Example 6.

**[0306]** The effect of truncated human collagen on Keratinocyte proliferation and UVB protection is determined according to the methods of Example 7.

**[0307]** The effect of truncated collagen on thymine dimer formation after exposure to UV radiation is determined according to the methods of Example 8.

**[0308]** It is understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and scope of the appended claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference in their entirety for all purposes.

### Example 11: Effect of Truncated Collagen on Inflammatory Cytokines

**[0309]** Keratinocytes and dermal fibroblasts play an important role in the immune response of the skin. In response to irritating chemicals or UV radiation (pro-inflammatory/pro-irritation stimuli), keratinocytes can release a vast array of cytokines. These cytokines are thought to help engage immune cells to the site of inflammation. Cytokines released by the keratinocytes include TNFα, IL-1α, IL-1β, IL-3, IL-6, IL-7, IL-8, IL-10, IL-18, and IL-1RA.

**[0310]** The testing model used for this study was the MatTek EpiDerm. This skin model consists of normal human-derived epidermal keratinocytes that have been cultured to form a multilayered, highly differentiated model of the human epidermis. Ultrastructural analysis has revealed the presence of keratohyalin granules, tonofilament bundles, desmosomes, and a multi-layered stratum corneum containing intercellular lamellar lipid layers arranged in patterns characteristic of in vivo epidermis. Markers of mature epidermis specific differentiation such as pro-filaggrin, the K1/K10 cytokeratin pair, involucrin, and type I epidermal transglutaminase have been localized in this model. The MatTek EpiDerm is also mitotically and metabolically active.

**[0311]** The MatTek EpiDerm tissues were used to assess the ability of various test materials to inhibit the release the inflammatory mediator IL-1α. Test materials were compared to an over the counter topical hydrocortisone preparation (positive control) as well as to untreated tissues (negative control 1) and untreated, non-inflamed tissues (negative control 2). This test was also used to assess the viability of the tissues after exposure to the test materials.

**[0312]** IL-1α, IL-6 and IL-8 are synthesized and stored in keratinocytes and have been identified as a mediators of skin irritation and inflammation. Release of these cytokines can be directly measured in tissue culture media via a colorimetric based enzyme linked immunosorbent assay (ELISA). Briefly, antibodies covalently linked to a solid support will bind IL-1α, IL-6 or IL-8 present in spent culture media samples. A second antibody that is covalently attached to an acetylcholinesterase enzyme will in turn detect the specific bound cytokines. Upon addition of an appropriate color substrate the acetylcholinesterase enzyme will generate a colored end product that can be measured spectrophotometrically.

**[0313]** MatTek EpiDerm Tissues were purchased from MatTek corporation and were stored at 4° C. until used. Prior to use, the tissues to be used were removed from the agarose-shipping tray and placed into a 6-well plate containing 0.9 ml of hydrocortisone free assay medium (37±2° C.). The tissues were allowed to incubate overnight at 37±2° C. and 5±1% $CO_2$. After this initial incubation, the assay medium was replaced with 0.9 ml of fresh hydrocortisone free medium (37±2° C.). Three tissues were prepared for each test material.

**[0314]** An inflammatory response in the tissues was initiated via UV irradiation (UVB). A UV lamp was used to give a 300 mJ/cm$^2$ dose of UVB radiation to the tissues. Immediately after the application of the inflammatory stimuli 50 μl or mg of test material was applied directly onto the surface of the tissue. An over the counter hydrocortisone cream was used as a positive control. For a negative control tissues were exposed to the inflammatory stimuli but were not treated with any type of anti-inflammatory material. One additional set of tissues was left without exposure to the inflammatory stimuli to provide a baseline measurement for the cytokines. The tissues were incubated at 37±2° C. and 5±1% $CO_2$ for 24 hours after exposure to the inflammatory stimuli. After the 24-hour incubation the cell culture medium was collect and stored at −75° C. until analyzed for cytokines.

**[0315]** The ELISA plates were prepared by diluting the appropriate capture antibody in PBS. Next, 100 μl of the diluted capture antibody was added to the wells of a 96-well ELISA plate and the plate was incubated overnight at room temperature. On the following day the plate was washed three times with 300 μl wash buffer (0.05% Tween 20 in PBS) and then blocked by adding 300 μl of blocking buffer (1% BSA in PBS) to each well. The plate was incubated with the blocking buffer for at least one hour. After the incubation the blocking buffer was removed and the plate was washed three times as described above.

**[0316]** A series of standards was prepared and 100 µl of each of these standards was dispensed into two wells (duplicates) in the appropriate 96-well plate. Subsequently, 100 µl of each sample was added to additional wells and the plate was incubated for two hours at room temperature. After the incubation the plate was washed three times as described above. Once the last wash was removed, 100 µl of a biotin conjugated detection antibody was added. After incubating the plate for two hours at room temperature the plate was washed again as described above. 100 µl of HRP-streptavidin was then added to each well and the plate was incubated for 20 minutes at room temperature. Once the last wash was removed, 100 µl of substrate solution (hydrogen peroxide+tetramethylbenzidine as a chromagen) was added to each well. Once a sufficient level of color development had occurred, 50 µl of stop solution (2N sulfuric acid) was added to each well and the plate was read at 460 nm.

**[0317]** After the 24 hour incubation, the tissues were rinsed twice with at least 100 µl of phosphate buffered saline to remove the test material and then transferred to a 6-well plate containing 1.0 ml of assay medium supplemented with MTT (1 mg/ml) and allowed to incubate for 3±0.25 hours at 37±2° C. and 5±1% $CO_2$. After the incubation, the tissues were rinsed at least twice with 100 µl of phosphate buffered saline, blotted dry, and then placed into a 24-well plate containing 2 ml of isopropanol per well. The 24-well plate was covered and allowed to incubate at room temperature for at least 2 hours on a rocking platform to extract the reduced MTT from the tissues. After the extraction, a 200 µl sample of the isopropanol/MTT mixture was transferred to a 96-well plate and the absorbance of the sample was read at 540 nm with a plate reader using 200 µl of isopropanol as the blank. The MTT assay is described in Example 6 herein. The cell viability results of the MTT assay were similar to the results obtained in Example 6

**[0318]** The results of the IL-1a assay are shown in Table 9 below. A 2% stock solution of the jellyfish collagen of SEQ ID NO: 91 is Sample 4 and Sample 3 is a 2% stock solution of the truncated jellyfish collagen of SEQ ID NO: 10. In Table 9 below, the indicated percentage is the percent dilution of the stock solution used for the test. For example, the 1% Sample 4 treatment is a 1% solution of the 2% stock truncated collagen solution. The untreated cells produced 18.2 pg/ml of Il-1a. Upon treatment with truncated collagen, all samples showed decreases in Il-1a production. The 1% Sample 4 treatment reduced IL-1A production to 13.4 pg/ml, which is significant with a p value of less than 0.05. The decrease in IL-1a production indicates that the truncated collagen has anti-inflammatory effects.

TABLE 9

IL-1a Assay

| Treatment | Il-1a pg/ml |
|---|---|
| Non-UVB Exposed | 4.9 ± 2.1 |
| Untreated | 18.2 ± 1.4 |
| 1% Hydrocortisone | 6.7 ± 0.6 |
| 5% Sample 4 | 18.1 ± 1.1 |
| 1% Sample 4 | 13.4 ± 0.9* |
| 0.5% Sample 4 | 15.7 ± 0.7 |
| 0.1% Sample 4 | 13.9 ± 1.7* |
| 5% Sample 3 | 15.8 ± 2.0 |

Denotes values that are significantly different from Untreated ($p < 0.05$)

## Example 11: Urban Dust Protection by Truncated Collagen

**[0319]** A keratinocyte cell culture model was used to assess the ability of truncated collagens to exert a protective effect by promoting cell survival after exposure to urban dust.

**[0320]** Human epidermal keratinocytes were pretreated with the test materials and then exposed to urban dust. At the end of the treatment period changes in cell viability were then determined via an MTT assay.

**[0321]** Keratinocytes were seeded into the individual wells of a 96 well plate in 100 µl of medium and incubated overnight at 37±2° C. and 5±1% $CO_2$. On the following day the media was removed via aspiration to eliminate any non-adherent cells and replaced with 100 µl of fresh medium. The cells were grown until confluent, with a media change every 48 to 72 hours.

Pretreatment with Test Material Followed by Urban Dust Treatment

**[0322]** Test materials were prepared at 2× their final desired concentrations in cell culture media. Urban dust (NIST 1649B from Sigma Chemicals) was also prepared at 2× solutions. For the pretreatment, 50 µl of 2× test material was combined with 50 µl of culture media and the cells were incubated for 24 hours. At the end of the pretreatment period the test material containing culture media was removed and replaced with 50 µl of 2× urban dust and 50 µl of media. Another set of cells was treated with media alone (non-dust exposed) and used as a reference control to represent 100% cell viability. The cells were then incubated for 24 hours and then subjected to an MTT assay to determine changes in cell viability.

**[0323]** At the end of the treatment period, the cell culture medium was removed and the cells were washed with PBS. After the wash, 100 µl of cell culture media supplemented with 0.5 mg/ml MTT was added to each well and the cells were incubated for 30 minutes at 37±2° C. and 5±1% $CO_2$. After the incubation, the media/MTT solution was removed and the cells were washed again once with PBS and then 100 µl of isopropyl alcohol was added to the wells to extract the purple formazin crystals. The 96-well plate was then read at 540 nm using isopropyl alcohol as a blank.

**[0324]** The mean MTT absorbance value for the non-dust exposed cells was calculated and used to represent 100% value for cell number. The individual MTT values from the cells undergoing the various treatments was then divided by the mean value for the non-dust exposed cells and expressed as a percent to determine the change in cell number caused by each treatment.

**[0325]** The MTT results for the pretreatment with the test material then dust treatments are presented in Table 10. Table 10 shows that as the cells were treated with increasing amounts of collagen, cell viability increased upon pretreatment with truncated collagen and subsequent exposure to urban dust. These results show that truncated collagen protects against the decline in cell viability associated with urban dust exposure.

TABLE 10

MTT Assay, Truncated Collagen Pretreatment

| Treatment | Viability (% Non-Dust Exposed) 4 mg/ml Urban Dust | Viability (% Non-Dust Exposed) 2 mg/ml Urban Dust |
|---|---|---|
| Non-Dust Exposed | 100 ± 4.4* | 100 ± 1.8 |
| Untreated | 59 ± 3.8 | 70 ± 0.9 |
| 0.1% Collagen | 61 ± 4.7 | 72 ± 3.5 |
| 0.5% Collagen | 59 ± 2.2 | 73 ± 2.2 |
| 1% Collagen | 58 ± 0.5 | 74 ± 2.6 |
| 5% Collagen | 66 ± 1.0 | 83 ± 6.5* |

*Denotes values that are significantly different from untreated group ($p < 0.05$)

## Example 12: Truncated *Chondrosia reniformis* (Kidney Sponge) Collagen

**[0326]** Truncated *Chondrosia reniformis* (Kidney Sponge) Fibrillar Collagen 1 with DsbA Secretion and FLAG Tag

**[0327]** The amino acid sequence of truncated *Chondrosia reniformis* fibrillar collagen 1 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 102. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 103 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 102. The fibrillary collagen nucleotide sequences are nucleotides 58-792 of SEQ ID NO: 103 and the amino acid sequences are amino acids 20-264 of SEQ ID NO: 102. The FLAG nucleotide sequences are nucleotides 793-819 of SEQ ID NO: 103 and the amino acid sequences are amino acids 265-273 of SEQ ID NO: 102.

(SEQ ID NO: 102)
MKKIWLALAGLVLAFSASAPVGRRGPKGSRGDPGDGGAAGPKGPEGV

DGLIGEPGQPGPIGAEGSSGLEGFLGDKGSKGARGGPGNRGRPGQDG

VPGQDGRAGEKGEGGETGDRGQQGLRGKVGDPGLVGDLGAQGPQGSQ

GLVGPPGIPGEPGSGGEPGDQGPRGPEGPQGSPGVRGGRGERGTPGA

VGPKGPPGKNGADGPRGLPGASGPPGSPGNQGPEGSRGADGNNGFPG

DDGENGLVGIPGEPGPKGARGTRGELGKTGDYKDDDDK

**[0328]** The nucleic acid sequence of truncated *Chondrosia reniformis* fibrillar collagen 1 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 103.

(SEQ ID NO: 103)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAG

CGCATCGGCGCCGGTTGGTCGTCGTGGTCCGAAAGGTAGCCGTGGTG

ATCCTGGTGATGGTGGTGCAGCAGGTCCTAAAGGTCCGGAAGGTGTT

GATGGTCTGATTGGTGAACCGGGTCAGCCTGGTCCGATTGGCGCAGA

AGGTAGCAGCGGTCTGGAAGGTTTTCTGGGTGATAAAGGTAGCAAAG

GTGCACGTGGTGGTCCGGGTAATCGCGGTCGTCCTGGTCAGGATGGT

GTTCCGGGTCAAGATGGTCGTGCCGGTGAAAAAGGTGAAGGTGGTGA

-continued

AACCGGTGATCGCGGTCAGCAGGGTCTGCGTGGTAAAGTTGGTGATC

CAGGTCTGGTGGGTGATCTGGGTGCACAGGGTCCGCAGGGTAGCCAA

GGTCTGGTTGGTCCGCCTGGTATTCCGGGTGAACCTGGTAGCGGTGG

CGAACCGGGTGATCAGGGTCCTCGCGGTCCAGAAGGTCCTCAGGGTT

CACCGGGTGTTCGCGGTGGTCGTGGTGAACGTGGTACACCGGGTGCA

GTTGGACCGAAAGGTCCGCCAGGTAAAAATGGTGCAGATGGTCCGCG

TGGTCTGCCTGGTGCAAGCGGTCCTCCGGGTAGTCCTGGTAACCAGG

GTCCTGAAGGTTCTCGTGGTGCCGATGGTAATAATGGTTTTCCAGGT

GATGATGGTGAAAATGGCCTGGTTGGTATCCCTGGCGAACCAGGTCC

AAAAGGCGCACGCGGTACACGCGGTGAACTGGGTAAAACCGGTGACT

ACAAAGACGACGACGACAAAtaa

**[0329]** The polynucleotide of SEQ ID NO: 103 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated *Chondrosia reniformis* fibrillar collagen 1 was purified as described herein. The purified fibrillary collagen produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 40 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

Truncated *Chondrosia reniformis* (Kidney Sponge) Fibrillar Collagen 2 with DsbA Secretion and FLAG Tag

**[0330]** The amino acid sequence of truncated *Chondrosia reniformis* fibrillar collagen 2 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 104. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 105 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 104. The fibrillary collagen nucleotide sequences are nucleotides 58-1323 of SEQ ID NO: 105 and the amino acid sequences are amino acids 20-441 of SEQ ID NO: 104. The FLAG nucleotide sequences are nucleotides 1324-1350 of SEQ ID NO: 105 and the amino acid sequences are amino acids 442-450 of SEQ ID NO: 105.

(SEQ ID NO: 104)
MKKIWLALAGLVLAFSASAGRGGPAGLQGAAGNPGDPGDRGQAGEIG

LPGTEGQRGQGGSRGDDGIGGQSGTDGDPGNDGVAGIRGARGEPGAT

GPEGAAGQKGDRGRFGEQGRPGNDGPPGRRGRVGNLGETGAEGDEGT

RGYTGDRGPEGAIGISGVTGNPGPQGIKGPPGDTGHPGRQGPSGPQG

PPGIPGTDGLTIHNLIKPPSQFFDATSSSDPLTDAVVESILKSFQYA

ELEIDLTKKPDGTMKYPAISCDDLHKDYPQLPSGNYTLDPNGGCKND

AFETYCEFNNSVKMCLTPKIPTLLPMGTYKYYVNSEGYYSPNDFGLN

LRFFEYYGSVTQLKFLQTKATRVTQTIRVLCKNYDPLHKQPVFIGMN

DETVMDEPRMEENQCQYFNGLSAHVELELSSNDPSYLPIYEMRLYLG

RKTNEELGIELGDLCFEYGDYKDDDDK

**[0331]** The nucleic acid sequence of truncated *Chondrosia reniformis* fibrillar collagen 2 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 105.

(SEQ ID NO: 105)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAG

CGCATCGGCGGGTCGTGGCGGTCCGGCAGGTCTGCAGGGTGCTGCAG

GTAATCCTGGCGACCCTGGCGATCGTGGTCAGGCAGGCGAAATTGGT

CTGCCAGGCACCGAAGGTCAGCGTGGTCAAGGTGGTTCACGTGGTGA

TGACGGTATTGGTGGTCAGAGCGGCACCGATGGCGATCCGGGTAACG

ATGGTGTTGCAGGTATTCGTGGTGCACGCGGAGAACCTGGTGCCACC

GGACCTGAAGGTGCAGCCGGTCAGAAAGGTGATCGTGGCCGTTTTGG

CGAACAGGGTCGTCCGGGAAATGATGGTCCACCGGGTCGCCGTGGCC

GTGTGGGCAATCTGGGTGAAACAGGTGCCGAAGGTGATGAAGGCACC

CGTGGTTATACAGGTGACCGTGGACCGGAAGGCGCAATTGGTATTAG

CGGTGTGACCGGTAATCCGGGTCCACAGGGCATTAAAGGCCCTCCGG

GTGATACGGGTCATCCGGGTCGTCAGGGACCGAGCGGTCCGCAAGGA

CCACCGGGTATTCCAGGTACAGATGGCCTGACCATTCATAATCTGAT

TAAACCGCCTAGCCAGTTTTTGATGCAACCAGCAGCAGCGATCCGC

TGACCGATGCAGTTGTTGAAAGCATTCTGAAATCTTTTCAGTATGCC

GAGCTGGAAATTGACCTGACCAAAAAACCGGATGGCACCATGAAATA

TCCGGCAATTAGCTGTGATGATCTGCACAAAGATTATCCGCAGCTGC

CGAGCGGTAATTATACCCTGGATCCGAATGGTGGTTGTAAAAATGAT

GCCTTTGAAACCTATTGCGAGTTCAACAATAGCGTGAAAATGTGTCT

GACCCCGAAAATTCCGACACTGCTGCCGATGGGCACCTATAAATACT

ATGTTAATAGCGAGGGTTACTACAGCCCGAATGATTTTGGTCTGAAT

CTGCGCTTTTTTGAGTATTATGGTAGCGTTACCCAGCTGAAATTTCT

GCAGACCAAAGCAACCCGTGTTACCCAGACCATTCGTGTTCTGTGTA

AAAACTATGATCCGCTGCATAAACAGCCGGTTTTTATTGGTATGAAT

GACGAAACCGTTATGGATGAACCGCGTATGGAAGAAAATCAGTGCCA

GTATTTTAACGGTCTGAGCGCACATGTTGAACTGGAACTGAGCAGCA

ATGATCCGAGCTATCTGCCGATTTATGAAATGCGTCTGTATCTGGGT

CGTAAAACCAATGAAGAACTGGGCATTGAACTGGGCGATCTGTGTTT

TGAATATGGTGACTACAAAGACGACGACGACAAAtaa

**[0332]** The polynucleotide of SEQ ID NO: 105 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated *Chondrosia reniformis* fibrillar collagen 2 was purified as described herein. The purified fibrillary collagen produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 55 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

### Truncated *Chondrosia reniformis* (Kidney Sponge) Non-Fibrillar Collagen 1 with DsbA Secretion and FLAG Tag

**[0333]** The amino acid sequence of truncated *Chondrosia reniformis* non-fibrillar collagen 1 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 106. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 107 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 106. The non-fibrillar collagen nucleotide sequences are nucleotides 58-831 of SEQ ID NO: 107 and the amino acid sequences are amino acids 20-277 of SEQ ID NO: 106. The FLAG nucleotide sequences are nucleotides 832-858 of SEQ ID NO: 107 and the amino acid sequences are amino acids 278-286 of SEQ ID NO: 106.

(SEQ ID NO: 106)
MKKIWLALAGLVLAFSASAEKTSSKVALMTVLVVITGALIIEGTSIT

RGSTHVNRGLRKRQTSEDNCEAVKVGLPGRDGREGPPGPPGPAGRDG

RDAVCSNQTTGLGAKGDRGPPGTPGFPGEVGRPGPPGADGIPGPQGE

RGAVGPGGKPGPRGEVGTPGADGADGATGATGVQGPDGAKGEKGASG

TAGLKGEKGDTCIPDSNSTLGMPGTPGAGGSKGQKGESGIVGPKGER

GEIGTPGHPGFRGADGEPGHKGVPGRAGAQGDRGDPGDDGLTGDYKD

DDDK

**[0334]** The nucleic acid sequence of truncated *Chondrosia reniformis* non-fibrillar collagen 1 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 107.

(SEQ ID NO: 107)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAG

CGCATCGGCGGAAAAAACCAGCAGCAAAGTTGCACTGATGACCGTTC

TGGTTGTTATTACCGGTGCACTGATTATTGAAGGCACCAGCATTACC

CGTGGTAGCACCCATGTTAATCGTGGTCTGCGTAAACGTCAGACCAG

CGAAGATAATTGTGAAGCAGTTAAAGTTGGTCTGCCAGGTCGTGATG

GTCGTGAAGGTCCTCCGGGTCCGCCTGGTCCGGCTGGCAGAGATGGC

CGTGATGCAGTTTGTAGCAATCAGACCACCGGTCTGGGTGCAAAAGG

TGATCGTGGTCCGCCAGGTACACCGGGTTTTCCGGGTGAAGTTGGCC

GTCCGGGTCCACCGGGTGCAGATGGTATTCCGGGTCCTCAGGGTGAA

CGTGGTGCAGTTGGTCCTGGTGGTAAACCTGGTCCGCGTGGTGAAGT

GGGCACCCCTGGTGCCGATGGCGCAGATGGTGCAACCGGTGCGACCG

GTGTTCAGGGTCCTGATGGTGCCAAAGGCGAAAAAGGTGCAAGCGGC

ACCGCAGGTCTGAAAGGTGAGAAAGGCGATACCTGTATTCCGGATAG

CAATAGCACCCTGGGTATGCCTGGTACACCAGGTGCCGGTGGTAGCA

AAGGCCAGAAAGGTGAAAGTGGTATTGTTGGTCCGAAAGGCGAACGC

GGTGAAATTGGCACACCGGGTCATCCTGGTTTTCGTGGTGCGGATGG

TGAACCAGGTCATAAAGGTGTTCCGGGTCGTGCCGGTGCGCAGGGTG

ATCGCGGTGATCCGGGTGATGATGGTCTGACCGGTGACTACAAAGAC

GACGACGACAAAtaa

**[0335]** The polynucleotide of SEQ ID NO: 107 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated *Chondrosia reniformis* non-fibrillar collagen 1 was purified as described herein. The purified non-fibrillar collagen produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 30 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

### Truncated *Chondrosia reniformis* (Kidney Sponge) Non Fibrillar Collagen 2 with DsbA Secretion and FLAG Tag

**[0336]** The amino acid sequence of truncated *Chondrosia reniformis* non-fibrillar collagen 2 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 108. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 109 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 108. The non-fibrillar collagen nucleotide sequences are nucleotides 58-1509 of SEQ ID NO: 109 and the amino acid sequences are amino acids 20-503 of SEQ ID NO: 108. The FLAG nucleotide sequences are nucleotides 1510-1536 of SEQ ID NO: 109 and the amino acid sequences are amino acids 504-512 of SEQ ID NO: 108.

(SEQ ID NO: 108)
MKKIWLALAGLVLAFSASAGFPGAPGADGAPGQKGELGAVGPQGTPG

LSGPSGPTGPPGPKGVRGAPGSSGAKGDAGNPGDDGPVGPQGVPGVD

GSPGQKGETGRVGPRGHDGINGTPGEDGATGFPGPDGAKGEKGTSGT

AGLKGEKGDTCIPDSNSTLGMPGTPGAGWSKGQKGESGIVGPKGEKG

EIGTPGPPGFRGADGEPGQRGEPGRAGAQGERGAPGNNGRDGFPGDP

GADGAPGQKGELGAIGHPGFSGPSGPSGPTGPPGPKGVRGAQGRPGD

RGSPGDVGPIGAPGPPGADGVPGLTGVQGRDGPKGESASSGAVYVRW

GRTTCPSGADVVYSGRAAGAKYDHSGGTSDHHCLPNNPQYLSEDDTN

ALGAQLYGVEYEIRDRSSPYNSLDQSDMPCVVCNANGRSQLLMVPAR

YTCPTGWSREYYGYMMSEGKAKNREGRKTTICMDFSAEAVPGSGANT

NPSPGIMMRANCNGLACPPYQSNTPLTCAVCTKGDYKDDDDK

**[0337]** The nucleic acid sequence of truncated *Chondrosia reniformis* non-fibrillar collagen 2 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 109.

(SEQ ID NO: 109)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAG

CGCATCGGCGGGTTTTCCTGGCGCTCCGGGTGCCGACGGTGCTCCGG

GTCAAAAAGGTGAACTGGGTGCCGTGGGTCCGCAGGGCACTCCGGGT

CTGAGTGGTCCTAGTGGTCCGACCGGTCCACCAGGTCCAAAAGGCGT

GCGTGGTGCACCGGGTAGCAGCGGAGCCAAAGGTGATGCAGGTAACC

CTGGTGATGACGGTCCGGTTGGTCCACAGGGCGTTCCAGGTGTTGAT

GGTAGCCCTGGCCAAAAGGGTGAAACCGGTCGTGTGGGTCCTCGTGG

TCATGATGGTATTAATGGCACCCCAGGTGAAGATGGTGCGACAGGCT

TTCCAGGTCCGGATGGCGCAAAGGGTGAGAAGGGCACCAGCGGTACA

GCTGGCCTGAAGGGCGAAAAGGGCGATACATGCATCCCGGATTCAAA

TTCAACACTGGGCATGCCAGGTACGCCTGGCGCAGGTTGGAGTAAAG

GACAAAAAGGCGAATCAGGCATTGTGGGACCTAAAGGCGAGAAGGGT

GAGATTGGTACTCCGGGACCGCCAGGCTTTCGCGGTGCAGACGGCGA

ACCGGGTCAGCGTGGCGAACCTGGTCGTGCAGGCGCACAAGGTGAAC

GCGGAGCCCCTGGTAATAATGGACGTGATGGCTTTCCTGGTGATCCA

GGTGCAGATGGCGCACCTGGCCAGAAAGGCGAACTGGGAGCAATTGG

TCATCCGGGATTTAGCGGTCCGTCAGGTCCGAGCGGACCGACAGGTC

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CTCCTGGACCGAAAGGTGTACGTGGCGCACAGGGTCGTCCTGGCGAT

CGTGGCAGTCCAGGTGATGTGGGTCCGATTGGTGCACCTGGTCCTCC

AGGTGCGGACGGCGTGCCTGGTTTAACAGGTGTGCAGGGTCGCGACG

GTCCTAAAGGTGAATCAGCAAGCAGCGGTGCAGTTTATGTTCGTTGG

GGTCGTACCACCTGTCCTAGCGGAGCAGATGTTGTTTATAGCGGTCG

CGCAGCCGGTGCAAAATATGATCATTCAGGTGGCACCTCAGATCATC

ATTGTCTGCCGAATAATCCGCAGTATCTGAGCGAAGATGATACCAAT

GCACTGGGTGCACAGCTGTATGGTGTGGAATATGAAATTCGTGATCG

TAGCAGCCCGTATAATAGCCTGGATCAGAGCGATATGCCGTGTGTTG

TTTGTAATGCAAATGGTCGTAGCCAGCTGCTGATGGTTCCGGCACGT

TATACATGCCCGACCGGTTGGAGCCGTGAATATTATGGTTATATGAT

GAGCGAAGGCAAAGCCAAAAATCGCGAAGGTCGTAAAACCACCATTT

GTATGGATTTTAGCGCAGAAGCAGTTCCTGGTAGCGGTGCAAATACC

AATCCGAGTCCGGGTATTATGATGCGTGCAAATTGTAATGGTCTGGC

ATGTCCGCCTTATCAGAGCAATACACCGCTGACCTGTGCCGTTTGTA

CCAAAGGTGACTACAAAGACGACGACGACAAAtaa

**[0338]** The polynucleotide of SEQ ID NO: 109 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated *Chondrosia reniformis* non-fibrillar collagen 2 was purified as described herein. The purified fibrillary collagen produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 60 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

## Example 13: Truncated *Rhincodon typus* (Whale Shark) Collagen

**[0339]** Truncated *Rhincodon typus* (Whale Shark) Collagen Type 1 Alpha 1 Truncation 1 with DsbA Secretion and FLAG Tag

**[0340]** The amino acid sequence of truncated *Rhincodon typus* collagen type 1 truncation 1 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 110. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 111 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 110. The collagen nucleotide sequences are nucleotides 58-630 of SEQ ID NO: 111 and the amino acid sequences are amino acids 20-210 of SEQ ID NO: 110. The FLAG nucleotide sequences are nucleotides 631-657 of SEQ ID NO: 111 and the amino acid sequences are amino acids 211-219 of SEQ ID NO: 110.

(SEQ ID NO: 110)
MKKIWLALAGLVLAFSASAGPAGAKGPSGDIGRPGESGSPGARGHSG

QPGRTGIAGNQGLPGTAGEEGRTGPPGPAGLRGQAGMMGFPGPKGAA

GLPGKPGDRGNVGLAGPRGAPGKDGEVGAQGPPGVAGPTGPRGETGL

AGSVGFQGMPGPSGAAGEPGKPGNQGLRGDAGSPGMIGPRGERGLPG

ERGASGAQGLLGPRGTSGAPGLGDYKDDDDK

**[0341]** The nucleic acid sequence of truncated *Rhincodon typus* collagen type 1 truncation 1 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 111.

(SEQ ID NO: 111)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAG

CGCATCGGCGGGTCCGGCAGGCGCAAAAGGTCCGAGCGGTGATATTG

GTCGTCCGGGTGAAAGCGGTAGTCCGGGTGCACGTGGTCATAGCGGT

CAGCCTGGTCGTACCGGTATTGCAGGTAATCAGGGTCTGCCTGGTAC

AGCCGGTGAAGAAGGTCGCACCGGTCCGCCAGGTCCTGCAGGTCTGC

GTGGTCAGGCAGGTATGATGGGTTTTCCGGGTCCGAAAGGTGCAGCG

GGTCTGCCAGGCAAACCGGGTGATCGTGGTAATGTTGGTCTGGCTGG

TCCGCGTGGTGCACCGGGTAAAGATGGTGAAGTTGGTGCACAGGGTC

CTCCGGGTGTTGCAGGTCCGACCGGTCCTCGTGGTGAAACCGGTCTG

GCAGGTAGCGTTGGTTTTCAGGGTATGCCAGGTCCGTCAGGTGCAGC

AGGCGAACCTGGTAAACCGGGTAACCAGGGCCTGCGTGGTGATGCCG

GTTCACCGGGTATGATTGGTCCACGCGGTGAACGTGGCCTGCCTGGC

GAACGTGGTGCAAGCGGTGCACAAGGTCTGCTGGGTCCACGTGGCAC

CTCAGGCGCACCAGGTCTGGGTGACTACAAAGACGACGACGACAAAt

aa

**[0342]** The polynucleotide of SEQ ID NO: 111 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated *Rhincodon typus* collagen type 1 truncation 1 was purified as described herein. The purified collagen produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 25 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

### Truncated *Rhincodon typus* (Whale Shark) Collagen Type 6 Alpha 1 Truncation 2 with DsbA Secretion and FLAG Tag

**[0343]** The amino acid sequence of truncated *Rhincodon typus* collagen type 6 truncation 2 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 112. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 113 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 112. The collagen nucleotide sequences are nucleotides 58-684 of SEQ ID NO: 113 and the amino acid sequences are amino acids 20-228 of SEQ ID NO: 112. The FLAG nucleotide sequences are nucleotides 685-711 of SEQ ID NO: 113 and the amino acid sequences are amino acids 229-237 of SEQ ID NO: 112.

(SEQ ID NO: 112)
MKKIWLALAGLVLAFSASAQGIPGSAGKEGGKGDPGPLGSPGKPGPD

GLRGFAGARGLPGAAGPPGLKGAEGPMGAPGLTGSTGERGPNGPAGA

IGLPGRPGGPGPPGPVGEKGDPGDKGLPGPAGDDGVQGAMGLPGPIG

SQGPPGDYGDKGELGKPGQKGSKGDKGESGPPGPIGIQGPIGHPGPI

GSDGSPGLRGYLGMRGQKGDDGIRGLPGSAGPVGLQGLPGGDYKDDD

DK

**[0344]** The nucleic acid sequence of truncated *Rhincodon typus* collagen type 6 truncation 2 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 113.

(SEQ ID NO: 113)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAG

CGCATCGGCGCAGGGTATTCCGGGTAGCGCAGGTAAAGAAGGTGGTA

AAGGCGATCCGGGTCCGCTGGGTTCACCGGGTAAACCGGGTCCTGAT

GGTCTGCGTGGTTTTGCCGGTGCACGTGGTCTGCCTGGTGCAGCAGG

TCCGCCTGGTCTGAAAGGTGCCGAAGGTCCGATGGGTGCTCCGGGTC

TGACCGGTAGCACCGGTGAACGCGGTCCGAATGGTCCGGCAGGCGCA

ATTGGTCTGCCAGGTCGTCCTGGTGGTCCGGGTCCTCCTGGTCCGGT

TGGTGAAAAAGGTGATCCTGGTGATAAAGGCCTGCCTGGTCCTGCCG

GTGATGATGGTGTTCAGGGTGCCATGGGCTTACCGGGTCCGATTGGT

AGCCAGGGTCCTCCGGGTGATTATGGCGATAAAGGTGAACTGGGTAA

ACCTGGCCAGAAAGGTAGCAAAGGTGACAAAGGCGAAAGCGGTCCGC

CAGGTCCGATCGGCATTCAGGGTCCTATTGGTCATCCAGGTCCAATT

GGTTCAGATGGCTCACCGGGACTGCGTGGCTATCTGGGTATGCGTGG

ACAGAAAGGTGATGACGGTATTCGTGGCCTGCCAGGTAGTGCAGGTC

CGGTGGGTCTGCAGGGACTGCCTGGTGGTGACTACAAAGACGACGAC

GACAAAtaa

**[0345]** The polynucleotide of SEQ ID NO: 113 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated *Rhincodon typus* collagen type 6 truncation 2 was purified as described herein. The purified collagen produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 35 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

### Truncated *Rhincodon typus* (Whale Shark) Collagen Type 6 Alpha 1 Truncation 3 with DsbA Secretion and FLAG Tag

**[0346]** The amino acid sequence of truncated *Rhincodon typus* collagen type 6 alpha 1 truncation 3 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 114. The DsbA secretion tag is encoded by nucleotides 1-57 of SEQ ID NO: 115 and the amino acid sequences are amino acids 1-19 of SEQ ID NO: 114. The collagen nucleotide sequences are nucleotides 58-735 of SEQ ID NO: 115 and the amino acid sequences are amino acids 20-245 of SEQ ID NO: 114. The FLAG nucleotide sequences are nucleotides 736-762 of SEQ ID NO: 115 and the amino acid sequences are amino acids 246-254 of SEQ ID NO: 114.

