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**OSBORN M J ET AL, "TALEN-based gene correction for epidermolysis bullosa", MOLECULAR THERAPY, ACADEMIC PRESS, US, (2013-01-01), vol. 21, no. 6, doi:10.1038/MT.2013.56, ISSN 1525-0016, pages 1151-1159.**



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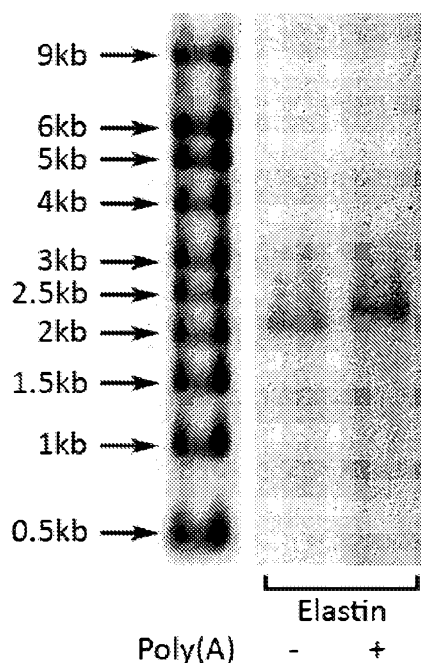
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(54) Title: METHODS AND PRODUCTS FOR NUCLEIC ACID PRODUCTION AND DELIVERY

FIG. 1



(57) Abstract: The present invention relates in part to nucleic acids, including nucleic acids encoding proteins, therapeutics and cosmetics comprising nucleic acids, methods for delivering nucleic acids to cells, tissues, organs, and patients, methods for inducing cells to express proteins using nucleic acids, methods, kits and devices for transfecting, gene editing, and reprogramming cells, and cells, organisms, therapeutics, and cosmetics produced using these methods, kits, and devices. Methods and products for altering the DNA sequence of a cell are described, as are methods and products for inducing cells to express proteins using synthetic RNA molecules, including cells present in vivo. Therapeutics comprising nucleic acids encoding gene-editing proteins are also described.

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**METHODS AND PRODUCTS FOR NUCLEIC ACID PRODUCTION AND DELIVERY****PRIORITY**

The present application claims priority to U.S. Provisional Application No. 61/934,397, filed on January 31, 2014, U.S. Provisional Application No. 62/038,608, filed on August 18, 2014, and U.S. Provisional Application No. 62/069,667, filed on October 28, 2014, the entire contents of which are hereby incorporated by reference in their entireties.

The present application is related to U.S. Application No. 13/465,490, filed on May 7, 2012, International Application No. PCT/US2012/067966, filed on December 5, 2012, U.S. Application No. 13/931,251, filed on June 28, 2013, and International Application No. PCT/US2013/068118, filed on November 1, 2013, the entire contents of which are hereby incorporated by reference in their entireties.

**FIELD OF THE INVENTION**

5 The present invention relates, in part, to methods, compositions, and products for producing and delivering nucleic acids to cells, tissues, organs, and patients, methods for expressing proteins in cells, tissues, organs, and patients, and cells, therapeutics, and cosmetics produced using these methods, compositions, and products.

**DESCRIPTION OF THE TEXT FILE SUBMITTED ELECTRONICALLY**

10 The contents of the text file submitted electronically herewith are incorporated herein by reference in their entirety: A computer readable format copy of the Sequence Listing (filename: FAB-008PC SequenceListing.txt; date recorded: January 30, 2015; file size: 929 KB).

**BACKGROUND***Synthetic RNA and Nucleic-Acid Therapeutics*

15 Ribonucleic acid (RNA) is ubiquitous in both prokaryotic and eukaryotic cells, where it encodes genetic information in the form of messenger RNA, binds and transports amino acids in the form of transfer RNA, assembles amino acids into proteins in the form of ribosomal RNA, and performs numerous other functions including gene expression regulation in the forms of microRNA and long non-coding RNA. RNA can be produced synthetically by methods including direct chemical synthesis and *in vitro* transcription, and can be administered to patients for therapeutic use. However, previously described synthetic RNA molecules are  
20 unstable and trigger a potent innate-immune response in human cells. In addition, methods for efficient non-viral delivery of nucleic acids to patients, organs, tissues, and cells *in vivo* have not been previously described. The many drawbacks of existing synthetic RNA technologies and methods for delivery of nucleic acids make them undesirable for therapeutic or cosmetic use.

*Cell Reprogramming and Cell-Based Therapies*

Cells can be reprogrammed by exposing them to specific extracellular cues and/or by ectopic expression of specific proteins, microRNAs, etc. While several reprogramming methods have been previously described, most that rely on ectopic expression require the introduction of exogenous DNA, which can carry mutation risks. DNA-free reprogramming methods based on direct delivery of reprogramming proteins have been reported. However, these methods are too inefficient and unreliable for commercial use. In addition, RNA-based reprogramming methods have been described (See, e.g., Angel. MIT Thesis. 2008. 1-56; Angel *et al.* PLoS ONE. 2010. 5,107; Warren *et al.* Cell Stem Cell. 2010. 7,618-630; Angel. MIT Thesis. 2011. 1-89; and Lee *et al.* Cell. 2012. 151,547-558; the contents of all of which are hereby incorporated by reference). However, existing RNA-based reprogramming methods are slow, unreliable, and inefficient when performed on adult cells, require many transfections (resulting in significant expense and opportunity for error), can reprogram only a limited number of cell types, can reprogram cells to only a limited number of cell types, require the use of immunosuppressants, and require the use of multiple human-derived components, including blood-derived HSA and human fibroblast feeders. The many drawbacks of previously disclosed RNA-based reprogramming methods make them undesirable for *in vivo* use.

*Gene Editing*

Several naturally occurring proteins contain DNA-binding domains that can recognize specific DNA sequences, for example, zinc fingers (ZFs) and transcription activator-like effectors (TALEs). Fusion proteins containing one or more of these DNA-binding domains and the cleavage domain of FokI endonuclease can be used to create a double-strand break in a desired region of DNA in a cell (See, e.g., US Patent Appl. Pub. No. US 2012/0064620, US Patent Appl. Pub. No. US 2011/0239315, US Patent No. 8,470,973, US Patent Appl. Pub. No. US 2013/0217119, US Patent No. 8,420,782, US Patent Appl. Pub. No. US 2011/0301073, US Patent Appl. Pub. No. US 2011/0145940, US Patent No. 8,450,471, US Patent No. 8,440,431, US Patent No. 8,440,432, and US Patent Appl. Pub. No. 2013/0122581, the contents of all of which are hereby incorporated by reference). However, current methods for gene editing cells are inefficient and carry a risk of uncontrolled mutagenesis, making them undesirable for both research and therapeutic use. Methods for DNA-free gene editing of somatic cells have not been previously explored, nor have methods for simultaneous or sequential gene editing and reprogramming of somatic cells. In addition, methods for directly gene editing cells in patients (*i.e.*, *in vivo*) have not been previously explored, and the development of such methods has been limited by a lack of acceptable targets, inefficient delivery, inefficient expression of the gene-editing protein/proteins, inefficient gene editing by the expressed gene-editing protein/proteins, due in part to poor binding of DNA-binding domains, excessive off-target effects, due in part to non-directed dimerization of the FokI cleavage domain and poor specificity of DNA-binding domains, and other factors.

Finally, the use of gene editing in anti-bacterial, anti-viral, and anti-cancer treatments has not been previously explored.

Accordingly, there remains a need for improved methods and compositions for the production and delivery of nucleic acids to cells, tissues, organs, and patients.

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is solely for the purpose of providing a context for the present invention. It is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present invention as it existed before the priority date of each claim of this specification

### SUMMARY OF THE INVENTION

The present invention provides, in part, compositions, methods, articles, and devices for delivering nucleic acids to cells, tissues, organs, and patients, methods for inducing cells to express proteins, methods, articles, and devices for producing these compositions, methods, articles, and devices, and compositions and articles, including cells, organisms, cosmetics and therapeutics, produced using these compositions, methods, articles, and devices. Unlike previously reported methods, certain embodiments of the present invention do not involve exposing cells to exogenous DNA or to allogeneic or animal-derived materials, making products produced according to the methods of the present invention useful for therapeutic and cosmetic applications.

In one aspect, there is provided an *in vivo* method for treating a dystrophic epidermolysis bullosa patient comprising delivering a synthetic RNA encoding collagen type VII to the patient's keratinocytes by injection to the epidermis, thereby resulting in the amelioration of one or more of the dystrophic epidermolysis bullosa patient's symptoms.

In another aspect, there is provided an *in vivo* method for treating epidermolysis bullosa, comprising delivering a synthetic RNA encoding a gene-editing protein that targets a COL7 gene to a patient in need thereof and inducing a single-strand or double-strand break in the COL7 gene of the patient's keratinocytes, thereby eliminating a mutation that is at least partially responsible for a disease phenotype, wherein: the synthetic RNA is delivered to the patient's keratinocytes by injection to the epidermis and the gene-editing protein comprises a DNA-binding domain and a nuclease domain.

In another aspect, there is provided an *in vivo* method for treating dystrophic epidermolysis bullosa, comprising delivering a synthetic RNA encoding a gene-editing protein that targets a COL7 gene to a patient in need thereof and delivering a COL7 repair template to the patient, thereby editing the COL7 gene, wherein: the synthetic RNA and repair template are delivered to the patient's keratinocytes by injection to the epidermis and the gene-editing protein comprises a DNA-binding domain and a nuclease domain and causes a double-strand break in the COL7 gene of the patient's keratinocytes.

In some aspects, there is provided a method for expressing a protein in a cell population of a patient, comprising introducing an RNA into the cell population, the RNA comprising one or more non-canonical nucleotides that do not induce significant cellular immune response and do not substantially reduce protein expression. In some embodiments, at least 50%, or at least 75%, or at least 90% of the non-canonical nucleotides are selected from one or more of 5-hydroxycytidine, 5-hydroxymethylcytidine, 5-carboxycytidine, 5-formylcytidine, 5-hydroxyuridine, 5-hydroxymethyluridine, 5-carboxyuridine, and 5-formyluridine, or in some embodiments selected from one or more of 5-hydroxymethylcytidine, 5-carboxycytidine, and 5-formylcytidine. Further embodiments relate to additional elements of the RNA, *e.g.* a 5' cap structure, a 3' poly(A) tail, and 5'-UTR and/or 3'-UTR, which optionally comprises one or more of a Kozak consensus sequence, a sequence that increases RNA stability *in vivo* (such as, by way of illustration, an alpha-globin or beta-globin 5'-UTR).

In some aspects, nucleic acid delivery patches are provided. In one aspect, devices for delivering nucleic acids using electric fields are provided. Other aspects pertain to methods and compositions for delivery of nucleic acids to the skin. Still further aspects pertain to methods and compositions for expression of proteins in the skin.

In one aspect, the invention provides methods and compositions for treating diseases and conditions in humans, including, but not limited to, prophylactic treatments, treatments for rare diseases, including, but not limited to, dermatologic rare diseases, and treatments for use in medical dermatology and aesthetic medicine. In another aspect, the invention provides cosmetics comprising nucleic acids. Still further aspects relate to methods and compositions for altering pigmentation, for example, for the treatment of pigmentation disorders. Still further aspects relate to methods and compositions for enhancing healing, including, but not limited to, healing in response to a wound or surgery. Other aspects relate to nucleic acids comprising one or more non-

canonical nucleotides. In one aspect, the invention provides nucleic acids comprising, for example, one or more of 5-hydroxycytidine, 5-hydroxymethylcytidine, 5-carboxycytidine, 5-formylcytidine, 5-hydroxyuridine, 5-hydroxymethyluridine, 5-carboxyuridine, and 5-formyluridine, or in some embodiments selected from one or more of 5-hydroxymethylcytidine, 5-carboxycytidine, and/or 5-formylcytidine.

- 5 The compositions of the present invention may alter, modify and/or change the appearance of a member of the integumentary system of a subject such as, but not limited to, skin, hair and nails. Such alteration, modification and/or change may be in the context of treatment methods and/or therapeutic uses as described herein including, by way of non-limiting example, dermatological treatments and cosmetics procedures.

- 10 In some aspects, synthetic RNA molecules with low toxicity and high translation efficiency are provided. In one aspect, a cell-culture medium for high-efficiency *in vivo* transfection, reprogramming, and gene editing of cells is provided. Other aspects pertain to methods for producing synthetic RNA molecules encoding reprogramming proteins. Still further aspects pertain to methods for producing synthetic RNA molecules encoding gene-editing proteins.

- 15 In one aspect, the invention provides high-efficiency gene-editing proteins comprising engineered nuclease cleavage domains. In another aspect, the invention provides high-fidelity gene-editing proteins comprising engineered nuclease cleavage domains. Other aspects relate to high-efficiency gene-editing proteins comprising engineered DNA-binding domains. Still further aspects pertain to high-fidelity gene-editing proteins comprising engineered DNA-binding domains. Still further aspects relate to gene-editing proteins comprising engineered repeat sequences. Some aspects relate to methods for altering the DNA sequence of a cell by transfecting the cell with or inducing the cell to express a gene-editing protein. Other aspects relate to methods for altering the DNA sequence of a cell that is present in an *in vitro* culture. Still further aspects relate to methods for altering the DNA sequence of a cell that is present *in vivo*.

- 25 In some aspects, the invention provides methods for treating cancer comprising administering to a patient a therapeutically effective amount of a gene-editing protein or a nucleic-acid encoding a gene-editing protein. In one aspect, the gene-editing protein is capable of altering the DNA sequence of a cancer associated gene. In another aspect, the cancer-associated gene is the BIRC5 gene. Still other aspects relate to therapeutics comprising nucleic acids and/or cells and methods of using therapeutics comprising nucleic acids and/or cells for the treatment of, for example, type 1 diabetes, heart disease, including ischemic and dilated cardiomyopathy, macular degeneration, Parkinson's disease, cystic fibrosis, sickle-cell anemia, thalassemia, Fanconi anemia, severe combined immunodeficiency, hereditary sensory neuropathy, xeroderma pigmentosum, Huntington's disease, muscular dystrophy, amyotrophic lateral sclerosis, Alzheimer's disease, cancer, and infectious diseases including hepatitis and HIV/AIDS. In some aspects, the nucleic acids comprise synthetic RNA. In other aspects, the nucleic acids are delivered to cells using a virus. In some



aspects, the virus is a replication-competent virus. In other aspects, the virus is a replication-incompetent virus.

The details of the invention are set forth in the accompanying description below. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, illustrative methods and materials are now described. Other features, objects, and advantages of the invention will be apparent from the description and from the claims. In the specification and the appended claims, the singular forms also include the plural unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

#### 10 DETAILED DESCRIPTION OF THE FIGURES

**FIG. 1** depicts RNA encoding human elastin protein and containing adenosine, 50% guanosine, 50% 7-deazaguanosine, 60% uridine, 40% 5-methyluridine, and 5-methylcytidine, resolved on a denaturing formaldehyde-agarose gel.