(SEQ ID NO: 114)
MKKIWLALAGLVLAFSASAKGETGEAGDPGTPGEPGIAGPKGDVGDK

GDAGPPGAAGPAGVKGPPGEDGAKGDVGPAGFPGDPGPTGEPGVPGM

DGGVGEKGSLGDPGLTGPRGASGEPGPPGSPGKRGPPGPAGPEGREG

LKGSKGSPGQEGPVGRTGPIGPQGSPGNVGPKGLRGIPGPTGEQGLL

GPPGQAGPPGPMGPPGMPGLRGAQGLKGDKGHVGLIGLIGPPGEMGE

KGDQGLPGIQGDYKDDDDK

**[0347]** The nucleic acid sequence of truncated *Rhincodon typus* collagen type 6 alpha 1 truncation 3 with DsbA secretion and FLAG tag is disclosed in SEQ ID NO: 115.

```
                                         (SEQ ID NO: 115)
ATGAAAAAGATTTGGCTGGCGCTGGCTGGTTTAGTTTTAGCGTTTAG

CGCATCGGCGAAAGGTGAAACCGGTGAAGCGGGTGATCCGGGTACAC

CGGGTGAACCTGGTATTGCAGGTCCGAAAGGTGATGTTGGTGATAAA

GGTGACGCAGGTCCGCCTGGTGCAGCAGGTCCGGCAGGCGTTAAAGG

TCCTCCGGGTGAAGATGGTGCAAAAGGCGACGTTGGTCCTGCAGGTT

TTCCTGGCGATCCGGGTCCGACTGGTGAACCGGGTGTGCCAGGTATG

GATGGTGGTGTGGGTGAAAAAGGTAGCCTGGGTGATCCTGGTCTGAC

CGGTCCGCGTGGCGCAAGTGGTGAACCAGGTCCACCGGGTAGTCCGG

GTAAACGTGGTCCTCCTGGACCGGCTGGTCCGGAAGGTCGTGAAGGT
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                    -continued
CTGAAAGGTAGCAAAGGTTCACCGGGTCAAGAAGGTCCGGTTGGTCG

TACCGGTCCGATTGGTCCGCAGGGCTCACCGGGTAATGTTGGTCCTA

AAGGTCTGCGTGGTATTCCGGGTCCTACAGGCGAACAGGGTCTGCTG

GGTCCGCCAGGCCAAGCAGGTCCTCCAGGTCCTATGGGTCCACCTGG

TATGCCTGGCCTGCGTGGTGCCCAGGGCCTGAAAGGCGATAAAGGCC

ATGTTGGTCTGATTGGCCTGATTGGTCCACCAGGTGAAATGGGAGAA

AAAGGCGATCAGGGCCTGCCTGGTATTCAGGGTGACTACAAAGACGA

CGACGACAAAtaa
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**[0348]** The polynucleotide of SEQ ID NO: 115 was subcloned into vector pET28a, expressed host *E. coli* cells and the truncated *Rhincodon typus* collagen type 1 truncation 1 was purified as described herein. The purified collagen produced a clear band on SDS-PAGE and an anti-FLAG western was observed at around 25 kilodaltons. There were no existing bands that appear at that location on the gel in the absence of expression of this protein.

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<160> NUMBER OF SEQ ID NOS: 153

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<211> LENGTH: 429
<212> TYPE: PRT
<213> ORGANISM: Podocoryna carnea

<400> SEQUENCE: 1

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Glu Lys Gly Glu Gln Gly Arg Thr Gly Ala Ala Gly Lys Gln Gly Ser
            20                  25                  30

Pro Gly Ala Asp Gly Ala Arg Gly Pro Leu Gly Ser Ile Gly Gln Gln
        35                  40                  45

Gly Ala Arg Gly Glu Pro Gly Asp Pro Gly Ser Pro Gly Leu Arg Gly
    50                  55                  60

Asp Thr Gly Leu Ala Gly Val Lys Gly Val Ala Gly Pro Ser Gly Arg
65                  70                  75                  80

Pro Gly Gln Pro Gly Ala Asn Gly Leu Pro Gly Val Asn Gly Arg Gly
                85                  90                  95

Gly Leu Arg Gly Lys Pro Gly Ala Lys Gly Ile Ala Gly Ser Asp Gly
            100                 105                 110

Glu Ala Gly Glu Ser Gly Ala Pro Gly Gln Ser Gly Pro Thr Gly Pro
        115                 120                 125

Arg Gly Gln Arg Gly Pro Ser Gly Glu Asp Gly Asn Pro Gly Leu Gln
    130                 135                 140

Gly Leu Pro Gly Ser Asp Gly Glu Pro Gly Glu Glu Gly Gln Pro Gly
145                 150                 155                 160

Arg Ser Gly Gln Pro Gly Gln Gln Gly Pro Arg Gly Ser Pro Gly Glu
                165                 170                 175

Val Gly Pro Arg Gly Ser Lys Gly Pro Ser Gly Asp Arg Gly Asp Arg
            180                 185                 190

Gly Glu Arg Gly Val Pro Gly Gln Thr Gly Ser Ala Gly Asn Val Gly
        195                 200                 205
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Glu Asp Gly Glu Gln Gly Gly Lys Gly Val Asp Gly Ala Ser Gly Pro
    210                 215                 220

Ser Gly Ala Leu Gly Ala Arg Gly Pro Pro Gly Ser Arg Gly Asp Thr
225                 230                 235                 240

Gly Ala Val Gly Pro Pro Gly Pro Thr Gly Arg Ser Gly Leu Pro Gly
                245                 250                 255

Asn Ala Gly Gln Lys Gly Pro Ser Gly Glu Pro Gly Ser Pro Gly Lys
            260                 265                 270

Ala Gly Ser Ala Gly Glu Gln Gly Pro Pro Gly Lys Asp Gly Ser Asn
        275                 280                 285

Gly Glu Pro Gly Ser Pro Gly Lys Glu Gly Glu Arg Gly Leu Ala Gly
    290                 295                 300

Pro Pro Gly Pro Asp Gly Arg Arg Gly Glu Thr Gly Ser Pro Gly Ile
305                 310                 315                 320

Ala Gly Ala Leu Gly Lys Pro Gly Leu Glu Gly Pro Lys Gly Tyr Pro
                325                 330                 335

Gly Leu Arg Gly Arg Asp Gly Thr Asn Gly Lys Arg Gly Glu Gln Gly
            340                 345                 350

Glu Thr Gly Pro Asp Gly Val Arg Gly Ile Pro Gly Asn Asp Gly Gln
        355                 360                 365

Ser Gly Lys Pro Gly Ile Asp Gly Ile Asp Gly Thr Asn Gly Gln Pro
    370                 375                 380

Gly Glu Ala Gly Tyr Gln Gly Gly Arg Gly Thr Arg Gly Gln Leu Gly
385                 390                 395                 400

Glu Thr Gly Asp Val Gly Gln Asn Gly Asp Arg Gly Ala Pro Gly Pro
                405                 410                 415

Asp Gly Ser Lys Gly Ser Ala Gly Arg Pro Gly Leu Arg
            420                 425


<210> SEQ ID NO 2
<211> LENGTH: 1289
<212> TYPE: DNA
<213> ORGANISM: Podocoryna carnea

<400> SEQUENCE: 2

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caaggacgaa ccggagctgc aggaaaacag ggaagccctg gagcagatgg agcaagaggc     120

cctcttggat caattggaca acaaggtgct cgtggagaac ctggtgatcc aggatctccc     180

ggcttaagag gagatactgg attggctgga gtcaaaggag tagcaggacc atctggtcga     240

cctggacaac ccggtgcaaa tggattacct ggtgtgaatg gcagaggcgg tttgagaggc     300

aaacctggtg ctaaaggaat tgctggcagt gatggagaag cgggagaatc tggcgcacct     360

ggacagtccg gacctaccgg tccacgtggt caacgaggac caagtggtga ggatggtaat     420

cctggattac agggattgcc tggttctgat ggagagcccg gagaggaagg acaacctgga     480

agatctggtc aaccaggaca gcaaggacca cgtggttccc ctggagaggt aggaccaaga     540

ggatctaaag gtccatcagg agatcgtggt gacaggggag agagaggtgt tcctggacaa     600

acaggttcgg ctggaaatgt aggagaagat ggagagcaag gaggcaaagg tgtcgatgga     660

gcgagtggac caagtggagc tcttggtgct cgtggtcccc caggaagtag aggtgacacc     720

ggggcagtgg gacctcccgg acctactggg cgatctggtt tacctggaaa cgcaggacaa     780
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aagggaccaa gtggtgaacc aggtagtcca ggaaaagcag gatcagctgg tgaacagggt 840

cctcctggta aagacggatc aaatggtgaa cctggatctc ctggcaaaga gggtgaacgt 900

ggtcttgctg gtccaccagg tccagatggc agacgtggtg aaacgggatc tccaggtatc 960

gctggtgctc ttggtaaacc aggtttggaa ggacctaaag gttatccagg attaagagga 1020

agagatggaa ccaatggcaa acgaggagaa caaggagaaa ctggtcctga tggagtcaga 1080

ggtattcctg gaaatgatgg acaatctggc aaaccaggta ttgatggtat tgacggaaca 1140

aatggtcaac caggtgaggc tggataccaa ggtggtagag gtacacgtgg tcagttaggt 1200

gaaactggtg atgtcggaca gaatggagat cgaggagctc ctggtcctga tggatctaaa 1260

ggttctgctg gtagaccagg acttcgtgg 1289

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 3

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cgcggcagcc atatgggtcc gcagggtgtt gttggtgcag atggtaaaga cggtaccccg 180

ggtgaaaaag gagaacaggg acgtacaggt gcagcaggta aacagggcag cccgggtgcc 240

gatggtgccc gtggcccgct gggtagcatt ggtcagcagg gtgcaagagg cgaaccgggc 300

gatccgggta gtccgggcct gcgtggtgat acgggtctgg ccggtgttaa aggcgttgca 360

ggtccttcag gtcgtccagg tcaaccgggt gcaaatggtc tgccgggtgt taatggtcgt 420

ggcggtctgc gtggcaaacc gggagcaaaa ggtattgcag gtagcgatgg agaagccggt 480

gaaagcggtg ccccgggtca gagtggtccg accggtccgc gcggtcagcg tggtccgtct 540

ggtgaagatg gcaatccggg tctgcagggt ctgcctggta gtgatggcga accaggtgaa 600

gaaggtcagc cgggtcgttc aggccagccg ggccagcagg gcccgcgtgg tagcccgggc 660

gaagttggcc cgcggggtag taaaggtcct agtggcgatc gcggtgatcg tggtgaacgc 720

ggtgttcctg gtcagaccgg tagcgcaggt aatgttggcg aagatggtga acagggtggc 780

aaaggtgttg atggtgcaag cggtccgagc ggtgcactgg gtgcacgtgg tcctccgggc 840

agccgtggtg acaccggtgc agttggtccg cctggcccga ccggccgtag tggcttaccg 900

ggtaatgcag gtcagaaagg tccgtcaggt gaacctggca gccctggtaa agcaggtagt 960

gccggtgagc agggtccgcc gggcaaagat ggtagtaatg gtgagccggg tagccctggc 1020

aaagaaggtg aacgtggtct ggcaggaccg ccgggtcctg atggtcgccg cggtgaaacg 1080

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cctggtctgc gcggtcgtga tggtaccaat ggcaaacgtg gcgaacaggg cgaaaccggt 1200

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ccggatggta gcaaaggtag cgccggtcgt ccgggtttac gttaa 1425

<210> SEQ ID NO 4
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<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 4

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cgcggcagcc atatgggtcc gcagggtgtt gttggtgcag atggtaaaga cggtaccccg 180

ggtgaaaaag gtgaacaggg tcgtaccggt gcagcaggta aacagggcag cccgggtgcc 240

gatggtgccc gtggcccgct gggtagcatt ggtcagcagg gtgcacgtgg cgaaccgggc 300

gatccgggta gcccgggcct gcgtggtgat acgggtctgg ccggtgttaa aggcgttgca 360

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ggcggtctgc gtggcaaacc gggtgcaaaa ggtattgcag gtagcgatgg cgaagccggt 480

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gaaggtcagc cgggtcgttc tggccagccg ggccagcagg gcccgcgtgg tagcccgggc 660

gaagttggcc cgcgcggttc taaaggtcct agcggcgatc gcggtgatcg tggtgaacgc 720

ggtgttcctg gtcagaccgg tagcgcaggt aatgttggcg aagatggtga acagggtggc 780

aaaggtgttg atggtgcaag cggtccgagc ggtgcactgg gtgcacgtgg tcctccgggc 840

agccgtggtg acaccggtgc agttggtccg cctggcccga ccggccgtag cggcctgccg 900

ggtaatgcag gtcagaaagg tccgtctggt gaacctggca gccctggtaa agcaggtagc 960

gccggtgagc agggtccgcc gggcaaagat ggtagcaatg gtgagccggg tagccctggc 1020

aaagaaggtg aacgtggtct ggcaggtccg ccgggtcctg atggtcgccg cggtgaaacg 1080

ggttctccgg gtattgccgg tgccctgggt aaaccaggtc tggaaggtcc gaaaggttat 1140

cctggtctgc gcggtcgtga tggtaccaat ggcaaacgtg gcgaacaggg cgaaaccggt 1200

ccagatggtg ttcgtggtat tccgggtaac gatggtcaga gcggtaaacc gggcattgat 1260

ggtattgatg gcaccaatgg tcagcctggc gaagcaggtt atcagggtgg tcgcggtacc 1320

cgtggtcagc tgggtgaaac cggtgatgtt ggtcagaatg gtgatcgcgg cgcaccgggt 1380

ccggatggta gcaaaggtag cgccggtcgt ccgggtctgc gttaa 1425

<210> SEQ ID NO 5
<211> LENGTH: 474
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 5

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1 5 10 15

Ala Ser Ala Ala Gln Tyr Glu Asp His His His His His His His His

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            20                  25                  30

His Ser Gly Ser Ser Leu Val Pro Arg Gly Ser His Met Gly Pro Gln
        35                  40                  45

Gly Val Val Gly Ala Asp Gly Lys Asp Gly Thr Pro Gly Glu Lys Gly
    50                  55                  60

Glu Gln Gly Arg Thr Gly Ala Ala Gly Lys Gln Gly Ser Pro Gly Ala
65                  70                  75                  80

Asp Gly Ala Arg Gly Pro Leu Gly Ser Ile Gly Gln Gln Gly Ala Arg
                85                  90                  95

Gly Glu Pro Gly Asp Pro Gly Ser Pro Gly Leu Arg Gly Asp Thr Gly
            100                 105                 110

Leu Ala Gly Val Lys Gly Val Ala Gly Pro Ser Gly Arg Pro Gly Gln
        115                 120                 125

Pro Gly Ala Asn Gly Leu Pro Gly Val Asn Gly Arg Gly Gly Leu Arg
    130                 135                 140

Gly Lys Pro Gly Ala Lys Gly Ile Ala Gly Ser Asp Gly Glu Ala Gly
145                 150                 155                 160

Glu Ser Gly Ala Pro Gly Gln Ser Gly Pro Thr Gly Pro Arg Gly Gln
                165                 170                 175

Arg Gly Pro Ser Gly Glu Asp Gly Asn Pro Gly Leu Gln Gly Leu Pro
            180                 185                 190

Gly Ser Asp Gly Glu Pro Gly Glu Glu Gly Gln Pro Gly Arg Ser Gly
        195                 200                 205

Gln Pro Gly Gln Gln Gly Pro Arg Gly Ser Pro Gly Glu Val Gly Pro
    210                 215                 220

Arg Gly Ser Lys Gly Pro Ser Gly Asp Arg Gly Asp Arg Gly Glu Arg
225                 230                 235                 240

Gly Val Pro Gly Gln Thr Gly Ser Ala Gly Asn Val Gly Glu Asp Gly
                245                 250                 255

Glu Gln Gly Gly Lys Gly Val Asp Gly Ala Ser Gly Pro Ser Gly Ala
            260                 265                 270

Leu Gly Ala Arg Gly Pro Pro Gly Ser Arg Gly Asp Thr Gly Ala Val
        275                 280                 285

Gly Pro Pro Gly Pro Thr Gly Arg Ser Gly Leu Pro Gly Asn Ala Gly
    290                 295                 300

Gln Lys Gly Pro Ser Gly Glu Pro Gly Ser Pro Gly Lys Ala Gly Ser
305                 310                 315                 320

Ala Gly Glu Gln Gly Pro Pro Gly Lys Asp Gly Ser Asn Gly Glu Pro
                325                 330                 335

Gly Ser Pro Gly Lys Glu Gly Glu Arg Gly Leu Ala Gly Pro Pro Gly
            340                 345                 350

Pro Asp Gly Arg Arg Gly Glu Thr Gly Ser Pro Gly Ile Ala Gly Ala
        355                 360                 365

Leu Gly Lys Pro Gly Leu Glu Gly Pro Lys Gly Tyr Pro Gly Leu Arg
    370                 375                 380

Gly Arg Asp Gly Thr Asn Gly Lys Arg Gly Glu Gln Gly Glu Thr Gly
385                 390                 395                 400

Pro Asp Gly Val Arg Gly Ile Pro Gly Asn Asp Gly Gln Ser Gly Lys
                405                 410                 415

Pro Gly Ile Asp Gly Ile Asp Gly Thr Asn Gly Gln Pro Gly Glu Ala
            420                 425                 430
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Gly Tyr Gln Gly Gly Arg Gly Thr Arg Gly Gln Leu Gly Glu Thr Gly
        435                 440                 445

Asp Val Gly Gln Asn Gly Asp Arg Gly Ala Pro Gly Pro Asp Gly Ser
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Lys Gly Ser Ala Gly Arg Pro Gly Leu Arg
465                 470


<210> SEQ ID NO 6
<211> LENGTH: 1362
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 6

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gaaaaaggag aacagggacg tacaggtgca gcaggtaaac agggcagccc gggtgccgat     180

ggtgcccgtg gcccgctggg tagcattggt cagcagggtg caagaggcga accgggcgat     240

ccgggtagtc cgggcctgcg tggtgatacg ggtctggccg gtgttaaagg cgttgcaggt     300

ccttcaggtc gtccaggtca accgggtgca aatggtctgc cgggtgttaa tggtcgtggc     360

ggtctgcgtg gcaaaccggg agcaaaaggt attgcaggta gcgatggaga agccggtgaa     420

agcggtgccc cgggtcagag tggtccgacc ggtccgcgcg gtcagcgtgg tccgtctggt     480

gaagatggca atccgggtct gcagggtctg cctggtagtg atggcgaacc aggtgaagaa     540

ggtcagccgg gtcgttcagg ccagccgggc cagcagggcc cgcgtggtag cccgggcgaa     600

gttggcccgc ggggtagtaa aggtcctagt ggcgatcgcg gtgatcgtgg tgaacgcggt     660

gttcctggtc agaccggtag cgcaggtaat gttggcgaag atggtgaaca gggtggcaaa     720

ggtgttgatg gtgcaagcgg tccgagcggt gcactgggtg cacgtggtcc tccgggcagc     780

cgtggtgaca ccggtgcagt tggtccgcct ggcccgaccg gccgtagtgg cttaccgggt     840

aatgcaggtc agaaaggtcc gtcaggtgaa cctggcagcc ctggtaaagc aggtagtgcc     900

ggtgagcagg gtccgccggg caaagatggt agtaatggtg agccgggtag ccctggcaaa     960

gaaggtgaac gtggtctggc aggaccgccg ggtcctgatg gtcgccgcgg tgaaacgggt    1020

tcaccgggta ttgccggtgc cctgggtaaa ccaggtctgg aaggtccgaa aggttatcct    1080

ggtctgcgcg gtcgtgatgg taccaatggc aaacgtggcg aacagggcga aaccggtcca    1140

gatggtgttc gtggtattcc gggtaacgat ggtcagagcg gtaaaccggg cattgatggt    1200

attgatggca ccaatggtca gcctggcgaa gcaggttatc agggtggtcg cggtacccgt    1260

ggtcagctgg gtgaaacagg tgatgttggt cagaatggtg atcgcggcgc accgggtccg    1320

gatggtagca aaggtagcgc cggtcgtccg ggtttacgtt aa                       1362


<210> SEQ ID NO 7
<211> LENGTH: 1362
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide
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<400> SEQUENCE: 7

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg 60

cagtatgaag atggtccgca gggtgttgtt ggtgcagatg gtaaagacgg taccccgggt 120

gaaaaaggtg aacagggtcg taccggtgca gcaggtaaac agggcagccc gggtgccgat 180

ggtgcccgtg gcccgctggg tagcattggt cagcagggtg cacgtggcga accgggcgat 240

ccgggtagcc cgggcctgcg tggtgatacg ggtctggccg gtgttaaagg cgttgcaggt 300

ccttctggtc gtccaggtca accgggtgca aatggtctgc cgggtgttaa tggtcgtggc 360

ggtctgcgtg gcaaaccggg tgcaaaaggt attgcaggta gcgatggcga agccggtgaa 420

agcggtgccc cgggtcagag cggtccgacc ggtccgcgcg gtcagcgtgg tccgtctggt 480

gaagatggca atccgggtct gcagggtctg cctggtagcg atggcgaacc aggtgaagaa 540

ggtcagccgg gtcgttctgg ccagccgggc cagcagggcc cgcgtggtag cccgggcgaa 600

gttggcccgc gcggttctaa aggtcctagc ggcgatcgcg gtgatcgtgg tgaacgcggt 660

gttcctggtc agaccggtag cgcaggtaat gttggcgaag atggtgaaca gggtggcaaa 720

ggtgttgatg gtgcaagcgg tccgagcggt gcactgggtg cacgtggtcc tccgggcagc 780

cgtggtgaca ccggtgcagt tggtccgcct ggcccgaccg gccgtagcgg cctgccgggt 840

aatgcaggtc agaaaggtcc gtctggtgaa cctggcagcc ctggtaaagc aggtagcgcc 900

ggtgagcagg gtccgccggg caaagatggt agcaatggtg agccgggtag ccctggcaaa 960

gaaggtgaac gtggtctggc aggtccgccg ggtcctgatg gtcgccgcgg tgaaacgggt 1020

tctccgggta ttgccggtgc cctgggtaaa ccaggtctgg aaggtccgaa aggttatcct 1080

ggtctgcgcg gtcgtgatgg taccaatggc aaacgtggcg aacagggcga aaccggtcca 1140

gatggtgttc gtggtattcc gggtaacgat ggtcagagcg gtaaaccggg cattgatggt 1200

attgatggca ccaatggtca gcctggcgaa gcaggttatc agggtggtcg cggtacccgt 1260

ggtcagctgg gtgaaaccgg tgatgttggt cagaatggtg atcgcggcgc accgggtccg 1320

gatggtagca aaggtagcgc cggtcgtccg ggtctgcgtt aa 1362

<210> SEQ ID NO 8
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 8

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1 5 10 15

Ala Ser Ala Ala Gln Tyr Glu Asp Gly Pro Gln Gly Val Val Gly Ala
20 25 30

Asp Gly Lys Asp Gly Thr Pro Gly Glu Lys Gly Glu Gln Gly Arg Thr
35 40 45

Gly Ala Ala Gly Lys Gln Gly Ser Pro Gly Ala Asp Gly Ala Arg Gly
50 55 60

Pro Leu Gly Ser Ile Gly Gln Gln Gly Ala Arg Gly Glu Pro Gly Asp
65 70 75 80

Pro Gly Ser Pro Gly Leu Arg Gly Asp Thr Gly Leu Ala Gly Val Lys
85 90 95

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Gly Val Ala Gly Pro Ser Gly Arg Pro Gly Gln Pro Gly Ala Asn Gly
            100                 105                 110

Leu Pro Gly Val Asn Gly Arg Gly Gly Leu Arg Gly Lys Pro Gly Ala
        115                 120                 125

Lys Gly Ile Ala Gly Ser Asp Gly Glu Ala Gly Glu Ser Gly Ala Pro
    130                 135                 140

Gly Gln Ser Gly Pro Thr Gly Pro Arg Gly Gln Arg Gly Pro Ser Gly
145                 150                 155                 160

Glu Asp Gly Asn Pro Gly Leu Gln Gly Leu Pro Gly Ser Asp Gly Glu
                165                 170                 175

Pro Gly Glu Glu Gly Gln Pro Gly Arg Ser Gly Gln Pro Gly Gln Gln
            180                 185                 190

Gly Pro Arg Gly Ser Pro Gly Glu Val Gly Pro Arg Gly Ser Lys Gly
        195                 200                 205

Pro Ser Gly Asp Arg Gly Asp Arg Gly Glu Arg Gly Val Pro Gly Gln
    210                 215                 220

Thr Gly Ser Ala Gly Asn Val Gly Glu Asp Gly Glu Gln Gly Gly Lys
225                 230                 235                 240

Gly Val Asp Gly Ala Ser Gly Pro Ser Gly Ala Leu Gly Ala Arg Gly
                245                 250                 255

Pro Pro Gly Ser Arg Gly Asp Thr Gly Ala Val Gly Pro Pro Gly Pro
            260                 265                 270

Thr Gly Arg Ser Gly Leu Pro Gly Asn Ala Gly Gln Lys Gly Pro Ser
        275                 280                 285

Gly Glu Pro Gly Ser Pro Gly Lys Ala Gly Ser Ala Gly Glu Gln Gly
    290                 295                 300

Pro Pro Gly Lys Asp Gly Ser Asn Gly Glu Pro Gly Ser Pro Gly Lys
305                 310                 315                 320

Glu Gly Glu Arg Gly Leu Ala Gly Pro Pro Gly Pro Asp Gly Arg Arg
                325                 330                 335

Gly Glu Thr Gly Ser Pro Gly Ile Ala Gly Ala Leu Gly Lys Pro Gly
            340                 345                 350

Leu Glu Gly Pro Lys Gly Tyr Pro Gly Leu Arg Gly Arg Asp Gly Thr
        355                 360                 365

Asn Gly Lys Arg Gly Glu Gln Gly Glu Thr Gly Pro Asp Gly Val Arg
    370                 375                 380

Gly Ile Pro Gly Asn Asp Gly Gln Ser Gly Lys Pro Gly Ile Asp Gly
385                 390                 395                 400

Ile Asp Gly Thr Asn Gly Gln Pro Gly Glu Ala Gly Tyr Gln Gly Gly
                405                 410                 415

Arg Gly Thr Arg Gly Gln Leu Gly Glu Thr Gly Asp Val Gly Gln Asn
            420                 425                 430

Gly Asp Arg Gly Ala Pro Gly Pro Asp Gly Ser Lys Gly Ser Ala Gly
        435                 440                 445

Arg Pro Gly Leu Arg
    450


<210> SEQ ID NO 9
<211> LENGTH: 825
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 9

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg 60

cagtatgaag atcaccatca ccaccaccac catcaccact ctggctcgag cctggtgccg 120

cgcggcagcc atatgggtcc gcagggtgtt gttggtgcag atggtaaaga cggtaccccg 180

ggtgaaaaag gagaacaggg acgtacaggt gcagcaggta aacagggcag cccgggtgcc 240

gatggtgccc gtggcccgct gggtagcatt ggtcagcagg gtgcaagagg cgaaccgggc 300

gatccgggta gtccgggcct gcgtggtgat acgggtctgg ccggtgttaa aggcgttgca 360

ggtccttcag gtcgtccagg tcaaccgggt gcaaatggtc tgccgggtgt taatggtcgt 420

ggcggtctgg aacgtggtct ggcaggaccg ccgggtcctg atggtcgccg cggtgaaacg 480

ggttcaccgg gtattgccgg tgccctgggt aaaccaggtc tggaaggtcc gaaaggttat 540

cctggtctgc gcggtcgtga tggtaccaat ggcaaacgtg gcgaacaggg cgaaaccggt 600

ccagatggtg ttcgtggtat tccgggtaac gatggtcaga gcggtaaacc gggcattgat 660

ggtattgatg gcaccaatgg tcagcctggc gaagcaggtt atcagggtgg tcgcggtacc 720

cgtggtcagc tgggtgaaac aggtgatgtt ggtcagaatg gtgatcgcgg cgcaccgggt 780

ccggatggta gcaaaggtag cgccggtcgt ccgggtttac gttaa 825

<210> SEQ ID NO 10
<211> LENGTH: 274
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 10

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1 5 10 15

Ala Ser Ala Ala Gln Tyr Glu Asp His His His His His His His His
20 25 30

His Ser Gly Ser Ser Leu Val Pro Arg Gly Ser His Met Gly Pro Gln
35 40 45

Gly Val Val Gly Ala Asp Gly Lys Asp Gly Thr Pro Gly Glu Lys Gly
50 55 60

Glu Gln Gly Arg Thr Gly Ala Ala Gly Lys Gln Gly Ser Pro Gly Ala
65 70 75 80

Asp Gly Ala Arg Gly Pro Leu Gly Ser Ile Gly Gln Gln Gly Ala Arg
85 90 95

Gly Glu Pro Gly Asp Pro Gly Ser Pro Gly Leu Arg Gly Asp Thr Gly
100 105 110

Leu Ala Gly Val Lys Gly Val Ala Gly Pro Ser Gly Arg Pro Gly Gln
115 120 125

Pro Gly Ala Asn Gly Leu Pro Gly Val Asn Gly Arg Gly Gly Leu Glu
130 135 140

Arg Gly Leu Ala Gly Pro Pro Gly Pro Asp Gly Arg Arg Gly Glu Thr
145 150 155 160

Gly Ser Pro Gly Ile Ala Gly Ala Leu Gly Lys Pro Gly Leu Glu Gly
165 170 175

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Pro Lys Gly Tyr Pro Gly Leu Arg Gly Arg Asp Gly Thr Asn Gly Lys
            180                 185                 190

Arg Gly Glu Gln Gly Glu Thr Gly Pro Asp Gly Val Arg Gly Ile Pro
        195                 200                 205

Gly Asn Asp Gly Gln Ser Gly Lys Pro Gly Ile Asp Gly Ile Asp Gly
    210                 215                 220

Thr Asn Gly Gln Pro Gly Glu Ala Gly Tyr Gln Gly Gly Arg Gly Thr
225                 230                 235                 240

Arg Gly Gln Leu Gly Glu Thr Gly Asp Val Gly Gln Asn Gly Asp Arg
                245                 250                 255

Gly Ala Pro Gly Pro Asp Gly Ser Lys Gly Ser Ala Gly Arg Pro Gly
            260                 265                 270

Leu Arg


<210> SEQ ID NO 11
<211> LENGTH: 642
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 11

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg      60

cagtatgaag atggtccgca gggtgttgtt ggtgcagatg gtaaagacgg taccccgggt     120

aatgcaggtc agaaaggtcc gtcaggtgaa cctggcagcc ctggtaaagc aggtagtgcc     180

ggtgagcagg gtccgccggg caaagatggt agtaatggtg agccgggtag ccctggcaaa     240

gaaggtgaac gtggtctggc aggaccgccg ggtcctgatg gtcgccgcgg tgaaacgggt     300

tcaccgggta ttgccggtgc cctgggtaaa ccaggtctgg aaggtccgaa aggttatcct     360

ggtctgcgcg gtcgtgatgg taccaatggc aaacgtggcg aacagggcga aaccggtcca     420

gatggtgttc gtggtattcc gggtaacgat ggtcagagcg gtaaaccggg cattgatggt     480

attgatggca ccaatggtca gcctggcgaa gcaggttatc agggtggtcg cggtacccgt     540

ggtcagctgg gtgaaacagg tgatgttggt cagaatggtg atcgcggcgc accgggtccg     600

gatggtagca aaggtagcgc cggtcgtccg ggtttacgtt aa                        642


<210> SEQ ID NO 12
<211> LENGTH: 213
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 12

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Ala Gln Tyr Glu Asp Gly Pro Gln Gly Val Val Gly Ala
            20                  25                  30

Asp Gly Lys Asp Gly Thr Pro Gly Asn Ala Gly Gln Lys Gly Pro Ser
        35                  40                  45

Gly Glu Pro Gly Ser Pro Gly Lys Ala Gly Ser Ala Gly Glu Gln Gly
    50                  55                  60
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Pro Pro Gly Lys Asp Gly Ser Asn Gly Glu Pro Gly Ser Pro Gly Lys
65                  70                  75                  80

Glu Gly Glu Arg Gly Leu Ala Gly Pro Pro Gly Pro Asp Gly Arg Arg
                85                  90                  95

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

Leu Glu Gly Pro Lys Gly Tyr Pro Gly Leu Arg Gly Arg Asp Gly Thr
        115                 120                 125

Asn Gly Lys Arg Gly Glu Gln Gly Glu Thr Gly Pro Asp Gly Val Arg
    130                 135                 140

Gly Ile Pro Gly Asn Asp Gly Gln Ser Gly Lys Pro Gly Ile Asp Gly
145                 150                 155                 160

Ile Asp Gly Thr Asn Gly Gln Pro Gly Glu Ala Gly Tyr Gln Gly Gly
                165                 170                 175

Arg Gly Thr Arg Gly Gln Leu Gly Glu Thr Gly Asp Val Gly Gln Asn
            180                 185                 190

Gly Asp Arg Gly Ala Pro Gly Pro Asp Gly Ser Lys Gly Ser Ala Gly
        195                 200                 205

Arg Pro Gly Leu Arg
    210


<210> SEQ ID NO 13
<211> LENGTH: 696
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 13

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg      60

cagtatgaag atggtgaaaa aggtgaaaag ggcgagaaag gtgagaaagg cgaaaagggt     120

gaaaaaggtc cgcagggtgt tgttggtgca gatggtaaag acggtacccc gggtaatgca     180

ggtcagaaag gtccgtcagg tgaacctggc agccctggta aagcaggtag tgccggtgag     240

cagggtccgc cgggcaaaga tggtagtaat ggtgagccgg gtagccctgg caaagaaggt     300

gaacgtggtc tggcaggacc gccgggtcct gatggtcgcc gcggtgaaac gggttcaccg     360

ggtattgccg gtgccctggg taaaccaggt ctggaaggtc cgaaaggtta tcctggtctg     420

cgcggtcgtg atggtaccaa tggcaaacgt ggcgaacagg gcgaaaccgg tccagatggt     480

gttcgtggta ttccgggtaa cgatggtcag agcggtaaac cgggcattga tggtattgat     540

ggcaccaatg gtcagcctgg cgaagcaggt tatcagggtg gtcgcggtac ccgtggtcag     600

ctgggtgaaa caggtgatgt tggtcagaat ggtgatcgcg gcgcaccggg tccggatggt     660

agcaaaggta gcgccggtcg tccgggttta cgttaa                               696


<210> SEQ ID NO 14
<211> LENGTH: 231
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 14
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Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Ala Gln Tyr Glu Asp Gly Glu Lys Gly Glu Lys Gly Glu
            20                  25                  30

Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Pro Gln Gly Val Val
        35                  40                  45

Gly Ala Asp Gly Lys Asp Gly Thr Pro Gly Asn Ala Gly Gln Lys Gly
    50                  55                  60

Pro Ser Gly Glu Pro Gly Ser Pro Gly Lys Ala Gly Ser Ala Gly Glu
65                  70                  75                  80

Gln Gly Pro Pro Gly Lys Asp Gly Ser Asn Gly Glu Pro Gly Ser Pro
                85                  90                  95

Gly Lys Glu Gly Glu Arg Gly Leu Ala Gly Pro Pro Gly Pro Asp Gly
            100                 105                 110

Arg Arg Gly Glu Thr Gly Ser Pro Gly Ile Ala Gly Ala Leu Gly Lys
        115                 120                 125

Pro Gly Leu Glu Gly Pro Lys Gly Tyr Pro Gly Leu Arg Gly Arg Asp
    130                 135                 140

Gly Thr Asn Gly Lys Arg Gly Glu Gln Gly Glu Thr Gly Pro Asp Gly
145                 150                 155                 160

Val Arg Gly Ile Pro Gly Asn Asp Gly Gln Ser Gly Lys Pro Gly Ile
                165                 170                 175

Asp Gly Ile Asp Gly Thr Asn Gly Gln Pro Gly Glu Ala Gly Tyr Gln
            180                 185                 190

Gly Gly Arg Gly Thr Arg Gly Gln Leu Gly Glu Thr Gly Asp Val Gly
        195                 200                 205

Gln Asn Gly Asp Arg Gly Ala Pro Gly Pro Asp Gly Ser Lys Gly Ser
    210                 215                 220

Ala Gly Arg Pro Gly Leu Arg
225                 230

<210> SEQ ID NO 15
<211> LENGTH: 696
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 15

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg 60

cagtatgaag atggtgataa aggtgataag ggcgacaaag gtgacaaagg cgataagggt 120

gataaaggtc cgcagggtgt tgttggtgca gatggtaaag acggtacccc gggtaatgca 180

ggtcagaaag gtccgtcagg tgaacctggc agccctggta aagcaggtag tgccggtgag 240

cagggtccgc cgggcaaaga tggtagtaat ggtgagccgg gtagccctgg caaagaaggt 300

gaacgtggtc tggcaggacc gccgggtcct gatggtcgcc gcggtgaaac gggttcaccg 360

ggtattgccg gtgccctggg taaaccaggt ctggaaggtc cgaaaggtta tcctggtctg 420

cgcggtcgtg atggtaccaa tggcaaacgt ggcgaacagg gcgaaaccgg tccagatggt 480

gttcgtggta ttccgggtaa cgatggtcag agcggtaaac cgggcattga tggtattgat 540

ggcaccaatg gtcagcctgg cgaagcaggt tatcagggtg gtcgcggtac ccgtggtcag 600

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ctgggtgaaa caggtgatgt tggtcagaat ggtgatcgcg gcgcaccggg tccggatggt    660

agcaaaggta gcgccggtcg tccgggttta cgttaa                              696


<210> SEQ ID NO 16
<211> LENGTH: 231
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 16

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Ala Gln Tyr Glu Asp Gly Asp Lys Gly Asp Lys Gly Asp
            20                  25                  30

Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Pro Gln Gly Val Val
        35                  40                  45

Gly Ala Asp Gly Lys Asp Gly Thr Pro Gly Asn Ala Gly Gln Lys Gly
    50                  55                  60

Pro Ser Gly Glu Pro Gly Ser Pro Gly Lys Ala Gly Ser Ala Gly Glu
65                  70                  75                  80

Gln Gly Pro Pro Gly Lys Asp Gly Ser Asn Gly Glu Pro Gly Ser Pro
                85                  90                  95

Gly Lys Glu Gly Glu Arg Gly Leu Ala Gly Pro Pro Gly Pro Asp Gly
            100                 105                 110

Arg Arg Gly Glu Thr Gly Ser Pro Gly Ile Ala Gly Ala Leu Gly Lys
        115                 120                 125

Pro Gly Leu Glu Gly Pro Lys Gly Tyr Pro Gly Leu Arg Gly Arg Asp
    130                 135                 140

Gly Thr Asn Gly Lys Arg Gly Glu Gln Gly Glu Thr Gly Pro Asp Gly
145                 150                 155                 160

Val Arg Gly Ile Pro Gly Asn Asp Gly Gln Ser Gly Lys Pro Gly Ile
                165                 170                 175

Asp Gly Ile Asp Gly Thr Asn Gly Gln Pro Gly Glu Ala Gly Tyr Gln
            180                 185                 190

Gly Gly Arg Gly Thr Arg Gly Gln Leu Gly Glu Thr Gly Asp Val Gly
        195                 200                 205

Gln Asn Gly Asp Arg Gly Ala Pro Gly Pro Asp Gly Ser Lys Gly Ser
    210                 215                 220

Ala Gly Arg Pro Gly Leu Arg
225                 230


<210> SEQ ID NO 17
<211> LENGTH: 2232
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 17

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg     60

cagtatgaag atcaccatca ccaccaccac catcaccact ctggctcgag cctggtgccg    120
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cgcggcagcc atatgtctgg ctcgagcagt aaaggtgaag aactgttcac cggtgttgtt 180

ccgatcctgg ttgaactgga tggtgatgtt aacggccaca aattctctgt tcgtggtgaa 240

ggtgaaggtg atgcaaccaa cggtaaactg accctgaaat tcatctgcac taccggtaaa 300

ctgccggttc catggccgac tctggtgact accctgacct atggtgttca gtgtttttct 360

cgttacccgg atcacatgaa gcagcatgat ttcttcaaat ctgcaatgcc ggaaggttat 420

gtacaggagc gcaccatttc tttcaaagac gatggcacct acaaaacccg tgcagaggtt 480

aaatttgaag gtgatactct ggtgaaccgt attgaactga aaggcattga tttcaaagag 540

gacggcaaca tcctgggcca caaactggaa tataacttca actcccataa cgtttacatc 600

accgcagaca aacagaagaa cggtatcaaa gctaacttca aaattcgcca taacgttgaa 660

gacggtagcg tacagctggc ggaccactac cagcagaaca ctccgatcgg tgatggtccg 720

gttctgctgc cggataacca ctacctgtcc acccagtcta aactgtccaa agacccgaac 780

gaaaagcgcg accacatggt gctgctggag ttcgttactg cagcaggtat cacgcacggc 840

atggatgaac tctacaaatc tggcgcgccg ggcggtccgc agggtgttgt tggtgcagat 900

ggtaaagacg gtaccccggg taatgcaggt cagaaaggtc cgtcaggtga acctggcagc 960

cctggtaaag caggtagtgc cggtgagcag ggtccgccgg gcaaagatgg tagtaatggt 1020

gagccgggta gccctggcaa agaaggtgaa cgtggtctgg caggaccgcc gggtcctgat 1080

ggtcgccgcg gtgaaacggg ttcaccgggt attgccggtg ccctgggtaa accaggtctg 1140

gaaggtccga aaggttatcc tggtctgcgc ggtcgtgatg gtaccaatgg caaacgtggc 1200

gaacagggcg aaaccggtcc agatggtgtt cgtggtattc cgggtaacga tggtcagagc 1260

ggtaaaccgg gcattgatgg tattgatggc accaatggtc agcctggcga agcaggttat 1320

cagggtggtc gcggtacccg tggtcagctg ggtgaaacag gtgatgttgg tcagaatggt 1380

gatcgcggcg caccgggtcc ggatggtagc aaaggtagcg ccggtcgtcc gggtttacgt 1440

cacccagaaa cgctggtgaa agtaaaagat gctgaagatc agttgggtgc acgagtgggt 1500

tacatcgaac tggatctcaa cagcggtaag atccttgaga gttttcgccc cgaagaacgt 1560

tttccaatga tgagcacttt taaagttctg ctatgtggcg cggtattatc ccgtattgac 1620

gccgggcaag agcaactcgg tcgccgcata cactattctc agaatgactt ggttgagtac 1680

tcaccagtca cagaaaagca tcttacggat ggcatgacag taagagaatt atgcagtgct 1740

gccataacca tgagtgataa cactgcggcc aacttacttc tgacaacgat cggaggaccg 1800

aaggagctaa ccgctttttt gcacaacatg ggggatcatg taactcgcct tgatcgttgg 1860

gaaccggagc tgaatgaagc cataccaaac gacgagcgtg acaccacgat gcctgtagca 1920

atggcaacaa cgttgcgcaa actattaact ggcgaactac ttactctagc ttcccggcaa 1980

caattaatag actggatgga ggcggataaa gttgcaggac cacttctgcg ctcggccctt 2040

ccggctggct ggtttattgc tgataaatct ggagccggtg agcgtgggtc tcgcggtatc 2100

attgcagcac tggggccaga tggtaagccc tcccgtatcg tagttatcta cacgacgggg 2160

agtcaggcaa ctatggatga acgaaataga cagatcgctg agataggtgc ctcactgatt 2220

aagcattggt aa 2232

<210> SEQ ID NO 18
<211> LENGTH: 743
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 18

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Ala Gln Tyr Glu Asp His His His His His His His His
            20                  25                  30

His Ser Gly Ser Ser Leu Val Pro Arg Gly Ser His Met Ser Gly Ser
        35                  40                  45

Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
    50                  55                  60

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Arg Gly Glu
65                  70                  75                  80

Gly Glu Gly Asp Ala Thr Asn Gly Lys Leu Thr Leu Lys Phe Ile Cys
                85                  90                  95

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
            100                 105                 110

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
        115                 120                 125

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
    130                 135                 140

Thr Ile Ser Phe Lys Asp Asp Gly Thr Tyr Lys Thr Arg Ala Glu Val
145                 150                 155                 160

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

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
            180                 185                 190

Phe Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
        195                 200                 205

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Val Glu Asp Gly Ser Val
    210                 215                 220

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
225                 230                 235                 240

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Lys Leu Ser
                245                 250                 255

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
            260                 265                 270

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ser Gly
        275                 280                 285

Ala Pro Gly Gly Pro Gln Gly Val Val Gly Ala Asp Gly Lys Asp Gly
    290                 295                 300

Thr Pro Gly Asn Ala Gly Gln Lys Gly Pro Ser Gly Glu Pro Gly Ser
305                 310                 315                 320

Pro Gly Lys Ala Gly Ser Ala Gly Glu Gln Gly Pro Pro Gly Lys Asp
                325                 330                 335

Gly Ser Asn Gly Glu Pro Gly Ser Pro Gly Lys Glu Gly Glu Arg Gly
            340                 345                 350

Leu Ala Gly Pro Pro Gly Pro Asp Gly Arg Arg Gly Glu Thr Gly Ser
        355                 360                 365
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Pro Gly Ile Ala Gly Ala Leu Gly Lys Pro Gly Leu Glu Gly Pro Lys
    370                 375                 380

Gly Tyr Pro Gly Leu Arg Gly Arg Asp Gly Thr Asn Gly Lys Arg Gly
385                 390                 395                 400

Glu Gln Gly Glu Thr Gly Pro Asp Gly Val Arg Gly Ile Pro Gly Asn
                405                 410                 415

Asp Gly Gln Ser Gly Lys Pro Gly Ile Asp Gly Ile Asp Gly Thr Asn
            420                 425                 430

Gly Gln Pro Gly Glu Ala Gly Tyr Gln Gly Gly Arg Gly Thr Arg Gly
        435                 440                 445

Gln Leu Gly Glu Thr Gly Asp Val Gly Gln Asn Gly Asp Arg Gly Ala
    450                 455                 460

Pro Gly Pro Asp Gly Ser Lys Gly Ser Ala Gly Arg Pro Gly Leu Arg
465                 470                 475                 480

His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
                485                 490                 495

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
            500                 505                 510

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
        515                 520                 525

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu
    530                 535                 540

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
545                 550                 555                 560

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
                565                 570                 575

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
            580                 585                 590

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
        595                 600                 605

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
    610                 615                 620

Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala
625                 630                 635                 640

Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
                645                 650                 655

Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
            660                 665                 670

Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
        675                 680                 685

Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
    690                 695                 700

Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
705                 710                 715                 720

Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly
                725                 730                 735

Ala Ser Leu Ile Lys His Trp
            740


<210> SEQ ID NO 19
<211> LENGTH: 2232
<212> TYPE: DNA
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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 19

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg 60

cagtatgaag atcaccatca ccaccaccac catcaccact ctggctcgag cctggtgccg 120

cgcggcagcc atatgtctgg ctcgagcagt aaaggtgaag aactgttcac cggtgttgtt 180

ccgatcctgg ttgaactgga tggtgatgtt aacggccaca aattctctgt tcgtggtgaa 240

ggtgaaggtg atgcaaccaa cggtaaactg accctgaaat tcatctgcac taccggtaaa 300

ctgccggttc catggccgac tctggtgact accctgacct atggtgttca gtgtttttct 360

cgttacccgg atcacatgaa gcagcatgat ttcttcaaat ctgcaatgcc ggaaggttat 420

gtacaggagc gcaccatttc tttcaaagac gatggcacct acaaaacccg tgcagaggtt 480

aaatttgaag gtgatactct ggtgaaccgt attgaactga aaggcattga tttcaaagag 540

gacggcaaca tcctgggcca caaactggaa tataacttca actcccataa cgtttacatc 600

accgcagaca aacagaagaa cggtatcaaa gctaacttca aaattcgcca taacgttgaa 660

gacggtagcg tacagctggc ggaccactac cagcagaaca ctccgatcgg tgatggtccg 720

gttctgctgc cggataacca ctacctgtcc acccagtcta aactgtccaa agacccgaac 780

gaaaagcgcg accacatggt gctgctggag ttcgttactg cagcaggtat cacgcacggc 840

atggatgaac tctacaaatc tggcgcgccg ggcggtccgc agggtgttgt tggtgcagat 900

ggtaaagacg gtaccccggg taatgcaggt cagaaaggtc cgtcaggtga acctggcagc 960

cctggtaaag caggtagtgc cggtgagcag ggtccgccgg gcaaagatgg tagtaatggt 1020

gagccgggta gccctggcaa agaaggtgaa cgtggtctgg caggaccgcc gggtcctgat 1080

ggtcgccgcg gtgaaacggg ttcaccgggt attgccggtg ccctgggtaa accaggtctg 1140

gaaggtccga aaggttatcc tggtctgcgc ggtcgtgatg gtaccaatgg caaacgtggc 1200

gaacagggcg aaaccggtcc agatggtgtt cgtggtattc cgggtaacga tggtcagagc 1260

ggtaaaccgg gcattgatgg tattgatggc accaatggtc agcctggcga agcaggttat 1320

cagggtggtc gcggtacccg tggtcagctg ggtgaaacag gtgatgttgg tcagaatggt 1380

gatcgcggcg caccgggtcc ggatggtagc aaaggtagcg ccggtcgtcc gggtttacgt 1440

cacccagaaa cgctggtgaa agtaaaagat gctgaagatc agttgggtgc acgagtgggt 1500

tacatcgaac tggatctcaa cagcggtaag atccttgaga gttttcgccc cgaagaacgt 1560

tttccaatga tgagcacttt taaagttctg ctatgtggcg cggtattatc ccgtattgac 1620

gccgggcaag agcaactcgg tcgccgcata cactattctc agaatgactt ggttgagtac 1680

tcaccagtca cagaaaagca tcttacggat ggcatgacag taagagaatt atgcagtgct 1740

gccataacca tgagtgataa cactgcggcc aacttacttc tgacaacgat cggaggaccg 1800

aaggagctaa ccgctttttt gcacaacatg ggggatcatg taactcgcct tgatcgttgg 1860

gaaccggagc tgaatgaagc cataccaaac gacgagcgtg acaccacgat gcctgtagca 1920

atggcaacaa cgttgcgcaa actattaact ggcgaactac ttactctagc ttcccggcaa 1980

caattaatag actggatgga ggcggataaa gttgcaggac cacttctgcg ctcggccctt 2040

ccggctggct ggtttattgc tgataaatct ggagccggtg agcgtgggtc tcgcggtatc 2100

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attgcagcac tggggccaga tggtaagccc tcccgtatcg tagttatcta cacgacgggg   2160

agtcaggcaa ctatggatga acgaaataga cagatcgctg agataggtgc ctcactgatt   2220

aagcattggt aa                                                       2232


<210> SEQ ID NO 20
<211> LENGTH: 743
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 20

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Ala Gln Tyr Glu Asp His His His His His His His His
            20                  25                  30

His Ser Gly Ser Ser Leu Val Pro Arg Gly Ser His Met Ser Gly Ser
        35                  40                  45

Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
    50                  55                  60

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Arg Gly Glu
65                  70                  75                  80

Gly Glu Gly Asp Ala Thr Asn Gly Lys Leu Thr Leu Lys Phe Ile Cys
                85                  90                  95

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
            100                 105                 110

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
        115                 120                 125

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
    130                 135                 140

Thr Ile Ser Phe Lys Asp Asp Gly Thr Tyr Lys Thr Arg Ala Glu Val
145                 150                 155                 160

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

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
            180                 185                 190

Phe Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
        195                 200                 205

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Val Glu Asp Gly Ser Val
    210                 215                 220

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
225                 230                 235                 240

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Lys Leu Ser
                245                 250                 255

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
            260                 265                 270

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ser Gly
        275                 280                 285

Ala Pro Gly Gly Pro Gln Gly Val Val Gly Ala Asp Gly Lys Asp Gly
    290                 295                 300

Thr Pro Gly Asn Ala Gly Gln Lys Gly Pro Ser Gly Glu Pro Gly Ser
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305                 310                 315                 320

Pro Gly Lys Ala Gly Ser Ala Gly Glu Gln Gly Pro Pro Gly Lys Asp
                325                 330                 335

Gly Ser Asn Gly Glu Pro Gly Ser Pro Gly Lys Glu Gly Glu Arg Gly
            340                 345                 350

Leu Ala Gly Pro Pro Gly Pro Asp Gly Arg Arg Gly Glu Thr Gly Ser
        355                 360                 365

Pro Gly Ile Ala Gly Ala Leu Gly Lys Pro Gly Leu Glu Gly Pro Lys
    370                 375                 380

Gly Tyr Pro Gly Leu Arg Gly Arg Asp Gly Thr Asn Gly Lys Arg Gly
385                 390                 395                 400

Glu Gln Gly Glu Thr Gly Pro Asp Gly Val Arg Gly Ile Pro Gly Asn
                405                 410                 415

Asp Gly Gln Ser Gly Lys Pro Gly Ile Asp Gly Ile Asp Gly Thr Asn
            420                 425                 430

Gly Gln Pro Gly Glu Ala Gly Tyr Gln Gly Gly Arg Gly Thr Arg Gly
        435                 440                 445

Gln Leu Gly Glu Thr Gly Asp Val Gly Gln Asn Gly Asp Arg Gly Ala
    450                 455                 460

Pro Gly Pro Asp Gly Ser Lys Gly Ser Ala Gly Arg Pro Gly Leu Arg
465                 470                 475                 480

His Pro Glu Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly
                485                 490                 495

Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu
            500                 505                 510

Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys
        515                 520                 525

Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu
    530                 535                 540

Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr
545                 550                 555                 560

Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu
                565                 570                 575

Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu
            580                 585                 590

Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His
        595                 600                 605

Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu
    610                 615                 620

Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala
625                 630                 635                 640

Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu
                645                 650                 655

Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala
            660                 665                 670

Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp
        675                 680                 685

Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu
    690                 695                 700

Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly
705                 710                 715                 720
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Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly
                725                 730                 735

Ala Ser Leu Ile Lys His Trp
            740


<210> SEQ ID NO 21
<211> LENGTH: 786
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

Met Ala Gly Leu Thr Ala Ala Ala Pro Arg Pro Gly Val Leu Leu Leu
1               5                   10                  15

Leu Leu Ser Ile Leu His Pro Ser Arg Pro Gly Gly Val Pro Gly Ala
            20                  25                  30

Ile Pro Gly Gly Val Pro Gly Gly Val Phe Tyr Pro Gly Ala Gly Leu
        35                  40                  45

Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro Gly Gly Lys Pro Leu Lys
    50                  55                  60

Pro Val Pro Gly Gly Leu Ala Gly Ala Gly Leu Gly Ala Gly Leu Gly
65                  70                  75                  80

Ala Phe Pro Ala Val Thr Phe Pro Gly Ala Leu Val Pro Gly Gly Val
                85                  90                  95

Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala Lys Ala Gly Ala Gly Leu
            100                 105                 110

Gly Gly Val Pro Gly Val Gly Gly Leu Gly Val Ser Ala Gly Ala Val
        115                 120                 125

Val Pro Gln Pro Gly Ala Gly Val Lys Pro Gly Lys Val Pro Gly Val
    130                 135                 140

Gly Leu Pro Gly Val Tyr Pro Gly Gly Val Leu Pro Gly Ala Arg Phe
145                 150                 155                 160

Pro Gly Val Gly Val Leu Pro Gly Val Pro Thr Gly Ala Gly Val Lys
                165                 170                 175

Pro Lys Ala Pro Gly Val Gly Gly Ala Phe Ala Gly Ile Pro Gly Val
            180                 185                 190

Gly Pro Phe Gly Gly Pro Gln Pro Gly Val Pro Leu Gly Tyr Pro Ile
        195                 200                 205

Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly Leu Pro Tyr Thr Thr Gly
    210                 215                 220

Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly Val Ala Gly Ala Ala Gly
225                 230                 235                 240

Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val Gly Pro Gln Ala Ala Ala
                245                 250                 255

Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe Gly Ala Gly Ala Ala Gly
            260                 265                 270

Val Leu Pro Gly Val Gly Gly Ala Gly Val Pro Gly Val Pro Gly Ala
        275                 280                 285

Ile Pro Gly Ile Gly Gly Ile Ala Gly Val Gly Thr Pro Ala Ala Ala
    290                 295                 300

Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Ala
305                 310                 315                 320

Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val Val Gly Val
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                325                 330                 335

Pro Gly Ala Gly Val Pro Gly Val Gly Val Pro Gly Ala Gly Ile Pro
            340                 345                 350

Val Val Pro Gly Ala Gly Ile Pro Gly Ala Ala Val Pro Gly Val Val
        355                 360                 365

Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys Tyr Gly
    370                 375                 380

Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly Val Gly
385                 390                 395                 400

Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile Pro Gly
                405                 410                 415

Val Ala Gly Val Pro Gly Val Gly Gly Val Pro Gly Val Gly Gly Val
            420                 425                 430

Pro Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala Ala Ala Lys
        435                 440                 445

Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly Val Leu Gly Gly Leu Val
    450                 455                 460

Pro Gly Pro Gln Ala Ala Val Pro Gly Val Pro Gly Thr Gly Gly Val
465                 470                 475                 480

Pro Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys
                485                 490                 495

Ala Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala Pro Gly Val
            500                 505                 510

Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Leu Ala Pro
        515                 520                 525

Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val
    530                 535                 540

Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala Lys Ser Ala
545                 550                 555                 560

Ala Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala Gly Leu Gly
                565                 570                 575

Ala Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro Gly Leu Gly
            580                 585                 590

Val Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly
        595                 600                 605

Phe Gly Ala Gly Ala Asp Glu Gly Val Arg Arg Ser Leu Ser Pro Glu
    610                 615                 620

Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln His Leu Pro Ser Thr Pro
625                 630                 635                 640

Ser Ser Pro Arg Val Pro Gly Ala Leu Ala Ala Ala Lys Ala Ala Lys
                645                 650                 655

Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly Ala Leu Gly
            660                 665                 670

Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro Ala Ala Ala
        675                 680                 685

Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val
    690                 695                 700

Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly Val Pro
705                 710                 715                 720

Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys Ala
                725                 730                 735
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Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala Gly
            740                 745                 750

Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu Ser
        755                 760                 765

Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys
    770                 775                 780

Arg Lys
785


<210> SEQ ID NO 22
<211> LENGTH: 2361
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

atggcgggtc tgacggcggc ggccccgcgg cccggagtcc tcctgctcct gctgtccatc      60

ctccacccct ctcggcctgg aggggtccct ggggccattc ctggtggagt tcctggagga     120

gtcttttatc caggggctgg tctcggagcc cttggaggag gagcgctggg gcctggaggc     180

aaacctctta agccagttcc cggagggctt gcgggtgctg gccttggggc agggctcggc     240

gccttccccg cagttacctt tccgggggct ctggtgcctg gtggagtggc tgacgctgct     300

gcagcctata aagctgctaa ggctggcgct gggcttggtg gtgtcccagg agttggtggc     360

ttaggagtgt ctgcaggtgc ggtggttcct cagcctggag ccggagtgaa gcctgggaaa     420

gtgccgggtg tggggctgcc aggtgtatac ccaggtggcg tgctcccagg agctcggttc     480

cccggtgtgg gggtgctccc tggagttccc actggagcag gagttaagcc caaggctcca     540

ggtgtaggtg gagcttttgc tggaatccca ggagttggac cctttggggg accgcaacct     600

ggagtcccac tggggtatcc catcaaggcc cccaagctgc ctggtggcta tggactgccc     660

tacaccacag ggaaactgcc ctatggctat gggcccggag gagtggctgg tgcagcgggc     720

aaggctggtt acccaacagg gacaggggtt ggcccccagg cagcagcagc agcggcagct     780

aaagcagcag caaagttcgg tgctggagca gccggagtcc tccctggtgt tggaggggct     840

ggtgttcctg gcgtgcctgg ggcaattcct ggaattggag gcatcgcagg cgttgggact     900

ccagctgcag ctgcagctgc agcagcagcc gctaaggcag ccaagtatgg agctgctgca     960

ggcttagtgc ctggtgggcc aggctttggc ccgggagtag ttggtgtccc aggagctggc    1020

gttccaggtg ttggtgtccc aggagctggg attccagttg tcccaggtgc tgggatccca    1080

ggtgctgcgg ttccaggggt tgtgtcacca gaagcagctg ctaaggcagc tgcaaaggca    1140

gccaaatacg gggccaggcc cggagtcgga gttggaggca ttcctactta cggggttgga    1200

gctgggggct ttcccggctt tggtgtcgga gtcggaggta tccctggagt cgcaggtgtc    1260

cctggtgtcg gaggtgttcc cggagtcgga ggtgtcccgg gagttggcat ttcccccgaa    1320

gctcaggcag cagctgccgc caaggctgcc aagtacggtg ctgcaggagc aggagtgctg    1380

ggtgggctag tgccaggtcc ccaggcggca gtcccaggtg tgccgggcac gggaggagtg    1440

ccaggagtgg ggaccccagc agctgcagct gctaaagcag ccgccaaagc cgcccagttt    1500

gggttagttc ctggtgtcgg cgtggctcct ggagttggcg tggctcctgg tgtcggtgtg    1560

gctcctggag ttggcttggc tcctggagtt ggcgtggctc ctggagttgg tgtggctcct    1620

ggcgttggcg tggctcccgg cattggccct ggtggagttg cagctgcagc aaaatccgct    1680
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gccaaggtgg ctgccaaagc ccagctccga gctgcagctg ggcttggtgc tggcatccct 1740

ggacttggag ttggtgtcgg cgtccctgga cttggagttg gtgctggtgt tcctggactt 1800

ggagttggtg ctggtgttcc tggcttcggg gcaggtgcag atgagggagt taggcggagc 1860

ctgtcccctg agctcaggga aggagatccc tcctcctctc agcacctccc cagcaccccc 1920

tcatcaccca gggtacctgg agccctggct gccgctaaag cagccaaata tggagcagca 1980

gtgcctgggg tccttggagg gctcggggct ctcggtggag taggcatccc aggcggtgtg 2040

gtgggagccg gacccgccgc cgccgctgcc gcagccaaag ctgctgccaa agccgcccag 2100

tttggcctag tgggagccgc tgggctcgga ggactcggag tcggagggct tggagttcca 2160

ggtgttgggg gccttggagg tatacctcca gctgcagccg ctaaagcagc taaatacggt 2220

gctgctggcc ttggaggtgt cctagggggt gccgggcagt tcccacttgg aggagtggca 2280

gcaagacctg gcttcggatt gtctcccatt ttcccaggtg ggcctgcct ggggaaagct 2340

tgtggccgga agagaaaatg a 2361

<210> SEQ ID NO 23
<211> LENGTH: 2418
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 23

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg 60

cagtatgaag atcaccatca ccaccaccac catcaccact ctggctcgag cctggtgccg 120

cgcggcagcc atatgggtgg cgtaccaggc gcaattcctg gggtgtccc aggcggtgtt 180

ttttatccgg gcgccggtct tggcgcactg ggtggcggtg cactgggccc gggcggcaaa 240

ccgctgaaac cggtaccagg tggtttagca ggcgccggct taggcgcagg tctgggagca 300

tttccggcag ttacctttcc aggggcactg gttcctggag gtgtggccga tgcagccgcg 360

gcatataaag ccgctaaagc cggtgcgggt ttaggaggcg tcccaggtgt cggtggcctg 420

ggtgttagcg ccggtgcagt tgttccgcag ccgggagcag gggttaaacc tggtaaagtg 480

ccgggagtag gtctgccagg cgtttatcct ggtggtgttt tgccgggtgc ccgttttccg 540

ggcgttggtg ttcttccagg cgtgccgacc ggagccggtg ttaaaccgaa agcccccggt 600

gttggaggtg catttgcagg catcccggga gttggcccgt ttggtggtcc gcaacctggg 660

gttccgttag gttatccgat taaagcaccg aaactgcccg gcggttatgg tctgccgtac 720

acaaccggta aactgccgta tggttatggc ccgggtggag ttgcgggtgc agcaggtaaa 780

gcgggttatc ctaccggaac cggtgtaggt ccgcaggccg ctgctgccgc cgccgcaaaa 840

gcagcggcta aatttggcgc cggagcagcg ggtgttctgc ctggagttgg tggtgcgggc 900

gtgccagggg tacctggtgc aattccgggt attggtggta ttgccggtgt cggcaccccg 960

gccgcggcag ctgcggcagc ggcggctgcc aaagctgcta aatacggtgc cgcggcgggt 1020

ctggtgccag gaggtccggg ttttggtccg ggagtggttg gcgtgcctgg cgcaggcgtt 1080

cctggtgtgg gcgttccagg tgcagggatt cctgttgtgc ctggtgccgg tattcccggc 1140

gcggccgttc cgggggtggt tagcccggaa gccgcagcga aggctgcggc aaaggcagca 1200

-continued

aagtatggcg cacgcccagg agtcggcgtg ggtggtatcc cgacctatgg ggtgggcgca 1260

gggggttttc ctggtttcgg cgtaggtgta ggaggtatac cgggcgtggc cggtgtacca 1320

ggggttggtg gcgtccctgg tgttggcggt gtgccaggtg ttggtatttc accggaagca 1380

caggcagcag ccgcagctaa ggcagcgaaa tatggtgccg ccggcgcagg agttttaggt 1440

gggctggttc cgggcccgca ggcagctgtg ccgggggttc caggcaccgg tggtgtccct 1500

ggagtcggta cgccggctgc agcggcagcc aaagcggctg cgaaagcagc acagtttggc 1560

ttagtaccgg gtgtgggagt tgcccccggc gttggcgttg ctccaggggt gggtgttgct 1620

cctggcgtcg gtctggctcc tggagtgggc gtagcacccg gtgtgggggt ggccccgggt 1680

gttggggttg caccgggtat cggtccgggc ggtgtcgcag cagcagctaa aagcgcggcg 1740

aaagttgcgg ccaaagccca actgcgcgcc gccgcgggcc tcggtgcagg tattccgggg 1800

ctgggtgtcg gagttggagt cccgggtttg ggcgtgggcg cgggagttcc gggactggga 1860

gtgggtgccg gagttcctgg ctttggtgca ggcgcagatg aaggtgttcg tcgtagcctg 1920

agtccggaac tgcgtgaagg tgatccgagt agcagccagc atctgccgag caccccgagc 1980

agcccgcgtg ttccgggtgc attagctgca gcaaaagccg ccaagtatgg tgcagccgtg 2040

ccgggcgtct taggtggtct gggcgccctg ggtggtgtag gcattccggg aggtgttgtg 2100

ggtgcaggac cggccgccgc agctgcggcc gccaaagcag ctgcaaaagc ggcccagttt 2160

ggtttagtgg gcgccgcagg tttaggcggt ttaggtgtgg gtggactggg tgtacctggc 2220

gtaggcggtc tgggtggaat tccgcccgca gcggccgcga aagcggcaaa atatggcgcg 2280

gcaggcctgg gcggcgtgct gggtggggca ggtcagtttc cgctgggcgg ggttgccgca 2340

cgtccgggat ttggtctgag cccgattttc cctggcggcg catgtctggg taaagcatgt 2400

ggtcgtaaac gtaaataa 2418

<210> SEQ ID NO 24
<211> LENGTH: 805
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 24

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1 5 10 15

Ala Ser Ala Ala Gln Tyr Glu Asp His His His His His His His His
20 25 30

His Ser Gly Ser Ser Leu Val Pro Arg Gly Ser His Met Gly Gly Val
35 40 45

Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe Tyr Pro Gly
50 55 60

Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro Gly Gly Lys
65 70 75 80

Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly Leu Gly Ala
85 90 95

Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala Leu Val Pro
100 105 110

Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala Lys Ala Gly
115 120 125

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Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly Val Ser Ala
    130                 135                 140

Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro Gly Lys Val
145                 150                 155                 160

Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val Leu Pro Gly
                165                 170                 175

Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro Thr Gly Ala
            180                 185                 190

Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe Ala Gly Ile
        195                 200                 205

Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val Pro Leu Gly
    210                 215                 220

Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly Leu Pro Tyr
225                 230                 235                 240

Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly Val Ala Gly
                245                 250                 255

Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val Gly Pro Gln
            260                 265                 270

Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe Gly Ala Gly
        275                 280                 285

Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val Pro Gly Val
    290                 295                 300

Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val Gly Thr Pro
305                 310                 315                 320

Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly
                325                 330                 335

Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val
            340                 345                 350

Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val Pro Gly Ala
        355                 360                 365

Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala Ala Val Pro
    370                 375                 380

Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala
385                 390                 395                 400

Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr
                405                 410                 415

Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly
            420                 425                 430

Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val Pro Gly Val
        435                 440                 445

Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala
    450                 455                 460

Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly Val Leu Gly
465                 470                 475                 480

Gly Leu Val Pro Gly Pro Gln Ala Ala Val Pro Gly Val Pro Gly Thr
                485                 490                 495

Gly Gly Val Pro Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Lys Ala
            500                 505                 510

Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala
        515                 520                 525
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Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly
    530                 535                 540

Leu Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly
545                 550                 555                 560

Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala
                565                 570                 575

Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala
            580                 585                 590

Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro
        595                 600                 605

Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly
    610                 615                 620

Val Pro Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg Arg Ser Leu
625                 630                 635                 640

Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln His Leu Pro
                645                 650                 655

Ser Thr Pro Ser Ser Pro Arg Val Pro Gly Ala Leu Ala Ala Ala Lys
            660                 665                 670

Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly
        675                 680                 685

Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro
    690                 695                 700

Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe
705                 710                 715                 720

Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu
                725                 730                 735

Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala
            740                 745                 750

Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly
        755                 760                 765

Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe
    770                 775                 780

Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys
785                 790                 795                 800

Gly Arg Lys Arg Lys
                805


<210> SEQ ID NO 25
<211> LENGTH: 2358
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 25

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg     60

cagtatgaag atatgggtgg cgtaccaggc gcaattcctg ggggtgtccc aggcggtgtt    120

ttttatccgg gcgccggtct tggcgcactg ggtggcggtg cactgggccc gggcggcaaa    180

ccgctgaaac cggtaccagg tggtttagca ggcgccggct taggcgcagg tctgggagca    240

tttccggcag ttacctttcc aggggcactg gttcctggag gtgtggccga tgcagccgcg    300

gcatataaag ccgctaaagc cggtgcgggt ttaggaggcg tcccaggtgt cggtggcctg    360
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ggtgttagcg ccggtgcagt tgttccgcag ccgggagcag gggttaaacc tggtaaagtg    420
ccgggagtag gtctgccagg cgtttatcct ggtggtgttt tgccgggtgc ccgttttccg    480
ggcgttggtg ttcttccagg cgtgccgacc ggagccggtg ttaaaccgaa agcccccggt    540
gttggaggtg catttgcagg catcccggga gttggcccgt ttggtggtcc gcaacctggg    600
gttccgttag gttatccgat taaagcaccg aaactgcccg gcggttatgg tctgccgtac    660
acaaccggta aactgccgta tggttatggc ccgggtggag ttgcgggtgc agcaggtaaa    720
gcgggttatc ctaccggaac cggtgtaggt ccgcaggccg ctgctgccgc cgccgcaaaa    780
gcagcggcta aatttggcgc cggagcagcg ggtgttctgc ctggagttgg tggtgcgggc    840
gtgccagggg tacctggtgc aattccgggt attggtggta ttgccggtgt cggcaccccg    900
gccgcggcag ctgcggcagc ggcggctgcc aaagctgcta aatacggtgc cgcggcgggt    960
ctggtgccag gaggtccggg ttttggtccg ggagtggttg gcgtgcctgg cgcaggcgtt   1020
cctggtgtgg gcgttccagg tgcagggatt cctgttgtgc ctggtgccgg tattcccggc   1080
gcggccgttc cgggggtggt tagcccggaa gccgcagcga aggctgcggc aaaggcagca   1140
aagtatggcg cacgcccagg agtcggcgtg ggtggtatcc cgacctatgg ggtgggcgca   1200
gggggttttc ctggtttcgg cgtaggtgta ggaggtatac cgggcgtggc cggtgtacca   1260
ggggttggtg gcgtccctgg tgttggcggt gtgccaggtg ttggtatttc accggaagca   1320
caggcagcag ccgcagctaa ggcagcgaaa tatggtgccg ccggcgcagg agttttaggt   1380
gggctggttc cgggcccgca ggcagctgtg ccgggggttc caggcaccgg tggtgtccct   1440
ggagtcggta cgccggctgc agcggcagcc aaagcggctg cgaaagcagc acagtttggc   1500
ttagtaccgg gtgtgggagt tgcccccggc gttggcgttg ctccaggggt gggtgttgct   1560
cctggcgtcg gtctggctcc tggagtgggc gtagcacccg gtgtgggggt ggcccgggt    1620
gttggggttg caccgggtat cggtccgggc ggtgtcgcag cagcagctaa aagcgcggcg   1680
aaagttgcgg ccaaagccca actgcgcgcc gccgcgggcc tcggtgcagg tattccgggg   1740
ctgggtgtcg gagttggagt cccgggtttg ggcgtgggcg cgggagttcc gggactggga   1800
gtgggtgccg gagttcctgg ctttggtgca ggcgcagatg aaggtgttcg tcgtagcctg   1860
agtccggaac tgcgtgaagg tgatccgagt agcagccagc atctgccgag caccccgagc   1920
agcccgcgtg ttccgggtgc attagctgca gcaaaagccg ccaagtatgg tgcagccgtg   1980
ccgggcgtct taggtggtct gggcgccctg ggtggtgtag gcattccggg aggtgttgtg   2040
ggtgcaggac cggccgccgc agctgcggcc gccaaagcag ctgcaaaagc ggcccagttt   2100
ggtttagtgg gcgccgcagg tttaggcggt ttaggtgtgg gtggactggg tgtacctggc   2160
gtaggcggtc tgggtggaat tccgcccgca gcggccgcga aagcggcaaa atatggcgcg   2220
gcaggcctgg gcggcgtgct gggtggggca ggtcagtttc cgctgggcgg ggttgccgca   2280
cgtccgggat ttggtctgag cccgattttc cctggcggcg catgtctggg taaagcatgt   2340
ggtcgtaaac gtaaataa                                                 2358
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<210> SEQ ID NO 26
<211> LENGTH: 785
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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      polypeptide

<400> SEQUENCE: 26

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Ala Gln Tyr Glu Asp Met Gly Gly Val Pro Gly Ala Ile
            20                  25                  30

Pro Gly Gly Val Pro Gly Gly Val Phe Tyr Pro Gly Ala Gly Leu Gly
        35                  40                  45

Ala Leu Gly Gly Gly Ala Leu Gly Pro Gly Gly Lys Pro Leu Lys Pro
    50                  55                  60

Val Pro Gly Gly Leu Ala Gly Ala Gly Leu Gly Ala Gly Leu Gly Ala
65                  70                  75                  80

Phe Pro Ala Val Thr Phe Pro Gly Ala Leu Val Pro Gly Gly Val Ala
                85                  90                  95

Asp Ala Ala Ala Ala Tyr Lys Ala Ala Lys Ala Gly Ala Gly Leu Gly
            100                 105                 110

Gly Val Pro Gly Val Gly Gly Leu Gly Val Ser Ala Gly Ala Val Val
        115                 120                 125

Pro Gln Pro Gly Ala Gly Val Lys Pro Gly Lys Val Pro Gly Val Gly
    130                 135                 140

Leu Pro Gly Val Tyr Pro Gly Gly Val Leu Pro Gly Ala Arg Phe Pro
145                 150                 155                 160

Gly Val Gly Val Leu Pro Gly Val Pro Thr Gly Ala Gly Val Lys Pro
                165                 170                 175

Lys Ala Pro Gly Val Gly Gly Ala Phe Ala Gly Ile Pro Gly Val Gly
            180                 185                 190

Pro Phe Gly Gly Pro Gln Pro Gly Val Pro Leu Gly Tyr Pro Ile Lys
        195                 200                 205

Ala Pro Lys Leu Pro Gly Gly Tyr Gly Leu Pro Tyr Thr Thr Gly Lys
    210                 215                 220

Leu Pro Tyr Gly Tyr Gly Pro Gly Gly Val Ala Gly Ala Ala Gly Lys
225                 230                 235                 240

Ala Gly Tyr Pro Thr Gly Thr Gly Val Gly Pro Gln Ala Ala Ala Ala
                245                 250                 255

Ala Ala Ala Lys Ala Ala Ala Lys Phe Gly Ala Gly Ala Ala Gly Val
            260                 265                 270

Leu Pro Gly Val Gly Gly Ala Gly Val Pro Gly Val Pro Gly Ala Ile
        275                 280                 285

Pro Gly Ile Gly Gly Ile Ala Gly Val Gly Thr Pro Ala Ala Ala Ala
    290                 295                 300

Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Ala Gly
305                 310                 315                 320

Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val Val Gly Val Pro
                325                 330                 335

Gly Ala Gly Val Pro Gly Val Gly Val Pro Gly Ala Gly Ile Pro Val
            340                 345                 350

Val Pro Gly Ala Gly Ile Pro Gly Ala Ala Val Pro Gly Val Val Ser
        355                 360                 365

Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala
    370                 375                 380
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Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly Val Gly Ala
385                 390                 395                 400

Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile Pro Gly Val
                405                 410                 415

Ala Gly Val Pro Gly Val Gly Gly Val Pro Gly Val Gly Gly Val Pro
            420                 425                 430

Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala Ala Ala Lys Ala
        435                 440                 445

Ala Lys Tyr Gly Ala Ala Gly Ala Gly Val Leu Gly Gly Leu Val Pro
    450                 455                 460

Gly Pro Gln Ala Ala Val Pro Gly Val Pro Gly Thr Gly Gly Val Pro
465                 470                 475                 480

Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala
                485                 490                 495

Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala Pro Gly Val Gly
            500                 505                 510

Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Leu Ala Pro Gly
        515                 520                 525

Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala
    530                 535                 540

Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala Lys Ser Ala Ala
545                 550                 555                 560

Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala Gly Leu Gly Ala
                565                 570                 575

Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro Gly Leu Gly Val
            580                 585                 590

Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Phe
        595                 600                 605

Gly Ala Gly Ala Asp Glu Gly Val Arg Arg Ser Leu Ser Pro Glu Leu
    610                 615                 620

Arg Glu Gly Asp Pro Ser Ser Ser Gln His Leu Pro Ser Thr Pro Ser
625                 630                 635                 640

Ser Pro Arg Val Pro Gly Ala Leu Ala Ala Ala Lys Ala Ala Lys Tyr
                645                 650                 655

Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly Ala Leu Gly Gly
            660                 665                 670

Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro Ala Ala Ala Ala
        675                 680                 685

Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Gly
    690                 695                 700

Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly Val Pro Gly
705                 710                 715                 720

Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys Ala Ala
                725                 730                 735

Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala Gly Gln
            740                 745                 750

Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro
        755                 760                 765

Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg
    770                 775                 780

Lys
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785

<210> SEQ ID NO 27
<211> LENGTH: 3945
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 27

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg 60

cagtatgaag atcaccatca ccaccaccac catcaccact ctggctcgag cctggtgccg 120

cgcggcagcc atatgtctgg ctcgagcagt aaaggtgaag aactgttcac cggtgttgtt 180

ccgatcctgg ttgaactgga tggtgatgtt aacggccaca aattctctgt tcgtggtgaa 240

ggtgaaggtg atgcaaccaa cggtaaactg accctgaaat tcatctgcac taccggtaaa 300

ctgccggttc catggccgac tctggtgact accctgacct atggtgttca gtgtttttct 360

cgttacccgg atcacatgaa gcagcatgat ttcttcaaat ctgcaatgcc ggaaggttat 420

gtacaggagc gcaccatttc tttcaaagac gatggcacct acaaaacccg tgcagaggtt 480

aaatttgaag gtgatactct ggtgaaccgt attgaactga aaggcattga tttcaaagag 540

gacggcaaca tcctgggcca caaactggaa tataacttca actcccataa cgtttacatc 600

accgcagaca aacagaagaa cggtatcaaa gctaacttca aaattcgcca taacgttgaa 660

gacggtagcg tacagctggc ggaccactac cagcagaaca ctccgatcgg tgatggtccg 720

gttctgctgc cggataacca ctacctgtcc acccagtcta aactgtccaa agacccgaac 780

gaaaagcgcg accacatggt gctgctggag ttcgttactg cagcaggtat cacgcacggc 840

atggatgaac tctacaaatc tggcgcgccg ggcggtggcg taccaggcgc aattcctggg 900

ggtgtcccag gcggtgtttt ttatccgggc gccggtcttg gcgcactggg tggcggtgca 960

ctgggcccgg gcggcaaacc gctgaaaccg gtaccaggtg gtttagcagg cgccggctta 1020

ggcgcaggtc tgggagcatt tccggcagtt acctttccag gggcactggt tcctggaggt 1080

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ccaggtgtcg gtggcctggg tgttagcgcc ggtgcagttg ttccgcagcc gggagcaggg 1200

gttaaacctg gtaaagtgcc gggagtaggt ctgccaggcg tttatcctgg tggtgttttg 1260

ccgggtgccc gttttccggg cgttggtgtt cttccaggcg tgccgaccgg agccggtgtt 1320

aaaccgaaag cccccggtgt tggaggtgca tttgcaggca tcccgggagt tggcccgttt 1380

ggtggtccgc aacctggggt tccgttaggt tatccgatta aagcaccgaa actgcccggc 1440

ggttatggtc tgccgtacac aaccggtaaa ctgccgtatg gttatggccc gggtggagtt 1500

gcgggtgcag caggtaaagc gggttatcct accggaaccg gtgtaggtcc gcaggccgct 1560

gctgccgccg ccgcaaaagc agcggctaaa tttggcgccg gagcagcggg tgttctgcct 1620

ggagttggtg gtgcgggcgt gccaggggta cctggtgcaa ttccgggtat tggtggtatt 1680

gccggtgtcg gcaccccggc cgcggcagct gcggcagcgg cggctgccaa agctgctaaa 1740

tacggtgccg cggcgggtct ggtgccagga ggtccgggtt ttggtccggg agtggttggc 1800

gtgcctggcg caggcgttcc tggtgtgggc gttccaggtg cagggattcc tgttgtgcct 1860

ggtgccggta ttcccggcgc ggccgttccg gggtggtta gcccggaagc cgcagcgaag 1920 gctgcggcaa aggcagcaaa gtatggcgca cgcccaggag tcggcgtggg tggtatcccg 1980

acctatgggg tgggcgcagg gggttttcct ggtttcggcg taggtgtagg aggtataccg 2040

ggcgtggccg gtgtaccagg ggttggtggc gtccctggtg ttggcggtgt gccaggtgtt 2100

ggtatttcac cggaagcaca ggcagcagcc gcagctaagg cagcgaaata tggtgccgcc 2160

ggcgcaggag ttttaggtgg gctggttccg ggcccgcagg cagctgtgcc gggggttcca 2220

ggcaccggtg gtgtccctgg agtcggtacg ccggctgcag cggcagccaa agcggctgcg 2280

aaagcagcac agtttggctt agtaccgggt gtgggagttg cccccggcgt tggcgttgct 2340

ccaggggtgg gtgttgctcc tggcgtcggt ctggctcctg gagtgggcgt agcacccggt 2400

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gcagctaaaa gcgcggcgaa agttgcggcc aaagcccaac tgcgcgccgc cgcgggcctc 2520

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ggtgttcgtc gtagcctgag tccggaactg cgtgaaggtg atccgagtag cagccagcat 2700

ctgccgagca ccccgagcag cccgcgtgtt ccgggtgcat tagctgcagc aaaagccgcc 2760

aagtatggtg cagccgtgcc gggcgtctta ggtggtctgg gcgccctggg tggtgtaggc 2820

attccgggag gtgttgtggg tgcaggaccg gccgccgcag ctgcggccgc caaagcagct 2880

gcaaaagcgg cccagtttgg tttagtgggc gccgcaggtt taggcggttt aggtgtgggt 2940

ggactgggtg tacctggcgt aggcggtctg ggtggaattc cgcccgcagc ggccgcgaaa 3000

gcggcaaaat atggcgcggc aggcctgggc ggcgtgctgg gtggggcagg tcagtttccg 3060

ctgggcgggg ttgccgcacg tccgggattt ggtctgagcc cgattttccc tggcggcgca 3120

tgtctgggta aagcatgtgg tcgtaaacgt aaacacccag aaacgctggt gaaagtaaaa 3180

gatgctgaag atcagttggg tgcacgagtg ggttacatcg aactggatct caacagcggt 3240

aagatccttg agagttttcg ccccgaagaa cgttttccaa tgatgagcac ttttaaagtt 3300

ctgctatgtg gcgcggtatt atcccgtatt gacgccgggc aagagcaact cggtcgccgc 3360

atacactatt ctcagaatga cttggttgag tactcaccag tcacagaaaa gcatcttacg 3420

gatggcatga cagtaagaga attatgcagt gctgccataa ccatgagtga taacactgcg 3480

gccaacttac ttctgacaac gatcggagga ccgaaggagc taaccgcttt tttgcacaac 3540

atgggggatc atgtaactcg ccttgatcgt tgggaaccgg agctgaatga agccatacca 3600

aacgacgagc gtgacaccac gatgcctgta gcaatggcaa caacgttgcg caaactatta 3660

actggcgaac tacttactct agcttcccgg caacaattaa tagactggat ggaggcggat 3720

aaagttgcag gaccacttct gcgctcggcc cttccggctg gctggtttat tgctgataaa 3780

tctggagccg gtgagcgtgg gtctcgcggt atcattgcag cactggggcc agatggtaag 3840

ccctcccgta tcgtagttat ctacacgacg gggagtcagg caactatgga tgaacgaaat 3900

agacagatcg ctgagatagg tgcctcactg attaagcatt ggtaa 3945

<210> SEQ ID NO 28
<211> LENGTH: 1314
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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      polypeptide

<400> SEQUENCE: 28

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Ala Gln Tyr Glu Asp His His His His His His His His
            20                  25                  30

His Ser Gly Ser Ser Leu Val Pro Arg Gly Ser His Met Ser Gly Ser
        35                  40                  45

Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
    50                  55                  60

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Arg Gly Glu
65                  70                  75                  80

Gly Glu Gly Asp Ala Thr Asn Gly Lys Leu Thr Leu Lys Phe Ile Cys
                85                  90                  95

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
            100                 105                 110

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
        115                 120                 125

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
    130                 135                 140

Thr Ile Ser Phe Lys Asp Asp Gly Thr Tyr Lys Thr Arg Ala Glu Val
145                 150                 155                 160

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

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
            180                 185                 190

Phe Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
        195                 200                 205

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Val Glu Asp Gly Ser Val
    210                 215                 220

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
225                 230                 235                 240

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Lys Leu Ser
                245                 250                 255

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
            260                 265                 270

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ser Gly
        275                 280                 285

Ala Pro Gly Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly
    290                 295                 300

Gly Val Phe Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala
305                 310                 315                 320

Leu Gly Pro Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala
                325                 330                 335

Gly Ala Gly Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe
            340                 345                 350

Pro Gly Ala Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr
        355                 360                 365

Lys Ala Ala Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly
    370                 375                 380
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Gly Leu Gly Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly
385                 390                 395                 400

Val Lys Pro Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro
                405                 410                 415

Gly Gly Val Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro
            420                 425                 430

Gly Val Pro Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly
        435                 440                 445

Gly Ala Phe Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln
    450                 455                 460

Pro Gly Val Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly
465                 470                 475                 480

Gly Tyr Gly Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly
                485                 490                 495

Pro Gly Gly Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly
            500                 505                 510

Thr Gly Val Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
        515                 520                 525

Ala Lys Phe Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly
    530                 535                 540

Ala Gly Val Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile
545                 550                 555                 560

Ala Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
                565                 570                 575

Lys Ala Ala Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro
            580                 585                 590

Gly Phe Gly Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly
        595                 600                 605

Val Gly Val Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile
    610                 615                 620

Pro Gly Ala Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys
625                 630                 635                 640

Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val
                645                 650                 655

Gly Gly Ile Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe
            660                 665                 670

Gly Val Gly Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val
        675                 680                 685

Gly Gly Val Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro
    690                 695                 700

Glu Ala Gln Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala
705                 710                 715                 720

Gly Ala Gly Val Leu Gly Gly Leu Val Pro Gly Pro Gln Ala Ala Val
                725                 730                 735

Pro Gly Val Pro Gly Thr Gly Gly Val Pro Gly Val Gly Thr Pro Ala
            740                 745                 750

Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val
        755                 760                 765

Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly
    770                 775                 780

Val Ala Pro Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala Pro Gly
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785                 790                 795                 800

Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly
                805                 810                 815

Gly Val Ala Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala
            820                 825                 830

Gln Leu Arg Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly
        835                 840                 845

Val Gly Val Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly
    850                 855                 860

Leu Gly Val Gly Ala Gly Val Pro Gly Phe Gly Ala Gly Ala Asp Glu
865                 870                 875                 880

Gly Val Arg Arg Ser Leu Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser
                885                 890                 895

Ser Ser Gln His Leu Pro Ser Thr Pro Ser Ser Pro Arg Val Pro Gly
            900                 905                 910

Ala Leu Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly
        915                 920                 925

Val Leu Gly Gly Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly
    930                 935                 940

Val Val Gly Ala Gly Pro Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
945                 950                 955                 960

Ala Lys Ala Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly
                965                 970                 975

Leu Gly Val Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly
            980                 985                 990

Ile Pro Pro Ala Ala Ala Ala Lys  Ala Ala Lys Tyr Gly  Ala Ala Gly
        995                 1000                 1005

Leu Gly  Gly Val Leu Gly Gly  Ala Gly Gln Phe Pro  Leu Gly Gly
    1010                 1015                 1020

Val Ala  Ala Arg Pro Gly Phe  Gly Leu Ser Pro Ile  Phe Pro Gly
    1025                 1030                 1035

Gly Ala  Cys Leu Gly Lys Ala  Cys Gly Arg Lys Arg  Lys His Pro
    1040                 1045                 1050

Glu Thr  Leu Val Lys Val Lys  Asp Ala Glu Asp Gln  Leu Gly Ala
    1055                 1060                 1065

Arg Val  Gly Tyr Ile Glu Leu  Asp Leu Asn Ser Gly  Lys Ile Leu
    1070                 1075                 1080

Glu Ser  Phe Arg Pro Glu Glu  Arg Phe Pro Met Met  Ser Thr Phe
    1085                 1090                 1095

Lys Val  Leu Leu Cys Gly Ala  Val Leu Ser Arg Ile  Asp Ala Gly
    1100                 1105                 1110

Gln Glu  Gln Leu Gly Arg Arg  Ile His Tyr Ser Gln  Asn Asp Leu
    1115                 1120                 1125

Val Glu  Tyr Ser Pro Val Thr  Glu Lys His Leu Thr  Asp Gly Met
    1130                 1135                 1140

Thr Val  Arg Glu Leu Cys Ser  Ala Ala Ile Thr Met  Ser Asp Asn
    1145                 1150                 1155

Thr Ala  Ala Asn Leu Leu Leu  Thr Thr Ile Gly Gly  Pro Lys Glu
    1160                 1165                 1170

Leu Thr  Ala Phe Leu His Asn  Met Gly Asp His Val  Thr Arg Leu
    1175                 1180                 1185
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Asp Arg  Trp Glu Pro Glu Leu  Asn Glu Ala Ile Pro  Asn Asp Glu
    1190                 1195                 1200

Arg Asp  Thr Thr Met Pro Val  Ala Met Ala Thr Thr  Leu Arg Lys
    1205                 1210                 1215

Leu Leu  Thr Gly Glu Leu Leu  Thr Leu Ala Ser Arg  Gln Gln Leu
    1220                 1225                 1230

Ile Asp  Trp Met Glu Ala Asp  Lys Val Ala Gly Pro  Leu Leu Arg
    1235                 1240                 1245

Ser Ala  Leu Pro Ala Gly Trp  Phe Ile Ala Asp Lys  Ser Gly Ala
    1250                 1255                 1260

Gly Glu  Arg Gly Ser Arg Gly  Ile Ile Ala Ala Leu  Gly Pro Asp
    1265                 1270                 1275

Gly Lys  Pro Ser Arg Ile Val  Val Ile Tyr Thr Thr  Gly Ser Gln
    1280                 1285                 1290

Ala Thr  Met Asp Glu Arg Asn  Arg Gln Ile Ala Glu  Ile Gly Ala
    1295                 1300                 1305

Ser Leu  Ile Lys His Trp
    1310
```

```
<210> SEQ ID NO 29
<211> LENGTH: 760
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 29

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1               5                   10                  15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95

Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
            100                 105                 110

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
        115                 120                 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
    130                 135                 140

Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145                 150                 155                 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
                165                 170                 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
            180                 185                 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
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        195                 200                 205

Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
    210                 215                 220

Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
225                 230                 235                 240

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val
                245                 250                 255

Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val
            260                 265                 270

Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
        275                 280                 285

Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly
    290                 295                 300

Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val
305                 310                 315                 320

Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala
                325                 330                 335

Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala
            340                 345                 350

Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile
        355                 360                 365

Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly
    370                 375                 380

Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val
385                 390                 395                 400

Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln
                405                 410                 415

Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly
            420                 425                 430

Val Leu Gly Gly Leu Val Pro Gly Pro Gln Ala Ala Val Pro Gly Val
        435                 440                 445

Pro Gly Thr Gly Gly Val Pro Gly Val Gly Thr Pro Ala Ala Ala Ala
    450                 455                 460

Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val
465                 470                 475                 480

Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro
                485                 490                 495

Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val
            500                 505                 510

Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala
        515                 520                 525

Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg
    530                 535                 540

Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val
545                 550                 555                 560

Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val
                565                 570                 575

Gly Ala Gly Val Pro Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg
            580                 585                 590

Arg Ser Leu Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln
        595                 600                 605
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His Leu Pro Ser Thr Pro Ser Ser Pro Arg Val Pro Gly Ala Leu Ala
    610                 615                 620

Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly
625                 630                 635                 640

Gly Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly
                645                 650                 655

Ala Gly Pro Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala
            660                 665                 670

Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val
        675                 680                 685

Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro
    690                 695                 700

Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly
705                 710                 715                 720

Val Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg
                725                 730                 735

Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly
            740                 745                 750

Lys Ala Cys Gly Arg Lys Arg Lys
        755                 760


<210> SEQ ID NO 30
<211> LENGTH: 2115
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 30

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc      60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta     120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc     180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct     240

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt     300

gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg     360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt     420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt     480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat     540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg     600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc     660

ggaaccggtg taggtccgca ggccgctgct gccgccgccg caaaagcagc ggctaaattt     720

ggcgccggag cagcgggtgt tctgcctgga gttggtggtg cgggcgtgcc aggggtacct     780

ggtgcaattc cgggtattgg tggtattgcc ggtgtcggca ccccggccgc ggcagctgcg     840

gcagcggcgg ctgccaaagc tgctaaatac ggtgccgcgg cgggtctggt gccaggaggt     900

ccgggttttg gtccgggagt ggttggcgtg cctggcgcag gcgttcctgg tgtgggcgtt     960

ccaggtgcag ggattcctgt tgtgcctggt gccggtattc ccggcgcggc cgttccgggg    1020
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gtggttagcc cggaagccgc agcgaaggct gcggcaaagg cagcaaagta tggcgcacgc   1080

ccaggagtcg gcgtgggtgg tatcccgacc tatggggtgg gcgcaggggg ttttcctggt   1140

ttcggcgtag gtgtaggagg tataccgggc gtggccggtg taccaggggt tggtggcgtc   1200

cctggtgttg gcggtgtgcc aggtgttggt atttcaccgg aagcacaggc agcagccgca   1260

gctaaggcag cgaaatatgg tgccgccggc gcaggagttt taggtgggct ggttccgggc   1320

ccgcaggcag ctgtgccggg ggttccaggc accggtggtg tccctggagt cggtacgccg   1380

gctgcagcgg cagccaaagc ggctgcgaaa gcagcacagt ttggcttagt accgggtgtg   1440

ggagttgccc ccggcgttgg cgttgctcca ggggtgggtg ttgctcctgg cgtcggtctg   1500

gctcctggag tgggcgtagc acccggtgtg ggggtggccc cgggtgttgg ggttgcaccg   1560

ggtatcggtc cgggcggtgt cgcagcagca gctaaaagcg cggcgaaagt tgcggccaaa   1620

gcccaactgc gcgccgccgc gggcctcggt gcaggtattc cggggctggg tgtcggagtt   1680

ggagtcccgg gtttgggcgt gggcgcggga gttccgggac tgggagtggg tgccggagtt   1740

cctggctttg gtgcaggcgc agatgaaggt gttcgtcgta gcctgagtcc ggaactgcgt   1800

gaaggtgatc cgagtagcag ccagcatctg ccgagcaccc cgagcagccc gcgtgttccg   1860

ggtgcattag ctgcagcaaa agccgccaag tatggtgcag ccgtgccggg cgtcttaggt   1920

ggtctgggcg ccctgggtgg tgtaggcatt ccgggaggtg ttgtgggtgc aggaccggcc   1980

gccgcagctg cggccgccaa agcagctgca aaagcggccc agtttggttt agtgggcgcc   2040

gcaggtttag gcggtttagg tgtgggtgga ctgggtgtac ctggcgtagg cggtctgggt   2100

ggaattccgc cctaa                                                    2115


<210> SEQ ID NO 31
<211> LENGTH: 704
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 31

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1               5                   10                  15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95

Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
            100                 105                 110

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
        115                 120                 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
    130                 135                 140
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Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145                 150                 155                 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
                165                 170                 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
            180                 185                 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
        195                 200                 205

Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
    210                 215                 220

Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
225                 230                 235                 240

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val
                245                 250                 255

Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val
            260                 265                 270

Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
        275                 280                 285

Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly
    290                 295                 300

Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val
305                 310                 315                 320

Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala
                325                 330                 335

Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala
            340                 345                 350

Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile
        355                 360                 365

Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly
    370                 375                 380

Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val
385                 390                 395                 400

Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln
                405                 410                 415

Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly
            420                 425                 430

Val Leu Gly Gly Leu Val Pro Gly Pro Gln Ala Ala Val Pro Gly Val
        435                 440                 445

Pro Gly Thr Gly Gly Val Pro Gly Val Gly Thr Pro Ala Ala Ala Ala
    450                 455                 460

Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val
465                 470                 475                 480

Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro
                485                 490                 495

Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val
            500                 505                 510

Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala
        515                 520                 525

Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg
    530                 535                 540

Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val
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545                 550                 555                 560

Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val
            565                 570                 575

Gly Ala Gly Val Pro Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg
        580                 585                 590

Arg Ser Leu Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln
    595                 600                 605

His Leu Pro Ser Thr Pro Ser Ser Pro Arg Val Pro Gly Ala Leu Ala
    610                 615                 620

Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly
625                 630                 635                 640

Gly Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly
            645                 650                 655

Ala Gly Pro Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala
        660                 665                 670

Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val
    675                 680                 685

Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro
    690                 695                 700

<210> SEQ ID NO 32
<211> LENGTH: 2115
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 32

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc 60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta 120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc 180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct 240

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt 300

gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg 360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt 420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt 480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat 540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg 600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc 660

ggaaccggtg taggtccgca ggccgctgct gccgccgccg caaaagcagc ggctaaattt 720

ggcgccggag cagcgggtgt tctgcctgga gttggtggtg cgggcgtgcc aggggtacct 780

ggtgcaattc cgggtattgg tggtattgcc ggtgtcggca ccccggccgc ggcagctgcg 840

gcagcggcgg ctgccaaagc tgctaaatac ggtgccgcgg cgggtctggt gccaggaggt 900

ccgggttttg gtccgggagt ggttggcgtg cctggcgcag gcgttcctgg tgtgggcgtt 960

ccaggtgcag ggattcctgt tgtgcctggt gccggtattc ccggcgcggc cgttccgggg 1020

gtggttagcc cggaagccgc agcgaaggct gcggcaaagg cagcaaagta tggcgcacgc 1080

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ccaggagtcg gcgtgggtgg tatcccgacc tatggggtgg gcgcaggggg ttttcctggt   1140

ttcggcgtag gtgtaggagg tataccgggc gtggccggtg taccaggggt tggtggcgtc   1200

cctggtgttg gcggtgtgcc aggtgttggt atttcaccgg aagcacaggc agcagccgca   1260

gctaaggcag cgaaatatgg tgccgccggc gcaggagttt taggtgggct ggttccgggc   1320

ccgcaggcag ctgtgccggg ggttccaggc accggtggtg tccctggagt cggtacgccg   1380

gctgcagcgg cagccaaagc ggctgcgaaa gcagcacagt ttggcttagt accgggtgtg   1440

ggagttgccc ccggcgttgg cgttgctcca ggggtgggtg ttgctcctgg cgtcggtctg   1500

gctcctggag tgggcgtagc acccggtgtg ggggtggccc cgggtgttgg ggttgcaccg   1560

ggtatcggtc cgggcggtgt cgcagcagca gctaaaagcg cggcgaaagt tgcggccaaa   1620

gcccaactgc gcgccgccgc gggcctcggt gcaggtattc cggggctggg tgtcggagtt   1680

ggagtcccgg gtttgggcgt gggcgcggga gttccgggac tgggagtggg tgccggagtt   1740

cctggctttg gtgcaggcgc agatgaaggt gttcgtcgta gcctgagtcc ggaactgcgt   1800

gaaggtgatc cgagtagcag ccagcatctg ccgagcaccc cgagcagccc gcgtgttccg   1860

ggtgcattag ctgcagcaaa agccgccaag tatggtgcag ccgtgccggg cgtcttaggt   1920

ggtctgggcg ccctgggtgg tgtaggcatt ccgggaggtg ttgtgggtgc aggaccggcc   1980

gccgcagctg cggccgccaa agcagctgca aaagcggccc agtttggttt agtgggcgcc   2040

gcaggtttag gcggtttagg tgtgggtgga ctgggtgtac ctggcgtagg cggtctgggt   2100

ggaattccgc cctaa                                                    2115


<210> SEQ ID NO 33
<211> LENGTH: 676
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 33

Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly Val Ser Ala Gly
1               5                   10                  15

Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro Gly Lys Val Pro
            20                  25                  30

Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val Leu Pro Gly Ala
        35                  40                  45

Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro Thr Gly Ala Gly
    50                  55                  60

Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe Ala Gly Ile Pro
65                  70                  75                  80

Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val Pro Leu Gly Tyr
                85                  90                  95

Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly Leu Pro Tyr Thr
            100                 105                 110

Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly Val Ala Gly Ala
        115                 120                 125

Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val Gly Pro Gln Ala
    130                 135                 140

Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe Gly Ala Gly Ala
145                 150                 155                 160
```