**FIG. 2** depicts primary adult human dermal fibroblasts transfected with the RNA of **FIG. 1**.

15 **FIG. 3** depicts the result of an immunocytochemical analysis of the primary adult human dermal fibroblasts of **FIG. 2** using an antibody targeting human elastin protein.

**FIG. 4** depicts primary human dermal fibroblasts transfected with synthetic RNA comprising cytidine, 5-methylcytidine ("5mC"), 5-hydroxymethylcytidine ("5hmC"), 5-carboxycytidine ("5cC") or 5-formylcytidine ("5fC") and encoding Oct4 protein. Cells were fixed and stained for Oct4 protein 24 hours after transfection.

20 **FIG. 5** depicts primary human dermal fibroblasts transfected with synthetic RNA comprising 5-hydroxymethylcytidine and encoding green fluorescent protein ("GFP"). Cells were imaged 24 hours after transfection.

**FIG. 6** depicts a region of the ventral forearm of a healthy, 33 year-old, male human subject treated with synthetic RNA comprising 5-hydroxymethylcytidine ("5hmC") and encoding GFP. Arrows indicate fluorescent cells.

25 **FIG. 7** depicts a region of the ventral forearm of a healthy, 33 year-old, male patient treated with synthetic RNA comprising 5-hydroxymethylcytidine ("5hmC") and encoding GFP. The top panel shows an untreated area on the same forearm, while the bottom panels show two fields within the treatment area. Fluorescent cells (indicated with arrows) are clearly visible in the bottom panels.

30 **FIG. 8** depicts primary human dermal fibroblasts transfected with synthetic RNA comprising 5-methyluridine and 5-hydroxymethylcytidine and encoding the indicated protein. Cells were fixed and stained using antibodies targeting the indicated protein 48 hours after transfection.

**FIG. 9** depicts primary human dermal fibroblasts transfected with synthetic RNA comprising 5-methyluridine and 5-hydroxymethylcytidine and encoding human tyrosinase. Cells were fixed and stained using an antibody targeting human tyrosinase 24 hours after transfection.

**FIG. 10** depicts primary human epidermal melanocytes.

- 5 **FIG. 11** depicts primary human dermal fibroblasts transfected with synthetic RNA comprising 5-hydroxymethylcytidine and encoding the indicated proteins.

**FIG. 12** depicts primary human dermal fibroblasts transfected daily with synthetic RNA comprising 5-hydroxymethylcytidine and encoding human tyrosinase. The number of transfections are shown above each sample. The cells were imaged 48 hours after the final transfection.

- 10 **FIG. 13** depicts primary human dermal fibroblasts transfected daily with synthetic RNA comprising the indicated nucleotides and encoding human tyrosinase. The cells were imaged 48 hours after transfection.

**FIG. 14** depicts IFNB1 expression and pigment production in primary human dermal fibroblasts transfected with synthetic RNA comprising the indicated nucleotides and encoding human tyrosinase. Values are normalized to the sample transfected with synthetic RNA comprising only canonical nucleotides ("A,G,U,C").

- 15 GAPDH was used as a loading control. Error bars indicate standard error (n=2).

**FIG. 15** depicts expression of the indicated genes, measured as in **FIG. 14**.

- FIG. 16** depicts a region of the ventral forearm of a healthy, 33 year-old, male human subject treated with synthetic RNA comprising 5-methyluridine and 5-hydroxymethylcytidine and encoding human tyrosinase (top panel), and an ephelis on the ventral forearm of the same subject (bottom panel). The same magnification was used for both images.
- 20

- FIG. 17** depicts primary human dermal fibroblasts transfected with synthetic RNA comprising 5-hydroxymethylcytidine and encoding collagen I (A1) (" + COL1 RNA"). Cells were fixed and stained using an antibody targeting collagen I between 24 and 72 hours after transfection. Two representative fields are shown for each of: the transfected cells and un-transfected cells ("Neg."). Arrows indicate extracellular deposits of collagen I.
- 25

**FIG. 18** depicts primary human dermal fibroblasts transfected with synthetic RNA comprising 5-hydroxymethylcytidine and encoding collagen VII (A1) (" + COL7 RNA"). Cells were fixed and stained using an antibody targeting collagen I between 24 and 72 hours after transfection. A representative field is shown for each of: the transfected cells and un-transfected cells ("Neg.).

**DETAILED DESCRIPTION OF THE INVENTION***Definitions*

By "molecule" is meant a molecular entity (molecule, ion, complex, etc.).

By "RNA molecule" is meant a molecule that comprises RNA.

- 5 By "synthetic RNA molecule" is meant an RNA molecule that is produced outside of a cell or that is produced inside of a cell using bioengineering, by way of non-limiting example, an RNA molecule that is produced in an *in vitro*-transcription reaction, an RNA molecule that is produced by direct chemical synthesis or an RNA molecule that is produced in a genetically-engineered *E.coli* cell.

By "transfection" is meant contacting a cell with a molecule, wherein the molecule is internalized by the cell.

- 10 By "upon transfection" is meant during or after transfection.

By "transfection reagent" is meant a substance or mixture of substances that associates with a molecule and facilitates the delivery of the molecule to and/or internalization of the molecule by a cell, by way of non-limiting example, a cationic lipid, a charged polymer or a cell-penetrating peptide.

By "reagent-based transfection" is meant transfection using a transfection reagent.

- 15 By "cell-culture medium" is meant a medium that can be used for cell culture, by way of non-limiting example, Dulbecco's Modified Eagle's Medium (DMEM) or DMEM + 10% fetal bovine serum (FBS), whether or not the medium is used *in vitro* or *in vivo*.

By "complexation medium" is meant a medium to which a transfection reagent and a molecule to be transfected are added and in which the transfection reagent associates with the molecule to be transfected.

- 20 By "transfection medium" is meant a medium that can be used for transfection, by way of non-limiting example, Dulbecco's Modified Eagle's Medium (DMEM), DMEM/F12, saline or water, whether or not the medium is used *in vitro* or *in vivo*.

- By "recombinant protein" is meant a protein or peptide that is not produced in animals or humans. Non-limiting examples include human transferrin that is produced in bacteria, human fibronectin that is produced  
25 in an *in vitro* culture of mouse cells, and human serum albumin that is produced in a rice plant.

By "lipid carrier" is meant a substance that can increase the solubility of a lipid or lipid-soluble molecule in an aqueous solution, by way of non-limiting example, human serum albumin or methyl-beta-cyclodextrin.

- By "Oct4 protein" is meant a protein that is encoded by the POU5F1 gene, or a natural or engineered variant, family-member, orthologue, fragment or fusion construct thereof, by way of non-limiting example, human  
30 Oct4 protein (SEQ ID NO: 8), mouse Oct4 protein, Oct1 protein, a protein encoded by POU5F1 pseudogene 2, a DNA-binding domain of Oct4 protein or an Oct4-GFP fusion protein. In some embodiments the Oct4

protein comprises an amino acid sequence that has at least 70% identity with SEQ ID NO: 8, or in other embodiments, at least 75%, 80%, 85%, 90%, or 95% identity with SEQ ID NO: 8. In some embodiments, the Oct4 protein comprises an amino acid sequence having from 1 to 20 amino acid insertions, deletions, or substitutions (collectively) with respect to SEQ ID NO: 8. Or in other embodiments, the Oct4 protein  
5 comprises an amino acid sequence having from 1 to 15 or from 1 to 10 amino acid insertions, deletions, or substitutions (collectively) with respect to SEQ ID NO: 8.

By "Sox2 protein" is meant a protein that is encoded by the SOX2 gene, or a natural or engineered variant, family-member, orthologue, fragment or fusion construct thereof, by way of non-limiting example, human Sox2 protein (SEQ ID NO: 9), mouse Sox2 protein, a DNA-binding domain of Sox2 protein or a Sox2-GFP  
10 fusion protein. In some embodiments the Sox2 protein comprises an amino acid sequence that has at least 70% identity with SEQ ID NO: 9, or in other embodiments, at least 75%, 80%, 85%, 90%, or 95% identity with SEQ ID NO: 9. In some embodiments, the Sox2 protein comprises an amino acid sequence having from 1 to 20 amino acid insertions, deletions, or substitutions (collectively) with respect to SEQ ID NO: 9. Or in other embodiments, the Sox2 protein comprises an amino acid sequence having from 1 to 15 or from 1 to 10 amino  
15 acid insertions, deletions, or substitutions (collectively) with respect to SEQ ID NO: 9.

By "Klf4 protein" is meant a protein that is encoded by the KLF4 gene, or a natural or engineered variant, family-member, orthologue, fragment or fusion construct thereof, by way of non-limiting example, human Klf4 protein (SEQ ID NO: 10), mouse Klf4 protein, a DNA-binding domain of Klf4 protein or a Klf4-GFP fusion protein. In some embodiments the Klf4 protein comprises an amino acid sequence that has at least 70%  
20 identity with SEQ ID NO: 10, or in other embodiments, at least 75%, 80%, 85%, 90%, or 95% identity with SEQ ID NO: 10. In some embodiments, the Klf4 protein comprises an amino acid sequence having from 1 to 20 amino acid insertions, deletions, or substitutions (collectively) with respect to SEQ ID NO: 10. Or in other embodiments, the Klf4 protein comprises an amino acid sequence having from 1 to 15 or from 1 to 10 amino acid insertions, deletions, or substitutions (collectively) with respect to SEQ ID NO: 10.

By "c-Myc protein" is meant a protein that is encoded by the MYC gene, or a natural or engineered variant, family-member, orthologue, fragment or fusion construct thereof, by way of non-limiting example, human c-Myc protein (SEQ ID NO: 11), mouse c-Myc protein, I-Myc protein, c-Myc (T58A) protein, a DNA-binding domain of c-Myc protein or a c-Myc-GFP fusion protein. In some embodiments the c-Myc protein comprises an amino acid sequence that has at least 70% identity with SEQ ID NO: 11, or in other embodiments, at least  
25 75%, 80%, 85%, 90%, or 95% identity with SEQ ID NO: 11. In some embodiments, the c-Myc protein comprises an amino acid having from 1 to 20 amino acid insertions, deletions, or substitutions (collectively) with respect to SEQ ID NO: 11. Or in other embodiments, the c-Myc protein comprises an amino acid sequence having from 1 to 15 or from 1 to 10 amino acid insertions, deletions, or substitutions (collectively) with respect to SEQ ID NO: 11.  
30

By "reprogramming" is meant causing a change in the phenotype of a cell, by way of non-limiting example, causing a  $\beta$ -cell progenitor to differentiate into a mature  $\beta$ -cell, causing a fibroblast to dedifferentiate into a pluripotent stem cell, causing a keratinocyte to transdifferentiate into a cardiac stem cell, causing the telomeres of a cell to lengthen or causing the axon of a neuron to grow.

- 5 By "reprogramming factor" is meant a molecule that, when a cell is contacted with the molecule and/or the cell expresses the molecule, can, either alone or in combination with other molecules, cause reprogramming, by way of non-limiting example, Oct4 protein.

By "feeder" is meant a cell that can be used to condition medium or to otherwise support the growth of other cells in culture.

- 10 By "conditioning" is meant contacting one or more feeders with a medium.

By "fatty acid" is meant a molecule that comprises an aliphatic chain of at least two carbon atoms, by way of non-limiting example, linoleic acid,  $\alpha$ -linolenic acid, octanoic acid, a leukotriene, a prostaglandin, cholesterol, a glucocorticoid, a resolvin, a protectin, a thromboxane, a lipoxin, a maresin, a sphingolipid, tryptophan, N-acetyl tryptophan or a salt, methyl ester or derivative thereof.

- 15 By "short-chain fatty acid" is meant a fatty acid that comprises an aliphatic chain of between two and 30 carbon atoms.

By "albumin" is meant a protein that is highly soluble in water, by way of non-limiting example, human serum albumin.

By "associated molecule" is meant a molecule that is non-covalently bound to another molecule.

- 20 By "associated-molecule-component of albumin" is meant one or more molecules that are bound to an albumin polypeptide, by way of non-limiting example, lipids, hormones, cholesterol, calcium ions, etc. that are bound to an albumin polypeptide.

By "treated albumin" is meant albumin that is treated to reduce, remove, replace or otherwise inactivate the associated-molecule-component of the albumin, by way of non-limiting example, human serum albumin that

- 25 is incubated at an elevated temperature, human serum albumin that is contacted with sodium octanoate or human serum albumin that is contacted with a porous material.

By "ion-exchange resin" is meant a material that, when contacted with a solution containing ions, can replace one or more of the ions with one or more different ions, by way of non-limiting example, a material that can replace one or more calcium ions with one or more sodium ions.

- 30 By "germ cell" is meant a sperm cell or an egg cell.

By "pluripotent stem cell" is meant a cell that can differentiate into cells of all three germ layers (endoderm, mesoderm, and ectoderm) *in vivo*.

By "somatic cell" is meant a cell that is not a pluripotent stem cell or a germ cell, by way of non-limiting example, a skin cell.

- 5 By "glucose-responsive insulin-producing cell" is meant a cell that, when exposed to a certain concentration of glucose, can produce and/or secrete an amount of insulin that is different from (either less than or more than) the amount of insulin that the cell produces and/or secretes when the cell is exposed to a different concentration of glucose, by way of non-limiting example, a  $\beta$ -cell.

- 10 By "hematopoietic cell" is meant a blood cell or a cell that can differentiate into a blood cell, by way of non-limiting example, a hematopoietic stem cell or a white blood cell.

By "cardiac cell" is meant a heart cell or a cell that can differentiate into a heart cell, by way of non-limiting example, a cardiac stem cell or a cardiomyocyte.

By "retinal cell" is meant a cell of the retina or a cell that can differentiate into a cell of the retina, by way of non-limiting example, a retinal pigmented epithelial cell.

- 15 By "skin cell" is meant a cell that is normally found in the skin, by way of non-limiting example, a fibroblast, a keratinocyte, a melanocyte, an adipocyte, a mesenchymal stem cell, an adipose stem cell or a blood cell.

By "Wnt signaling agonist" is meant a molecule that can perform one or more of the biological functions of one or more members of the Wnt family of proteins, by way of non-limiting example, Wnt1, Wnt2, Wnt3, Wnt3a or 2-amino-4-[3,4-(methylenedioxy)benzylamino]-6-(3-methoxyphenyl)pyrimidine.

- 20 By "IL-6 signaling agonist" is meant a molecule that can perform one or more of the biological functions of IL-6 protein, by way of non-limiting example, IL-6 protein or IL-6 receptor (also known as soluble IL-6 receptor, IL-6R, IL-6R alpha, etc.).