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```
Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val Pro Gly Val Pro
                165                 170                 175

Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val Gly Thr Pro Ala
            180                 185                 190

Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala
        195                 200                 205

Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val Val
    210                 215                 220

Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val Pro Gly Ala Gly
225                 230                 235                 240

Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala Ala Val Pro Gly
                245                 250                 255

Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys
            260                 265                 270

Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly
        275                 280                 285

Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile
    290                 295                 300

Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val Pro Gly Val Gly
305                 310                 315                 320

Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala Ala
                325                 330                 335

Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly Val Leu Gly Gly
            340                 345                 350

Leu Val Pro Gly Pro Gln Ala Ala Val Pro Gly Val Pro Gly Thr Gly
        355                 360                 365

Gly Val Pro Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Lys Ala Ala
    370                 375                 380

Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala Pro
385                 390                 395                 400

Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Leu
                405                 410                 415

Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val
            420                 425                 430

Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala Lys
        435                 440                 445

Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala Gly
    450                 455                 460

Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro Gly
465                 470                 475                 480

Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val
                485                 490                 495

Pro Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg Arg Ser Leu Ser
            500                 505                 510

Pro Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln His Leu Pro Ser
        515                 520                 525

Thr Pro Ser Ser Pro Arg Val Pro Gly Ala Leu Ala Ala Ala Lys Ala
    530                 535                 540

Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly Ala
545                 550                 555                 560
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```
Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro Ala
                565                 570                 575

Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly
            580                 585                 590

Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly
        595                 600                 605

Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala
    610                 615                 620

Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly
625                 630                 635                 640

Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly
                645                 650                 655

Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly
            660                 665                 670

Arg Lys Arg Lys
        675


<210> SEQ ID NO 34
<211> LENGTH: 2031
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 34

ggtttaggag gcgtcccagg tgtcggtggc ctgggtgtta gcgccggtgc agttgttccg     60

cagccgggag caggggttaa acctggtaaa gtgccgggag taggtctgcc aggcgtttat    120

cctggtggtg ttttgccggg tgcccgtttt ccgggcgttg gtgttcttcc aggcgtgccg    180

accggagccg gtgttaaacc gaaagccccc ggtgttggag gtgcatttgc aggcatcccg    240

ggagttggcc cgtttggtgg tccgcaacct ggggttccgt taggttatcc gattaaagca    300

ccgaaactgc ccggcggtta tggtctgccg tacacaaccg gtaaactgcc gtatggttat    360

ggcccgggtg gagttgcggg tgcagcaggt aaagcgggtt atcctaccgg aaccggtgta    420

ggtccgcagg ccgctgctgc cgccgccgca aaagcagcgg ctaaatttgg cgccggagca    480

gcgggtgttc tgcctggagt tggtggtgcg ggcgtgccag gggtacctgg tgcaattccg    540

ggtattggtg gtattgccgg tgtcggcacc ccggccgcgg cagctgcggc agcggcggct    600

gccaaagctg ctaaatacgg tgccgcggcg ggtctggtgc caggaggtcc gggttttggt    660

ccgggagtgg ttggcgtgcc tggcgcaggc gttcctggtg tgggcgttcc aggtgcaggg    720

attcctgttg tgcctggtgc cggtattccc ggcgcggccg ttccgggggt ggttagcccg    780

gaagccgcag cgaaggctgc ggcaaaggca gcaaagtatg gcgcacgccc aggagtcggc    840

gtgggtggta tcccgaccta tggggtgggc gcagggggtt ttcctggttt cggcgtaggt    900

gtaggaggta taccgggcgt ggccggtgta ccaggggttg gtggcgtccc tggtgttggc    960

ggtgtgccag gtgttggtat ttcaccggaa gcacaggcag cagccgcagc taaggcagcg   1020

aaatatggtg ccgccggcgc aggagtttta ggtgggctgg ttccgggccc gcaggcagct   1080

gtgccggggg ttccaggcac cggtggtgtc cctggagtcg gtacgccggc tgcagcggca   1140

gccaaagcgg ctgcgaaagc agcacagttt ggcttagtac cgggtgtggg agttgccccc   1200

ggcgttggcg ttgctccagg ggtgggtgtt gctcctggcg tcggtctggc tcctggagtg   1260
```

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```
ggcgtagcac ccggtgtggg ggtggccccg ggtgttgggg ttgcaccggg tatcggtccg   1320

ggcggtgtcg cagcagcagc taaaagcgcg gcgaaagttg cggccaaagc ccaactgcgc   1380

gccgccgcgg gcctcggtgc aggtattccg gggctgggtg tcggagttgg agtcccgggt   1440

ttgggcgtgg gcgcgggagt tccgggactg ggagtgggtg ccggagttcc tggctttggt   1500

gcaggcgcag atgaaggtgt tcgtcgtagc ctgagtccgg aactgcgtga aggtgatccg   1560

agtagcagcc agcatctgcc gagcaccccg agcagcccgc gtgttccggg tgcattagct   1620

gcagcaaaag ccgccaagta tggtgcagcc gtgccgggcg tcttaggtgg tctgggcgcc   1680

ctgggtggtg taggcattcc gggaggtgtt gtgggtgcag gaccggccgc cgcagctgcg   1740

gccgccaaag cagctgcaaa agcggcccag tttggtttag tgggcgccgc aggtttaggc   1800

ggtttaggtg tgggtggact gggtgtacct ggcgtaggcg gtctgggtgg aattccgccc   1860

gcagcggccg cgaaagcggc aaaatatggc gcggcaggcc tgggcggcgt gctgggtggg   1920

gcaggtcagt ttccgctggg cggggttgcc gcacgtccgg gatttggtct gagcccgatt   1980

ttccctggcg gcgcatgtct gggtaaagca tgtggtcgta aacgtaaata a            2031
```

```
<210> SEQ ID NO 35
<211> LENGTH: 659
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 35

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1               5                   10                  15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95

Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
            100                 105                 110

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
        115                 120                 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
    130                 135                 140

Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145                 150                 155                 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
                165                 170                 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
            180                 185                 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
        195                 200                 205
```

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Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
    210                 215                 220

Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
225                 230                 235                 240

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val
                245                 250                 255

Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val
            260                 265                 270

Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
        275                 280                 285

Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly
    290                 295                 300

Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val
305                 310                 315                 320

Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala
                325                 330                 335

Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala
            340                 345                 350

Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile
        355                 360                 365

Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly
    370                 375                 380

Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val
385                 390                 395                 400

Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln
                405                 410                 415

Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly
            420                 425                 430

Val Leu Gly Gly Leu Val Pro Gly Pro Gln Ala Ala Val Pro Gly Val
        435                 440                 445

Pro Gly Thr Gly Gly Val Pro Gly Val Gly Thr Pro Ala Ala Ala Ala
    450                 455                 460

Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val
465                 470                 475                 480

Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro
                485                 490                 495

Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val
            500                 505                 510

Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala
        515                 520                 525

Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg
    530                 535                 540

Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val
545                 550                 555                 560

Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val
                565                 570                 575

Gly Ala Gly Val Pro Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg
            580                 585                 590

Arg Ser Leu Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln
        595                 600                 605
```

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```
His Leu Pro Ser Thr Pro Ser Ser Pro Arg Val Pro Gly Ala Leu Ala
    610                 615                 620

Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly
625                 630                 635                 640

Gly Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly
                645                 650                 655

Ala Gly Pro


<210> SEQ ID NO 36
<211> LENGTH: 1980
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 36

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc     60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta    120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc    180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct    240

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt    300

gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg    360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt    420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt    480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat    540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg    600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc    660

ggaaccggtg taggtccgca ggccgctgct gccgccgccg caaaagcagc ggctaaattt    720

ggcgccggag cagcgggtgt tctgcctgga gttggtggtg cgggcgtgcc aggggtacct    780

ggtgcaattc cgggtattgg tggtattgcc ggtgtcggca ccccggccgc ggcagctgcg    840

gcagcggcgg ctgccaaagc tgctaaatac ggtgccgcgg cgggtctggt gccaggaggt    900

ccgggttttg gtccgggagt ggttggcgtg cctggcgcag gcgttcctgg tgtgggcgtt    960

ccaggtgcag ggattcctgt tgtgcctggt gccggtattc ccggcgcggc cgttccgggg   1020

gtggttagcc cggaagccgc agcgaaggct gcggcaaagg cagcaaagta tggcgcacgc   1080

ccaggagtcg gcgtgggtgg tatcccgacc tatggggtgg gcgcaggggg ttttcctggt   1140

ttcggcgtag gtgtaggagg tataccgggc gtggccggtg taccaggggt tggtggcgtc   1200

cctggtgttg gcggtgtgcc aggtgttggt atttcaccgg aagcacaggc agcagccgca   1260

gctaaggcag cgaaatatgg tgccgccggc gcaggagttt taggtgggct ggttccgggc   1320

ccgcaggcag ctgtgccggg ggttccaggc accggtggtg tccctggagt cggtacgccg   1380

gctgcagcgg cagccaaagc ggctgcgaaa gcagcacagt ttggcttagt accgggtgtg   1440

ggagttgccc ccggcgttgg cgttgctcca ggggtgggtg ttgctcctgg cgtcggtctg   1500

gctcctggag tgggcgtagc acccggtgtg ggggtggccc cgggtgttgg ggttgcaccg   1560

ggtatcggtc cgggcggtgt cgcagcagca gctaaaagcg cggcgaaagt tgcggccaaa   1620
```

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```
gcccaactgc gcgccgccgc gggcctcggt gcaggtattc cggggctggg tgtcggagtt   1680

ggagtcccgg gtttgggcgt gggcgcggga gttccgggac tgggagtggg tgccggagtt   1740

cctggctttg gtgcaggcgc agatgaaggt gttcgtcgta gcctgagtcc ggaactgcgt   1800

gaaggtgatc cgagtagcag ccagcatctg ccgagcaccc cgagcagccc gcgtgttccg   1860

ggtgcattag ctgcagcaaa agccgccaag tatggtgcag ccgtgccggg cgtcttaggt   1920

ggtctgggcg ccctgggtgg tgtaggcatt ccgggaggtg ttgtgggtgc aggaccgtaa   1980


<210> SEQ ID NO 37
<211> LENGTH: 622
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 37

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1               5                   10                  15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95

Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
            100                 105                 110

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
        115                 120                 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
    130                 135                 140

Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145                 150                 155                 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
                165                 170                 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
            180                 185                 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
        195                 200                 205

Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
    210                 215                 220

Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
225                 230                 235                 240

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val
                245                 250                 255

Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val
            260                 265                 270

Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
        275                 280                 285
```

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```
Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly
    290                 295                 300

Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val
305                 310                 315                 320

Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala
                325                 330                 335

Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala
            340                 345                 350

Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile
        355                 360                 365

Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly
    370                 375                 380

Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val
385                 390                 395                 400

Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln
                405                 410                 415

Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly
            420                 425                 430

Val Leu Gly Gly Leu Val Pro Gly Pro Gln Ala Ala Val Pro Gly Val
        435                 440                 445

Pro Gly Thr Gly Gly Val Pro Gly Val Gly Thr Pro Ala Ala Ala Ala
    450                 455                 460

Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val
465                 470                 475                 480

Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro
                485                 490                 495

Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val
            500                 505                 510

Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala
        515                 520                 525

Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg
    530                 535                 540

Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val
545                 550                 555                 560

Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val
                565                 570                 575

Gly Ala Gly Val Pro Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg
            580                 585                 590

Arg Ser Leu Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln
        595                 600                 605

His Leu Pro Ser Thr Pro Ser Ser Pro Arg Val Pro Gly Ala
    610                 615                 620


<210> SEQ ID NO 38
<211> LENGTH: 1869
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 38

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc      60
```

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ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta 120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc 180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct 240

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt 300

gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg 360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt 420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt 480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat 540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg 600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc 660

ggaaccggtg taggtccgca ggccgctgct gccgccgccg caaaagcagc ggctaaattt 720

ggcgccggag cagcgggtgt tctgcctgga gttggtggtg cgggcgtgcc aggggtacct 780

ggtgcaattc cgggtattgg tggtattgcc ggtgtcggca ccccggccgc ggcagctgcg 840

gcagcggcgg ctgccaaagc tgctaaatac ggtgccgcgg cgggtctggt gccaggaggt 900

ccgggttttg gtccgggagt ggttggcgtg cctggcgcag gcgttcctgg tgtgggcgtt 960

ccaggtgcag ggattcctgt tgtgcctggt gccggtattc ccggcgcggc cgttccgggg 1020

gtggttagcc cggaagccgc agcgaaggct gcggcaaagg cagcaaagta tggcgcacgc 1080

ccaggagtcg gcgtgggtgg tatcccgacc tatggggtgg gcgcaggggg ttttcctggt 1140

ttcggcgtag gtgtaggagg tataccgggc gtggccggtg taccaggggt tggtggcgtc 1200

cctggtgttg gcggtgtgcc aggtgttggt atttcaccgg aagcacaggc agcagccgca 1260

gctaaggcag cgaaatatgg tgccgccggc gcaggagttt taggtgggct ggttccgggc 1320

ccgcaggcag ctgtgccggg ggttccaggc accggtggtg tccctggagt cggtacgccg 1380

gctgcagcgg cagccaaagc ggctgcgaaa gcagcacagt ttggcttagt accgggtgtg 1440

ggagttgccc ccggcgttgg cgttgctcca ggggtgggtg ttgctcctgg cgtcggtctg 1500

gctcctggag tgggcgtagc acccggtgtg gggggtggccc cgggtgttgg ggttgcaccg 1560

ggtatcggtc cgggcggtgt cgcagcagca gctaaaagcg cggcgaaagt tgcggccaaa 1620

gcccaactgc gcgccgccgc gggcctcggt gcaggtattc cggggctggg tgtcggagtt 1680

ggagtcccgg gtttgggcgt gggcgcggga gttccgggac tgggagtggg tgccggagtt 1740

cctggctttg gtgcaggcgc agatgaaggt gttcgtcgta gcctgagtcc ggaactgcgt 1800

gaaggtgatc cgagtagcag ccagcatctg ccgagcaccc cgagcagccc gcgtgttccg 1860

ggtgcataa 1869

<210> SEQ ID NO 39
<211> LENGTH: 527
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 39

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1 5 10 15

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```
Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95

Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
            100                 105                 110

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
        115                 120                 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
    130                 135                 140

Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145                 150                 155                 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
                165                 170                 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
            180                 185                 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
        195                 200                 205

Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
    210                 215                 220

Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
225                 230                 235                 240

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val
                245                 250                 255

Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val
            260                 265                 270

Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
        275                 280                 285

Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly
    290                 295                 300

Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val
305                 310                 315                 320

Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala
                325                 330                 335

Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala
            340                 345                 350

Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile
        355                 360                 365

Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly
    370                 375                 380

Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val
385                 390                 395                 400

Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln
                405                 410                 415
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Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly
            420                 425                 430

Val Leu Gly Gly Leu Val Pro Gly Pro Gln Ala Ala Val Pro Gly Val
        435                 440                 445

Pro Gly Thr Gly Gly Val Pro Gly Val Gly Thr Pro Ala Ala Ala Ala
    450                 455                 460

Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val
465                 470                 475                 480

Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro
                485                 490                 495

Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val
            500                 505                 510

Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val
        515                 520                 525
```

<210> SEQ ID NO 40
<211> LENGTH: 1584
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 40

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc 60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta 120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc 180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct 240

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt 300

gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg 360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt 420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt 480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat 540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg 600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc 660

ggaaccggtg taggtccgca ggccgctgct gccgccgccg caaaagcagc ggctaaattt 720

ggcgccggag cagcgggtgt tctgcctgga gttggtggtg cgggcgtgcc aggggtacct 780

ggtgcaattc cgggtattgg tggtattgcc ggtgtcggca ccccggccgc ggcagctgcg 840

gcagcggcgg ctgccaaagc tgctaaatac ggtgccgcgg cgggtctggt gccaggaggt 900

ccgggttttg gtccgggagt ggttggcgtg cctggcgcag gcgttcctgg tgtgggcgtt 960

ccaggtgcag ggattcctgt tgtgcctggt gccggtattc ccggcgcggc cgttccgggg 1020

gtggttagcc cggaagccgc agcgaaggct gcggcaaagg cagcaaagta tggcgcacgc 1080

ccaggagtcg gcgtgggtgg tatcccgacc tatggggtgg gcgcaggggg ttttcctggt 1140

ttcggcgtag gtgtaggagg tataccgggc gtggccggtg taccaggggt tggtggcgtc 1200

cctggtgttg gcggtgtgcc aggtgttggt atttcaccgg aagcacaggc agcagccgca 1260

gctaaggcag cgaaatatgg tgccgccggc gcaggagttt taggtgggct ggttccgggc 1320

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ccgcaggcag ctgtgccggg ggttccaggc accggtggtg tccctggagt cggtacgccg   1380

gctgcagcgg cagccaaagc ggctgcgaaa gcagcacagt ttggcttagt accgggtgtg   1440

ggagttgccc ccggcgttgg cgttgctcca ggggtgggtg ttgctcctgg cgtcggtctg   1500

gctcctggag tgggcgtagc acccggtgtg ggggtggccc cgggtgttgg ggttgcaccg   1560

ggtatcggtc cgggcggtgt ctaa                                          1584


<210> SEQ ID NO 41
<211> LENGTH: 515
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 41

Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val Pro Gly Val Pro Gly
1               5                   10                  15

Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val Gly Thr Pro Ala Ala
            20                  25                  30

Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala
        35                  40                  45

Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val Val Gly
    50                  55                  60

Val Pro Gly Ala Gly Val Pro Gly Val Gly Val Pro Gly Ala Gly Ile
65                  70                  75                  80

Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala Ala Val Pro Gly Val
                85                  90                  95

Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys Tyr
            100                 105                 110

Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly Val
        115                 120                 125

Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile Pro
    130                 135                 140

Gly Val Ala Gly Val Pro Gly Val Gly Gly Val Pro Gly Val Gly Gly
145                 150                 155                 160

Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala Ala Ala
                165                 170                 175

Lys Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly Val Leu Gly Gly Leu
            180                 185                 190

Val Pro Gly Pro Gln Ala Ala Val Pro Gly Val Pro Gly Thr Gly Gly
        195                 200                 205

Val Pro Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Lys Ala Ala Ala
    210                 215                 220

Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala Pro Gly
225                 230                 235                 240

Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Leu Ala
                245                 250                 255

Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly
            260                 265                 270

Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala Lys Ser
        275                 280                 285

Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala Gly Leu
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    290                 295                 300

Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro Gly Leu
305                 310                 315                 320

Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro
                325                 330                 335

Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg Arg Ser Leu Ser Pro
            340                 345                 350

Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln His Leu Pro Ser Thr
        355                 360                 365

Pro Ser Ser Pro Arg Val Pro Gly Ala Leu Ala Ala Ala Lys Ala Ala
    370                 375                 380

Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly Ala Leu
385                 390                 395                 400

Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro Ala Ala
                405                 410                 415

Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu
            420                 425                 430

Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly Val
        435                 440                 445

Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys
    450                 455                 460

Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala
465                 470                 475                 480

Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu
                485                 490                 495

Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg
            500                 505                 510

Lys Arg Lys
        515


<210> SEQ ID NO 42
<211> LENGTH: 1548
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 42

ggtgttctgc ctggagttgg tggtgcgggc gtgccagggg tacctggtgc aattccgggt     60

attggtggta ttgccggtgt cggcaccccg gccgcggcag ctgcggcagc ggcggctgcc    120

aaagctgcta aatacggtgc cgcggcgggt ctggtgccag gaggtccggg ttttggtccg    180

ggagtggttg gcgtgcctgg cgcaggcgtt cctggtgtgg gcgttccagg tgcagggatt    240

cctgttgtgc ctggtgccgg tattcccggc gcggccgttc cgggggtggt tagcccggaa    300

gccgcagcga aggctgcggc aaaggcagca aagtatggcg cacgcccagg agtcggcgtg    360

ggtggtatcc cgacctatgg ggtgggcgca gggggttttc ctggtttcgg cgtaggtgta    420

ggaggtatac cgggcgtggc cggtgtacca ggggttggtg gcgtccctgg tgttggcggt    480

gtgccaggtg ttggtatttc accggaagca caggcagcag ccgcagctaa ggcagcgaaa    540

tatggtgccg ccggcgcagg agttttaggt gggctggttc cgggcccgca ggcagctgtg    600

ccgggggttc caggcaccgg tggtgtccct ggagtcggta cgccggctgc agcggcagcc    660
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aaagcggctg cgaaagcagc acagtttggc ttagtaccgg gtgtgggagt tgcccccggc    720

gttggcgttg ctccaggggt gggtgttgct cctggcgtcg gtctggctcc tggagtgggc    780

gtagcacccg gtgtgggggt ggccccgggt gttggggttg caccgggtat cggtccgggc    840

ggtgtcgcag cagcagctaa aagcgcggcg aaagttgcgg ccaaagccca actgcgcgcc    900

gccgcgggcc tcggtgcagg tattccgggg ctgggtgtcg gagttggagt cccgggtttg    960

ggcgtgggcg cgggagttcc gggactggga gtgggtgccg gagttcctgg ctttggtgca   1020

ggcgcagatg aaggtgttcg tcgtagcctg agtccggaac tgcgtgaagg tgatccgagt   1080

agcagccagc atctgccgag caccccgagc agcccgcgtg ttccgggtgc attagctgca   1140

gcaaaagccg ccaagtatgg tgcagccgtg ccgggcgtct taggtggtct gggcgccctg   1200

ggtggtgtag gcattccggg aggtgttgtg ggtgcaggac cggccgccgc agctgcggcc   1260

gccaaagcag ctgcaaaagc ggcccagttt ggtttagtgg gcgccgcagg tttaggcggt   1320

ttaggtgtgg gtggactggg tgtacctggc gtaggcggtc tgggtggaat tccgcccgca   1380

gcggccgcga aagcggcaaa atatggcgcg gcaggcctgg gcggcgtgct gggtggggca   1440

ggtcagtttc cgctgggcgg ggttgccgca cgtccgggat ttggtctgag cccgattttc   1500

cctggcggcg catgtctggg taaagcatgt ggtcgtaaac gtaaataa                1548


<210> SEQ ID NO 43
<211> LENGTH: 466
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 43

Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val Val Gly Val
1               5                   10                  15

Pro Gly Ala Gly Val Pro Gly Val Gly Val Pro Gly Ala Gly Ile Pro
            20                  25                  30

Val Val Pro Gly Ala Gly Ile Pro Gly Ala Ala Val Pro Gly Val Val
        35                  40                  45

Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys Tyr Gly
    50                  55                  60

Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly Val Gly
65                  70                  75                  80

Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile Pro Gly
                85                  90                  95

Val Ala Gly Val Pro Gly Val Gly Gly Val Pro Gly Val Gly Gly Val
            100                 105                 110

Pro Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala Ala Ala Lys
        115                 120                 125

Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly Val Leu Gly Gly Leu Val
    130                 135                 140

Pro Gly Pro Gln Ala Ala Val Pro Gly Val Pro Gly Thr Gly Gly Val
145                 150                 155                 160

Pro Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys
                165                 170                 175

Ala Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala Pro Gly Val
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            180                 185                 190

Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Leu Ala Pro
        195                 200                 205

Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val
    210                 215                 220

Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala Lys Ser Ala
225                 230                 235                 240

Ala Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala Gly Leu Gly
                245                 250                 255

Ala Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro Gly Leu Gly
            260                 265                 270

Val Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly
        275                 280                 285

Phe Gly Ala Gly Ala Asp Glu Gly Val Arg Arg Ser Leu Ser Pro Glu
    290                 295                 300

Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln His Leu Pro Ser Thr Pro
305                 310                 315                 320

Ser Ser Pro Arg Val Pro Gly Ala Leu Ala Ala Ala Lys Ala Ala Lys
                325                 330                 335

Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly Ala Leu Gly
            340                 345                 350

Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro Ala Ala Ala
        355                 360                 365

Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val
    370                 375                 380

Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly Val Pro
385                 390                 395                 400

Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys Ala
                405                 410                 415

Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala Gly
            420                 425                 430

Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu Ser
        435                 440                 445

Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys
    450                 455                 460

Arg Lys
465


<210> SEQ ID NO 44
<211> LENGTH: 1401
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 44

ggtctggtgc caggaggtcc gggttttggt ccgggagtgg ttggcgtgcc tggcgcaggc     60

gttcctggtg tgggcgttcc aggtgcaggg attcctgttg tgcctggtgc cggtattccc    120

ggcgcggccg ttccgggggt ggttagcccg gaagccgcag cgaaggctgc ggcaaaggca    180

gcaaagtatg gcgcacgccc aggagtcggc gtgggtggta tcccgaccta tggggtgggc    240

gcagggggtt ttcctggttt cggcgtaggt gtaggaggta taccgggcgt ggccggtgta    300
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ccaggggttg gtggcgtccc tggtgttggc ggtgtgccag gtgttggtat ttcaccggaa    360

gcacaggcag cagccgcagc taaggcagcg aaatatggtg ccgccggcgc aggagtttta    420

ggtgggctgg ttccgggccc gcaggcagct gtgccggggg ttccaggcac cggtggtgtc    480

cctggagtcg gtacgccggc tgcagcggca gccaaagcgg ctgcgaaagc agcacagttt    540

ggcttagtac cgggtgtggg agttgccccc ggcgttggcg ttgctccagg ggtgggtgtt    600

gctcctggcg tcggtctggc tcctggagtg ggcgtagcac ccggtgtggg ggtggccccg    660

ggtgttgggg ttgcaccggg tatcggtccg ggcggtgtcg cagcagcagc taaaagcgcg    720

gcgaaagttg cggccaaagc ccaactgcgc gccgccgcgg gcctcggtgc aggtattccg    780

gggctgggtg tcggagttgg agtcccgggt ttgggcgtgg gcgcgggagt tccgggactg    840

ggagtgggtg ccggagttcc tggctttggt gcaggcgcag atgaaggtgt tcgtcgtagc    900

ctgagtccgg aactgcgtga aggtgatccg agtagcagcc agcatctgcc gagcaccccg    960

agcagcccgc gtgttccggg tgcattagct gcagcaaaag ccgccaagta tggtgcagcc   1020

gtgccgggcg tcttaggtgg tctgggcgcc ctgggtggtg taggcattcc gggaggtgtt   1080

gtgggtgcag gaccggccgc cgcagctgcg gccgccaaag cagctgcaaa agcggcccag   1140

tttggtttag tgggcgccgc aggtttaggc ggtttaggtg tgggtggact gggtgtacct   1200

ggcgtaggcg gtctgggtgg aattccgccc gcagcggccg cgaaagcggc aaaatatggc   1260

gcggcaggcc tgggcggcgt gctgggtggg gcaggtcagt ttccgctggg cggggttgcc   1320

gcacgtccgg gatttggtct gagcccgatt ttccctggcg gcgcatgtct gggtaaagca   1380

tgtggtcgta aacgtaaata a                                              1401
```

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<210> SEQ ID NO 45
<211> LENGTH: 460
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 45

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1               5                   10                  15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95

Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
            100                 105                 110

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
        115                 120                 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
    130                 135                 140
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Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145 150 155 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
165 170 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
180 185 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
195 200 205

Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
210 215 220

Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
225 230 235 240

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val
245 250 255

Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val
260 265 270

Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
275 280 285

Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly
290 295 300

Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val
305 310 315 320

Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala
325 330 335

Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala
340 345 350

Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile
355 360 365

Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly
370 375 380

Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val
385 390 395 400

Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln
405 410 415

Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly
420 425 430

Val Leu Gly Gly Leu Val Pro Gly Pro Gln Ala Ala Val Pro Gly Val
435 440 445

Pro Gly Thr Gly Gly Val Pro Gly Val Gly Thr Pro
450 455 460

<210> SEQ ID NO 46
<211> LENGTH: 1383
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 46

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc 60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta 120

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ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc     180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct     240

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt     300

gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg     360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt     420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt     480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat     540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg     600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc     660

ggaaccggtg taggtccgca ggccgctgct gccgccgccg caaaagcagc ggctaaattt     720

ggcgccggag cagcgggtgt tctgcctgga gttggtggtg cgggcgtgcc aggggtacct     780

ggtgcaattc cgggtattgg tggtattgcc ggtgtcggca ccccggccgc ggcagctgcg     840

gcagcggcgg ctgccaaagc tgctaaatac ggtgccgcgg cgggtctggt gccaggaggt     900

ccgggttttg gtccgggagt ggttggcgtg cctggcgcag gcgttcctgg tgtgggcgtt     960

ccaggtgcag ggattcctgt tgtgcctggt gccggtattc ccggcgcggc cgttccgggg    1020

gtggttagcc cggaagccgc agcgaaggct gcggcaaagg cagcaaagta tggcgcacgc    1080

ccaggagtcg gcgtgggtgg tatcccgacc tatggggtgg gcgcaggggg ttttcctggt    1140

ttcggcgtag gtgtaggagg tataccgggc gtggccggtg taccaggggt tggtggcgtc    1200

cctggtgttg gcggtgtgcc aggtgttggt atttcaccgg aagcacaggc agcagccgca    1260

gctaaggcag cgaaatatgg tgccgccggc gcaggagttt taggtgggct ggttccgggc    1320

ccgcaggcag ctgtgccggg ggttccaggc accggtggtg tccctggagt cggtacgccg    1380

taa                                                                  1383
```

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<210> SEQ ID NO 47
<211> LENGTH: 416
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 47

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1               5                   10                  15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95

Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
            100                 105                 110
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Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
        115                 120                 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
    130                 135                 140

Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145                 150                 155                 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
                165                 170                 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
            180                 185                 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
        195                 200                 205

Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
    210                 215                 220

Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
225                 230                 235                 240

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val
                245                 250                 255

Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val
            260                 265                 270

Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
        275                 280                 285

Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly
    290                 295                 300

Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val
305                 310                 315                 320

Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala
                325                 330                 335

Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala
            340                 345                 350

Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile
        355                 360                 365

Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly
    370                 375                 380

Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val
385                 390                 395                 400

Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln
                405                 410                 415


<210> SEQ ID NO 48
<211> LENGTH: 1251
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 48

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc      60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta     120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc     180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct     240
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                                -continued

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt    300

gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg    360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt    420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt    480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat    540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg    600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc    660

ggaaccggtg taggtccgca ggccgctgct gccgccgccg caaaagcagc ggctaaattt    720

ggcgccggag cagcgggtgt tctgcctgga gttggtggtg cgggcgtgcc aggggtacct    780

ggtgcaattc cgggtattgg tggtattgcc ggtgtcggca ccccggccgc ggcagctgcg    840

gcagcggcgg ctgccaaagc tgctaaatac ggtgccgcgg cgggtctggt gccaggaggt    900

ccgggttttg gtccgggagt ggttggcgtg cctggcgcag gcgttcctgg tgtgggcgtt    960

ccaggtgcag ggattcctgt tgtgcctggt gccggtattc ccggcgcggc cgttccgggg   1020

gtggttagcc cggaagccgc agcgaaggct gcggcaaagg cagcaaagta tggcgcacgc   1080

ccaggagtcg gcgtgggtgg tatcccgacc tatggggtgg gcgcaggggg ttttcctggt   1140

ttcggcgtag gtgtaggagg tataccgggc gtggccggtg taccaggggt tggtggcgtc   1200

cctggtgttg gcggtgtgcc aggtgttggt atttcaccgg aagcacagta a            1251


<210> SEQ ID NO 49
<211> LENGTH: 401
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 49

Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly Val Gly Ala
1               5                   10                  15

Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile Pro Gly Val
            20                  25                  30

Ala Gly Val Pro Gly Val Gly Gly Val Pro Gly Val Gly Gly Val Pro
        35                  40                  45

Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala Ala Ala Lys Ala
    50                  55                  60

Ala Lys Tyr Gly Ala Ala Gly Ala Gly Val Leu Gly Gly Leu Val Pro
65                  70                  75                  80

Gly Pro Gln Ala Ala Val Pro Gly Val Pro Gly Thr Gly Gly Val Pro
                85                  90                  95

Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala
            100                 105                 110

Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala Pro Gly Val Gly
        115                 120                 125

Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Leu Ala Pro Gly
    130                 135                 140

Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala
145                 150                 155                 160

Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala Lys Ser Ala Ala
```

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                165                 170                 175

Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala Gly Leu Gly Ala
            180                 185                 190

Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro Gly Leu Gly Val
        195                 200                 205

Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Phe
    210                 215                 220

Gly Ala Gly Ala Asp Glu Gly Val Arg Arg Ser Leu Ser Pro Glu Leu
225                 230                 235                 240

Arg Glu Gly Asp Pro Ser Ser Ser Gln His Leu Pro Ser Thr Pro Ser
                245                 250                 255

Ser Pro Arg Val Pro Gly Ala Leu Ala Ala Ala Lys Ala Ala Lys Tyr
            260                 265                 270

Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly Ala Leu Gly Gly
        275                 280                 285

Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro Ala Ala Ala Ala
    290                 295                 300

Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Gly
305                 310                 315                 320

Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly Val Pro Gly
                325                 330                 335

Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys Ala Ala
            340                 345                 350

Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala Gly Gln
        355                 360                 365

Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro
    370                 375                 380

Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg
385                 390                 395                 400

Lys


<210> SEQ ID NO 50
<211> LENGTH: 1206
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 50

cgcccaggag tcggcgtggg tggtatcccg acctatgggg tgggcgcagg gggttttcct      60

ggtttcggcg taggtgtagg aggtataccg ggcgtggccg gtgtaccagg ggttggtggc     120

gtccctggtg ttggcggtgt gccaggtgtt ggtatttcac cggaagcaca ggcagcagcc     180

gcagctaagg cagcgaaata tggtgccgcc ggcgcaggag ttttaggtgg gctggttccg     240

ggcccgcagg cagctgtgcc gggggttcca ggcaccggtg gtgtccctgg agtcggtacg     300

ccggctgcag cggcagccaa agcggctgcg aaagcagcac agtttggctt agtaccgggt     360

gtgggagttg cccccggcgt tggcgttgct ccaggggtgg gtgttgctcc tggcgtcggt     420

ctggctcctg gagtgggcgt agcacccggt gtgggggtgg ccccgggtgt tggggttgca     480

ccgggtatcg gtccgggcgg tgtcgcagca gcagctaaaa gcgcggcgaa agttgcggcc     540

aaagcccaac tgcgcgccgc cgcgggcctc ggtgcaggta ttccggggct gggtgtcgga     600
```

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gttggagtcc cgggtttggg cgtgggcgcg ggagttccgg gactgggagt gggtgccgga    660

gttcctggct ttggtgcagg cgcagatgaa ggtgttcgtc gtagcctgag tccggaactg    720

cgtgaaggtg atccgagtag cagccagcat ctgccgagca ccccgagcag cccgcgtgtt    780

ccgggtgcat tagctgcagc aaaagccgcc aagtatggtg cagccgtgcc gggcgtctta    840

ggtggtctgg gcgccctggg tggtgtaggc attccgggag gtgttgtggg tgcaggaccg    900

gccgccgcag ctgcggccgc caaagcagct gcaaaagcgg cccagtttgg tttagtgggc    960

gccgcaggtt taggcggttt aggtgtgggt ggactgggtg tacctggcgt aggcggtctg   1020

ggtggaattc cgcccgcagc ggccgcgaaa gcggcaaaat atggcgcggc aggcctgggc   1080

ggcgtgctgg gtggggcagg tcagtttccg ctgggcgggg ttgccgcacg tccgggattt   1140

ggtctgagcc cgattttccc tggcggcgca tgtctgggta aagcatgtgg tcgtaaacgt   1200

aaataa                                                              1206
```

```
<210> SEQ ID NO 51
<211> LENGTH: 371
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 51

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1               5                   10                  15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95

Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
            100                 105                 110

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
        115                 120                 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
    130                 135                 140

Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145                 150                 155                 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
                165                 170                 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
            180                 185                 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
        195                 200                 205

Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
    210                 215                 220
```

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```
Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
225                 230                 235                 240

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val
                245                 250                 255

Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val
            260                 265                 270

Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
        275                 280                 285

Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly
    290                 295                 300

Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val
305                 310                 315                 320

Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala
                325                 330                 335

Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala
            340                 345                 350

Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile
        355                 360                 365

Pro Thr Tyr
    370
```

<210> SEQ ID NO 52
<211> LENGTH: 1116
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 52

```
ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc     60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta    120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc    180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct    240

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt    300

gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg    360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt    420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt    480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat    540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg    600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc    660

ggaaccggtg taggtccgca ggccgctgct gccgccgccg caaaagcagc ggctaaattt    720

ggcgccggag cagcgggtgt tctgcctgga gttggtggtg cgggcgtgcc aggggtacct    780

ggtgcaattc cgggtattgg tggtattgcc ggtgtcggca ccccggccgc ggcagctgcg    840

gcagcggcgg ctgccaaagc tgctaaatac ggtgccgcgg cgggtctggt gccaggaggt    900

ccgggttttg gtccgggagt ggttggcgtg cctggcgcag gcgttcctgg tgtgggcgtt    960

ccaggtgcag ggattcctgt tgtgcctggt gccggtattc ccggcgcggc cgttccgggg   1020

gtggttagcc cggaagccgc agcgaaggct gcggcaaagg cagcaaagta tggcgcacgc   1080
```

-continued

```
ccaggagtcg gcgtgggtgg tatcccgacc tattaa                           1116


<210> SEQ ID NO 53
<211> LENGTH: 345
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 53

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1               5                   10                  15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95

Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
            100                 105                 110

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
        115                 120                 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
    130                 135                 140

Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145                 150                 155                 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
                165                 170                 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
            180                 185                 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
        195                 200                 205

Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
    210                 215                 220

Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
225                 230                 235                 240

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val
                245                 250                 255

Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val
            260                 265                 270

Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
        275                 280                 285

Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly
    290                 295                 300

Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val
305                 310                 315                 320

Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala
                325                 330                 335
```

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Ala Val Pro Gly Val Val Ser Pro Glu
340 345

<210> SEQ ID NO 54
<211> LENGTH: 1038
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 54

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc 60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta 120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc 180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct 240

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt 300

gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg 360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt 420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt 480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat 540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg 600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc 660

ggaaccggtg taggtccgca ggccgctgct gccgccgccg caaaagcagc ggctaaattt 720

ggcgccggag cagcgggtgt tctgcctgga gttggtggtg cgggcgtgcc aggggtacct 780

ggtgcaattc cgggtattgg tggtattgcc ggtgtcggca ccccggccgc ggcagctgcg 840

gcagcggcgg ctgccaaagc tgctaaatac ggtgccgcgg cgggtctggt gccaggaggt 900

ccgggttttg gtccgggagt ggttggcgtg cctggcgcag gcgttcctgg tgtgggcgtt 960

ccaggtgcag ggattcctgt tgtgcctggt gccggtattc ccggcgcggc cgttccgggg 1020

gtggttagcc cggaataa 1038

<210> SEQ ID NO 55
<211> LENGTH: 336
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 55

Lys Tyr Gly Ala Ala Gly Ala Gly Val Leu Gly Gly Leu Val Pro Gly
1 5 10 15

Pro Gln Ala Ala Val Pro Gly Val Pro Gly Thr Gly Gly Val Pro Gly
20 25 30

Val Gly Thr Pro Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala
35 40 45

Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala Pro Gly Val Gly Val
50 55 60

Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Leu Ala Pro Gly Val
65 70 75 80

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```
Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro
                85                  90                  95

Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala Lys Ser Ala Ala Lys
            100                 105                 110

Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala Gly Leu Gly Ala Gly
        115                 120                 125

Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro Gly Leu Gly Val Gly
    130                 135                 140

Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Phe Gly
145                 150                 155                 160

Ala Gly Ala Asp Glu Gly Val Arg Arg Ser Leu Ser Pro Glu Leu Arg
                165                 170                 175

Glu Gly Asp Pro Ser Ser Ser Gln His Leu Pro Ser Thr Pro Ser Ser
            180                 185                 190

Pro Arg Val Pro Gly Ala Leu Ala Ala Ala Lys Ala Ala Lys Tyr Gly
        195                 200                 205

Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly Ala Leu Gly Gly Val
    210                 215                 220

Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro Ala Ala Ala Ala Ala
225                 230                 235                 240

Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Gly Ala
                245                 250                 255

Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly Val Pro Gly Val
            260                 265                 270

Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys Ala Ala Lys
        275                 280                 285

Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala Gly Gln Phe
    290                 295                 300

Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile
305                 310                 315                 320

Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys
                325                 330                 335
```

```
<210> SEQ ID NO 56
<211> LENGTH: 1011
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 56

aaatatggtg ccgccggcgc aggagtttta ggtgggctgg ttccgggccc gcaggcagct      60

gtgccggggg ttccaggcac cggtggtgtc cctggagtcg gtacgccggc tgcagcggca     120

gccaaagcgg ctgcgaaagc agcacagttt ggcttagtac cgggtgtggg agttgccccc     180

ggcgttggcg ttgctccagg ggtgggtgtt gctcctggcg tcggtctggc tcctggagtg     240

ggcgtagcac ccggtgtggg ggtggccccg ggtgttgggg ttgcaccggg tatcggtccg     300

ggcggtgtcg cagcagcagc taaaagcgcg gcgaaagttg cggccaaagc ccaactgcgc     360

gccgccgcgg gcctcggtgc aggtattccg gggctgggtg tcggagttgg agtcccgggt     420

ttgggcgtgg gcgcgggagt tccgggactg ggagtgggtg ccggagttcc tggctttggt     480
```