- 25 By "TGF- $\beta$  signaling agonist" is meant a molecule that can perform one or more of the biological functions of one or more members of the TGF- $\beta$  superfamily of proteins, by way of non-limiting example, TGF- $\beta$ 1, TGF- $\beta$ 3, Activin A, BMP-4 or Nodal.

By "immunosuppressant" is meant a substance that can suppress one or more aspects of an immune system, and that is not normally present in a mammal, by way of non-limiting example, B18R or dexamethasone.

By "single-strand break" is meant a region of single-stranded or double-stranded DNA in which one or more of the covalent bonds linking the nucleotides has been broken in one of the one or two strands.

- 30 By "double-strand break" is meant a region of double-stranded DNA in which one or more of the covalent bonds linking the nucleotides has been broken in each of the two strands.

By "nucleotide" is meant a nucleotide or a fragment or derivative thereof, by way of non-limiting example, a nucleobase, a nucleoside, a nucleotide-triphosphate, etc.

By "nucleoside" is meant a nucleotide or a fragment or derivative thereof, by way of non-limiting example, a nucleobase, a nucleoside, a nucleotide-triphosphate, etc.

- 5 By "gene editing" is meant altering the DNA sequence of a cell, by way of non-limiting example, by transfecting the cell with a protein that causes a mutation in the DNA of the cell.

- By "gene-editing protein" is meant a protein that can, either alone or in combination with one or more other molecules, alter the DNA sequence of a cell, by way of non-limiting example, a nuclease, a transcription activator-like effector nuclease (TALEN), a zinc-finger nuclease, a meganuclease, a nickase, a clustered  
10 regularly interspaced short palindromic repeat (CRISPR)-associated protein or a natural or engineered variant, family-member, orthologue, fragment or fusion construct thereof.

By "repair template" is meant a nucleic acid containing a region of at least about 70% homology with a sequence that is within 10kb of a target site of a gene-editing protein.

- By "repeat sequence" is meant an amino-acid sequence that is present in more than one copy in a protein, to  
15 within at least about 10% homology, by way of non-limiting example, a monomer repeat of a transcription activator-like effector.

- By "DNA-binding domain" is meant a region of a molecule that is capable of binding to a DNA molecule, by way of non-limiting example, a protein domain comprising one or more zinc fingers, a protein domain comprising one or more transcription activator-like (TAL) effector repeat sequences or a binding pocket of a  
20 small molecule that is capable of binding to a DNA molecule.

- By "binding site" is meant a nucleic-acid sequence that is capable of being recognized by a gene-editing protein, DNA-binding protein, DNA-binding domain or a biologically active fragment or variant thereof or a nucleic-acid sequence for which a gene-editing protein, DNA-binding protein, DNA-binding domain or a biologically active fragment or variant thereof has high affinity, by way of non-limiting example, an about 20-  
25 base-pair sequence of DNA in exon 1 of the human BIRC5 gene.

By "target" is meant a nucleic acid that contains a binding site.

- Other definitions are set forth in U.S. Application No. 13/465,490, U.S. Provisional Application No. 61/664,494, U.S. Provisional Application No. 61/721,302, International Application No. PCT/US12/67966, U.S. Provisional Application No. 61/785,404, U.S. Provisional Application No. 61/842,874, International Application No.  
30 PCT/US13/68118, U.S. Provisional Application No. 61/934,397, U.S. Application No. 14/296,220, U.S. Provisional Application No. 62/038,608, and U.S. Provisional Application No. 62/069,667, the contents of which are hereby incorporated by reference in their entireties.

Glycation and glycosylation are processes by which one or more sugar molecules are bound to a protein. It has now been discovered that altering the number or location of glycation and glycosylation sites can increase or decrease the stability of a protein. Certain embodiments are therefore directed to a protein with one or more glycation or glycosylation sites. In one embodiment, the protein is engineered to have more glycation or glycosylation sites than a natural variant of the protein. In another embodiment, the protein is engineered to have fewer glycation or glycosylation sites than a natural variant of the protein. In yet another embodiment, the protein has increased stability. In yet another embodiment, the protein has decreased stability.

It has been further discovered that in certain situations, including one or more steroids and/or one or more antioxidants in the transfection medium can increase *in vivo* transfection efficiency, *in vivo* reprogramming efficiency, and *in vivo* gene-editing efficiency. Certain embodiments are therefore directed to contacting a cell or patient with a glucocorticoid, such as hydrocortisone, prednisone, prednisolone, methylprednisolone, dexamethasone or betamethasone. Other embodiments are directed to a method for inducing a cell to express a protein of interest by contacting a cell with a medium containing a steroid and contacting the cell with one or more nucleic acid molecules. In one embodiment, the nucleic acid molecule comprises synthetic RNA. In another embodiment, the steroid is hydrocortisone. In yet another embodiment, the hydrocortisone is present in the medium at a concentration of between about 0.1uM and about 10uM, or about 1uM. Other embodiments are directed to a method for inducing a cell *in vivo* to express a protein of interest by contacting the cell with a medium containing an antioxidant and contacting the cell with one or more nucleic acid molecules. In one embodiment, the antioxidant is ascorbic acid or ascorbic-acid-2-phosphate. In another embodiment, the ascorbic acid or ascorbic-acid-2-phosphate is present in the medium at a concentration of between about 0.5mg/L and about 500mg/L, including about 50mg/L. Still other embodiments are directed to a method for reprogramming and/or gene-editing a cell *in vivo* by contacting the cell with a medium containing a steroid and/or an antioxidant and contacting the cell with one or more nucleic acid molecules, wherein the one or more nucleic acid molecules encodes one or more reprogramming and/or gene-editing proteins. In certain embodiments, the cell is present in an organism, and the steroid and/or antioxidant are delivered to the organism.

Adding transferrin to the complexation medium has been reported to increase the efficiency of plasmid transfection in certain situations. It has now been discovered that adding transferrin to the complexation medium can also increase the efficiency of *in vivo* transfection with synthetic RNA molecules. Certain embodiments are therefore directed to a method for inducing a cell *in vivo* to express a protein of interest by adding one or more synthetic RNA molecules and a transfection reagent to a solution containing transferrin. In one embodiment, the transferrin is present in the solution at a concentration of between about 1mg/L and about 100mg/L, such as about 5mg/L. In another embodiment, the transferrin is recombinant.



Cells, tissues, organs, and organisms, including, but not limited to, humans, have several characteristics that can inhibit or prevent the delivery of nucleic acids, including, for example, the stratum corneum, which can serve as a barrier to foreign organisms and nucleic acids. These characteristics can thus inhibit the effects of therapeutics and cosmetics comprising nucleic acids. It has now been discovered that many of these characteristics can be circumvented or overcome using a patch comprising a flexible membrane and a plurality of needles, and that such a patch can serve as an effective and safe article for the delivery of nucleic acids. Certain embodiments are therefore directed to a nucleic acid delivery patch. In one embodiment, the nucleic acid delivery patch comprises a flexible membrane. In another embodiment, the nucleic acid delivery patch comprises a plurality of needles. In yet another embodiment, the plurality of needles are attached to the flexible membrane. In some embodiments, the patch comprises a nucleic acid. In one embodiment, the nucleic acid is present in solution. In one embodiment, the plurality of needles include one or more needles having a lumen. In another embodiment, the patch further comprises a second flexible membrane. In yet another embodiment, the flexible membrane and the second flexible membrane are arranged to form a cavity. In a further embodiment, the cavity contains a nucleic acid. In a still further embodiment, the membrane comprises one or more holes through which a nucleic acid can pass. In a still further embodiment, one or more holes and one or more needles having a lumen are arranged to allow the passage of a solution containing a nucleic acid through at least one of the one or more holes and through at least one of the one or more needles having a lumen. In some embodiments, the patch is configured to deliver a solution to the skin. In one embodiment, the solution comprises a nucleic acid. In another embodiment, the solution comprises a vehicle. In yet another embodiment, the vehicle is a lipid or lipidoid. In a still further embodiment, the vehicle is a lipid-based transfection reagent.

The cell membrane can serve as a barrier to foreign nucleic acids. It has now been discovered that combining the patch of the present invention with an electric field can increase the efficiency of nucleic acid delivery. Certain embodiments are therefore directed to a nucleic acid delivery patch comprising a plurality of needles, wherein at least two needles form part of a high-voltage circuit. In one embodiment, the high-voltage circuit generates a voltage greater than about 10V. In another embodiment, the high-voltage circuit generates a voltage greater than about 20V. In yet another embodiment, an electric field is produced between two of the needles. In a further embodiment, the magnitude of the electric field is at least about 100V/cm. In a still further embodiment, the magnitude of the electric field is at least about 200V/cm. In some embodiments, the patch is configured to deliver a nucleic acid to the epidermis. In other embodiments, the patch is configured to deliver a nucleic acid to the dermis. In still other embodiments, the patch is configured to deliver a nucleic acid to sub-dermal tissue. In still other embodiments, the patch is configured to deliver a nucleic acid to muscle. Certain embodiments are directed to a nucleic acid delivery patch comprising a plurality of electrodes. In one embodiment, the plurality of electrodes is attached to a flexible membrane. Other embodiments are

directed to a nucleic acid delivery patch comprising a rigid structure. In one embodiment, a plurality of electrodes are attached to the rigid structure.

Other embodiments are directed to a method for delivering a nucleic acid to a cell *in vivo* comprising applying a nucleic acid to a tissue containing a cell *in vivo*. In one embodiment, the method further comprises applying a transient electric field in the vicinity of the cell. In another embodiment, the method results in the cell *in vivo* internalizing the nucleic acid. In yet another embodiment, the nucleic acid comprises synthetic RNA. In a further embodiment, the method further results in the cell internalizing a therapeutically or cosmetically effective amount of the nucleic acid. In one embodiment, the cell is a skin cell. In another embodiment, the cell is a muscle cell. In yet another embodiment, the cell is a dermal fibroblast. In a further embodiment, the cell is a keratinocyte. In a still further embodiment, the cell is a myoblast. In some embodiments, the nucleic acid comprises a protein of interest. In one embodiment, the protein of interest is a fluorescent protein. In another embodiment, the protein of interest is an extracellular-matrix protein. In yet another embodiment, the protein of interest is a member of the group: elastin, collagen, laminin, fibronectin, vitronectin, lysyl oxidase, elastin binding protein, a growth factor, fibroblast growth factor, transforming growth factor beta, granulocyte colony-stimulating factor, a matrix metalloproteinase, an actin, fibrillin, microfibril-associated glycoprotein, a lysyl-oxidase-like protein, platelet-derived growth factor, a lipase, an uncoupling protein, thermogenin, and a protein involved with pigment production. In some embodiments, the method further comprises delivering the nucleic acid to the epidermis. In other embodiments, the method further comprises delivering the nucleic acid to the dermis. In still other embodiments, the method further comprises delivering the nucleic acid below the dermis. In one embodiment, the delivering is by injection. In another embodiment, the delivering is by injection using a micro-needle array. In yet another embodiment, the delivering is by topical administration. In a further embodiment, the delivering comprises disruption or removal of a part of the tissue. In a still further embodiment, the delivering comprises disruption or removal of the stratum corneum. In some embodiments, the nucleic acid is present in solution. In one embodiment, the solution comprises a growth factor. In another embodiment, the growth factor is a member of the group: a fibroblast growth factor and a transforming growth factor. In yet another embodiment, the growth factor is a member of the group: basis fibroblast growth factor and transforming growth factor beta. In other embodiments, the solution comprises cholesterol.

In another embodiment, the method further comprises contacting the cell with one or more nucleic acid molecules. In yet another embodiment, at least one of the one or more nucleic acid molecules encodes a protein of interest. In a further embodiment, the method results in the cell expressing the protein of interest. In a still further embodiment, the method results in the cell expressing a therapeutically or cosmetically effective amount of the protein of interest.

In another embodiment, the cell is contacted with a nucleic acid molecule. In yet another embodiment, the method results in the cell internalizing the nucleic acid molecule. In a further embodiment, the method results

in the cell internalizing a therapeutically or cosmetically effective amount of the nucleic acid molecule. In one embodiment, the nucleic acid encodes a protein of interest. In one embodiment, the nucleic acid molecule comprises a member of the group: a dsDNA molecule, a ssDNA molecule, a dsRNA molecule, a ssRNA molecule, a plasmid, an oligonucleotide, a synthetic RNA molecule, a miRNA molecule, an mRNA molecule, and an siRNA molecule.

Synthetic RNA comprising only canonical nucleotides can bind to pattern recognition receptors, can be recognized as a pathogen-associated molecular pattern, and can trigger a potent immune response in cells, which can result in translation block, the secretion of inflammatory cytokines, and cell death. It has now been discovered that synthetic RNA comprising certain non-canonical nucleotides can evade detection by the innate immune system, and can be translated at high efficiency into protein. It has been further discovered that synthetic RNA comprising at least one member of the group: 5-hydroxycytidine, 5-hydroxymethylcytidine, 5-carboxycytidine, 5-formylcytidine, 5-hydroxyuridine, 5-hydroxymethyluridine, 5-carboxyuridine, and 5-formyluridine can evade detection by the innate immune system, and can be translated at high efficiency into protein. Certain embodiments are therefore directed to a method for inducing a cell to express a protein of interest comprising contacting a cell with synthetic RNA. Other embodiments are directed to a method for transfecting a cell with synthetic RNA comprising contacting a cell with a solution comprising one or more synthetic RNA molecules. Still other embodiments are directed to a method for treating a patient comprising administering to the patient synthetic RNA. In one embodiment, the synthetic RNA comprises at least one member of the group: 5-hydroxycytidine, 5-hydroxymethylcytidine, 5-carboxycytidine, 5-formylcytidine, 5-hydroxyuridine, 5-hydroxymethyluridine, 5-carboxyuridine, and 5-formyluridine. In another embodiment, the synthetic RNA encodes a protein of interest. Exemplary RNAs may contain combinations and levels of non-canonical and non-canonical nucleotides as described elsewhere herein, including with respect to the expression of any protein of interest described herein. In yet another embodiment, the method results in the expression of the protein of interest. In a further embodiment, the method results in the expression of the protein of interest in the patient's skin.

It has now been further discovered that contacting a cell with a steroid can suppress the innate immune response to foreign nucleic acids, and can increase the efficiency of nucleic acid delivery and translation. Certain embodiments are therefore directed to contacting a cell with a steroid. Other embodiments are directed to administering a steroid to a patient. In one embodiment, the steroid is hydrocortisone. In another embodiment, the steroid is dexamethasone. Still other embodiments are directed to administering to a patient a member of the group: an antibiotic, an antimycotic, and an RNase inhibitor.