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```
gcaggcgcag atgaaggtgt tcgtcgtagc ctgagtccgg aactgcgtga aggtgatccg    540

agtagcagcc agcatctgcc gagcaccccg agcagcccgc gtgttccggg tgcattagct    600

gcagcaaaag ccgccaagta tggtgcagcc gtgccgggcg tcttaggtgg tctgggcgcc    660

ctgggtggtg taggcattcc gggaggtgtt gtgggtgcag gaccggccgc cgcagctgcg    720

gccgccaaag cagctgcaaa agcggcccag tttggtttag tgggcgccgc aggtttaggc    780

ggtttaggtg tgggtggact gggtgtacct ggcgtaggcg gtctgggtgg aattccgccc    840

gcagcggccg cgaaagcggc aaaatatggc gcggcaggcc tgggcggcgt gctgggtggg    900

gcaggtcagt ttccgctggg cggggttgcc gcacgtccgg gatttggtct gagcccgatt    960

ttccctggcg gcgcatgtct gggtaaagca tgtggtcgta aacgtaaata a            1011


<210> SEQ ID NO 57
<211> LENGTH: 288
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 57

Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala Pro Gly Val Gly Val
1               5                   10                  15

Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Leu Ala Pro Gly Val
            20                  25                  30

Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro
        35                  40                  45

Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala Lys Ser Ala Ala Lys
    50                  55                  60

Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala Gly Leu Gly Ala Gly
65                  70                  75                  80

Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro Gly Leu Gly Val Gly
                85                  90                  95

Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Phe Gly
            100                 105                 110

Ala Gly Ala Asp Glu Gly Val Arg Arg Ser Leu Ser Pro Glu Leu Arg
        115                 120                 125

Glu Gly Asp Pro Ser Ser Ser Gln His Leu Pro Ser Thr Pro Ser Ser
    130                 135                 140

Pro Arg Val Pro Gly Ala Leu Ala Ala Ala Lys Ala Ala Lys Tyr Gly
145                 150                 155                 160

Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly Ala Leu Gly Gly Val
                165                 170                 175

Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro Ala Ala Ala Ala Ala
            180                 185                 190

Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Gly Ala
        195                 200                 205

Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly Val Pro Gly Val
    210                 215                 220

Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys Ala Ala Lys
225                 230                 235                 240

Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala Gly Gln Phe
                245                 250                 255
```

-continued

```
Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile
            260                 265                 270

Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys
        275                 280                 285


<210> SEQ ID NO 58
<211> LENGTH: 867
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 58

cagtttggct tagtaccggg tgtgggagtt gcccccggcg ttggcgttgc tccaggggtg      60

ggtgttgctc ctggcgtcgg tctggctcct ggagtgggcg tagcacccgg tgtgggggtg     120

gccccgggtg ttggggttgc accgggtatc ggtccgggcg gtgtcgcagc agcagctaaa     180

agcgcggcga aagttgcggc caaagcccaa ctgcgcgccg ccgcgggcct cggtgcaggt     240

attccggggc tgggtgtcgg agttggagtc ccgggtttgg gcgtgggcgc gggagttccg     300

ggactgggag tgggtgccgg agttcctggc tttggtgcag gcgcagatga aggtgttcgt     360

cgtagcctga gtccggaact gcgtgaaggt gatccgagta gcagccagca tctgccgagc     420

accccgagca gcccgcgtgt tccgggtgca ttagctgcag caaaagccgc caagtatggt     480

gcagccgtgc cgggcgtctt aggtggtctg ggcgccctgg gtggtgtagg cattccggga     540

ggtgttgtgg gtgcaggacc ggccgccgca gctgcggccg ccaaagcagc tgcaaaagcg     600

gcccagtttg gtttagtggg cgccgcaggt ttaggcggtt taggtgtggg tggactgggt     660

gtacctggcg taggcggtct gggtggaatt ccgcccgcag cggccgcgaa agcggcaaaa     720

tatggcgcgg caggcctggg cggcgtgctg ggtggggcag gtcagtttcc gctgggcggg     780

gttgccgcac gtccgggatt tggtctgagc ccgattttcc ctggcggcgc atgtctgggt     840

aaagcatgtg gtcgtaaacg taaataa                                         867


<210> SEQ ID NO 59
<211> LENGTH: 275
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 59

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1               5                   10                  15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95
```

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Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
100 105 110

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
115 120 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
130 135 140

Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145 150 155 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
165 170 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
180 185 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
195 200 205

Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
210 215 220

Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
225 230 235 240

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val
245 250 255

Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val
260 265 270

Gly Thr Pro
275

<210> SEQ ID NO 60
<211> LENGTH: 828
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 60

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc 60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta 120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc 180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct 240

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt 300

gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg 360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt 420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt 480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat 540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg 600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc 660

ggaaccggtg taggtccgca ggccgctgct gccgccgccg caaaagcagc ggctaaattt 720

ggcgccggag cagcgggtgt tctgcctgga gttggtggtg cgggcgtgcc aggggtacct 780

ggtgcaattc cgggtattgg tggtattgcc ggtgtcggca ccccgtaa 828

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<210> SEQ ID NO 61
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 61

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1               5                   10                  15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95

Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
            100                 105                 110

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
        115                 120                 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
    130                 135                 140

Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145                 150                 155                 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
                165                 170                 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
            180                 185                 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
        195                 200                 205

Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
    210                 215                 220

Gly Pro Gln
225


<210> SEQ ID NO 62
<211> LENGTH: 684
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 62

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc      60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta     120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc     180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct     240

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt     300
```

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gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg    360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt    420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt    480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat    540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg    600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc    660

ggaaccggtg taggtccgca gtaa                                            684
```

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<210> SEQ ID NO 63
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 63

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

Val Gly Val Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly
            20                  25                  30

Leu Gly Val Gly Ala Gly Val Pro Gly Phe Gly Ala Gly Ala Asp Glu
        35                  40                  45

Gly Val Arg Arg Ser Leu Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser
    50                  55                  60

Ser Ser Gln His Leu Pro Ser Thr Pro Ser Ser Pro Arg Val Pro Gly
65                  70                  75                  80

Ala Leu Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly
                85                  90                  95

Val Leu Gly Gly Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly
            100                 105                 110

Val Val Gly Ala Gly Pro Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
        115                 120                 125

Ala Lys Ala Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly
    130                 135                 140

Leu Gly Val Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly
145                 150                 155                 160

Ile Pro Pro Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly
                165                 170                 175

Leu Gly Gly Val Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly Val
            180                 185                 190

Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala
        195                 200                 205

Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys
    210                 215


<210> SEQ ID NO 64
<211> LENGTH: 660
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide
```

<400> SEQUENCE: 64

caactgcgcg ccgccgcggg cctcggtgca ggtattccgg ggctgggtgt cggagttgga 60

gtcccgggtt tgggcgtggg cgcgggagtt ccgggactgg gagtgggtgc cggagttcct 120

ggctttggtg caggcgcaga tgaaggtgtt cgtcgtagcc tgagtccgga actgcgtgaa 180

ggtgatccga gtagcagcca gcatctgccg agcaccccga gcagcccgcg tgttccgggt 240

gcattagctg cagcaaaagc cgccaagtat ggtgcagccg tgccgggcgt cttaggtggt 300

ctgggcgccc tgggtggtgt aggcattccg ggaggtgttg tgggtgcagg accggccgcc 360

gcagctgcgg ccgccaaagc agctgcaaaa gcggcccagt ttggtttagt gggcgccgca 420

ggtttaggcg gtttaggtgt gggtggactg ggtgtacctg gcgtaggcgg tctgggtgga 480

attccgcccg cagcggccgc gaaagcggca aaatatggcg cggcaggcct gggcggcgtg 540

ctgggtgggg caggtcagtt tccgctgggc ggggttgccg cacgtccggg atttggtctg 600

agcccgattt tccctggcgg cgcatgtctg ggtaaagcat gtggtcgtaa acgtaaataa 660

<210> SEQ ID NO 65
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 65

```
Val Pro Gly Val Leu Gly Gly Leu Gly Ala Leu Gly Gly Val Gly Ile
1               5                   10                  15

Pro Gly Gly Val Val Gly Ala Gly Pro Ala Ala Ala Ala Ala Ala Ala
            20                  25                  30

Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Gly Ala Ala Gly
        35                  40                  45

Leu Gly Gly Leu Gly Val Gly Gly Leu Gly Val Pro Gly Val Gly Gly
    50                  55                  60

Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly
65                  70                  75                  80

Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala Gly Gln Phe Pro Leu
                85                  90                  95

Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro
            100                 105                 110

Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys
        115                 120                 125
```

<210> SEQ ID NO 66
<211> LENGTH: 381
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 66

gtgccgggcg tcttaggtgg tctgggcgcc ctgggtggtg taggcattcc gggaggtgtt 60

gtgggtgcag gaccggccgc cgcagctgcg gccgccaaag cagctgcaaa agcggcccag 120

tttggtttag tgggcgccgc aggtttaggc ggtttaggtg tgggtggact gggtgtacct 180

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ggcgtaggcg gtctgggtgg aattccgccc gcagcggccg cgaaagcggc aaaatatggc 240

gcggcaggcc tgggcggcgt gctgggtggg gcaggtcagt ttccgctggg cggggttgcc 300

gcacgtccgg gatttggtct gagcccgatt ttccctggcg gcgcatgtct gggtaaagca 360

tgtggtcgta aacgtaaata a 381

<210> SEQ ID NO 67
<211> LENGTH: 87
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 67

Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly
1 5 10 15

Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala
20 25 30

Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val
35 40 45

Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro
50 55 60

Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys
65 70 75 80

Ala Cys Gly Arg Lys Arg Lys
85

<210> SEQ ID NO 68
<211> LENGTH: 264
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 68

cagtttggtt tagtgggcgc cgcaggttta ggcggtttag gtgtgggtgg actgggtgta 60

cctggcgtag gcggtctggg tggaattccg cccgcagcgg ccgcgaaagc ggcaaaatat 120

ggcgcggcag gcctgggcgg cgtgctgggt ggggcaggtc agtttccgct gggcggggtt 180

gccgcacgtc cgggatttgg tctgagcccg attttccctg gcggcgcatg tctgggtaaa 240

gcatgtggtc gtaaacgtaa ataa 264

<210> SEQ ID NO 69
<211> LENGTH: 72
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 69

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1 5 10 15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
20 25 30

-continued

```
Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp
65                  70


<210> SEQ ID NO 70
<211> LENGTH: 219
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 70

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc      60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta     120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc     180

tttccagggg cactggttcc tggaggtgtg gccgattaa                            219


<210> SEQ ID NO 71
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 71

Gly Leu Gly Gly Val Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly
1               5                   10                  15

Val Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly
            20                  25                  30

Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys
        35                  40


<210> SEQ ID NO 72
<211> LENGTH: 135
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 72

ggcctgggcg gcgtgctggg tggggcaggt cagtttccgc tgggcggggt tgccgcacgt      60

ccgggatttg gtctgagccc gattttccct ggcggcgcat gtctgggtaa agcatgtggt     120

cgtaaacgta aataa                                                      135


<210> SEQ ID NO 73
<211> LENGTH: 636
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 73
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```
atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg      60

cagtatgaag atgcaggttt tccgggtctg cctggtccgg caggcgaacc gggtcgtcat     120

ggtaaagatg gtctgatggg tagtccgggt tttaaaggtg aagcaggttc accgggtgca     180

cctggtcagg atggcacccg tggtgaaccg ggtattccgg gatttccggg taatcgtggc     240

ctgatgggtc agaaaggtga aattggtccg cctggtcagc agggtaaaaa aggcgcaccg     300

ggtatgccag gactgatggg ttcaaatggc agtccgggtc agccaggcac accgggttca     360

aaaggtagca aaggcgaacc tggtattcag ggtatgcctg gtgcaagcgg tctgaaaggc     420

gagccaggtg ccaccggttc tccgggtgaa ccaggttata tgggtctgcc aggtatccaa     480

ggcaaaaaag gtgataaagg taatcagggc gaaaaaggca ttcagggcca gaaaggcgaa     540

aatggccgtc agggtattcc aggccagcag ggcatccagg gtcatcatgg tgcaaaaggt     600

gaacgtggtg aaaagggcga accaggtgtt cgttaa                               636


<210> SEQ ID NO 74
<211> LENGTH: 211
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 74

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Ala Gln Tyr Glu Asp Ala Gly Phe Pro Gly Leu Pro Gly
            20                  25                  30

Pro Ala Gly Glu Pro Gly Arg His Gly Lys Asp Gly Leu Met Gly Ser
        35                  40                  45

Pro Gly Phe Lys Gly Glu Ala Gly Ser Pro Gly Ala Pro Gly Gln Asp
    50                  55                  60

Gly Thr Arg Gly Glu Pro Gly Ile Pro Gly Phe Pro Gly Asn Arg Gly
65                  70                  75                  80

Leu Met Gly Gln Lys Gly Glu Ile Gly Pro Pro Gly Gln Gln Gly Lys
                85                  90                  95

Lys Gly Ala Pro Gly Met Pro Gly Leu Met Gly Ser Asn Gly Ser Pro
            100                 105                 110

Gly Gln Pro Gly Thr Pro Gly Ser Lys Gly Ser Lys Gly Glu Pro Gly
        115                 120                 125

Ile Gln Gly Met Pro Gly Ala Ser Gly Leu Lys Gly Glu Pro Gly Ala
    130                 135                 140

Thr Gly Ser Pro Gly Glu Pro Gly Tyr Met Gly Leu Pro Gly Ile Gln
145                 150                 155                 160

Gly Lys Lys Gly Asp Lys Gly Asn Gln Gly Glu Lys Gly Ile Gln Gly
                165                 170                 175

Gln Lys Gly Glu Asn Gly Arg Gln Gly Ile Pro Gly Gln Gln Gly Ile
            180                 185                 190

Gln Gly His His Gly Ala Lys Gly Glu Arg Gly Glu Lys Gly Glu Pro
        195                 200                 205

Gly Val Arg
    210
```

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<210> SEQ ID NO 75
<211> LENGTH: 565
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 75

tgcaggtttt ccgggtctgc ctggtccggc aggcgaaccg ggtcgtcatg gtaaagatgg     60

tctgatgggt agtccgggtt ttaaaggtga agcaggttca ccgggtgcac ctggtcagga    120

tggcacccgt ggtgaaccgg gtattccggg atttccgggt aatcgtggcc tgatgggtca    180

gaaaggtgaa attggtccgc ctggtcagca gggtaaaaaa ggcgcaccgg gtatgccagg    240

actgatgggt tcaaatggca gtccgggtca gccaggcaca ccgggttcaa aaggtagcaa    300

aggcgaacct ggtattcagg gtatgcctgg tgcaagcggt ctgaaaggcg agccaggtgc    360

caccggttct ccgggtgaac caggttatat gggtctgcca ggtatccaag gcaaaaaagg    420

tgataaaggt aatcagggcg aaaaaggcat tcagggccag aaaggcgaaa atggccgtca    480

gggtattcca ggccagcagg gcatccaggg tcatcatggt gcaaaaggtg aacgtggtga    540

aaagggcgaa ccaggtgttc gttaa                                          565


<210> SEQ ID NO 76
<211> LENGTH: 187
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 76

Ala Gly Phe Pro Gly Leu Pro Gly Pro Ala Gly Glu Pro Gly Arg His
1               5                   10                  15

Gly Lys Asp Gly Leu Met Gly Ser Pro Gly Phe Lys Gly Glu Ala Gly
            20                  25                  30

Ser Pro Gly Ala Pro Gly Gln Asp Gly Thr Arg Gly Glu Pro Gly Ile
        35                  40                  45

Pro Gly Phe Pro Gly Asn Arg Gly Leu Met Gly Gln Lys Gly Glu Ile
    50                  55                  60

Gly Pro Pro Gly Gln Gln Gly Lys Lys Gly Ala Pro Gly Met Pro Gly
65                  70                  75                  80

Leu Met Gly Ser Asn Gly Ser Pro Gly Gln Pro Gly Thr Pro Gly Ser
                85                  90                  95

Lys Gly Ser Lys Gly Glu Pro Gly Ile Gln Gly Met Pro Gly Ala Ser
            100                 105                 110

Gly Leu Lys Gly Glu Pro Gly Ala Thr Gly Ser Pro Gly Glu Pro Gly
        115                 120                 125

Tyr Met Gly Leu Pro Gly Ile Gln Gly Lys Lys Gly Asp Lys Gly Asn
    130                 135                 140

Gln Gly Glu Lys Gly Ile Gln Gly Gln Lys Gly Glu Asn Gly Arg Gln
145                 150                 155                 160

Gly Ile Pro Gly Gln Gln Gly Ile Gln Gly His His Gly Ala Lys Gly
                165                 170                 175

Glu Arg Gly Glu Lys Gly Glu Pro Gly Val Arg
            180                 185
```

-continued

<210> SEQ ID NO 77
<211> LENGTH: 639
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 77

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg 60

cagtatgaag atatgggtcc gcctggtagc cgtggtgcaa gtggtccggc aggcgttcgt 120

ggtccgaatg gtgatgcagg tcgtccgggt gaaccgggtc tgatgggtcc tcgtggtctg 180

cctggttcac cgggtaatat tggtcctgca ggtaaagaag gtccggttgg tctgccaggt 240

attgatggcc gtccgggtcc gattggtcca gccggtgcac gtggtgaacc tggcaatatt 300

ggttttccgg gtcctaaagg tccgaccggt gatccgggta aaaatggtga taaaggtcat 360

gcaggtctgg caggcgcacg cggtgcacct ggtccggatg gtaataatgg tgcacagggt 420

ccaccgggtc cgcagggtgt tcaaggtggt aaaggcgaac agggtcctgc cggtcctccg 480

ggttttcagg gactgcctgg tccgagcggt cctgcgggtg aagttggtaa acctggtgaa 540

cgcggtctgc atggtgaatt tggcctgcct gggcctgcag gtccgcgtgg cgaacgtggt 600

ccgccaggtg aaagcggtgc agcaggtccg acaggttaa 639

<210> SEQ ID NO 78
<211> LENGTH: 212
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 78

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1 5 10 15

Ala Ser Ala Ala Gln Tyr Glu Asp Met Gly Pro Pro Gly Ser Arg Gly
20 25 30

Ala Ser Gly Pro Ala Gly Val Arg Gly Pro Asn Gly Asp Ala Gly Arg
35 40 45

Pro Gly Glu Pro Gly Leu Met Gly Pro Arg Gly Leu Pro Gly Ser Pro
50 55 60

Gly Asn Ile Gly Pro Ala Gly Lys Glu Gly Pro Val Gly Leu Pro Gly
65 70 75 80

Ile Asp Gly Arg Pro Gly Pro Ile Gly Pro Ala Gly Ala Arg Gly Glu
85 90 95

Pro Gly Asn Ile Gly Phe Pro Gly Pro Lys Gly Pro Thr Gly Asp Pro
100 105 110

Gly Lys Asn Gly Asp Lys Gly His Ala Gly Leu Ala Gly Ala Arg Gly
115 120 125

Ala Pro Gly Pro Asp Gly Asn Asn Gly Ala Gln Gly Pro Pro Gly Pro
130 135 140

Gln Gly Val Gln Gly Gly Lys Gly Glu Gln Gly Pro Ala Gly Pro Pro
145 150 155 160

Gly Phe Gln Gly Leu Pro Gly Pro Ser Gly Pro Ala Gly Glu Val Gly

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                165                 170                 175

Lys Pro Gly Glu Arg Gly Leu His Gly Glu Phe Gly Leu Pro Gly Pro
            180                 185                 190

Ala Gly Pro Arg Gly Glu Arg Gly Pro Pro Gly Glu Ser Gly Ala Ala
        195                 200                 205

Gly Pro Thr Gly
    210


<210> SEQ ID NO 79
<211> LENGTH: 567
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 79

atgggtccgc ctggtagccg tggtgcaagt ggtccggcag gcgttcgtgg tccgaatggt     60

gatgcaggtc gtccgggtga accgggtctg atgggtcctc gtggtctgcc tggttcaccg    120

ggtaatattg gtcctgcagg taaagaaggt ccggttggtc tgccaggtat tgatggccgt    180

ccgggtccga ttggtccagc cggtgcacgt ggtgaacctg gcaatattgg ttttccgggt    240

cctaaaggtc cgaccggtga tccgggtaaa aatggtgata aaggtcatgc aggtctggca    300

ggcgcacgcg gtgcacctgg tccggatggt aataatggtg cacagggtcc accgggtccg    360

cagggtgttc aaggtggtaa aggcgaacag ggtcctgccg gtcctccggg ttttcaggga    420

ctgcctggtc cgagcggtcc tgcgggtgaa gttggtaaac ctggtgaacg cggtctgcat    480

ggtgaatttg gcctgcctgg gcctgcaggt ccgcgtggcg aacgtggtcc gccaggtgaa    540

agcggtgcag caggtccgac aggttaa                                        567


<210> SEQ ID NO 80
<211> LENGTH: 188
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 80

Met Gly Pro Pro Gly Ser Arg Gly Ala Ser Gly Pro Ala Gly Val Arg
1               5                   10                  15

Gly Pro Asn Gly Asp Ala Gly Arg Pro Gly Glu Pro Gly Leu Met Gly
            20                  25                  30

Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly Lys
        35                  40                  45

Glu Gly Pro Val Gly Leu Pro Gly Ile Asp Gly Arg Pro Gly Pro Ile
    50                  55                  60

Gly Pro Ala Gly Ala Arg Gly Glu Pro Gly Asn Ile Gly Phe Pro Gly
65                  70                  75                  80

Pro Lys Gly Pro Thr Gly Asp Pro Gly Lys Asn Gly Asp Lys Gly His
                85                  90                  95

Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn
            100                 105                 110

Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Gly Lys Gly
        115                 120                 125
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Glu Gln Gly Pro Ala Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro
    130                 135                 140

Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His
145                 150                 155                 160

Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly
                165                 170                 175

Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly
            180                 185


<210> SEQ ID NO 81
<211> LENGTH: 612
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 81

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggcg      60

cagtatgaag atggttttca gggtcctgcc ggtgaaccgg gtgaacctgg tcagacaggt     120

ccggcaggcg cacgtggtcc tgcaggtcct cctggtaaag ccggtgaaga tggtcatccg     180

ggtaaaccgg gtcgtcctgg tgaacgtggt gttgttggtc cgcagggtgc ccgtggtttt     240

ccgggtactc cgggtctgcc aggttttaaa ggtattcgtg gtcataatgg tctggatggt     300

ctgaaaggtc agcctggtgc accgggtgtt aaaggtgaac caggtgctcc gggtgaaaat     360

ggcacaccgg gtcagaccgg tgcgcgtggt ctgcctggcg aacgcggtcg tgttggtgca     420

cctggtccag ccggtgcacg cggtagtgat ggtagcgttg gtccggttgg tccagcgggt     480

ccgattggta gcgcaggtcc accgggtttt ccaggcgcac cgggtccgaa aggtgaaatt     540

ggtgcagttg gtaatgcagg ccctgccggt ccagcaggac cgcgtggtga agttggcctg     600

cctggtctgt aa                                                         612


<210> SEQ ID NO 82
<211> LENGTH: 203
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 82

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Ala Gln Tyr Glu Asp Gly Phe Gln Gly Pro Ala Gly Glu
            20                  25                  30

Pro Gly Glu Pro Gly Gln Thr Gly Pro Ala Gly Ala Arg Gly Pro Ala
        35                  40                  45

Gly Pro Pro Gly Lys Ala Gly Glu Asp Gly His Pro Gly Lys Pro Gly
    50                  55                  60

Arg Pro Gly Glu Arg Gly Val Val Gly Pro Gln Gly Ala Arg Gly Phe
65                  70                  75                  80

Pro Gly Thr Pro Gly Leu Pro Gly Phe Lys Gly Ile Arg Gly His Asn
                85                  90                  95

Gly Leu Asp Gly Leu Lys Gly Gln Pro Gly Ala Pro Gly Val Lys Gly
```

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100 105 110

Glu Pro Gly Ala Pro Gly Glu Asn Gly Thr Pro Gly Gln Thr Gly Ala
115 120 125

Arg Gly Leu Pro Gly Glu Arg Gly Arg Val Gly Ala Pro Gly Pro Ala
130 135 140

Gly Ala Arg Gly Ser Asp Gly Ser Val Gly Pro Val Gly Pro Ala Gly
145 150 155 160

Pro Ile Gly Ser Ala Gly Pro Pro Gly Phe Pro Gly Ala Pro Gly Pro
165 170 175

Lys Gly Glu Ile Gly Ala Val Gly Asn Ala Gly Pro Ala Gly Pro Ala
180 185 190

Gly Pro Arg Gly Glu Val Gly Leu Pro Gly Leu
195 200

<210> SEQ ID NO 83
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 83

ggttttcagg gtcctgccgg tgaaccgggt gaacctggtc agacaggtcc ggcaggcgca 60

cgtggtcctg caggtcctcc tggtaaagcc ggtgaagatg gtcatccggg taaaccgggt 120

cgtcctggtg aacgtggtgt tgttggtccg cagggtgccc gtggttttcc gggtactccg 180

ggtctgccag gttttaaagg tattcgtggt cataatggtc tggatggtct gaaaggtcag 240

cctggtgcac cgggtgttaa aggtgaacca ggtgctccgg gtgaaaatgg cacaccgggt 300

cagaccggtg cgcgtggtct gcctggcgaa cgcggtcgtg ttggtgcacc tggtccagcc 360

ggtgcacgcg gtagtgatgg tagcgttggt ccggttggtc cagcgggtcc gattggtagc 420

gcaggtccac cgggttttcc aggcgcaccg ggtccgaaag gtgaaattgg tgcagttggt 480

aatgcaggcc ctgccggtcc agcaggaccg cgtggtgaag ttggcctgcc tggtctgtaa 540

<210> SEQ ID NO 84
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polypeptide

<400> SEQUENCE: 84

Gly Phe Gln Gly Pro Ala Gly Glu Pro Gly Glu Pro Gly Gln Thr Gly
1 5 10 15

Pro Ala Gly Ala Arg Gly Pro Ala Gly Pro Pro Gly Lys Ala Gly Glu
20 25 30

Asp Gly His Pro Gly Lys Pro Gly Arg Pro Gly Glu Arg Gly Val Val
35 40 45

Gly Pro Gln Gly Ala Arg Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly
50 55 60

Phe Lys Gly Ile Arg Gly His Asn Gly Leu Asp Gly Leu Lys Gly Gln
65 70 75 80

Pro Gly Ala Pro Gly Val Lys Gly Glu Pro Gly Ala Pro Gly Glu Asn

```
                85                  90                  95

Gly Thr Pro Gly Gln Thr Gly Ala Arg Gly Leu Pro Gly Glu Arg Gly
            100                 105                 110

Arg Val Gly Ala Pro Gly Pro Ala Gly Ala Arg Gly Ser Asp Gly Ser
        115                 120                 125

Val Gly Pro Val Gly Pro Ala Gly Pro Ile Gly Ser Ala Gly Pro Pro
    130                 135                 140

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

Asn Ala Gly Pro Ala Gly Pro Ala Gly Pro Arg Gly Glu Val Gly Leu
                165                 170                 175

Pro Gly Leu


<210> SEQ ID NO 85
<211> LENGTH: 689
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 85

gtccgcaggg tgttgttggt gcagatggta aagacggtac cccgggtgaa aaaggagaac      60

agggacgtac aggtgcagca ggtaaacagg gcagcccggg tgccgatggt gcccgtggcc     120

cgctgggtag cattggtcag cagggtgcaa gaggcgaacc gggcgatccg ggtagtccgg     180

gcctgcgtgg tgatacgggt ctggccggtg ttaaaggcgt tgcaggtcct tcaggtcgtc     240

caggtcaacc gggtgcaaat ggtctgccgg gtgttaatgg tcgtggcggt ctggaacgtg     300

gtctggcagg accgccgggt cctgatggtc gccgcggtga aacgggttca ccgggtattg     360

ccggtgccct gggtaaacca ggtctggaag gtccgaaagg ttatcctggt ctgcgcggtc     420

gtgatggtac caatggcaaa cgtggcgaac agggcgaaac cggtccagat ggtgttcgtg     480

gtattccggg taacgatggt cagagcggta aaccgggcat tgatggtatt gatggcacca     540

atggtcagcc tggcgaagca ggttatcagg gtggtcgcgg tacccgtggt cagctgggtg     600

aaacaggtga tgttggtcag aatggtgatc gcggcgcacc gggtccggat ggtagcaaag     660

gtagcgccgg tcgtccgggt ttacgttaa                                       689


<210> SEQ ID NO 86
<211> LENGTH: 229
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 86

Gly Pro Gln Gly Val Val Gly Ala Asp Gly Lys Asp Gly Thr Pro Gly
1               5                   10                  15

Glu Lys Gly Glu Gln Gly Arg Thr Gly Ala Ala Gly Lys Gln Gly Ser
            20                  25                  30

Pro Gly Ala Asp Gly Ala Arg Gly Pro Leu Gly Ser Ile Gly Gln Gln
        35                  40                  45

Gly Ala Arg Gly Glu Pro Gly Asp Pro Gly Ser Pro Gly Leu Arg Gly
    50                  55                  60
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Asp Thr Gly Leu Ala Gly Val Lys Gly Val Ala Gly Pro Ser Gly Arg
65                  70                  75                  80

Pro Gly Gln Pro Gly Ala Asn Gly Leu Pro Gly Val Asn Gly Arg Gly
                85                  90                  95

Gly Leu Glu Arg Gly Leu Ala Gly Pro Pro Gly Pro Asp Gly Arg Arg
            100                 105                 110

Gly Glu Thr Gly Ser Pro Gly Ile Ala Gly Ala Leu Gly Lys Pro Gly
        115                 120                 125

Leu Glu Gly Pro Lys Gly Tyr Pro Gly Leu Arg Gly Arg Asp Gly Thr
    130                 135                 140

Asn Gly Lys Arg Gly Glu Gln Gly Glu Thr Gly Pro Asp Gly Val Arg
145                 150                 155                 160

Gly Ile Pro Gly Asn Asp Gly Gln Ser Gly Lys Pro Gly Ile Asp Gly
                165                 170                 175

Ile Asp Gly Thr Asn Gly Gln Pro Gly Glu Ala Gly Tyr Gln Gly Gly
            180                 185                 190

Arg Gly Thr Arg Gly Gln Leu Gly Glu Thr Gly Asp Val Gly Gln Asn
        195                 200                 205

Gly Asp Arg Gly Ala Pro Gly Pro Asp Gly Ser Lys Gly Ser Ala Gly
    210                 215                 220

Arg Pro Gly Leu Arg
225


<210> SEQ ID NO 87
<211> LENGTH: 2283
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 87

ggtggcgtac caggcgcaat tcctgggggt gtcccaggcg gtgtttttta tccgggcgcc     60

ggtcttggcg cactgggtgg cggtgcactg ggcccgggcg gcaaaccgct gaaaccggta    120

ccaggtggtt tagcaggcgc cggcttaggc gcaggtctgg gagcatttcc ggcagttacc    180

tttccagggg cactggttcc tggaggtgtg gccgatgcag ccgcggcata taaagccgct    240

aaagccggtg cgggtttagg aggcgtccca ggtgtcggtg gcctgggtgt tagcgccggt    300

gcagttgttc cgcagccggg agcaggggtt aaacctggta aagtgccggg agtaggtctg    360

ccaggcgttt atcctggtgg tgttttgccg ggtgcccgtt ttccgggcgt tggtgttctt    420

ccaggcgtgc cgaccggagc cggtgttaaa ccgaaagccc ccggtgttgg aggtgcattt    480

gcaggcatcc cgggagttgg cccgtttggt ggtccgcaac ctggggttcc gttaggttat    540

ccgattaaag caccgaaact gcccggcggt tatggtctgc cgtacacaac cggtaaactg    600

ccgtatggtt atggcccggg tggagttgcg ggtgcagcag gtaaagcggg ttatcctacc    660

ggaaccggtg taggtccgca ggccgctgct gccgccgccg caaaagcagc ggctaaattt    720

ggcgccggag cagcgggtgt tctgcctgga gttggtggtg cgggcgtgcc aggggtacct    780

ggtgcaattc cgggtattgg tggtattgcc ggtgtcggca ccccggccgc ggcagctgcg    840

gcagcggcgg ctgccaaagc tgctaaatac ggtgccgcgg cgggtctggt gccaggaggt    900

ccgggttttg gtccgggagt ggttggcgtg cctggcgcag gcgttcctgg tgtgggcgtt    960
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ccaggtgcag ggattcctgt tgtgcctggt gccggtattc ccggcgcggc cgttccgggg   1020

gtggttagcc cggaagccgc agcgaaggct gcggcaaagg cagcaaagta tggcgcacgc   1080

ccaggagtcg gcgtgggtgg tatcccgacc tatggggtgg gcgcaggggg ttttcctggt   1140

ttcggcgtag gtgtaggagg tataccgggc gtggccggtg taccaggggt tggtggcgtc   1200

cctggtgttg gcggtgtgcc aggtgttggt atttcaccgg aagcacaggc agcagccgca   1260

gctaaggcag cgaaatatgg tgccgccggc gcaggagttt taggtgggct ggttccgggc   1320

ccgcaggcag ctgtgccggg ggttccaggc accggtggtg tccctggagt cggtacgccg   1380

gctgcagcgg cagccaaagc ggctgcgaaa gcagcacagt ttggcttagt accgggtgtg   1440

ggagttgccc ccggcgttgg cgttgctcca ggggtgggtg ttgctcctgg cgtcggtctg   1500

gctcctggag tgggcgtagc acccggtgtg gggtggccc cgggtgttgg ggttgcaccg   1560

ggtatcggtc cgggcggtgt cgcagcagca gctaaaagcg cggcgaaagt tgcggccaaa   1620

gcccaactgc gcgccgccgc gggcctcggt gcaggtattc cggggctggg tgtcggagtt   1680

ggagtcccgg gtttgggcgt gggcgcggga gttccgggac tgggagtggg tgccggagtt   1740

cctggctttg gtgcaggcgc agatgaaggt gttcgtcgta gcctgagtcc ggaactgcgt   1800

gaaggtgatc cgagtagcag ccagcatctg ccgagcaccc cgagcagccc gcgtgttccg   1860

ggtgcattag ctgcagcaaa agccgccaag tatggtgcag ccgtgccggg cgtcttaggt   1920

ggtctgggcg ccctgggtgg tgtaggcatt ccgggaggtg ttgtgggtgc aggaccggcc   1980

gccgcagctg cggccgccaa agcagctgca aaagcggccc agtttggttt agtgggcgcc   2040

gcaggtttag gcggtttagg tgtgggtgga ctgggtgtac ctggcgtagg cggtctgggt   2100

ggaattccgc ccgcagcggc cgcgaaagcg gcaaaatatg gcgcggcagg cctgggcggc   2160

gtgctgggtg gggcaggtca gtttccgctg ggcggggttg ccgcacgtcc gggatttggt   2220

ctgagcccga ttttccctgg cggcgcatgt ctgggtaaag catgtggtcg taaacgtaaa   2280

taa                                                                 2283


<210> SEQ ID NO 88
<211> LENGTH: 760
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 88

Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly Gly Val Phe
1               5                   10                  15

Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala Leu Gly Pro
            20                  25                  30

Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala Gly Ala Gly
        35                  40                  45

Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe Pro Gly Ala
    50                  55                  60

Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala
65                  70                  75                  80

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
                85                  90                  95
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```
Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro
            100                 105                 110

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
        115                 120                 125

Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro
    130                 135                 140

Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe
145                 150                 155                 160

Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val
                165                 170                 175

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
            180                 185                 190

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly
        195                 200                 205

Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val
    210                 215                 220

Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
225                 230                 235                 240

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val
                245                 250                 255

Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val
            260                 265                 270

Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala
        275                 280                 285

Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly
    290                 295                 300

Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val
305                 310                 315                 320

Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala
                325                 330                 335

Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala
            340                 345                 350

Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile
        355                 360                 365

Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly
    370                 375                 380

Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val
385                 390                 395                 400

Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln
                405                 410                 415

Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Ala Gly
            420                 425                 430

Val Leu Gly Gly Leu Val Pro Gly Pro Gln Ala Ala Val Pro Gly Val
        435                 440                 445

Pro Gly Thr Gly Gly Val Pro Gly Val Gly Thr Pro Ala Ala Ala Ala
    450                 455                 460

Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val
465                 470                 475                 480

Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro
                485                 490                 495

Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val
```

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500 505 510

Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala
515 520 525

Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg
530 535 540

Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val
545 550 555 560

Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val
565 570 575

Gly Ala Gly Val Pro Gly Phe Gly Ala Gly Ala Asp Glu Gly Val Arg
580 585 590

Arg Ser Leu Ser Pro Glu Leu Arg Glu Gly Asp Pro Ser Ser Ser Gln
595 600 605

His Leu Pro Ser Thr Pro Ser Ser Pro Arg Val Pro Gly Ala Leu Ala
610 615 620

Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly
625 630 635 640

Gly Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly
645 650 655

Ala Gly Pro Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala
660 665 670

Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val
675 680 685

Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro
690 695 700

Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly
705 710 715 720

Val Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg
725 730 735

Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly
740 745 750

Lys Ala Cys Gly Arg Lys Arg Lys
755 760

<210> SEQ ID NO 89
<211> LENGTH: 429
<212> TYPE: PRT
<213> ORGANISM: Podocoryna carnea

<400> SEQUENCE: 89

Gly Pro Gln Gly Val Val Gly Ala Asp Gly Lys Asp Gly Thr Pro Gly
1 5 10 15

Glu Lys Gly Glu Gln Gly Arg Thr Gly Ala Ala Gly Lys Gln Gly Ser
20 25 30

Pro Gly Ala Asp Gly Ala Arg Gly Pro Leu Gly Ser Ile Gly Gln Gln
35 40 45

Gly Ala Arg Gly Glu Pro Gly Asp Pro Gly Ser Pro Gly Leu Arg Gly
50 55 60

Asp Thr Gly Leu Ala Gly Val Lys Gly Val Ala Gly Pro Ser Gly Arg
65 70 75 80

Pro Gly Gln Pro Gly Ala Asn Gly Leu Pro Gly Val Asn Gly Arg Gly
85 90 95

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Gly Leu Arg Gly Lys Pro Gly Ala Lys Gly Ile Ala Gly Ser Asp Gly
            100                 105                 110

Glu Ala Gly Glu Ser Gly Ala Pro Gly Gln Ser Gly Pro Thr Gly Pro
        115                 120                 125

Arg Gly Gln Arg Gly Pro Ser Gly Glu Asp Gly Asn Pro Gly Leu Gln
    130                 135                 140

Gly Leu Pro Gly Ser Asp Gly Glu Pro Gly Glu Glu Gly Gln Pro Gly
145                 150                 155                 160

Arg Ser Gly Gln Pro Gly Gln Gln Gly Pro Arg Gly Ser Pro Gly Glu
                165                 170                 175

Val Gly Pro Arg Gly Ser Lys Gly Pro Ser Gly Asp Arg Gly Asp Arg
            180                 185                 190

Gly Glu Arg Gly Val Pro Gly Gln Thr Gly Ser Ala Gly Asn Val Gly
        195                 200                 205

Glu Asp Gly Glu Gln Gly Gly Lys Gly Val Asp Gly Ala Ser Gly Pro
    210                 215                 220

Ser Gly Ala Leu Gly Ala Arg Gly Pro Pro Gly Ser Arg Gly Asp Thr
225                 230                 235                 240

Gly Ala Val Gly Pro Pro Gly Pro Thr Gly Arg Ser Gly Leu Pro Gly
                245                 250                 255

Asn Ala Gly Gln Lys Gly Pro Ser Gly Glu Pro Gly Ser Pro Gly Lys
            260                 265                 270

Ala Gly Ser Ala Gly Glu Gln Gly Pro Pro Gly Lys Asp Gly Ser Asn
        275                 280                 285

Gly Glu Pro Gly Ser Pro Gly Lys Glu Gly Glu Arg Gly Leu Ala Gly
    290                 295                 300

Pro Pro Gly Pro Asp Gly Arg Arg Gly Glu Thr Gly Ser Pro Gly Ile
305                 310                 315                 320

Ala Gly Ala Leu Gly Lys Pro Gly Leu Glu Gly Pro Lys Gly Tyr Pro
                325                 330                 335

Gly Leu Arg Gly Arg Asp Gly Thr Asn Gly Lys Arg Gly Glu Gln Gly
            340                 345                 350

Glu Thr Gly Pro Asp Gly Val Arg Gly Ile Pro Gly Asn Asp Gly Gln
        355                 360                 365

Ser Gly Lys Pro Gly Ile Asp Gly Ile Asp Gly Thr Asn Gly Gln Pro
    370                 375                 380

Gly Glu Ala Gly Tyr Gln Gly Gly Arg Gly Thr Arg Gly Gln Leu Gly
385                 390                 395                 400

Glu Thr Gly Asp Val Gly Gln Asn Gly Asp Arg Gly Ala Pro Gly Pro
                405                 410                 415

Asp Gly Ser Lys Gly Ser Ala Gly Arg Pro Gly Leu Arg
            420                 425


<210> SEQ ID NO 90
<211> LENGTH: 570
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 90

ggtccgcagg gtgttgttgg tgcagatggt aaagacggta ccccgggtaa tgcaggtcag     60
```

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```
aaaggtccgt caggtgaacc tggcagccct ggtaaagcag gtagtgccgg tgagcagggt    120

ccgccgggca aagatggtag taatggtgag ccgggtagcc ctggcaaaga aggtgaacgt    180

ggtctggcag gaccgccggg tcctgatggt cgccgcggtg aaacgggttc accgggtatt    240

gccggtgccc tgggtaaacc aggtctggaa ggtccgaaag gttatcctgg tctgcgcggt    300

cgtgatggta ccaatggcaa acgtggcgaa cagggcgaaa ccggtccaga tggtgttcgt    360

ggtattccgg gtaacgatgg tcagagcggt aaaccgggca ttgatggtat tgatggcacc    420

aatggtcagc ctggcgaagc aggttatcag ggtggtcgcg gtacccgtgg tcagctgggt    480

gaaacaggtg atgttggtca gaatggtgat cgcggcgcac cgggtccgga tggtagcaaa    540

ggtagcgccg gtcgtccggg tttacgttaa                                     570


<210> SEQ ID NO 91
<211> LENGTH: 189
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 91

Gly Pro Gln Gly Val Val Gly Ala Asp Gly Lys Asp Gly Thr Pro Gly
1               5                   10                  15

Asn Ala Gly Gln Lys Gly Pro Ser Gly Glu Pro Gly Ser Pro Gly Lys
            20                  25                  30

Ala Gly Ser Ala Gly Glu Gln Gly Pro Pro Gly Lys Asp Gly Ser Asn
        35                  40                  45

Gly Glu Pro Gly Ser Pro Gly Lys Glu Gly Glu Arg Gly Leu Ala Gly
    50                  55                  60

Pro Pro Gly Pro Asp Gly Arg Arg Gly Glu Thr Gly Ser Pro Gly Ile
65                  70                  75                  80

Ala Gly Ala Leu Gly Lys Pro Gly Leu Glu Gly Pro Lys Gly Tyr Pro
                85                  90                  95

Gly Leu Arg Gly Arg Asp Gly Thr Asn Gly Lys Arg Gly Glu Gln Gly
            100                 105                 110

Glu Thr Gly Pro Asp Gly Val Arg Gly Ile Pro Gly Asn Asp Gly Gln
        115                 120                 125

Ser Gly Lys Pro Gly Ile Asp Gly Ile Asp Gly Thr Asn Gly Gln Pro
    130                 135                 140

Gly Glu Ala Gly Tyr Gln Gly Gly Arg Gly Thr Arg Gly Gln Leu Gly
145                 150                 155                 160

Glu Thr Gly Asp Val Gly Gln Asn Gly Asp Arg Gly Ala Pro Gly Pro
                165                 170                 175

Asp Gly Ser Lys Gly Ser Ala Gly Arg Pro Gly Leu Arg
            180                 185


<210> SEQ ID NO 92
<211> LENGTH: 228
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 92
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```
Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Gly Asp Gln Gly Pro Val Gly Arg Thr Gly Glu Val Gly
            20                  25                  30

Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro Ser Gly Glu
        35                  40                  45

Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln Gly Leu Leu
    50                  55                  60

Gly Ala Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg Gly Glu Arg Gly
65                  70                  75                  80

Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro Leu Gly Ile
                85                  90                  95

Ala Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Ala Val Gly Ser Pro
            100                 105                 110

Gly Val Asn Gly Ala Pro Gly Glu Ala Gly Arg Asp Gly Asn Pro Gly
        115                 120                 125

Asn Asp Gly Pro Pro Gly Arg Asp Gly Gln Pro Gly His Lys Gly Glu
    130                 135                 140

Arg Gly Tyr Pro Gly Asn Ile Gly Pro Val Gly Ala Ala Gly Ala Pro
145                 150                 155                 160

Gly Pro His Gly Pro Val Gly Pro Ala Gly Lys His Gly Asn Arg Gly
                165                 170                 175

Glu Thr Gly Pro Ser Gly Pro Val Gly Pro Ala Gly Ala Val Gly Pro
            180                 185                 190

Arg Gly Pro Ser Gly Pro Gln Gly Ile Arg Gly Asp Lys Gly Glu Pro
        195                 200                 205

Gly Glu Lys Gly Pro Arg Gly Leu Pro Gly Leu Gly Asp Tyr Lys Asp
    210                 215                 220

Asp Asp Asp Lys
225
```

<210> SEQ ID NO 93
<211> LENGTH: 687
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 93

```
atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcgggt      60

gatcagggtc cggttggtcg taccggtgaa gttggtgcag tcgggccgcc gggttttgcg     120

ggtgaaaaag gcccgtcagg tgaagcaggc accgctggcc ctcctggcac gcctggccca     180

cagggtttac tgggcgcacc tggaattctg ggactgccgg gcagccgtgg agaacgcggt     240

ttaccaggtg ttgccggtgc cgttggtgaa cctggtccac tgggcattgc agggccgcct     300

ggcgcacggg gaccgcctgg tgctgttggt agtccgggtg tgaatggtgc tccgggtgaa     360

gccggtcgtg acggtaatcc gggaaatgac ggcccgccag gccgcgatgg tcagccgggt     420

cataaaggtg agcgtggtta cccaggtaat attggtccag tcggtgccgc cggtgcgccg     480

ggtcctcatg gccctgtcgg tccagccggt aaacatggta atcgcggtga gacaggtccg     540

tcaggaccag tgggccctgc tggcgcagtc ggtccgcgcg ggccgagtgg ccctcagggt     600
```

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```
attcgtggcg ataaagggga accgggcgaa aaagggccgc ggggtctgcc aggcctgggt    660

gactacaaag acgacgacga caaataa                                        687


<210> SEQ ID NO 94
<211> LENGTH: 228
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 94

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

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

Gly His His Gly Asp Gln Gly Ala Pro Gly Ser Val Gly Pro Ala Gly
        35                  40                  45

Pro Arg Gly Pro Ala Gly Pro Ser Gly Pro Ala Gly Lys Asp Gly Arg
    50                  55                  60

Thr Gly His Pro Gly Thr Val Gly Pro Ala Gly Ile Arg Gly Pro Gln
65                  70                  75                  80

Gly His Gln Gly Pro Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
                85                  90                  95

Pro Pro Gly Val Ser Gly Gly Gly Tyr Asp Phe Gly Tyr Asp Gly Asp
            100                 105                 110

Phe Tyr Arg Ala Asp Gln Pro Arg Ser Ala Pro Ser Leu Arg Pro Lys
        115                 120                 125

Asp Tyr Glu Val Asp Ala Thr Leu Lys Ser Leu Asn Asn Gln Ile Glu
    130                 135                 140

Thr Leu Leu Thr Pro Glu Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys
145                 150                 155                 160

Arg Asp Leu Arg Leu Ser His Pro Glu Trp Ser Ser Gly Tyr Tyr Trp
                165                 170                 175

Ile Asp Pro Asn Gln Gly Cys Thr Met Asp Ala Ile Lys Val Tyr Cys
            180                 185                 190

Asp Phe Ser Thr Gly Glu Thr Cys Ile Arg Ala Gln Pro Glu Asn Ile
        195                 200                 205

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

Asp Asp Asp Lys
225


<210> SEQ ID NO 95
<211> LENGTH: 687
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 95

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcgaaa     60

ggtcacaatg gactgcaagg cctgccaggt attgcaggtc atcatggtga tcaaggtgcc    120

ccgggaagcg ttggtccggc ggggccgaga ggccctgcgg gaccttcagg tccggcaggc    180
```

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```
aaagatggtc ggacaggcca tccgggcacc gttggccctg caggaattcg tggaccgcag    240

ggtcatcagg gacctgctgg tccgccaggt cccccgggcc ctccgggacc accgggtgtt    300

agtggtggtg gttatgattt tggctatgat ggtgattttt atcgtgcaga tcagccgcgt    360

agcgcaccga gcctgcgtcc taaagattat gaagttgatg caaccctgaa aagcctgaat    420

aatcagattg aaacactgct gacaccggaa ggtagccgta aaaatccggc ccgtacctgt    480

cgtgatctgc gtctgagcca cccggaatgg agcagcggtt attattggat tgatccgaat    540

caaggttgta ccatggatgc aattaaagtt tattgtgatt ttagcacagg tgaaacatgt    600

atccgtgcac agccggaaaa tattccggcc aaaaattggt atcgtagtag caaagatggt    660

gactacaaag acgacgacga caaataa                                        687


<210> SEQ ID NO 96
<211> LENGTH: 262
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 96

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Tyr Glu Val Asp Ala Thr Leu Lys Ser Leu Asn Asn Gln
            20                  25                  30

Ile Glu Thr Leu Leu Thr Pro Glu Gly Ser Arg Lys Asn Pro Ala Arg
        35                  40                  45

Thr Cys Arg Asp Leu Arg Leu Ser His Pro Glu Trp Ser Ser Gly Tyr
    50                  55                  60

Tyr Trp Ile Asp Pro Asn Gln Gly Cys Thr Met Asp Ala Ile Lys Val
65                  70                  75                  80

Tyr Cys Asp Phe Ser Thr Gly Glu Thr Cys Ile Arg Ala Gln Pro Glu
                85                  90                  95

Asn Ile Pro Ala Lys Asn Trp Tyr Arg Ser Ser Lys Asp Lys Lys His
            100                 105                 110

Val Trp Leu Gly Glu Thr Ile Asn Ala Gly Ser Gln Phe Glu Tyr Asn
        115                 120                 125

Val Glu Gly Val Thr Ser Lys Glu Met Ala Thr Gln Leu Ala Phe Met
    130                 135                 140

Arg Leu Leu Ala Asn Tyr Ala Ser Gln Asn Ile Thr Tyr His Cys Lys
145                 150                 155                 160

Asn Ser Ile Ala Tyr Met Asp Glu Glu Thr Gly Asn Leu Lys Lys Ala
                165                 170                 175

Val Ile Leu Gln Gly Ser Asn Asp Val Glu Leu Val Ala Glu Gly Asn
            180                 185                 190

Ser Arg Phe Thr Tyr Thr Val Leu Val Asp Gly Cys Ser Lys Lys Thr
        195                 200                 205

Asn Glu Trp Gly Lys Thr Ile Ile Glu Tyr Lys Thr Asn Lys Pro Ser
    210                 215                 220

Arg Leu Pro Phe Leu Asp Ile Ala Pro Leu Asp Ile Gly Gly Ala Asp
225                 230                 235                 240

Gln Glu Phe Phe Val Asp Ile Gly Pro Val Cys Phe Lys Gly Asp Tyr
```

-continued

```
                245                 250                 255

Lys Asp Asp Asp Asp Lys
            260
```

<210> SEQ ID NO 97
<211> LENGTH: 788
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 97

```
tgaaaaagat ttggctggcg ctggctggtt tagttttagc gtttagcgca tcggcgtatg     60

aagttgatgc aaccctgaaa agcctgaata atcagattga aacactgctg acaccggaag    120

gtagccgtaa aaatccggcc cgtacctgtc gtgatctgcg tctgagccac ccggaatgga    180

gcagcggtta ttattggatt gatccgaatc aaggttgtac catggatgca attaaagttt    240

attgtgattt tagcacaggt gaaacatgta tccgtgcaca gccggaaaat attccggcca    300

aaaattggta tcgtagtagc aaagataaaa aacatgtgtg gctgggtgaa accattaatg    360

caggtagcca gtttgaatac aatgttgaag gtgttaccag caaagaaatg gcaacacagc    420

tggcatttat gcgtctgctg gcaaattatg caagccagaa tattacatat cattgtaaaa    480

atagcattgc atatatggat gaagaaaccg gtaatctgaa aaaagcagtt attctgcagg    540

gtagcaatga tgttgaactg gttgccgaag gtaatagccg ttttacatat accgttctgg    600

ttgatggttg tagcaaaaaa accaatgaat ggggtaaaac catcattgaa tataaaacca    660

acaaaccgag ccgtctgccg tttctggata tcgctccgct ggatattggt ggtgccgatc    720

aggaattttt tgtcgatatc ggtcctgtgt gttttaaagg tgactacaaa gacgacgacg    780

acaaataa                                                              788
```

<210> SEQ ID NO 98
<211> LENGTH: 228
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 98

```
Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Gly Gly Val Pro Gly Ala Ile Pro Gly Gly Val Pro Gly
            20                  25                  30

Gly Val Phe Tyr Pro Gly Ala Gly Leu Gly Ala Leu Gly Gly Gly Ala
        35                  40                  45

Leu Gly Pro Gly Gly Lys Pro Leu Lys Pro Val Pro Gly Gly Leu Ala
    50                  55                  60

Gly Ala Gly Leu Gly Ala Gly Leu Gly Ala Phe Pro Ala Val Thr Phe
65                  70                  75                  80

Pro Gly Ala Leu Val Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr
                85                  90                  95

Lys Ala Ala Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly
            100                 105                 110
```

-continued

Gly Leu Gly Val Ser Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly
        115                 120                 125

Val Lys Pro Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro
    130                 135                 140

Gly Gly Val Leu Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro
145                 150                 155                 160

Gly Val Pro Thr Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly
                165                 170                 175

Gly Ala Phe Ala Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln
            180                 185                 190

Pro Gly Val Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly
        195                 200                 205

Gly Tyr Gly Leu Pro Tyr Thr Thr Gly Lys Leu Gly Asp Tyr Lys Asp
    210                 215                 220

Asp Asp Asp Lys
225

<210> SEQ ID NO 99
<211> LENGTH: 687
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 99

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcgggt     60

ggcgtaccag gcgcaattcc tgggggtgtc ccaggcggtg ttttttatcc gggcgccggt    120

cttggcgcac tgggtggcgg tgcactgggc ccgggcggca aaccgctgaa accggtacca    180

ggtggtttag caggcgccgg cttaggcgca ggtctgggag catttccggc agttaccttt    240

ccaggggcac tggttcctgg aggtgtggcc gatgcagccg cggcatataa agccgctaaa    300

gccggtgcgg gtttaggagg cgtcccaggt gtcggtggcc tgggtgttag cgccggtgca    360

gttgttccgc agccgggagc aggggttaaa cctggtaaag tgccgggagt aggtctgcca    420

ggcgtttatc ctggtggtgt tttgccgggt gcccgttttc cgggcgttgg tgttcttcca    480

ggcgtgccga ccggagccgg tgttaaaccg aaagcccccg gtgttggagg tgcatttgca    540

ggcatcccgg gagttggccc gtttggtggt ccgcaacctg ggttccgtt aggttatccg    600

attaaagcac cgaaactgcc cggcggttat ggtctgccgt acacaaccgg taaactgggt    660

gactacaaag acgacgacga caaataa                                        687

<210> SEQ ID NO 100
<211> LENGTH: 228
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 100

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Pro Tyr Gly Tyr Gly Pro Gly Gly Val Ala Gly Ala Ala
            20                  25                  30

-continued

```
Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val Gly Pro Gln Ala Ala
        35                  40                  45

Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe Gly Ala Gly Ala Ala
    50                  55                  60

Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val Pro Gly Val Pro Gly
65                  70                  75                  80

Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val Gly Thr Pro Ala Ala
                85                  90                  95

Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala
            100                 105                 110

Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val Val Gly
        115                 120                 125

Val Pro Gly Ala Gly Val Pro Gly Val Gly Val Pro Gly Ala Gly Ile
    130                 135                 140

Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala Ala Val Pro Gly Val
145                 150                 155                 160

Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys Tyr
                165                 170                 175

Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly Val
            180                 185                 190

Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile Pro
        195                 200                 205

Gly Val Ala Gly Val Pro Gly Val Gly Gly Val Gly Asp Tyr Lys Asp
    210                 215                 220

Asp Asp Asp Lys
225


<210> SEQ ID NO 101
<211> LENGTH: 687
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 101

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcgccg      60

tatggttatg gcccgggtgg agttgcgggt gcagcaggta aagcgggtta tcctaccgga     120

accggtgtag gtccgcaggc cgctgctgcc gccgccgcaa aagcagcggc taaatttggc     180

gccggagcag cgggtgttct gcctggagtt ggtggtgcgg gcgtgccagg ggtacctggt     240

gcaattccgg gtattggtgg tattgccggt gtcggcaccc cggccgcggc agctgcggca     300

gcggcggctg ccaaagctgc taaatacggt gccgcggcgg gtctggtgcc aggaggtccg     360

ggttttggtc cgggagtggt tggcgtgcct ggcgcaggcg ttcctggtgt gggcgttcca     420

ggtgcaggga ttcctgttgt gcctggtgcc ggtattcccg gcgcggccgt tccgggggtg     480

gttagcccgg aagccgcagc gaaggctgcg gcaaaggcag caaagtatgg cgcacgccca     540

ggagtcggcg tgggtggtat cccgacctat ggggtgggcg caggggggttt tcctggtttc     600

ggcgtaggtg taggaggtat accgggcgtg gccggtgtac caggggttgg tggcgtcggt     660

gactacaaag acgacgacga caaataa                                          687


<210> SEQ ID NO 102
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<211> LENGTH: 273
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 102

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Pro Val Gly Arg Arg Gly Pro Lys Gly Ser Arg Gly Asp
            20                  25                  30

Pro Gly Asp Gly Gly Ala Ala Gly Pro Lys Gly Pro Glu Gly Val Asp
        35                  40                  45

Gly Leu Ile Gly Glu Pro Gly Gln Pro Gly Pro Ile Gly Ala Glu Gly
    50                  55                  60

Ser Ser Gly Leu Glu Gly Phe Leu Gly Asp Lys Gly Ser Lys Gly Ala
65                  70                  75                  80

Arg Gly Gly Pro Gly Asn Arg Gly Arg Pro Gly Gln Asp Gly Val Pro
                85                  90                  95

Gly Gln Asp Gly Arg Ala Gly Glu Lys Gly Glu Gly Gly Glu Thr Gly
            100                 105                 110

Asp Arg Gly Gln Gln Gly Leu Arg Gly Lys Val Gly Asp Pro Gly Leu
        115                 120                 125

Val Gly Asp Leu Gly Ala Gln Gly Pro Gln Gly Ser Gln Gly Leu Val
    130                 135                 140

Gly Pro Pro Gly Ile Pro Gly Glu Pro Gly Ser Gly Gly Glu Pro Gly
145                 150                 155                 160

Asp Gln Gly Pro Arg Gly Pro Glu Gly Pro Gln Gly Ser Pro Gly Val
                165                 170                 175

Arg Gly Gly Arg Gly Glu Arg Gly Thr Pro Gly Ala Val Gly Pro Lys
            180                 185                 190

Gly Pro Pro Gly Lys Asn Gly Ala Asp Gly Pro Arg Gly Leu Pro Gly
        195                 200                 205

Ala Ser Gly Pro Pro Gly Ser Pro Gly Asn Gln Gly Pro Glu Gly Ser
    210                 215                 220

Arg Gly Ala Asp Gly Asn Asn Gly Phe Pro Gly Asp Asp Gly Glu Asn
225                 230                 235                 240

Gly Leu Val Gly Ile Pro Gly Glu Pro Gly Pro Lys Gly Ala Arg Gly
                245                 250                 255

Thr Arg Gly Glu Leu Gly Lys Thr Gly Asp Tyr Lys Asp Asp Asp Asp
            260                 265                 270

Lys


<210> SEQ ID NO 103
<211> LENGTH: 822
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 103

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcgccg      60

gttggtcgtc gtggtccgaa aggtagccgt ggtgatcctg gtgatggtgg tgcagcaggt     120
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cctaaaggtc cggaaggtgt tgatggtctg attggtgaac cgggtcagcc tggtccgatt    180

ggcgcagaag gtagcagcgg tctggaaggt tttctgggtg ataaaggtag caaaggtgca    240

cgtggtggtc cgggtaatcg cggtcgtcct ggtcaggatg gtgttccggg tcaagatggt    300

cgtgccggtg aaaaaggtga aggtggtgaa accggtgatc gcggtcagca gggtctgcgt    360

ggtaaagttg gtgatccagg tctggtgggt gatctgggtg cacagggtcc gcagggtagc    420

caaggtctgg ttggtccgcc tggtattccg ggtgaacctg gtagcggtgg cgaaccgggt    480

gatcagggtc ctcgcggtcc agaaggtcct cagggttcac cgggtgttcg cggtggtcgt    540

ggtgaacgtg gtacaccggg tgcagttgga ccgaaaggtc cgccaggtaa aaatggtgca    600

gatggtccgc gtggtctgcc tggtgcaagc ggtcctccgg gtagtcctgg taaccagggt    660

cctgaaggtt ctcgtggtgc cgatggtaat aatggttttc caggtgatga tggtgaaaat    720

ggcctggttg gtatccctgg cgaaccaggt ccaaaaggcg cacgcggtac acgcggtgaa    780

ctgggtaaaa ccggtgacta caaagacgac gacgacaaat aa                       822
```

```
<210> SEQ ID NO 104
<211> LENGTH: 450
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 104

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Gly Arg Gly Gly Pro Ala Gly Leu Gln Gly Ala Ala Gly
            20                  25                  30

Asn Pro Gly Asp Pro Gly Asp Arg Gly Gln Ala Gly Glu Ile Gly Leu
        35                  40                  45

Pro Gly Thr Glu Gly Gln Arg Gly Gln Gly Gly Ser Arg Gly Asp Asp
    50                  55                  60

Gly Ile Gly Gly Gln Ser Gly Thr Asp Gly Asp Pro Gly Asn Asp Gly
65                  70                  75                  80

Val Ala Gly Ile Arg Gly Ala Arg Gly Glu Pro Gly Ala Thr Gly Pro
                85                  90                  95

Glu Gly Ala Ala Gly Gln Lys Gly Asp Arg Gly Arg Phe Gly Glu Gln
            100                 105                 110

Gly Arg Pro Gly Asn Asp Gly Pro Pro Gly Arg Arg Gly Arg Val Gly
        115                 120                 125

Asn Leu Gly Glu Thr Gly Ala Glu Gly Asp Glu Gly Thr Arg Gly Tyr
    130                 135                 140

Thr Gly Asp Arg Gly Pro Glu Gly Ala Ile Gly Ile Ser Gly Val Thr
145                 150                 155                 160

Gly Asn Pro Gly Pro Gln Gly Ile Lys Gly Pro Pro Gly Asp Thr Gly
                165                 170                 175

His Pro Gly Arg Gln Gly Pro Ser Gly Pro Gln Gly Pro Pro Gly Ile
            180                 185                 190

Pro Gly Thr Asp Gly Leu Thr Ile His Asn Leu Ile Lys Pro Pro Ser
        195                 200                 205

Gln Phe Phe Asp Ala Thr Ser Ser Ser Asp Pro Leu Thr Asp Ala Val
```

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```
    210                 215                 220

Val Glu Ser Ile Leu Lys Ser Phe Gln Tyr Ala Glu Leu Glu Ile Asp
225                 230                 235                 240

Leu Thr Lys Lys Pro Asp Gly Thr Met Lys Tyr Pro Ala Ile Ser Cys
                245                 250                 255

Asp Asp Leu His Lys Asp Tyr Pro Gln Leu Pro Ser Gly Asn Tyr Thr
            260                 265                 270

Leu Asp Pro Asn Gly Gly Cys Lys Asn Asp Ala Phe Glu Thr Tyr Cys
        275                 280                 285

Glu Phe Asn Asn Ser Val Lys Met Cys Leu Thr Pro Lys Ile Pro Thr
    290                 295                 300

Leu Leu Pro Met Gly Thr Tyr Lys Tyr Tyr Val Asn Ser Glu Gly Tyr
305                 310                 315                 320

Tyr Ser Pro Asn Asp Phe Gly Leu Asn Leu Arg Phe Phe Glu Tyr Tyr
                325                 330                 335

Gly Ser Val Thr Gln Leu Lys Phe Leu Gln Thr Lys Ala Thr Arg Val
            340                 345                 350

Thr Gln Thr Ile Arg Val Leu Cys Lys Asn Tyr Asp Pro Leu His Lys
        355                 360                 365

Gln Pro Val Phe Ile Gly Met Asn Asp Glu Thr Val Met Asp Glu Pro
    370                 375                 380

Arg Met Glu Glu Asn Gln Cys Gln Tyr Phe Asn Gly Leu Ser Ala His
385                 390                 395                 400

Val Glu Leu Glu Leu Ser Ser Asn Asp Pro Ser Tyr Leu Pro Ile Tyr
                405                 410                 415

Glu Met Arg Leu Tyr Leu Gly Arg Lys Thr Asn Glu Glu Leu Gly Ile
            420                 425                 430

Glu Leu Gly Asp Leu Cys Phe Glu Tyr Gly Asp Tyr Lys Asp Asp Asp
        435                 440                 445

Asp Lys
    450


<210> SEQ ID NO 105
<211> LENGTH: 1353
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 105

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcgggt      60

cgtggcggtc cggcaggtct gcagggtgct gcaggtaatc ctggcgaccc tggcgatcgt     120

ggtcaggcag gcgaaattgg tctgccaggc accgaaggtc agcgtggtca aggtggttca     180

cgtggtgatg acggtattgg tggtcagagc ggcaccgatg gcgatccggg taacgatggt     240

gttgcaggta ttcgtggtgc acgcggagaa cctggtgcca ccggacctga aggtgcagcc     300

ggtcagaaag gtgatcgtgg ccgttttggc gaacagggtc gtccgggaaa tgatggtcca     360

ccgggtcgcc gtggccgtgt gggcaatctg ggtgaaacag gtgccgaagg tgatgaaggc     420

acccgtggtt atacaggtga ccgtggaccg gaaggcgcaa ttggtattag cggtgtgacc     480

ggtaatccgg gtccacaggg cattaaaggc cctccgggtg atacgggtca tccgggtcgt     540
```

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cagggaccga gcggtccgca aggaccaccg ggtattccag gtacagatgg cctgaccatt 600

cataatctga ttaaaccgcc tagccagttt tttgatgcaa ccagcagcag cgatccgctg 660

accgatgcag ttgttgaaag cattctgaaa tcttttcagt atgccgagct ggaaattgac 720

ctgaccaaaa aaccggatgg caccatgaaa tatccggcaa ttagctgtga tgatctgcac 780

aaagattatc cgcagctgcc gagcggtaat tataccctgg atccgaatgg tggttgtaaa 840

aatgatgcct ttgaaaccta ttgcgagttc aacaatagcg tgaaaatgtg tctgaccccg 900

aaaattccga cactgctgcc gatgggcacc tataaatact atgttaatag cgagggttac 960

tacagcccga atgattttgg tctgaatctg cgctttttttg agtattatgg tagcgttacc 1020

cagctgaaat ttctgcagac caaagcaacc cgtgttaccc agaccattcg tgttctgtgt 1080

aaaaactatg atccgctgca taaacagccg gtttttattg gtatgaatga cgaaaccgtt 1140

atggatgaac cgcgtatgga agaaaatcag tgccagtatt ttaacggtct gagcgcacat 1200

gttgaactgg aactgagcag caatgatccg agctatctgc cgatttatga aatgcgtctg 1260

tatctgggtc gtaaaaccaa tgaagaactg ggcattgaac tgggcgatct gtgttttgaa 1320

tatggtgact acaaagacga cgacgacaaa taa 1353

<210> SEQ ID NO 106
<211> LENGTH: 286
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 106

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Glu Lys Thr Ser Ser Lys Val Ala Leu Met Thr Val Leu
            20                  25                  30

Val Val Ile Thr Gly Ala Leu Ile Ile Glu Gly Thr Ser Ile Thr Arg
        35                  40                  45

Gly Ser Thr His Val Asn Arg Gly Leu Arg Lys Arg Gln Thr Ser Glu
    50                  55                  60

Asp Asn Cys Glu Ala Val Lys Val Gly Leu Pro Gly Arg Asp Gly Arg
65                  70                  75                  80

Glu Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Arg Asp Gly Arg Asp
                85                  90                  95

Ala Val Cys Ser Asn Gln Thr Thr Gly Leu Gly Ala Lys Gly Asp Arg
            100                 105                 110

Gly Pro Pro Gly Thr Pro Gly Phe Pro Gly Glu Val Gly Arg Pro Gly
        115                 120                 125

Pro Pro Gly Ala Asp Gly Ile Pro Gly Pro Gln Gly Glu Arg Gly Ala
    130                 135                 140

Val Gly Pro Gly Gly Lys Pro Gly Pro Arg Gly Glu Val Gly Thr Pro
145                 150                 155                 160

Gly Ala Asp Gly Ala Asp Gly Ala Thr Gly Ala Thr Gly Val Gln Gly
                165                 170                 175

Pro Asp Gly Ala Lys Gly Glu Lys Gly Ala Ser Gly Thr Ala Gly Leu
            180                 185                 190

Lys Gly Glu Lys Gly Asp Thr Cys Ile Pro Asp Ser Asn Ser Thr Leu

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```
        195                 200                 205

Gly Met Pro Gly Thr Pro Gly Ala Gly Gly Ser Lys Gly Gln Lys Gly
    210                 215                 220

Glu Ser Gly Ile Val Gly Pro Lys Gly Glu Arg Gly Glu Ile Gly Thr
225                 230                 235                 240

Pro Gly His Pro Gly Phe Arg Gly Ala Asp Gly Glu Pro Gly His Lys
                245                 250                 255

Gly Val Pro Gly Arg Ala Gly Ala Gln Gly Asp Arg Gly Asp Pro Gly
            260                 265                 270

Asp Asp Gly Leu Thr Gly Asp Tyr Lys Asp Asp Asp Asp Lys
        275                 280                 285


<210> SEQ ID NO 107
<211> LENGTH: 861
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 107

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcggaa      60

aaaaccagca gcaaagttgc actgatgacc gttctggttg ttattaccgg tgcactgatt     120

attgaaggca ccagcattac ccgtggtagc acccatgtta atcgtggtct gcgtaaacgt     180

cagaccagcg aagataattg tgaagcagtt aaagttggtc tgccaggtcg tgatggtcgt     240

gaaggtcctc cgggtccgcc tggtccggct ggcagagatg gccgtgatgc agtttgtagc     300

aatcagacca ccggtctggg tgcaaaaggt gatcgtggtc cgccaggtac accgggtttt     360

ccgggtgaag ttggccgtcc gggtccaccg ggtgcagatg gtattccggg tcctcagggt     420

gaacgtggtg cagttggtcc tggtggtaaa cctggtccgc gtggtgaagt gggcacccct     480

ggtgccgatg gcgcagatgg tgcaaccggt gcgaccggtg ttcagggtcc tgatggtgcc     540

aaaggcgaaa aaggtgcaag cggcaccgca ggtctgaaag gtgagaaagg cgatacctgt     600

attccggata gcaatagcac cctgggtatg cctggtacac caggtgccgg tggtagcaaa     660

ggccagaaag gtgaaagtgg tattgttggt ccgaaaggcg aacgcggtga aattggcaca     720

ccgggtcatc ctggttttcg tggtgcggat ggtgaaccag gtcataaagg tgttccgggt     780

cgtgccggtg cgcagggtga tcgcggtgat ccgggtgatg atggtctgac cggtgactac     840

aaagacgacg acgacaaata a                                               861


<210> SEQ ID NO 108
<211> LENGTH: 512
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 108

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Gly Phe Pro Gly Ala Pro Gly Ala Asp Gly Ala Pro Gly
            20                  25                  30

Gln Lys Gly Glu Leu Gly Ala Val Gly Pro Gln Gly Thr Pro Gly Leu
```