Other embodiments are directed to a method for delivering a nucleic acid to a cell *in vivo*. Still other embodiments are directed to a method for inducing a cell *in vivo* to express a protein of interest. Still other embodiments are directed to a method for treating a patient. In one embodiment, the method comprises

disrupting the stratum corneum. In another embodiment, the method comprises contacting a cell with a nucleic acid. In yet another embodiment, the method results in the cell internalizing the nucleic acid. In a further embodiment, the method results in the cell expressing the protein of interest. In a still further embodiment, the method results in the expression of the protein of interest in the patient. In a still further  
5 embodiment, the method results in the amelioration of one or more of the patient's symptoms. In a still further embodiment, the patient is in need of the protein of interest. In a still further embodiment, the patient is deficient in the protein of interest.

Still other embodiments are directed to a method for treating a patient comprising delivering to a patient a composition. In one embodiment, the composition comprises albumin that is treated with an ion-exchange  
10 resin or charcoal. In another embodiment, the composition comprises one or more nucleic acid molecules. In yet another embodiment, at least one of the one or more nucleic acid molecules encodes a protein of interest. In one embodiment, the method results in the expression of the protein in the patient's skin. In another embodiment, the method results in the expression of a therapeutically or cosmetically effective amount of the protein of interest in the patient. In yet another embodiment, the method comprises administering a steroid. In  
15 a further embodiment, the steroid is a member of the group: hydrocortisone and dexamethasone.

Certain embodiments are directed to a synthetic RNA molecule. In one embodiment, the synthetic RNA molecule encodes a protein of interest. In another embodiment, the synthetic RNA molecule comprises a member of the group: 5-hydroxycytidine, 5-hydroxymethylcytidine, 5-carboxycytidine, 5-formylcytidine, 5-  
20 hydroxyuridine, 5-hydroxymethyluridine, 5-carboxyuridine, and 5-formyluridine. Other embodiments are directed to a cosmetic composition. In one embodiment, the cosmetic composition comprises albumin. In another embodiment, the albumin is treated with an ion-exchange resin or charcoal. In yet another embodiment, the cosmetic composition comprises a nucleic acid molecule. In a further embodiment, the cosmetic composition comprises both albumin and a nucleic acid molecule. Still other embodiments are directed to a cosmetic treatment article comprising a cosmetic composition contained in a device configured  
25 to deliver the composition to a patient. Still other embodiments are directed to a device configured to deliver a cosmetic composition to a patient. In one embodiment, the nucleic acid molecule encodes a member of the group: elastin, collagen, tyrosinase, melanocortin 1 receptor, and hyaluronan synthase.

Certain proteins have long half-lives, and can persist in tissues for several hours, days, weeks, months or years. It has now been discovered that certain methods of treating a patient can result in accumulation of one  
30 or more proteins, including, for example, one or more beneficial proteins. Certain embodiments are therefore directed to a method for treating a patient comprising delivering to a patient in a series of doses a nucleic acid encoding one or more proteins. In one embodiment the nucleic acid comprises synthetic RNA. In another embodiment, a first dose is given at a first time-point. In yet another embodiment, a second dose is given at a second time-point. In a further embodiment, the amount of at least one of the one or more proteins in the

patient at the second time-point is greater than the amount of said protein at the first time-point. In a still further embodiment, the method results in the accumulation of said protein in the patient.

Other embodiments are directed to a therapeutic composition comprising a nucleic acid molecule encoding one or more proteins, wherein at least one of the one or more proteins is an extracellular matrix protein. Still other embodiments are directed to a cosmetic composition comprising a nucleic acid molecule encoding one or more proteins, wherein at least one of the one or more proteins is an extracellular matrix protein.

Pigmentation disorders can cause severe symptoms in patients. It has now been discovered that pigmentation disorders can be treated by delivering to a patient a nucleic acid encoding tyrosinase. Certain embodiments are therefore directed to a method for treating a pigmentation disorder. Other embodiments are directed to a method for altering the pigmentation of a patient. In one embodiment, the method comprises delivering to a patient a nucleic acid encoding tyrosinase. Other embodiments are directed to a cosmetic composition comprising a nucleic acid encoding tyrosinase. Still other embodiments are directed to a therapeutic composition comprising a nucleic acid encoding tyrosinase. Still other embodiments are directed to a method for increasing the ultraviolet absorption of a patient's skin. In one embodiment the method comprises delivering to a patient a nucleic acid encoding tyrosinase. In another embodiment, the method results in an increase in the ultraviolet absorption of the patient's skin. Still other embodiments are directed to a method for reducing photodamage to a person's skin upon exposure to ultraviolet light. In one embodiment, the method results in the reduction of photodamage to the person's skin upon exposure to ultraviolet light. Still other embodiments are directed to a method for treating xeroderma pigmentosum. In one embodiment, the method comprises delivering to a patient a nucleic acid encoding tyrosinase. Still other embodiments are directed to a method for treating epidermolysis bullosa. In one embodiment, the method comprises delivering to a patient a nucleic acid encoding collagen type VII. In another embodiment, the method comprises delivering to a patient a nucleic acid encoding melanocortin 1 receptor. Still other embodiments are directed to a method for treating xerosis. In one embodiment, the method comprises delivering to a patient a nucleic acid encoding a hyaluronan synthase. In another embodiment, the patient is diagnosed with atopic dermatitis. In yet another embodiment, the patient is diagnosed with ichthyosis. Certain embodiments are directed to a method for treating a cosmetic condition. Other embodiments are directed to a method for inducing tissue healing. In one embodiment, the method comprises delivering to a patient a nucleic acid encoding a hyaluronan synthase. In another embodiment, the cosmetic condition is a member of the group: wrinkles, sagging skin, thin skin, discoloration, and dry skin. In yet another embodiment, the patient has had cataract surgery. In some embodiments, the nucleic acid is synthetic RNA. In other embodiments, the method results in the amelioration of one or more of the patient's symptoms. Other embodiments are directed to a method for treating an indication by delivering to a cell or a patient a nucleic acid encoding a protein or a peptide. Still other embodiments are directed to a composition comprising a nucleic acid encoding a protein or a peptide. Indications that can be treated using the methods and compositions of the present invention and proteins and

peptides that can be encoded by compositions of the present invention are set forth in Table 1, and are given by way of example, and not by way of limitation. In one embodiment, the indication is selected from Table 1. In another embodiment the protein or peptide is selected from Table 1. In yet another embodiment, the indication and the protein or peptide are selected from the same row of Table 1. In a further embodiment, the protein of interest is a member of the group: UCP1, UCP2, and UCP3. Other embodiments are directed to methods for inducing a cell to express a plurality of proteins of interest. In one embodiment, the proteins of interest include at least two members of the group: a lipase, UCP1, UCP2, and UCP3. In another embodiment, the proteins of interest include a lipase and a member of the group: UCP1, UCP2, and UCP3. In another embodiment, the protein is a gene-editing protein. In yet another embodiment, the gene-editing protein targets a gene that is at least partly responsible for a disease phenotype. In yet another embodiment, the gene-editing protein targets a gene that encodes a protein selected from Table 1. In still another embodiment, the gene-editing protein corrects or eliminates, either alone or in combination with one or more other molecules or gene-editing proteins, a mutation that is at least partly responsible for a disease phenotype.

Table 1. Illustrative Indications

Illustrative Indication	Illustrative Protein / Peptide
Acne	Retinol Dehydrogenase 10
Aging	Elastin
Aging	Collagen Type I
Aging	Collagen Type III
Aging	Collagen Type VII
Aging	Hyaluronan Synthase
Aging	Telomerase Reverse Transcriptase
Albinism	Tyrosinase
Alport Syndrome	Collagen Type IV
Anemia	Erythropoietin
Atopic Dermatitis	Filaggrin
Cutis Laxa	Elastin
Dystrophic Epidermolysis Bullosa	Collagen Type VII
Ehlers-Danlos Syndrome	Collagen Type V
Ehlers-Danlos Syndrome	Collagen Type I
Epidermolysis bullosa, lethal acantholytic	ADAM17
Epidermolysis bullosa, type IV	Collagen Type III
Erythropoietic Protoporphyrria	Ferrochelatase
Excess Fat	Thermogenin
Excess Fat	Lipase
Hypotrichosis	ADAM17

Ichthyosis Vulgaris	Filaggrin
Infections	Genetic Antibiotics (e.g. Anti-Sigma Factors)
Inflammatory and Bullous Skin Bowel Syndrome	Desmoglein 2
Keratosis Pilaris	Retinol Dehydrogenase 10
Oily Skin	Retinol Dehydrogenase 10
Osteoarthritis	Hyaluronan Synthase
Pemphigus Vulgaris	Plakophilin-1
Pseudoxanthoma elasticum	Elastin
Psoriasis	Retinol Dehydrogenase 10
Scar Treatment	Tyrosinase
Scarring	Elastin
Scarring	Collagen Type I
Scarring	Collagen Type III
Skin Cancer	Interferon
Striate Palmoplantar Keratoderma	ADAM17
Tanning	Tyrosinase
Vitiligo	Melanocyte-Stimulating Hormone
Vitiligo	Tyrosinase
Warts	Interferon
Wound Healing	Elastin
Wound Healing	Collagen Type I
Wound Healing	Collagen Type III
Xeroderma Pigmentosum	DNA Polymerase Eta

Additional illustrative targets of the present invention include the cosmetic targets listed in Table 6 of International Patent Publication No. WO 2013/151671, the contents of which are hereby incorporated by reference in their entirety.

- 5 Further, the present compositions and methods may be used to alter a biological and/or physiological process to, for example, reduce skin sagging, increase skin thickness, increase skin volume, reduce the number of wrinkles, the length of wrinkles and/or the depth of wrinkles, increase skin tightness, firmness, tone and/or elasticity, increase skin hydration and ability to retain moisture, water flow and osmotic balance, increase the levels of skin lipids; increase the extracellular matrix and/or adhesion and communication
- 10 polypeptides; increase skin energy production; utilization and conservation; improve oxygen utilization; improve skin cell life; improve skin cell immunity defense, heat shock stress response, antioxidant defense capacity to neutralize free radicals, and/or toxic defense; improve the protection and recovery from ultraviolet rays; improve skin cell communication and skin cell innervations; improve cell cohesion/adhesion; improve calcium mineral and other mineral metabolism; improve cell turnover; and improve cell circadian rhythms.

- Further still, in some embodiments, the present compositions may be used to treat a disease, disorder and/or condition and/or may alter, modify or change the appearance of a member of the integumentary system of a subject suffering from a disease, disorder and/or condition such as, but not limited to, acne vulgaris, acne aestivalis, acne conglobata, acne cosmetic, acne fulminans, acne keloidalis nuchae, acne mechanica, acne medicamentosa, acne miliaris necrotica, acne necrotica, acne rosacea, actinic keratosis, acne vulgaris, acne aestivalis, acne conglobata, acne cosmetic, acne fulminans, acne keloidalis nuchae, acne mechanica, acne medicamentosa, acne miliaris necrotica, acne necrotica, acne rosacea, acute urticaria, allergic contact dermatitis, alopecia areata, angioedema, athlete's foot, atopic dermatitis, autoeczematization, baby acne, balding, blastomycosis, blackheads, birthmarks and other skin pigmentation problems, boils, bruises, bug bites and stings, burns, cellulitis, chiggers, chloracne, cholinergic or stress urticaria, chronic urticaria, cold type urticaria, confluent and reticulated papillomatosis, corns, cysts, dandruff, dermatitis herpetiformis, dermatographism, dyshidrotic eczema, diaper rash, dry skin, dyshidrosis, ectodermal dysplasia such as, hypohidrotic ectodermal dysplasia and X-linked hypohidrotic ectodermal dysplasia, eczema, epidermodysplasia verruciformis, erythema nodosum, excoriated acne, exercise-induced anaphylaxis, folliculitis, excess skin oil, folliculitis, freckles, frostbite, fungal nails, hair density, hair growth rate, halogen acne, hair loss, heat rash, hematoma, herpes simplex infections (e.g. non-genital), hidradenitis suppurativa, hives, hyperhidrosis, hyperpigmentation, hypohidrotic ectodermal dysplasia, hypopigmentation, impetigo, ingrown hair, heat type urticaria, ingrown toenail, infantile acne or neonatal acne, itch, irritant contact dermatitis, jock itch, keloid, keratosis pilaris, lichen planus, lichen sclerosus, lupus miliaris disseminatus faciei, melasma, moles, molluscum contagiosum, nail growth rate, nail health, neurodermatitis, nummular eczema, occupational acne, oil acne, onychomycosis, physical urticaria, pilonidal cyst, pityriasis rosea, pityriasis versicolor, poison ivy, pomade acne, pseudofolliculitis barbae or acne keloidalis nuchae, psoriasis, psoriatic arthritis, pressure or delayed pressure urticaria, puncture wounds such as cuts and scrapes, rash, rare or water type urticaria, rhinoplasty, ringworm, rosacea, Rothmund-Thomson syndrome, sagging of the skin, scabies, scars, seborrhea, seborrheic dermatitis, shingles, skin cancer, skin tag, solar type urticaria, spider bite, stretch marks, sunburn, tar acne, tropical acne, thinning of skin, thrush, tinea versicolor, transient acantholytic dermatosis, tycoon's cap or acne necrotica miliaris, uneven skin tone, varicose veins, venous eczema, vibratory angioedema, vitiligo, warts, Weber-Christian disease, wrinkles, x-linked hypohidrotic ectodermal dysplasia, xerotic eczema, yeast infection and general signs of aging.
- In some embodiments, there is provided methods of treating dry skin with the present compositions. In some embodiments profilaggrin (a protein which is converted to filaggrin) is a protein of interest (e.g. when treating ichthyosis vulgaris).

In some embodiments, there is provided methods of treating any one of the various types of psoriasis (e.g. plaque psoriasis, guttate psoriasis, pustular psoriasis, inverse psoriasis, and erythrodermic psoriasis). In



various embodiments, the protein of interest is any of the products of the genes psoriasis susceptibility 1 through 9 (PSORS1 - PSORS9).

Various embodiments relate to the treatment of eczema (e.g. atopic dermatitis, nummular eczema, dyshidrotic eczema, seborrheic dermatitis, irritant contact dermatitis, allergic contact dermatitis, dyshidrosis, 5 venous eczema, dermatitis herpetiformis, neurodermatitis, autoeczematization and xerotic eczema) and, optionally, one or more of the following may be targeted: filaggrin; three genetic variants, ovo-like 1 (OVOL1), actin-like 9 (ACTL9) and kinesin family member 3 A (KIF3A) have been associated with eczema; and the genes brain-derived neurotrophic factor (BDNF) and tachykinin, precursor 1 (TAC1).

Hives, or urticaria, including, but not limited to, acute urticaria, chronic urticaria and angioedema, physical 10 urticaria, pressure or delayed pressure urticaria, cholinergic or stress urticaria, cold type urticaria, heat type urticaria, solar type urticaria, rare or water type urticaria, vibratory angioedema, exercise-induced anaphylaxis and dermatographism may be treated with the present compositions by, for example, targeting PLCG-2.

Various embodiments relate to the treatment of rosacea, which includes, but is not limited to, erythematotelangiectatic rosacea, papulopustular rosacea, phymatous rosacea, and ocular rosacea. 15 Optionally, cathelicidin antimicrobial peptide (CAMP) and/or kallikrein-related peptidase 5 (also known as stratum corneum tryptic enzyme (SCTE)) are proteins of interest.

In some embodiments, there is provided methods of treating acne with the present compositions. For example, acne may include, but is not limited to, acneiform eruptions, acne aestivalis, acne conglobata, acne cosmetic, acne fulminans, acne keloidalis nuchae, acne mechanica, acne medicamentosa, acne miliaris 20 necrotica, acne necrotica, acne rosacea, baby acne, blackheads, chloracne, excoriated acne, halogen acne, infantile acne or neonatal acne, lupus miliaris disseminatus faciei, occupational acne, oil acne, pomade acne, tar acne, tropical acne, tycoon's cap or acne necrotica miliaris, pseudofolliculitis barbae or acne keloidalis nuchae, and hidradenitis suppurativa. In these embodiments, the protein of interest may be one or more matrix metalloproteinases (MMP), e.g., matrix metalloproteinase-1 (MMP-1 or interstitial collagenase), matrix metalloproteinase-9 (MMP-9), and matrix metalloproteinase-13 (MMP-13). 25

In further embodiments, vitiligo is treated with the present compositions, e.g. wherein the NLR family, pyrin domain containing 1 gene (NALP1) gene is targeted.

In some embodiments, the present compositions find use in the treatment of hypohidrotic ectodermal dysplasia (HED), e.g. via the ectodysplasin A gene (EDA), receptor (EDAR), and receptor associated death 30 domain (EDARADD).

In some embodiments, the present compositions find use in the treatment of balding, or hair thinning (e.g. male pattern baldness, or androgenetic alopecia (AGA)) and, optionally, one or more of the following may be

the protein of interest: androgen receptor (AR), ectodysplasin A2 receptor (EDA2R) and lysophosphatidic acid receptor 6 (P2RY5).

The present compositions also find use in methods of treating scars and stretch marks (striae), e.g. via collagen, ribosomal s6 kinase, secreted phosphoprotein 1 (also known as osteopontin), or transforming growth factor beta 3.

Epidermodysplasia verruciformis (also known as Lutz-Lewandowsky epidermodysplasia), a rare autosomal recessive genetic hereditary skin disorder, may also be treated with compositions of the present invention, e.g. by targeted transmembrane channel-like 6 (EVER1) or transmembrane channel-like 8 (EVER2) genes.

In some embodiments, skin sagging, thinning or wrinkling may be treated with present composition, e.g. by targeting one or more of the proteins of interest such as collagen, elastin, fibroblast growth factor 7, TIMP metalloproteinase inhibitors, matrix metalloproteinases, superoxide dismutase and other extracellular matrix proteins and proteoglycans.

Further embodiments are used in tanning of the skin, such as via melanocyte-stimulating hormone and/or pro-opiomelanocortin.

In some embodiments, the present compositions may be used for wound treatment. In some embodiments, methods of treating wounds with the present compositions comprises additional steps of, for example, cleaning the wound bed to facilitate wound healing and closure, including, but not limited to: debridement, sharp debridement (surgical removal of dead or infected tissue from a wound), optionally including chemical debriding agents, such as enzymes, to remove necrotic tissue; wound dressings to provide the wound with a moist, warm environment and to promote tissue repair and healing (e.g., wound dressings comprising hydrogels (e.g., AQUASORB®; DUODERM®), hydrocolloids (e.g., AQUACEL®; COMFEEL®), foams (e.g., LYOFAM®; SPYROSORB®), and alginates (e.g., ALGISITE®; CURASORB®); administration of growth factors to stimulate cell division and proliferation and to promote wound healing e.g. becaplermin; and (iv) soft-tissue wound coverage, a skin graft may be necessary to obtain coverage of clean, non-healing wounds (e.g., autologous skin grafts, cadaveric skin graft, bioengineered skin substitutes (e.g., APLIGRAF®; DERMAGRAFT®)).

In various embodiments, a variety of cancers are treated with the present compositions (e.g., colorectal cancer, gallbladder cancer, lung cancer, pancreatic cancer, and stomach cancer). In some embodiments, skin cancer is treated with the present compositions. For instance, basal cell cancer (BCC), squamous cell cancer (SCC), and melanoma. In some embodiments, the present compositions are used adjuvant to complete circumferential peripheral and deep margin assessment, Mohs surgery, radiation (e.g. external beam radiotherapy or brachytherapy), chemotherapy (including but not limited to topical chemotherapy, e.g. with imiquimod or 5-fluorouracil), and cryotherapy. The present compositions also find use in the treatment of

various stages of cancers, including skin cancers (e.g. basal cell cancer (BCC), squamous cell cancer (SCC), and melanoma), such as a stage of the American Joint Committee on Cancer (AJCC) TNM system (e.g. one or more of TX, T0, Tis, T1, T1a, T1b, T2, T2A, T2B, T3, T3a, T3b, T4, T4a, T4b, NX, N0, N1, N2, N3, M0, M1a, M1b, M1c) and/or a staging system (e.g. Stage 0, Stage IA, Stage IB, Stage IIA, Stage IIB, Stage IIC, Stage IIIA, Stage IIIB, Stage IIIC, Stage IV).

In various embodiments, one or more rare diseases are treated with the present compositions, including, by way of illustration, Erythropoietic Protoporphyrria, Hailey-Hailey Disease, Epidermolysis Bullosa (EB), Xeroderma Pigmentosum, Ehlers-Danlos Syndrome, Cutis Laxa, Protein C & Protein S Deficiency, Alport Syndrome, Striate Palmoplantar Keratoderma, Lethal Acantholytic EB, Pseudoxanthoma Elasticum (PXE), Ichthyosis Vulgaris, Pemphigus Vulgaris, and Basal Cell Nevus Syndrome.

In certain situations, it may be desirable to replace animal-derived components with non-animal-derived and/or recombinant components, in part because non-animal-derived and/or recombinant components can be produced with a higher degree of consistency than animal-derived components, and in part because non-animal-derived and/or recombinant components carry less risk of contamination with toxic and/or pathogenic substances than do animal-derived components. Certain embodiments are therefore directed to a protein that is non-animal-derived and/or recombinant. Other embodiments are directed to a medium, wherein some or all of the components of the medium are non-animal-derived and/or recombinant.

Other embodiments are directed to a method for transfecting a cell *in vivo*. In one embodiment, a cell *in vivo* is transfected with one or more nucleic acids, and the transfection is performed using a transfection reagent, such as a lipid-based transfection reagent. In one embodiment, the one or more nucleic acids includes at least one RNA molecule. In another embodiment, the cell is transfected with one or more nucleic acids, and the one or more nucleic acids encodes at least one of: p53, TERT, a cytokine, a secreted protein, a membrane-bound protein, an enzyme, a gene-editing protein, a chromatin-modifying protein, a DNA-binding protein, a transcription factor, a histone deacetylase, a pathogen-associated molecular pattern, and a tumor-associated antigen or a biologically active fragment, analogue, variant or family-member thereof. In another embodiment, the cell is transfected repeatedly, such as at least about 2 times during about 10 consecutive days, or at least about 3 times during about 7 consecutive days, or at least about 4 times during about 6 consecutive days.

Reprogramming can be performed by transfecting cells with one or more nucleic acids encoding one or more reprogramming factors. Examples of reprogramming factors include, but are not limited to: Oct4 protein, Sox2 protein, Klf4 protein, c-Myc protein, l-Myc protein, TERT protein, Nanog protein, Lin28 protein, Ulf1 protein, Aicda protein, miR200 micro-RNA, miR302 micro-RNA, miR367 micro-RNA, miR369 micro-RNA and biologically active fragments, analogues, variants and family-members thereof. Certain embodiments are therefore directed to a method for reprogramming a cell *in vivo*. In one embodiment, the cell *in vivo* is

reprogrammed by transfecting the cell with one or more nucleic acids encoding one or more reprogramming factors. In one embodiment, the one or more nucleic acids includes an RNA molecule that encodes Oct4 protein. In another embodiment, the one or more nucleic acids also includes one or more RNA molecules that encodes Sox2 protein, Klf4 protein, and c-Myc protein. In yet another embodiment, the one or more nucleic acids also includes an RNA molecule that encodes Lin28 protein. In one embodiment, the cell is a human skin cell, and the human skin cell is reprogrammed to a pluripotent stem cell. In another embodiment, the cell is a human skin cell, and the human skin cell is reprogrammed to a glucose-responsive insulin-producing cell. Examples of other cells that can be reprogrammed and other cells to which a cell can be reprogrammed include, but are not limited to: skin cells, pluripotent stem cells, mesenchymal stem cells,  $\beta$ -cells, retinal pigmented epithelial cells, hematopoietic cells, cardiac cells, airway epithelial cells, neural stem cells, neurons, glial cells, bone cells, blood cells, and dental pulp stem cells. In one embodiment, the cell is contacted with a medium that supports the reprogrammed cell. In one embodiment, the medium also supports the cell.

Importantly, infecting skin cells with viruses encoding Oct4, Sox2, Klf4, and c-Myc, combined with culturing the cells in a medium that supports the growth of cardiomyocytes, has been reported to cause reprogramming of the skin cells to cardiomyocytes, without first reprogramming the skin cells to pluripotent stem cells (See Efs *et al* Nat Cell Biol. 2011;13:215-22, the contents of which are hereby incorporated by reference). In certain situations, direct reprogramming (reprogramming one somatic cell to another somatic cell without first reprogramming the somatic cell to a pluripotent stem cell, also known as "transdifferentiation") may be desirable, in part because culturing pluripotent stem cells can be time-consuming and expensive, the additional handling involved in establishing and characterizing a stable pluripotent stem cell line can carry an increased risk of contamination, and the additional time in culture associated with first producing pluripotent stem cells can carry an increased risk of genomic instability and the acquisition of mutations, including point mutations, copy-number variations, and karyotypic abnormalities. Certain embodiments are therefore directed to a method for reprogramming a somatic cell *in vivo*, wherein the cell is reprogrammed to a somatic cell, and wherein a characterized pluripotent stem-cell line is not produced.

It has been further discovered that, in certain situations, fewer total transfections may be required to reprogram a cell according to the methods of the present invention than according to other methods. Certain embodiments are therefore directed to a method for reprogramming a cell *in vivo*, wherein between about 1 and about 12 transfections are performed during about 20 consecutive days, or between about 4 and about 10 transfections are performed during about 15 consecutive days, or between about 4 and about 8 transfections are performed during about 10 consecutive days. It is recognized that when a cell is contacted with a medium containing nucleic acid molecules, the cell may likely come into contact with and/or internalize more than one nucleic acid molecule either simultaneously or at different times. A cell can therefore be

contacted with a nucleic acid more than once, e.g. repeatedly, even when a cell is contacted only once with a medium containing nucleic acids.

Of note, nucleic acids can contain one or more non-canonical, or "modified", residues (e.g. a residue other than adenine, guanine, thymine, uracil, and cytosine or the standard nucleoside, nucleotide, deoxynucleoside or deoxynucleotide derivatives thereof). Of particular note, pseudouridine-5'-triphosphate can be substituted for uridine-5'-triphosphate in an *in vitro*-transcription reaction to yield synthetic RNA, wherein up to 100% of the uridine residues of the synthetic RNA may be replaced with pseudouridine residues. *In vitro*-transcription can yield RNA with residual immunogenicity, even when pseudouridine and 5-methylcytidine are completely substituted for uridine and cytidine, respectively (See, e.g., Angel. Reprogramming Human Somatic Cells to Pluripotency Using RNA [Doctoral Thesis]. Cambridge, MA: MIT; 2011, the contents of which are hereby incorporated by reference). For this reason, it is common to add an immunosuppressant to the transfection medium when transfecting cells with RNA. In certain situations, adding an immunosuppressant to the transfection medium may not be desirable, in part because the recombinant immunosuppressant most commonly used for this purpose, B18R, can be expensive and difficult to manufacture. It has now been discovered that cells *in vivo* can be transfected and/or reprogrammed according to the methods of the present invention, without using B18R or any other immunosuppressant. It has been further discovered that reprogramming cells *in vivo* according to the methods of the present invention without using immunosuppressants can be rapid, efficient, and reliable. Certain embodiments are therefore directed to a method for transfecting a cell *in vivo*, wherein the transfection medium does not contain an immunosuppressant. Other embodiments are directed to a method for reprogramming a cell *in vivo*, wherein the transfection medium does not contain an immunosuppressant. In certain situations, for example when using a high cell density, it may be beneficial to add an immunosuppressant to the transfection medium. Certain embodiments are therefore directed to a method for transfecting a cell *in vivo*, wherein the transfection medium contains an immunosuppressant. Other embodiments are directed to a method for reprogramming a cell *in vivo*, wherein the transfection medium contains an immunosuppressant. In one embodiment, the immunosuppressant is B18R or a biologically active fragment, analogue, variant or family-member thereof or dexamethasone or a derivative thereof. In one embodiment, the transfection medium does not contain an immunosuppressant, and the nucleic-acid dose is chosen to prevent excessive toxicity. In another embodiment, the nucleic-acid dose is less than about 1mg/cm<sup>2</sup> of tissue or less than about 1mg/100,000 cells or less than about 10mg/kg.

Reprogrammed cells produced according to certain embodiments of the present invention are suitable for therapeutic and/or cosmetic applications as they do not contain exogenous DNA sequences, and they are not exposed to animal-derived or human-derived products, which may be undefined, and which may contain toxic and/or pathogenic contaminants. Furthermore, the high speed, efficiency, and reliability of certain embodiments of the present invention may reduce the risk of acquisition and accumulation of mutations and

other chromosomal abnormalities. Certain embodiments of the present invention can thus be used to generate cells that have a safety profile adequate for use in therapeutic and/or cosmetic applications. For example, reprogramming cells using RNA and the medium of the present invention, wherein the medium does not contain animal or human-derived components, can yield cells that have not been exposed to allogeneic material. Certain embodiments are therefore directed to a reprogrammed cell that has a desirable safety profile. In one embodiment, the reprogrammed cell has a normal karyotype. In another embodiment, the reprogrammed cell has fewer than about 5 copy-number variations (CNVs) relative to the patient genome, such as fewer than about 3 copy-number variations relative to the patient genome, or no copy-number variations relative to the patient genome. In yet another embodiment, the reprogrammed cell has a normal karyotype and fewer than about 100 single nucleotide variants in coding regions relative to the patient genome, or fewer than about 50 single nucleotide variants in coding regions relative to the patient genome, or fewer than about 10 single nucleotide variants in coding regions relative to the patient genome.