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```
        35                  40                  45

Ser Gly Pro Ser Gly Pro Thr Gly Pro Pro Gly Pro Lys Gly Val Arg
    50                  55                  60

Gly Ala Pro Gly Ser Ser Gly Ala Lys Gly Asp Ala Gly Asn Pro Gly
65                  70                  75                  80

Asp Asp Gly Pro Val Gly Pro Gln Gly Val Pro Gly Val Asp Gly Ser
                85                  90                  95

Pro Gly Gln Lys Gly Glu Thr Gly Arg Val Gly Pro Arg Gly His Asp
            100                 105                 110

Gly Ile Asn Gly Thr Pro Gly Glu Asp Gly Ala Thr Gly Phe Pro Gly
        115                 120                 125

Pro Asp Gly Ala Lys Gly Glu Lys Gly Thr Ser Gly Thr Ala Gly Leu
    130                 135                 140

Lys Gly Glu Lys Gly Asp Thr Cys Ile Pro Asp Ser Asn Ser Thr Leu
145                 150                 155                 160

Gly Met Pro Gly Thr Pro Gly Ala Gly Trp Ser Lys Gly Gln Lys Gly
                165                 170                 175

Glu Ser Gly Ile Val Gly Pro Lys Gly Glu Lys Gly Glu Ile Gly Thr
            180                 185                 190

Pro Gly Pro Pro Gly Phe Arg Gly Ala Asp Gly Glu Pro Gly Gln Arg
        195                 200                 205

Gly Glu Pro Gly Arg Ala Gly Ala Gln Gly Glu Arg Gly Ala Pro Gly
    210                 215                 220

Asn Asn Gly Arg Asp Gly Phe Pro Gly Asp Pro Gly Ala Asp Gly Ala
225                 230                 235                 240

Pro Gly Gln Lys Gly Glu Leu Gly Ala Ile Gly His Pro Gly Phe Ser
                245                 250                 255

Gly Pro Ser Gly Pro Ser Gly Pro Thr Gly Pro Pro Gly Pro Lys Gly
            260                 265                 270

Val Arg Gly Ala Gln Gly Arg Pro Gly Asp Arg Gly Ser Pro Gly Asp
        275                 280                 285

Val Gly Pro Ile Gly Ala Pro Gly Pro Pro Gly Ala Asp Gly Val Pro
    290                 295                 300

Gly Leu Thr Gly Val Gln Gly Arg Asp Gly Pro Lys Gly Glu Ser Ala
305                 310                 315                 320

Ser Ser Gly Ala Val Tyr Val Arg Trp Gly Arg Thr Thr Cys Pro Ser
                325                 330                 335

Gly Ala Asp Val Val Tyr Ser Gly Arg Ala Ala Gly Ala Lys Tyr Asp
            340                 345                 350

His Ser Gly Gly Thr Ser Asp His His Cys Leu Pro Asn Asn Pro Gln
        355                 360                 365

Tyr Leu Ser Glu Asp Asp Thr Asn Ala Leu Gly Ala Gln Leu Tyr Gly
    370                 375                 380

Val Glu Tyr Glu Ile Arg Asp Arg Ser Ser Pro Tyr Asn Ser Leu Asp
385                 390                 395                 400

Gln Ser Asp Met Pro Cys Val Val Cys Asn Ala Asn Gly Arg Ser Gln
                405                 410                 415

Leu Leu Met Val Pro Ala Arg Tyr Thr Cys Pro Thr Gly Trp Ser Arg
            420                 425                 430

Glu Tyr Tyr Gly Tyr Met Met Ser Glu Gly Lys Ala Lys Asn Arg Glu
        435                 440                 445
```

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```
Gly Arg Lys Thr Thr Ile Cys Met Asp Phe Ser Ala Glu Ala Val Pro
    450                 455                 460

Gly Ser Gly Ala Asn Thr Asn Pro Ser Pro Gly Ile Met Met Arg Ala
465                 470                 475                 480

Asn Cys Asn Gly Leu Ala Cys Pro Pro Tyr Gln Ser Asn Thr Pro Leu
                485                 490                 495

Thr Cys Ala Val Cys Thr Lys Gly Asp Tyr Lys Asp Asp Asp Asp Lys
            500                 505                 510


<210> SEQ ID NO 109
<211> LENGTH: 1539
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 109

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcgggt     60

tttcctggcg ctccgggtgc cgacggtgct ccgggtcaaa aaggtgaact gggtgccgtg    120

ggtccgcagg gcactccggg tctgagtggt cctagtggtc cgaccggtcc accaggtcca    180

aaaggcgtgc gtggtgcacc gggtagcagc ggagccaaag gtgatgcagg taaccctggt    240

gatgacggtc cggttggtcc acagggcgtt ccaggtgttg atggtagccc tggccaaaag    300

ggtgaaaccg gtcgtgtggg tcctcgtggt catgatggta ttaatggcac cccaggtgaa    360

gatggtgcga caggctttcc aggtccggat ggcgcaaagg gtgagaaggg caccagcggt    420

acagctggcc tgaagggcga aaagggcgat acatgcatcc cggattcaaa ttcaacactg    480

ggcatgccag gtacgcctgg cgcaggttgg agtaaaggac aaaaaggcga atcaggcatt    540

gtgggaccta aaggcgagaa gggtgagatt ggtactccgg gaccgccagg ctttcgcggt    600

gcagacggcg aaccgggtca gcgtggcgaa cctggtcgtg caggcgcaca aggtgaacgc    660

ggagcccctg gtaataatgg acgtgatggc tttcctggtg atccaggtgc agatggcgca    720

cctggccaga aaggcgaact gggagcaatt ggtcatccgg gatttagcgg tccgtcaggt    780

ccgagcggac cgacaggtcc tcctggaccg aaaggtgtac gtggcgcaca gggtcgtcct    840

ggcgatcgtg gcagtccagg tgatgtgggt ccgattggtg cacctggtcc tccaggtgcg    900

gacggcgtgc ctggtttaac aggtgtgcag ggtcgcgacg gtcctaaagg tgaatcagca    960

agcagcggtg cagtttatgt tcgttggggt cgtaccacct gtcctagcgg agcagatgtt   1020

gtttatagcg gtcgcgcagc cggtgcaaaa tatgatcatt caggtggcac ctcagatcat   1080

cattgtctgc cgaataatcc gcagtatctg agcgaagatg ataccaatgc actgggtgca   1140

cagctgtatg gtgtggaata tgaaattcgt gatcgtagca gcccgtataa tagcctggat   1200

cagagcgata tgccgtgtgt tgtttgtaat gcaaatggtc gtagccagct gctgatggtt   1260

ccggcacgtt atacatgccc gaccggttgg agccgtgaat attatggtta tatgatgagc   1320

gaaggcaaag ccaaaaatcg cgaaggtcgt aaaaccacca tttgtatgga ttttagcgca   1380

gaagcagttc ctggtagcgg tgcaaatacc aatccgagtc cgggtattat gatgcgtgca   1440

aattgtaatg gtctggcatg tccgccttat cagagcaata caccgctgac ctgtgccgtt   1500

tgtaccaaag gtgactacaa agacgacgac gacaaataa                           1539
```

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<210> SEQ ID NO 110
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 110

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Gly Pro Ala Gly Ala Lys Gly Pro Ser Gly Asp Ile Gly
            20                  25                  30

Arg Pro Gly Glu Ser Gly Ser Pro Gly Ala Arg Gly His Ser Gly Gln
        35                  40                  45

Pro Gly Arg Thr Gly Ile Ala Gly Asn Gln Gly Leu Pro Gly Thr Ala
    50                  55                  60

Gly Glu Glu Gly Arg Thr Gly Pro Pro Gly Pro Ala Gly Leu Arg Gly
65                  70                  75                  80

Gln Ala Gly Met Met Gly Phe Pro Gly Pro Lys Gly Ala Ala Gly Leu
                85                  90                  95

Pro Gly Lys Pro Gly Asp Arg Gly Asn Val Gly Leu Ala Gly Pro Arg
            100                 105                 110

Gly Ala Pro Gly Lys Asp Gly Glu Val Gly Ala Gln Gly Pro Pro Gly
        115                 120                 125

Val Ala Gly Pro Thr Gly Pro Arg Gly Glu Thr Gly Leu Ala Gly Ser
    130                 135                 140

Val Gly Phe Gln Gly Met Pro Gly Pro Ser Gly Ala Ala Gly Glu Pro
145                 150                 155                 160

Gly Lys Pro Gly Asn Gln Gly Leu Arg Gly Asp Ala Gly Ser Pro Gly
                165                 170                 175

Met Ile Gly Pro Arg Gly Glu Arg Gly Leu Pro Gly Glu Arg Gly Ala
            180                 185                 190

Ser Gly Ala Gln Gly Leu Leu Gly Pro Arg Gly Thr Ser Gly Ala Pro
        195                 200                 205

Gly Leu Gly Asp Tyr Lys Asp Asp Asp Asp Lys
    210                 215


<210> SEQ ID NO 111
<211> LENGTH: 660
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 111

atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcgggt      60

ccggcaggcg caaaaggtcc gagcggtgat attggtcgtc cgggtgaaag cggtagtccg     120

ggtgcacgtg gtcatagcgg tcagcctggt cgtaccggta ttgcaggtaa tcagggtctg     180

cctggtacag ccggtgaaga aggtcgcacc ggtccgccag gtcctgcagg tctgcgtggt     240

caggcaggta tgatgggttt tccgggtccg aaaggtgcag cgggtctgcc aggcaaaccg     300

ggtgatcgtg gtaatgttgg tctggctggt ccgcgtggtg caccgggtaa agatggtgaa     360
```

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gttggtgcac agggtcctcc gggtgttgca ggtccgaccg gtcctcgtgg tgaaaccggt    420

ctggcaggta gcgttggttt tcagggtatg ccaggtccgt caggtgcagc aggcgaacct    480

ggtaaaccgg gtaaccaggg cctgcgtggt gatgccggtt caccgggtat gattggtcca    540

cgcggtgaac gtggcctgcc tggcgaacgt ggtgcaagcg gtgcacaagg tctgctgggt    600

ccacgtggca cctcaggcgc accaggtctg ggtgactaca aagacgacga cgacaaataa    660
```

<210> SEQ ID NO 112
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 112

```
Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Gln Gly Ile Pro Gly Ser Ala Gly Lys Glu Gly Gly Lys
            20                  25                  30

Gly Asp Pro Gly Pro Leu Gly Ser Pro Gly Lys Pro Gly Pro Asp Gly
        35                  40                  45

Leu Arg Gly Phe Ala Gly Ala Arg Gly Leu Pro Gly Ala Ala Gly Pro
    50                  55                  60

Pro Gly Leu Lys Gly Ala Glu Gly Pro Met Gly Ala Pro Gly Leu Thr
65                  70                  75                  80

Gly Ser Thr Gly Glu Arg Gly Pro Asn Gly Pro Ala Gly Ala Ile Gly
                85                  90                  95

Leu Pro Gly Arg Pro Gly Gly Pro Gly Pro Pro Gly Pro Val Gly Glu
            100                 105                 110

Lys Gly Asp Pro Gly Asp Lys Gly Leu Pro Gly Pro Ala Gly Asp Asp
        115                 120                 125

Gly Val Gln Gly Ala Met Gly Leu Pro Gly Pro Ile Gly Ser Gln Gly
    130                 135                 140

Pro Pro Gly Asp Tyr Gly Asp Lys Gly Glu Leu Gly Lys Pro Gly Gln
145                 150                 155                 160

Lys Gly Ser Lys Gly Asp Lys Gly Glu Ser Gly Pro Pro Gly Pro Ile
                165                 170                 175

Gly Ile Gln Gly Pro Ile Gly His Pro Gly Pro Ile Gly Ser Asp Gly
            180                 185                 190

Ser Pro Gly Leu Arg Gly Tyr Leu Gly Met Arg Gly Gln Lys Gly Asp
        195                 200                 205

Asp Gly Ile Arg Gly Leu Pro Gly Ser Ala Gly Pro Val Gly Leu Gln
    210                 215                 220

Gly Leu Pro Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys
225                 230                 235
```

<210> SEQ ID NO 113
<211> LENGTH: 714
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polynucleotide

<400> SEQUENCE: 113

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```
atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcgcag      60

ggtattccgg gtagcgcagg taaagaaggt ggtaaaggcg atccgggtcc gctgggttca     120

ccgggtaaac cgggtcctga tggtctgcgt ggttttgccg gtgcacgtgg tctgcctggt     180

gcagcaggtc cgcctggtct gaaaggtgcc gaaggtccga tgggtgctcc gggtctgacc     240

ggtagcaccg gtgaacgcgg tccgaatggt ccggcaggcg caattggtct gccaggtcgt     300

cctggtggtc cgggtcctcc tggtccggtt ggtgaaaaag gtgatcctgg tgataaaggc     360

ctgcctggtc ctgccggtga tgatggtgtt cagggtgcca tgggcttacc gggtccgatt     420

ggtagccagg gtcctccggg tgattatggc gataaaggtg aactgggtaa acctggccag     480

aaaggtagca aaggtgacaa aggcgaaagc ggtccgccag gtccgatcgg cattcagggt     540

cctattggtc atccaggtcc aattggttca gatggctcac cgggactgcg tggctatctg     600

ggtatgcgtg gacagaaagg tgatgacggt attcgtggcc tgccaggtag tgcaggtccg     660

gtgggtctgc agggactgcc tggtggtgac tacaaagacg acgacgacaa ataa           714
```

```
<210> SEQ ID NO 114
<211> LENGTH: 254
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide

<400> SEQUENCE: 114

Met Lys Lys Ile Trp Leu Ala Leu Ala Gly Leu Val Leu Ala Phe Ser
1               5                   10                  15

Ala Ser Ala Lys Gly Glu Thr Gly Glu Ala Gly Asp Pro Gly Thr Pro
            20                  25                  30

Gly Glu Pro Gly Ile Ala Gly Pro Lys Gly Asp Val Gly Asp Lys Gly
        35                  40                  45

Asp Ala Gly Pro Pro Gly Ala Ala Gly Pro Ala Gly Val Lys Gly Pro
    50                  55                  60

Pro Gly Glu Asp Gly Ala Lys Gly Asp Val Gly Pro Ala Gly Phe Pro
65                  70                  75                  80

Gly Asp Pro Gly Pro Thr Gly Glu Pro Gly Val Pro Gly Met Asp Gly
                85                  90                  95

Gly Val Gly Glu Lys Gly Ser Leu Gly Asp Pro Gly Leu Thr Gly Pro
            100                 105                 110

Arg Gly Ala Ser Gly Glu Pro Gly Pro Pro Gly Ser Pro Gly Lys Arg
        115                 120                 125

Gly Pro Pro Gly Pro Ala Gly Pro Glu Gly Arg Glu Gly Leu Lys Gly
    130                 135                 140

Ser Lys Gly Ser Pro Gly Gln Glu Gly Pro Val Gly Arg Thr Gly Pro
145                 150                 155                 160

Ile Gly Pro Gln Gly Ser Pro Gly Asn Val Gly Pro Lys Gly Leu Arg
                165                 170                 175

Gly Ile Pro Gly Pro Thr Gly Glu Gln Gly Leu Leu Gly Pro Pro Gly
            180                 185                 190

Gln Ala Gly Pro Pro Gly Pro Met Gly Pro Pro Gly Met Pro Gly Leu
        195                 200                 205

Arg Gly Ala Gln Gly Leu Lys Gly Asp Lys Gly His Val Gly Leu Ile
```

-continued

```
    210                 215                 220

Gly Leu Ile Gly Pro Pro Gly Glu Met Gly Glu Lys Gly Asp Gln Gly
225                 230                 235                 240

Leu Pro Gly Ile Gln Gly Asp Tyr Lys Asp Asp Asp Asp Lys
                245                 250
```

<210> SEQ ID NO 115
<211> LENGTH: 765
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
polynucleotide

<400> SEQUENCE: 115

```
atgaaaaaga tttggctggc gctggctggt ttagttttag cgtttagcgc atcggcgaaa     60

ggtgaaaccg gtgaagcggg tgatccgggt acaccgggtg aacctggtat tgcaggtccg    120

aaaggtgatg ttggtgataa aggtgacgca ggtccgcctg gtgcagcagg tccggcaggc    180

gttaaaggtc ctccgggtga agatggtgca aaaggcgacg ttggtcctgc aggttttcct    240

ggcgatccgg gtccgactgg tgaaccgggt gtgccaggta tggatggtgg tgtgggtgaa    300

aaaggtagcc tgggtgatcc tggtctgacc ggtccgcgtg gcgcaagtgg tgaaccaggt    360

ccaccgggta gtccgggtaa acgtggtcct cctggaccgg ctggtccgga aggtcgtgaa    420

ggtctgaaag gtagcaaagg ttcaccgggt caagaaggtc cggttggtcg taccggtccg    480

attggtccgc agggctcacc gggtaatgtt ggtcctaaag gtctgcgtgg tattccgggt    540

cctacaggcg aacagggtct gctgggtccg ccaggccaag caggtcctcc aggtcctatg    600

ggtccacctg gtatgcctgg cctgcgtggt gcccagggcc tgaaaggcga taaaggccat    660

gttggtctga ttggcctgat tggtccacca ggtgaaatgg gagaaaaagg cgatcagggc    720

ctgcctggta ttcagggtga ctacaaagac gacgacgaca aataa                    765
```

<210> SEQ ID NO 116
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(30)
<223> OTHER INFORMATION: This sequence may encompass 2-30 residues

<400> SEQUENCE: 116

```
His His His His His His His His His His His His His His His His
1               5                   10                  15

His His His His His His His His His His His His His His
            20                  25                  30
```

<210> SEQ ID NO 117
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE

-continued

```
<222> LOCATION: (1)..(20)
<223> OTHER INFORMATION: This sequence may encompass 2-20 residues

<400> SEQUENCE: 117

His His His His His His His His His His His His His His His His
1               5                   10                  15

His His His His
            20


<210> SEQ ID NO 118
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(15)
<223> OTHER INFORMATION: This sequence may encompass 5-15 residues

<400> SEQUENCE: 118

His His His His His His His His His His His His His His His
1               5                   10                  15


<210> SEQ ID NO 119
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(18)
<223> OTHER INFORMATION: This sequence may encompass 5-18 residues

<400> SEQUENCE: 119

His His His His His His His His His His His His His His His His
1               5                   10                  15

His His


<210> SEQ ID NO 120
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(16)
<223> OTHER INFORMATION: This sequence may encompass 5-16 residues

<400> SEQUENCE: 120

His His His His His His His His His His His His His His His His
1               5                   10                  15


<210> SEQ ID NO 121
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      His tag
<220> FEATURE:
```

-continued

```
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(14)
<223> OTHER INFORMATION: This sequence may encompass 5-14 residues

<400> SEQUENCE: 121

His His His His His His His His His His His His His His
1               5                   10


<210> SEQ ID NO 122
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(13)
<223> OTHER INFORMATION: This sequence may encompass 5-13 residues

<400> SEQUENCE: 122

His His His His His His His His His His His His His
1               5                   10


<210> SEQ ID NO 123
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(12)
<223> OTHER INFORMATION: This sequence may encompass 5-12 residues

<400> SEQUENCE: 123

His His His His His His His His His His His His
1               5                   10


<210> SEQ ID NO 124
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(11)
<223> OTHER INFORMATION: This sequence may encompass 5-11 residues

<400> SEQUENCE: 124

His His His His His His His His His His His
1               5                   10


<210> SEQ ID NO 125
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(10)
<223> OTHER INFORMATION: This sequence may encompass 5-10 residues
```

-continued

```
<400> SEQUENCE: 125

His His His His His His His His His His
1               5                   10


<210> SEQ ID NO 126
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(12)
<223> OTHER INFORMATION: This sequence may encompass 6-12 residues

<400> SEQUENCE: 126

His His His His His His His His His His His His
1               5                   10


<210> SEQ ID NO 127
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(11)
<223> OTHER INFORMATION: This sequence may encompass 6-11 residues

<400> SEQUENCE: 127

His His His His His His His His His His His
1               5                   10


<210> SEQ ID NO 128
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      His tag
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(10)
<223> OTHER INFORMATION: This sequence may encompass 7-10 residues

<400> SEQUENCE: 128

His His His His His His His His His His
1               5                   10


<210> SEQ ID NO 129
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      9xHis tag

<400> SEQUENCE: 129

His His His His His His His His His
1               5


<210> SEQ ID NO 130
<211> LENGTH: 150
```

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(150)
<223> OTHER INFORMATION: This sequence may encompass 2-50 "Gly Glu Lys"
      repeating units

<400> SEQUENCE: 130

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
1               5                   10                  15

Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu
            20                  25                  30

Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
        35                  40                  45

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
    50                  55                  60

Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu
65                  70                  75                  80

Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
                85                  90                  95

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
            100                 105                 110

Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu
        115                 120                 125

Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
    130                 135                 140

Gly Glu Lys Gly Glu Lys
145                 150


<210> SEQ ID NO 131
<211> LENGTH: 150
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(150)
<223> OTHER INFORMATION: This sequence may encompass 2-50 "Gly Asp Lys"
      repeating units

<400> SEQUENCE: 131

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
1               5                   10                  15

Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp
            20                  25                  30

Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
        35                  40                  45

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
    50                  55                  60

Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp
65                  70                  75                  80

Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
                85                  90                  95
```

```
Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
            100                 105                 110

Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp
        115                 120                 125

Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
    130                 135                 140

Gly Asp Lys Gly Asp Lys
145                 150


<210> SEQ ID NO 132
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(120)
<223> OTHER INFORMATION: This sequence may encompass 2-40 "Gly Glu Lys"
      repeating units

<400> SEQUENCE: 132

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
1               5                   10                  15

Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu
            20                  25                  30

Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
        35                  40                  45

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
    50                  55                  60

Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu
65                  70                  75                  80

Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
                85                  90                  95

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
            100                 105                 110

Glu Lys Gly Glu Lys Gly Glu Lys
        115                 120


<210> SEQ ID NO 133
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(120)
<223> OTHER INFORMATION: This sequence may encompass 2-40 "Gly Asp Lys"
      repeating units

<400> SEQUENCE: 133

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
1               5                   10                  15

Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp
            20                  25                  30

Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
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        35                  40                  45

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
    50                  55                  60

Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp
65                  70                  75                  80

Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
                85                  90                  95

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
            100                 105                 110

Asp Lys Gly Asp Lys Gly Asp Lys
        115                 120


<210> SEQ ID NO 134
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(90)
<223> OTHER INFORMATION: This sequence may encompass 2-30 “Gly Glu Lys”
      repeating units

<400> SEQUENCE: 134

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
1               5                   10                  15

Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu
            20                  25                  30

Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
        35                  40                  45

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
    50                  55                  60

Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu
65                  70                  75                  80

Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
                85                  90


<210> SEQ ID NO 135
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(90)
<223> OTHER INFORMATION: This sequence may encompass 2-30 “Gly Asp Lys”
      repeating units

<400> SEQUENCE: 135

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
1               5                   10                  15

Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp
            20                  25                  30

Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
        35                  40                  45
```

```
Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
    50                  55                  60

Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp
65                  70                  75                  80

Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
                85                  90


<210> SEQ ID NO 136
<211> LENGTH: 60
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(60)
<223> OTHER INFORMATION: This sequence may encompass 2-20 “Gly Glu Lys”
      repeating units

<400> SEQUENCE: 136

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
1               5                   10                  15

Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu
            20                  25                  30

Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
        35                  40                  45

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
    50                  55                  60


<210> SEQ ID NO 137
<211> LENGTH: 60
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(60)
<223> OTHER INFORMATION: This sequence may encompass 2-20 “Gly Asp Lys”
      repeating units

<400> SEQUENCE: 137

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
1               5                   10                  15

Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp
            20                  25                  30

Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
        35                  40                  45

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
    50                  55                  60


<210> SEQ ID NO 138
<211> LENGTH: 45
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(45)
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<223> OTHER INFORMATION: This sequence may encompass 2-15 "Gly Glu Lys"
      repeating units

<400> SEQUENCE: 138

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
1               5                   10                  15

Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu
            20                  25                  30

Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
        35                  40                  45


<210> SEQ ID NO 139
<211> LENGTH: 45
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(45)
<223> OTHER INFORMATION: This sequence may encompass 2-15 "Gly Asp Lys"
      repeating units

<400> SEQUENCE: 139

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
1               5                   10                  15

Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp
            20                  25                  30

Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
        35                  40                  45


<210> SEQ ID NO 140
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(30)
<223> OTHER INFORMATION: This sequence may encompass 2-10 "Gly Glu Lys"
      repeating units

<400> SEQUENCE: 140

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
1               5                   10                  15

Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
            20                  25                  30


<210> SEQ ID NO 141
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      polypeptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(30)
<223> OTHER INFORMATION: This sequence may encompass 2-10 "Gly Asp Lys"
      repeating units

<400> SEQUENCE: 141
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Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
1               5                   10                  15

Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
            20                  25                  30


<210> SEQ ID NO 142
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(27)
<223> OTHER INFORMATION: This sequence may encompass 2-9 “Gly Glu Lys”
      repeating units

<400> SEQUENCE: 142

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
1               5                   10                  15

Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
            20                  25


<210> SEQ ID NO 143
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(27)
<223> OTHER INFORMATION: This sequence may encompass 2-9 “Gly Asp Lys”
      repeating units

<400> SEQUENCE: 143

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
1               5                   10                  15

Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
            20                  25


<210> SEQ ID NO 144
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(24)
<223> OTHER INFORMATION: This sequence may encompass 2-8 “Gly Glu Lys”
      repeating units

<400> SEQUENCE: 144

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
1               5                   10                  15

Glu Lys Gly Glu Lys Gly Glu Lys
            20


<210> SEQ ID NO 145
<211> LENGTH: 24
```

```
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(24)
<223> OTHER INFORMATION: This sequence may encompass 2-8 "Gly Asp Lys"
      repeating units

<400> SEQUENCE: 145

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
1               5                   10                  15

Asp Lys Gly Asp Lys Gly Asp Lys
            20


<210> SEQ ID NO 146
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(21)
<223> OTHER INFORMATION: This sequence may encompass 2-7 "Gly Glu Lys"
      repeating units

<400> SEQUENCE: 146

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
1               5                   10                  15

Glu Lys Gly Glu Lys
            20


<210> SEQ ID NO 147
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(21)
<223> OTHER INFORMATION: This sequence may encompass 2-7 "Gly Asp Lys"
      repeating units

<400> SEQUENCE: 147

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
1               5                   10                  15

Asp Lys Gly Asp Lys
            20


<210> SEQ ID NO 148
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(18)
<223> OTHER INFORMATION: This sequence may encompass 2-6 "Gly Glu Lys"
      repeating units
```

<400> SEQUENCE: 148

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly
1               5                   10                  15

Glu Lys

<210> SEQ ID NO 149
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(18)
<223> OTHER INFORMATION: This sequence may encompass 2-6 “Gly Asp Lys”
      repeating units

<400> SEQUENCE: 149

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly
1               5                   10                  15

Asp Lys

<210> SEQ ID NO 150
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(15)
<223> OTHER INFORMATION: This sequence may encompass 2-5 “Gly Glu Lys”
      repeating units

<400> SEQUENCE: 150

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
1               5                   10                  15

<210> SEQ ID NO 151
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(15)
<223> OTHER INFORMATION: This sequence may encompass 2-5 “Gly Asp Lys”
      repeating units

<400> SEQUENCE: 151

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
1               5                   10                  15

<210> SEQ ID NO 152
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:

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<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(12)
<223> OTHER INFORMATION: This sequence may encompass 2-4 "Gly Glu Lys"
      repeating units

<400> SEQUENCE: 152

Gly Glu Lys Gly Glu Lys Gly Glu Lys Gly Glu Lys
1               5                   10


<210> SEQ ID NO 153
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
      peptide
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(12)
<223> OTHER INFORMATION: This sequence may encompass 2-4 "Gly Asp Lys"
      repeating units

<400> SEQUENCE: 153

Gly Asp Lys Gly Asp Lys Gly Asp Lys Gly Asp Lys
1               5                   10
```

What is claimed is:

**1**. A recombinant cell comprising at least one copy of a heterologous nucleic acid sequence encoding a recombinant polypeptide comprising an amino acid sequence according to a human type 21 alpha 1 collagen, or a fragment thereof.

**2**. The recombinant cell of claim **1**, wherein the recombinant cell is a microbial cell.

**3**. The recombinant cell of claim **2**, wherein the microbial cell is a bacterial cell.

**4**. The recombinant cell of claim **3**, wherein the bacterial cell is of the species *Escherichia coli.*

**5**. The recombinant cell of claim **1**, wherein the heterologous nucleic acid sequence comprises SEQ ID NO: 75.

**6**. The recombinant cell of claim **1**, wherein the heterologous nucleic acid sequence is codon-optimized for expression in a cell.

**7**. The recombinant cell of claim **1**, wherein the recombinant polypeptide is full-length human type 21 alpha 1 collagen.

**8**. The recombinant cell of claim **1**, wherein the recombinant polypeptide is non-naturally occurring.

**9**. The recombinant cell of claim **1**, wherein the recombinant polypeptide comprises an amino acid sequence comprising a truncation relative to a full-length human type 21 alpha 1 collagen.

**10**. The recombinant cell of claim **9**, wherein the truncation comprises a truncation at an N-terminal end relative to a full-length human type 21 alpha 1 collagen, a truncation at a C-terminal end relative to a full-length human type 21 alpha 1 collagen, an internal truncation relative to a full-length human type 21 alpha 1 collagen, or any combination thereof.

**11**. The recombinant cell of claim **9**, wherein the truncation comprises a truncation of between 50 amino acids and 800 amino acids relative to a full-length human type 21 alpha 1 collagen.

**12**. The recombinant cell of claim **9**, wherein the truncation comprises a truncation at an N-terminal end relative to a full-length human type 21 alpha 1 collagen, and a truncation at a C-terminal end relative to a full-length human type 21 alpha 1 collagen.

**13**. The recombinant cell of claim **12**, wherein the truncation at an N-terminal end relative to a full-length human type 21 alpha 1 collagen is a truncation of between 50 amino acids and 600 amino acids.

**14**. The recombinant cell of claim **12**, wherein the truncation at a C-terminal end relative to a full-length human type 21 alpha collagen is a truncation of between 50 amino acids and 250 amino acids.

**15**. The recombinant cell of claim **9**, wherein the truncation is a truncation at an N-terminal end of between 50 amino acids and 600 amino acids relative to a full-length human type 21 alpha 1 collagen, and a truncation at a C-terminal end of between 50 amino acids and 250 amino acids relative to a full-length human type 21 alpha 1 collagen.

**16**. The recombinant cell of claim **1**, wherein the recombinant polypeptide comprises an amino acid sequence according to SEQ ID NO: 76 or a fragment thereof.

**17**. The recombinant cell of claim **1**, wherein the recombinant polypeptide consists of an amino acid sequence according to SEQ ID NO: 76.

**18**. The recombinant cell of claim **1**, wherein the recombinant polypeptide further comprises a secretion tag.

**19**. The recombinant cell of claim **18**, wherein the secretion tag is a DsbA secretion tag.

**20**. The recombinant cell of claim **18**, wherein the recombinant cell is capable of secreting the recombinant polypeptide extracellularly.

**21**. A composition comprising a recombinant cell of claim **1**, and a culture media comprising a recombinant polypeptide comprising an amino acid sequence according to a human type 21 alpha 1 collagen, or a fragment thereof.

**22**. The composition of claim **21**, wherein the recombinant cell is a bacterial cell of the species *Escherichia coli.*

**23**. The composition of claim **22**, wherein the heterologous nucleic acid sequence is a nucleic acid sequence according to SEQ ID NO: 75, and the recombinant polypeptide has an amino acid sequence according to SEQ ID NO: 76.

**24**. A method for producing a recombinant polypeptide, the method comprising:

a. incubating a recombinant cell of claim **1** in a culture media wherein the recombinant cell secretes the recombinant polypeptide into the culture media;
b. collecting the culture media comprising the recombinant polypeptide secreted thereto; and
c. purifying the recombinant polypeptide from the culture media.

**25**. The method of claim **24**, wherein the recombinant cell is a bacterial cell of the species *Escherichia coli.*

**26**. The method of claim **25**, wherein the heterologous nucleic acid sequence is a nucleic acid sequence according to SEQ ID NO: 75, and the recombinant polypeptide has an amino acid sequence according to SEQ ID NO: 76.

* * * * *