Endotoxins and nucleases can co-purify and/or become associated with other proteins, such as serum albumin. Recombinant proteins, in particular, can often have high levels of associated endotoxins and nucleases, due in part to the lysis of cells that can take place during their production. Endotoxins and nucleases can be reduced, removed, replaced or otherwise inactivated by many of the methods of the present invention, including, for example, by acetylation, by addition of a stabilizer such as sodium octanoate, followed by heat treatment, by the addition of nuclease inhibitors to the albumin solution and/or medium, by crystallization, by contacting with one or more ion-exchange resins, by contacting with charcoal, by preparative electrophoresis or by affinity chromatography. It has now been discovered that partially or completely reducing, removing, replacing or otherwise inactivating endotoxins and/or nucleases from a medium and/or from one or more components of a medium can increase the efficiency with which cells can be transfected and reprogrammed. Certain embodiments are therefore directed to a method for transfecting a cell *in vivo* with one or more nucleic acids, wherein the transfection medium is treated to partially or completely reduce, remove, replace or otherwise inactivate one or more endotoxins and/or nucleases. Other embodiments are directed to a medium that causes minimal degradation of nucleic acids. In one embodiment, the medium contains less than about 1EU/mL, or less than about 0.1EU/mL, or less than about 0.01EU/mL.

In certain situations, protein-based lipid carriers such as serum albumin can be replaced with non-protein-based lipid carriers such as methyl-beta-cyclodextrin. The medium of the present invention can also be used without a lipid carrier, for example, when transfection is performed using a method that may not require or may not benefit from the presence of a lipid carrier, for example, using one or more lipid-based transfection reagents, polymer-based transfection reagents or peptide-based transfection reagents or using electroporation. Many protein-associated molecules, such as metals, can be highly toxic to cells *in vivo*. This toxicity can cause decreased viability, as well as the acquisition of mutations. Certain embodiments thus have the additional benefit of producing cells that are free from toxic molecules.

The associated-molecule component of a protein can be measured by suspending the protein in solution and measuring the conductivity of the solution. Certain embodiments are therefore directed to a medium that contains a protein, wherein about a 10% solution of the protein in water has a conductivity of less than about 500  $\mu\text{mho/cm}$ . In one embodiment, the solution has a conductivity of less than about 50  $\mu\text{mho/cm}$ . In another  
5 embodiment, less than about 0.65% of the dry weight of the protein comprises lipids and/or less than about 0.35% of the dry weight of the protein comprises free fatty acids.

The amount of nucleic acid delivered to cells *in vivo* can be increased to increase the desired effect of the nucleic acid. However, increasing the amount of nucleic acid delivered to cells *in vivo* beyond a certain point can cause a decrease in the viability of the cells, due in part to toxicity of the transfection reagent. It has now  
10 been discovered that when a nucleic acid is delivered to a population of cells *in vivo* in a fixed volume (for example, cells in a region of tissue), the amount of nucleic acid delivered to each cell can depend on the total amount of nucleic acid delivered to the population of cells and to the density of the cells, with a higher cell density resulting in less nucleic acid being delivered to each cell. In certain embodiments, a cell *in vivo* is transfected with one or more nucleic acids more than once. Under certain conditions, for example when the  
15 cells are proliferating, the cell density may change from one transfection to the next. Certain embodiments are therefore directed to a method for transfecting a cell *in vivo* with a nucleic acid, wherein the cell is transfected more than once, and wherein the amount of nucleic acid delivered to the cell is different for two of the transfections. In one embodiment, the cell proliferates between two of the transfections, and the amount of nucleic acid delivered to the cell is greater for the second of the two transfections than for the first of the  
20 two transfections. In another embodiment, the cell is transfected more than twice, and the amount of nucleic acid delivered to the cell is greater for the second of three transfections than for the first of the same three transfections, and the amount of nucleic acid delivered to the cells is greater for the third of the same three transfections than for the second of the same three transfections. In yet another embodiment, the cell is transfected more than once, and the maximum amount of nucleic acid delivered to the cell during each  
25 transfection is sufficiently low to yield at least about 80% viability for at least two consecutive transfections.

It has now been discovered that modulating the amount of nucleic acid delivered to a population of proliferating cells *in vivo* in a series of transfections can result in both an increased effect of the nucleic acid and increased viability of the cells. It has been further discovered that, in certain situations, when cells *in vivo* are contacted with one or more nucleic acids encoding one or more reprogramming factors in a series of  
30 transfections, the efficiency of reprogramming can be increased when the amount of nucleic acid delivered in later transfections is greater than the amount of nucleic acid delivered in earlier transfections, for at least part of the series of transfections. Certain embodiments are therefore directed to a method for reprogramming a cell *in vivo*, wherein one or more nucleic acids is repeatedly delivered to the cell in a series of transfections, and the amount of the nucleic acid delivered to the cell is greater for at least one later transfection than for at  
35 least one earlier transfection. In one embodiment, the cell is transfected between about 2 and about 10 times,

or between about 3 and about 8 times, or between about 4 and about 6 times. In another embodiment, the one or more nucleic acids includes at least one RNA molecule, the cell is transfected between about 2 and about 10 times, and the amount of nucleic acid delivered to the cell in each transfection is the same as or greater than the amount of nucleic acid delivered to the cell in the most recent previous transfection. In yet another embodiment, the amount of nucleic acid delivered to the cell in the first transfection is between about 20ng/cm<sup>2</sup> and about 250ng/cm<sup>2</sup>, or between 100ng/cm<sup>2</sup> and 600ng/cm<sup>2</sup>. In yet another embodiment, the cell is transfected about 5 times at intervals of between about 12 and about 48 hours, and the amount of nucleic acid delivered to the cell is about 25ng/cm<sup>2</sup> for the first transfection, about 50ng/cm<sup>2</sup> for the second transfection, about 100ng/cm<sup>2</sup> for the third transfection, about 200ng/cm<sup>2</sup> for the fourth transfection, and about 400ng/cm<sup>2</sup> for the fifth transfection. In yet another embodiment, the cell is further transfected at least once after the fifth transfection, and the amount of nucleic acid delivered to the cell is about 400ng/cm<sup>2</sup>.

Certain embodiments are directed to a method for transfecting a cell *in vivo* with a nucleic acid, wherein the amount of nucleic acid is determined by measuring the cell density, and choosing the amount of nucleic acid to transfect based on the measurement of cell density. In one embodiment, the cell density is measured by optical means. In another embodiment, the cell is transfected repeatedly, the cell density increases between two transfections, and the amount of nucleic acid transfected is greater for the second of the two transfections than for the first of the two transfections.

It has now been discovered that, in certain situations, the *in vivo* transfection efficiency and viability of cells contacted with the medium of the present invention can be improved by conditioning the medium. Certain embodiments are therefore directed to a method for conditioning a medium. Other embodiments are directed to a medium that is conditioned. In one embodiment, the feeders are fibroblasts, and the medium is conditioned for approximately 24 hours. Other embodiments are directed to a method for transfecting a cell *in vivo*, wherein the transfection medium is conditioned. Other embodiments are directed to a method for reprogramming and/or gene-editing a cell *in vivo*, wherein the medium is conditioned. In one embodiment, the feeders are mitotically inactivated, for example, by exposure to a chemical such as mitomycin-C or by exposure to gamma radiation. In certain embodiments, it may be beneficial to use only autologous materials, in part to, for example and not wishing to be bound by theory, avoid the risk of disease transmission from the feeders to the cell or the patient. Certain embodiments are therefore directed to a method for transfecting a cell *in vivo*, wherein the transfection medium is conditioned, and wherein the feeders are derived from the same individual as the cell being transfected. Other embodiments are directed to a method for reprogramming and/or gene-editing a cell *in vivo*, wherein the medium is conditioned, and wherein the feeders are derived from the same individual as the cell being reprogrammed and/or gene-edited.

Several molecules can be added to media by conditioning. Certain embodiments are therefore directed to a medium that is supplemented with one or more molecules that are present in a conditioned medium. In one



embodiment, the medium is supplemented with Wnt1, Wnt2, Wnt3, Wnt3a or a biologically active fragment, analogue, variant, agonist, or family-member thereof. In another embodiment, the medium is supplemented with TGF- $\beta$  or a biologically active fragment, analogue, variant, agonist, or family-member thereof. In yet another embodiment, a cell *in vivo* is reprogrammed according to the method of the present invention, wherein the medium is not supplemented with TGF- $\beta$  for between about 1 and about 5 days, and is then supplemented with TGF- $\beta$  for at least about 2 days. In yet another embodiment, the medium is supplemented with IL-6, IL-6R or a biologically active fragment, analogue, variant, agonist, or family-member thereof. In yet another embodiment, the medium is supplemented with a sphingolipid or a fatty acid. In still another embodiment, the sphingolipid is lysophosphatidic acid, lysosphingomyelin, sphingosine-1-phosphate or a biologically active analogue, variant or derivative thereof.

In addition to mitotically inactivating cells, under certain conditions, irradiation can change the gene expression of cells, causing cells to produce less of certain proteins and more of certain other proteins than non-irradiated cells, for example, members of the Wnt family of proteins. In addition, certain members of the Wnt family of proteins can promote the growth and transformation of cells. It has now been discovered that, in certain situations, the efficiency of reprogramming can be greatly increased by contacting a cell *in vivo* with a medium that is conditioned using irradiated feeders instead of mitomycin-c-treated feeders. It has been further discovered that the increase in reprogramming efficiency observed when using irradiated feeders is caused in part by Wnt proteins that are secreted by the feeders. Certain embodiments are therefore directed to a method for reprogramming a cell *in vivo*, wherein the cell is contacted with Wnt1, Wnt2, Wnt3, Wnt3a or a biologically active fragment, analogue, variant, family-member or agonist thereof, including agonists of downstream targets of Wnt proteins, and/or agents that mimic one or more of the biological effects of Wnt proteins, for example, 2-amino-4-[3,4-(methylenedioxy)benzylamino]-6-(3-methoxyphenyl)pyrimidine.

Because of the low efficiency of many DNA-based reprogramming methods, these methods may be difficult or impossible to use with cells derived from patient samples, which may contain only a small number of cells. In contrast, the high efficiency of certain embodiments of the present invention can allow reliable reprogramming of a small number of cells, including single cells. Certain embodiments are directed to a method for reprogramming a small number of cells. Other embodiments are directed to a method for reprogramming a single cell. In one embodiment, the cell is contacted with one or more enzymes. In another embodiment, the enzyme is collagenase. In yet another embodiment, the collagenase is animal-component free. In one embodiment, the collagenase is present at a concentration of between about 0.1mg/mL and about 10mg/mL, or between about 0.5mg/mL and about 5mg/mL. In another embodiment, the cell is a blood cell. In yet another embodiment, the cell is contacted with a medium containing one or more proteins that is derived from the patient's blood. In still another embodiment, the cell is contacted with a medium comprising: DMEM/F12 + 2mM L-alanyl-L-glutamine + between about 5% and about 25% patient-derived serum, or between about 10% and about 20% patient-derived serum, or about 20% patient-derived serum.

It has now been discovered that, in certain situations, transfecting cells *in vivo* with a mixture of RNA encoding Oct4, Sox2, Klf4, and c-Myc using the medium of the present invention can cause the rate of proliferation of the cells to increase. When the amount of RNA delivered to the cells is too low to ensure that all of the cells are transfected, only a fraction of the cells may show an increased proliferation rate. In certain situations, such as when generating a personalized therapeutic, increasing the proliferation rate of cells may be desirable, in part because doing so can reduce the time necessary to generate the therapeutic, and therefore can reduce the cost of the therapeutic. Certain embodiments are therefore directed to a method for transfecting a cell *in vivo* with a mixture of RNA encoding Oct4, Sox2, Klf4, and c-Myc. In one embodiment, the cell exhibits an increased proliferation rate. In another embodiment, the cell is reprogrammed.

- Many diseases are associated with one or more mutations. Mutations can be corrected by contacting a cell with a nucleic acid that encodes a protein that, either alone or in combination with other molecules, corrects the mutation (an example of gene-editing). Examples of such proteins include: zinc finger nucleases and TALENs. Certain embodiments are therefore directed to a method for transfecting a cell *in vivo* with a nucleic acid, wherein the nucleic acid encodes a protein that, either alone or in combination with other molecules, creates a single-strand or double-strand break in a DNA molecule. In a one embodiment, the protein is a zinc finger nuclease or a TALEN. In another embodiment, the nucleic acid is an RNA molecule. In yet another embodiment, the single-strand or double-strand break is within about 5,000,000 bases of the transcription start site of a gene selected from the group: CCR5, CXCR4, GAD1, GAD2, CFTR, HBA1, HBA2, HBB, HBD, FANCA, XPA, XPB, XPC, ERCC2, POLH, HTT, DMD, SOD1, APOE, PRNP, BRCA1, and BRCA2 or an analogue, variant or family-member thereof. In yet another embodiment, the cell is transfected with a nucleic acid that acts as a repair template by either causing the insertion of a DNA sequence in the region of the single-strand or double-strand break or by causing the DNA sequence in the region of the single-strand or double-strand break to otherwise change. In yet another embodiment, the cell is reprogrammed, and subsequently, the cell is gene-edited. In yet another embodiment, the cell is gene-edited, and subsequently, the cell is reprogrammed. In yet another embodiment, the gene-editing and reprogramming are performed within about 7 days of each other. In yet another embodiment, the gene-editing and reprogramming occur simultaneously or on the same day. In yet another embodiment, the cell is a skin cell, the skin cell is gene-edited to disrupt the CCR5 gene, the skin cell is reprogrammed to a hematopoietic stem cell, thus producing a therapeutic for HIV/AIDS, and the therapeutic is used to treat a patient with HIV/AIDS. In yet another embodiment, the skin cell is derived from the same patient whom the therapeutic is used to treat.

Genes that can be edited according to the methods of the present invention to produce therapeutics of the present invention include genes that can be edited to restore normal function, as well as genes that can be edited to reduce or eliminate function. Such genes include, but are not limited to beta globin (HBB), mutations in which can cause sickle cell disease (SCD) and  $\beta$ -thalassemia, breast cancer 1, early onset (BRCA1) and breast cancer 2, early onset (BRCA2), mutations in which can increase susceptibility to breast cancer, C-C

chemokine receptor type 5 (CCR5) and C-X-C chemokine receptor type 4 (CXCR4), mutations in which can confer resistance to HIV infection, cystic fibrosis transmembrane conductance regulator (CFTR), mutations in which can cause cystic fibrosis, dystrophin (DMD), mutations in which can cause muscular dystrophy, including Duchenne muscular dystrophy and Becker's muscular dystrophy, glutamate decarboxylase 1 and glutamate decarboxylase 2 (GAD1, GAD2), mutations in which can prevent autoimmune destruction of  $\beta$ -cells, hemoglobin alpha 1, hemoglobin alpha 2, and hemoglobin delta (HBA1, HBA2, and HBD), mutations in which can cause thalassemia, Huntington (HTT), mutations in which can cause Huntington's disease, superoxide dismutase 1 (SOD1), mutations in which can cause amyotrophic lateral sclerosis (ALS), XPA, XPB, XPC, XPD (ERCC6) and polymerase (DNA directed), eta (POLH), mutations in which can cause xeroderma pigmentosum, leucine-rich repeat kinase 2 (LRRK2), mutations in which can cause Parkinson's disease, and Fanconi anemia, complementation groups A, B, C, D1, D2, E, F, G, I, J, L, M, N, P (FANCA, FANCB, FANCC, FANCD1, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCJ, FANCL, FANCM, FANCN, FANCP), and RAD51 homolog C (*S. cerevisiae*) (RAD51C), mutations in which can cause Fanconi anemia.

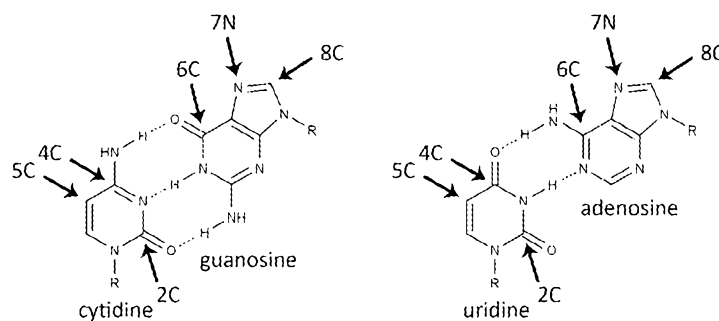
Certain embodiments are directed to a therapeutic comprising a nucleic acid. In one embodiment, the nucleic acid encodes one or more gene-editing proteins. Other embodiments are directed to a therapeutic comprising one or more cells that are transfected, reprogrammed, and/or gene-edited *in vivo* according to the methods of the present invention. In one embodiment, a cell is transfected, reprogrammed, and/or gene-edited, and the transfected, reprogrammed, and/or gene-edited cell is introduced into a patient. In another embodiment, the cell is harvested from the same patient into whom the transfected, reprogrammed and/or gene-edited cell is introduced. Examples of diseases that can be treated with therapeutics of the present invention include, but are not limited to Alzheimer's disease, spinal cord injury, amyotrophic lateral sclerosis, cystic fibrosis, heart disease, including ischemic and dilated cardiomyopathy, macular degeneration, Parkinson's disease, Huntington's disease, diabetes, sickle-cell anemia, thalassemia, Fanconi anemia, xeroderma pigmentosum, muscular dystrophy, severe combined immunodeficiency, hereditary sensory neuropathy, cancer, and HIV/AIDS. In certain embodiments, the therapeutic comprises a cosmetic. In one embodiment, a cell is harvested from a patient, the cell is reprogrammed and expanded to a large number of adipose cells to produce a cosmetic, and the cosmetic is introduced into the patient. In still another embodiment, the cosmetic is used for tissue reconstruction.

While detailed examples are provided herein for the production of specific types of cells and for the production of therapeutics comprising specific types of cells, it is recognized that the methods of the present invention can be used to produce many other types of cells, and to produce therapeutics comprising one or more of many other types of cells, for example, by reprogramming a cell according to the methods of the present invention, and culturing the cell under conditions that mimic one or more aspects of development by providing conditions that resemble the conditions present in the cellular microenvironment during development.

Certain embodiments are directed to a library of cells with a variety of human leukocyte antigen (HLA) types ("HLA-matched libraries"). An HLA-matched library may be beneficial in part because it can provide for the rapid production and/or distribution of therapeutics without the patient having to wait for a therapeutic to be produced from the patient's cells. Such a library may be particularly beneficial for the production of cosmetics and for the treatment of heart disease and diseases of the blood and/or immune system for which patients may benefit from the immediate availability of a therapeutic or cosmetic.

Certain non-canonical nucleotides, when incorporated into synthetic RNA molecules, can reduce the toxicity of the synthetic RNA molecules, in part by interfering with binding of proteins that detect exogenous nucleic acids, for example, protein kinase R, Rig-1 and the oligoadenylate synthetase family of proteins. Non-canonical nucleotides that have been reported to reduce the toxicity of synthetic RNA molecules when incorporated therein include: pseudouridine, 5-methyluridine, 2-thiouridine, 5-methylcytidine, N6-methyladenosine, and certain combinations thereof. However, the chemical characteristics of non-canonical nucleotides that can enable them to lower the *in vivo* toxicity of synthetic RNA molecules have, until this point, remained unknown. Furthermore, incorporation of large amounts of most non-canonical nucleotides, for example, 5-methyluridine, 2-thiouridine, 5-methylcytidine, and N6-methyladenosine, can reduce the efficiency with which synthetic RNA molecules can be translated into protein, limiting the utility of synthetic RNA molecules containing these nucleotides in applications that require protein expression. In addition, while pseudouridine can be completely substituted for uridine in synthetic RNA molecules without reducing the efficiency with which the synthetic RNA molecules can be translated into protein, in certain situations, for example, when performing frequent, repeated transfections, synthetic RNA molecules containing only adenosine, guanosine, cytidine, and pseudouridine can exhibit excessive toxicity.

It has now been discovered that synthetic RNA molecules containing one or more non-canonical nucleotides that include one or more substitutions at the 2C and/or 4C and/or 5C positions in the case of a pyrimidine or the 6C and/or 7N and/or 8C positions in the case of a purine can be less toxic than synthetic RNA molecules containing only canonical nucleotides, due in part to the ability of substitutions at these positions to interfere with recognition of synthetic RNA molecules by proteins that detect exogenous nucleic acids, and furthermore, that substitutions at these positions can have minimal impact on the efficiency with which the synthetic RNA molecules can be translated into protein, due in part to the lack of interference of substitutions at these positions with base-pairing and base-stacking interactions.



Examples of non-canonical nucleotides that include one or more substitutions at the 2C and/or 4C and/or 5C positions in the case of a pyrimidine or the 6C and/or 7N and/or 8C positions in the case of a purine include, but are not limited to: 2-thiouridine, 5-azauridine, pseudouridine, 4-thiouridine, 5-methyluridine, 5-aminouridine, 5-hydroxyuridine, 5-methyl-5-azauridine, 5-amino-5-azauridine, 5-hydroxy-5-azauridine, 5-methylpseudouridine, 5-aminopseudouridine, 5-hydroxypseudouridine, 4-thio-5-azauridine, 4-thiopseudouridine, 4-thio-5-methyluridine, 4-thio-5-aminouridine, 4-thio-5-hydroxyuridine, 4-thio-5-methyl-5-azauridine, 4-thio-5-amino-5-azauridine, 4-thio-5-hydroxy-5-azauridine, 4-thio-5-methylpseudouridine, 4-thio-5-aminopseudouridine, 4-thio-5-hydroxypseudouridine, 2-thiocytidine, 5-azacytidine, pseudoisocytidine, N4-methylcytidine, N4-aminocytidine, N4-hydroxycytidine, 5-methylcytidine, 5-aminocytidine, 5-hydroxycytidine, 5-methyl-5-azacytidine, 5-amino-5-azacytidine, 5-hydroxy-5-azacytidine, 5-methylpseudoisocytidine, 5-aminopseudoisocytidine, 5-hydroxypseudoisocytidine, N4-methyl-5-azacytidine, N4-methylpseudoisocytidine, 2-thio-5-azacytidine, 2-thiopseudoisocytidine, 2-thio-N4-methylcytidine, 2-thio-N4-aminocytidine, 2-thio-N4-hydroxycytidine, 2-thio-5-methylcytidine, 2-thio-5-aminocytidine, 2-thio-5-hydroxycytidine, 2-thio-5-methyl-5-azacytidine, 2-thio-5-amino-5-azacytidine, 2-thio-5-hydroxy-5-azacytidine, 2-thio-5-methylpseudoisocytidine, 2-thio-5-aminopseudoisocytidine, 2-thio-5-hydroxypseudoisocytidine, 2-thio-N4-methyl-5-azacytidine, 2-thio-N4-methylpseudoisocytidine, N4-methyl-5-methylcytidine, N4-methyl-5-aminocytidine, N4-methyl-5-hydroxycytidine, N4-methyl-5-methyl-5-azacytidine, N4-methyl-5-amino-5-azacytidine, N4-methyl-5-hydroxy-5-azacytidine, N4-methyl-5-methylpseudoisocytidine, N4-methyl-5-aminopseudoisocytidine, N4-methyl-5-hydroxypseudoisocytidine, N4-amino-5-azacytidine, N4-aminopseudoisocytidine, N4-amino-5-methylcytidine, N4-amino-5-aminocytidine, N4-amino-5-hydroxycytidine, N4-amino-5-methyl-5-azacytidine, N4-amino-5-amino-5-azacytidine, N4-amino-5-hydroxy-5-azacytidine, N4-amino-5-methylpseudoisocytidine, N4-amino-5-aminopseudoisocytidine, N4-amino-5-hydroxypseudoisocytidine, N4-hydroxy-5-azacytidine, N4-hydroxypseudoisocytidine, N4-hydroxy-5-methylcytidine, N4-hydroxy-5-aminocytidine, N4-hydroxy-5-hydroxycytidine, N4-hydroxy-5-methyl-5-azacytidine, N4-hydroxy-5-amino-5-azacytidine, N4-hydroxy-5-hydroxy-5-azacytidine, N4-hydroxy-5-methylpseudoisocytidine, N4-hydroxy-5-aminopseudoisocytidine, N4-hydroxy-5-hydroxypseudoisocytidine, 2-thio-N4-methyl-5-methylcytidine, 2-thio-N4-methyl-5-aminocytidine, 2-thio-N4-methyl-5-hydroxycytidine, 2-thio-N4-methyl-5-methyl-5-azacytidine, 2-thio-N4-methyl-5-amino-5-azacytidine, 2-thio-N4-methyl-5-hydroxy-5-azacytidine, 2-thio-N4-methyl-5-methylpseudoisocytidine, 2-thio-

N4-methyl-5-aminopseudoisocytidine, 2-thio-N4-methyl-5-hydroxypseudoisocytidine, 2-thio-N4-amino-5-azacytidine, 2-thio-N4-aminopseudoisocytidine, 2-thio-N4-amino-5-methylcytidine, 2-thio-N4-amino-5-aminocytidine, 2-thio-N4-amino-5-hydroxycytidine, 2-thio-N4-amino-5-methyl-5-azacytidine, 2-thio-N4-amino-5-amino-5-azacytidine, 2-thio-N4-amino-5-hydroxy-5-azacytidine, 2-thio-N4-amino-5-methylpseudoisocytidine, 2-thio-N4-amino-5-aminopseudoisocytidine, 2-thio-N4-amino-5-hydroxypseudoisocytidine, 2-thio-N4-hydroxy-5-azacytidine, 2-thio-N4-hydroxypseudoisocytidine, 2-thio-N4-hydroxy-5-methylcytidine, N4-hydroxy-5-aminocytidine, 2-thio-N4-hydroxy-5-hydroxycytidine, 2-thio-N4-hydroxy-5-methyl-5-azacytidine, 2-thio-N4-hydroxy-5-amino-5-azacytidine, 2-thio-N4-hydroxy-5-hydroxy-5-azacytidine, 2-thio-N4-hydroxy-5-methylpseudoisocytidine, 2-thio-N4-hydroxy-5-aminopseudoisocytidine, 2-thio-N4-hydroxy-5-hydroxypseudoisocytidine, N6-methyladenosine, N6-aminoadenosine, N6-hydroxyadenosine, 7-deazaadenosine, 8-azaadenosine, N6-methyl-7-deazaadenosine, N6-methyl-8-azaadenosine, 7-deaza-8-azaadenosine, N6-methyl-7-deaza-8-azaadenosine, N6-amino-7-deazaadenosine, N6-amino-8-azaadenosine, N6-amino-7-deaza-8-azaadenosine, N6-hydroxyadenosine, N6-hydroxy-7-deazaadenosine, N6-hydroxy-8-azaadenosine, N6-hydroxy-7-deaza-8-azaadenosine, 6-thioguanosine, 7-deazaguanosine, 8-azaguanosine, 6-thio-7-deazaguanosine, 6-thio-8-azaguanosine, 7-deaza-8-azaguanosine, and 6-thio-7-deaza-8-azaguanosine. Note that alternative naming schemes exist for certain non-canonical nucleotides. For example, in certain situations, 5-methylpseudouridine can be referred to as "3-methylpseudouridine" or "N3-methylpseudouridine" or "1-methylpseudouridine" or "N1-methylpseudouridine".

Nucleotides that contain the prefix "amino" can refer to any nucleotide that contains a nitrogen atom bound to the atom at the stated position of the nucleotide, for example, 5-aminocytidine can refer to 5-aminocytidine, 5-methylaminocytidine, and 5-nitrocytidine. Similarly, nucleotides that contain the prefix "methyl" can refer to any nucleotide that contains a carbon atom bound to the atom at the stated position of the nucleotide, for example, 5-methylcytidine can refer to 5-methylcytidine, 5-ethylcytidine, and 5-hydroxymethylcytidine, nucleotides that contain the prefix "thio" can refer to any nucleotide that contains a sulfur atom bound to the atom at the given position of the nucleotide, and nucleotides that contain the prefix "hydroxy" can refer to any nucleotide that contains an oxygen atom bound to the atom at the given position of the nucleotide, for example, 5-hydroxyuridine can refer to 5-hydroxyuridine and uridine with a methyl group bound to an oxygen atom, wherein the oxygen atom is bound to the atom at the 5C position of the uridine.

Certain embodiments are therefore directed to a synthetic RNA molecule, wherein the synthetic RNA molecule contains one or more nucleotides that includes one or more substitutions at the 2C and/or 4C and/or 5C positions in the case of a pyrimidine or the 6C and/or 7N and/or 8C positions in the case of a purine. Other embodiments are directed to a therapeutic, wherein the therapeutic contains one or more synthetic RNA molecules, and wherein the one or more synthetic RNA molecules contains one or more nucleotides that includes one or more substitutions at the 2C and/or 4C and/or 5C positions in the case of a pyrimidine or the 6C and/or 7N and/or 8C positions in the case of a purine. In one embodiment, the

therapeutic comprises a transfection reagent. In another embodiment, the transfection reagent comprises a cationic lipid, liposome or micelle. In still another embodiment, the liposome or micelle comprises folate and the therapeutic composition has anti-cancer activity. In another embodiment, the one or more nucleotides includes at least one of pseudouridine, 2-thiouridine, 4-thiouridine, 5-azauridine, 5-hydroxyuridine, 5-methyluridine, 5-aminouridine, 2-thiopseudouridine, 4-thiopseudouridine, 5-hydroxypseudouridine, 5-methylpseudouridine, 5-aminopseudouridine, pseudoisocytidine, N4-methylcytidine, 2-thiocytidine, 5-azacytidine, 5-hydroxycytidine, 5-aminocytidine, 5-methylcytidine, N4-methylpseudoisocytidine, 2-thiopseudoisocytidine, 5-hydroxypseudoisocytidine, 5-aminopseudoisocytidine, 5-methylpseudoisocytidine, 7-deazaadenosine, 7-deazaguanosine, 6-thioguanosine, and 6-thio-7-deazaguanosine. In another embodiment, the one or more nucleotides includes at least one of pseudouridine, 2-thiouridine, 4-thiouridine, 5-azauridine, 5-hydroxyuridine, 5-methyluridine, 5-aminouridine, 2-thiopseudouridine, 4-thiopseudouridine, 5-hydroxypseudouridine, 5-methylpseudouridine, and 5-aminopseudouridine and at least one of pseudoisocytidine, N4-methylcytidine, 2-thiocytidine, 5-azacytidine, 5-hydroxycytidine, 5-aminocytidine, 5-methylcytidine, N4-methylpseudoisocytidine, 2-thiopseudoisocytidine, 5-hydroxypseudoisocytidine, 5-aminopseudoisocytidine, and 5-methylpseudoisocytidine. In still another embodiment, the one or more nucleotides include at least one of pseudouridine, 2-thiouridine, 4-thiouridine, 5-azauridine, 5-hydroxyuridine, 5-methyluridine, 5-aminouridine, 2-thiopseudouridine, 4-thiopseudouridine, 5-hydroxypseudouridine, and 5-methylpseudouridine, 5-aminopseudouridine and at least one of pseudoisocytidine, N4-methylcytidine, 2-thiocytidine, 5-azacytidine, 5-hydroxycytidine, 5-aminocytidine, 5-methylcytidine, N4-methylpseudoisocytidine, 2-thiopseudoisocytidine, 5-hydroxypseudoisocytidine, 5-aminopseudoisocytidine, and 5-methylpseudoisocytidine. In yet another embodiment, the one or more nucleotides includes: 5-methylcytidine and 7-deazaguanosine. In another embodiment, the one or more nucleotides also includes pseudouridine or 4-thiouridine or 5-methyluridine or 5-aminouridine or 4-thiopseudouridine or 5-methylpseudouridine or 5-aminopseudouridine. In a still another embodiment, the one or more nucleotides also includes 7-deazaadenosine. In another embodiment, the one or more nucleotides includes: pseudoisocytidine and 7-deazaguanosine and 4-thiouridine. In yet another embodiment, the one or more nucleotides includes: pseudoisocytidine or 7-deazaguanosine and pseudouridine. In still another embodiment, the one or more nucleotides includes: 5-methyluridine and 5-methylcytidine and 7-deazaguanosine. In a further embodiment, the one or more nucleotides includes: pseudouridine or 5-methylpseudouridine and 5-methylcytidine and 7-deazaguanosine. In another embodiment, the one or more nucleotides includes: pseudoisocytidine and 7-deazaguanosine and pseudouridine. In one embodiment, the synthetic RNA molecule is present *in vivo*.

Certain non-canonical nucleotides can be incorporated more efficiently than other non-canonical nucleotides into synthetic RNA molecules by RNA polymerases that are commonly used for *in vitro* transcription, due in part to the tendency of these certain non-canonical nucleotides to participate in standard base-pairing

- interactions and base-stacking interactions, and to interact with the RNA polymerase in a manner similar to that in which the corresponding canonical nucleotide interacts with the RNA polymerase. As a result, certain nucleotide mixtures containing one or more non-canonical nucleotides can be beneficial in part because *in vitro*-transcription reactions containing these nucleotide mixtures can yield a large quantity of synthetic RNA.
- 5 Certain embodiments are therefore directed to a nucleotide mixture containing one or more nucleotides that includes one or more substitutions at the 2C and/or 4C and/or 5C positions in the case of a pyrimidine or the 6C and/or 7N and/or 8C positions in the case of a purine. Nucleotide mixtures include, but are not limited to (numbers preceding each nucleotide indicate an exemplary fraction of the non-canonical nucleotide triphosphate in an *in vitro*-transcription reaction, for example, 0.2 pseudoisocytidine refers to a reaction
- 10 containing adenosine-5'-triphosphate, guanosine-5'-triphosphate, uridine-5'-triphosphate, cytidine-5'-triphosphate, and pseudoisocytidine-5'-triphosphate, wherein pseudoisocytidine-5'-triphosphate is present in the reaction at an amount approximately equal to 0.2 times the total amount of pseudoisocytidine-5'-triphosphate + cytidine-5'-triphosphate that is present in the reaction, with amounts measured either on a molar or mass basis, and wherein more than one number preceding a nucleoside indicates a range of
- 15 exemplary fractions): 1.0 pseudouridine, 0.1 – 0.8 2-thiouridine, 0.1 – 0.8 5-methyluridine, 0.2 – 1.0 5-hydroxyuridine, 0.1 – 1.0 5-aminouridine, 0.1 – 1.0 4-thiouridine, 0.1 – 1.0 2-thiopseudouridine, 0.1 – 1.0 4-thiopseudouridine, 0.1 – 1.0 5-hydroxypseudouridine, 0.2 – 1 5-methylpseudouridine, 0.1 – 1.0 5-aminopseudouridine, 0.2 – 1.0 2-thiocytidine, 0.1 – 0.8 pseudoisocytidine, 0.2 – 1.0 5-methylcytidine, 0.2 – 1.0 5-hydroxycytidine, 0.1 – 1.0 5-aminocytidine, 0.2 – 1.0 N4-methylcytidine, 0.2 – 1.0 5-methylpseudoisocytidine, 0.2 – 1.0 5-hydroxypseudoisocytidine, 0.2 – 1.0 5-aminopseudoisocytidine, 0.2 – 1.0 N4-methylpseudoisocytidine, 0.2 – 1.0 2-thiopseudoisocytidine, 0.2 – 1.0 7-deazaguanosine, 0.2 – 1.0 6-thioguanosine, 0.2 – 1.0 6-thio-7-deazaguanosine, 0.2 – 1.0 8-azaguanosine, 0.2 – 1.0 7-deaza-8-azaguanosine, 0.2 – 1.0 6-thio-8-azaguanosine, 0.1 – 0.5 7-deazaadenosine, and 0.1 – 0.5 N6-methyladenosine.
- 25 In various embodiments, the synthetic RNA composition or synthetic polynucleotide composition (e.g., which may be prepared by *in vitro* transcription) contains substantially or entirely the canonical nucleotide at positions having adenine or "A" in the genetic code. The term "substantially" in this context refers to at least 90%. In these embodiments, the synthetic RNA composition or synthetic polynucleotide composition may further contain (e.g., consist of) 7-deazaguanosine at positions with "G" in the genetic code as well as the
- 30 corresponding canonical nucleotide "G", and the canonical and non-canonical nucleotide at positions with G may be in the range of 5:1 to 1:5, or in some embodiments in the range of 2:1 to 1:2. In these embodiments, the synthetic RNA composition or synthetic polynucleotide composition may further contain (e.g., consist of) one or more (e.g., two, three or four) of 5-hydroxymethylcytidine, 5-hydroxycytidine, 5-carboxycytidine, and 5-formylcytidine at positions with "C" in the genetic code as well as the canonical nucleotide "C", and the
- 35 canonical and non-canonical nucleotide at positions with C may be in the range of 5:1 to 1:5, or in some



embodiments in the range of 2:1 to 1:2. In some embodiments, the level of non-canonical nucleotide at positions of "C" are as described in the preceding paragraph. In these embodiments, the synthetic RNA composition or synthetic polynucleotide composition may further contain (e.g., consist of) one or more (e.g., two, three, or four) of 5-hydroxymethyluridine, 5-hydroxyuridine, 5-carboxyuridine, and 5-formyluridine at positions with "U" in the genetic code as well as the canonical nucleotide "U", and the canonical and non-canonical nucleotide at positions with "U" may be in the range of 5:1 to 1:5, or in some embodiments in the range of 2:1 to 1:2. In some embodiments, the level of non-canonical nucleotide at positions of "U" are as described in the preceding paragraph.

It has now been discovered that combining certain non-canonical nucleotides can be beneficial in part because the contribution of non-canonical nucleotides to lowering the toxicity of synthetic RNA molecules can be additive. Certain embodiments are therefore directed to a nucleotide mixture, wherein the nucleotide mixture contains more than one of the non-canonical nucleotides listed above, for example, the nucleotide mixture contains both pseudoisocytidine and 7-deazaguanosine or the nucleotide mixture contains both N4-methylcytidine and 7-deazaguanosine, etc. In one embodiment, the nucleotide mixture contains more than one of the non-canonical nucleotides listed above, and each of the non-canonical nucleotides is present in the mixture at the fraction listed above, for example, the nucleotide mixture contains 0.1 – 0.8 pseudoisocytidine and 0.2 – 1.0 7-deazaguanosine or the nucleotide mixture contains 0.2 – 1.0 N4-methylcytidine and 0.2 – 1.0 7-deazaguanosine, etc.

In certain situations, for example, when it may not be necessary or desirable to maximize the yield of an *in vitro*-transcription reaction, nucleotide fractions other than those given above may be used. The exemplary fractions and ranges of fractions listed above relate to nucleotide-triphosphate solutions of typical purity (greater than 90% purity). Larger fractions of these and other nucleotides can be used by using nucleotide-triphosphate solutions of greater purity, for example, greater than about 95% purity or greater than about 98% purity or greater than about 99% purity or greater than about 99.5% purity, which can be achieved, for example, by purifying the nucleotide triphosphate solution using existing chemical-purification technologies such as high-pressure liquid chromatography (HPLC) or by other means. In one embodiment, nucleotides with multiple isomers are purified to enrich the desired isomer.

Other embodiments are directed to a method for inducing a cell *in vivo* to express a protein of interest by contacting the cell with a synthetic RNA molecule that contains one or more non-canonical nucleotides that includes one or more substitutions at the 2C and/or 4C and/or 5C positions in the case of a pyrimidine or the 6C and/or 7N and/or 8C positions in the case of a purine. Still other embodiments are directed to a method for transfecting, reprogramming, and/or gene-editing a cell *in vivo* by contacting the cell with a synthetic RNA molecule that contains one or more non-canonical nucleotides that includes one or more substitutions at the 2C and/or 4C and/or 5C positions in the case of a pyrimidine or the 6C and/or 7N and/or 8C positions in the

case of a purine. In one embodiment, the synthetic RNA molecule is produced by *in vitro* transcription. In one embodiment, the synthetic RNA molecule encodes one or more reprogramming factors. In another embodiment, the one or more reprogramming factors includes Oct4 protein. In another embodiment, the cell is also contacted with a synthetic RNA molecule that encodes Sox2 protein. In yet another embodiment, the cell is also contacted with a synthetic RNA molecule that encodes Klf4 protein. In yet another embodiment, the cell is also contacted with a synthetic RNA molecule that encodes c-Myc protein. In yet another embodiment, the cell is also contacted with a synthetic RNA molecule that encodes Lin28 protein.

Enzymes such as T7 RNA polymerase may preferentially incorporate canonical nucleotides in an *in vitro*-transcription reaction containing both canonical and non-canonical nucleotides. As a result, an *in vitro*-transcription reaction containing a certain fraction of a non-canonical nucleotide may yield RNA containing a different, often lower, fraction of the non-canonical nucleotide than the fraction at which the non-canonical nucleotide was present in the reaction. In certain embodiments, references to nucleotide incorporation fractions (for example, "a synthetic RNA molecule containing 50% pseudoisocytidine" or "0.1 – 0.8 pseudoisocytidine") therefore can refer both to RNA molecules containing the stated fraction of the nucleotide, and to RNA molecules synthesized in a reaction containing the stated fraction of the nucleotide (or nucleotide derivative, for example, nucleotide-triphosphate), even though such a reaction may yield RNA containing a different fraction of the nucleotide than the fraction at which the non-canonical nucleotide was present in the reaction.

Different nucleotide sequences can encode the same protein by utilizing alternative codons. In certain embodiments, references to nucleotide incorporation fractions therefore can refer both to RNA molecules containing the stated fraction of the nucleotide, and to RNA molecules encoding the same protein as a different RNA molecule, wherein the different RNA molecule contains the stated fraction of the nucleotide.

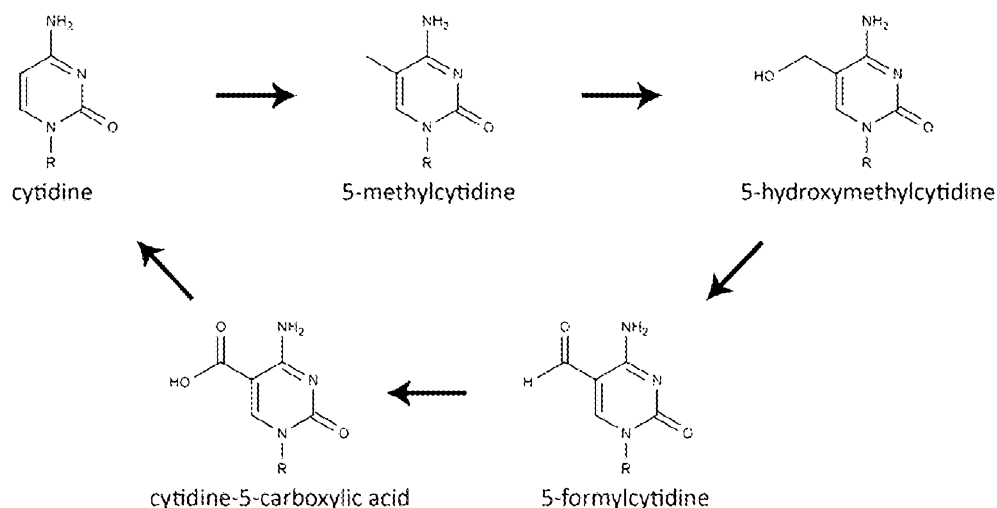
Certain embodiments are directed to a kit containing one or more materials needed to practice the present invention. In one embodiment, the kit contains one or more synthetic RNA molecules. In one embodiment, the kit contains one or more synthetic RNA molecules that encode one or more reprogramming factors and/or gene-editing proteins. In another embodiment, the one or more synthetic RNA molecules contain one or more non-canonical nucleotides that include one or more substitutions at the 2C and/or 4C and/or 5C positions in the case of a pyrimidine or the 6C and/or 7N and/or 8C positions in the case of a purine. In another embodiment, the kit contains one or more of: a transfection medium, a transfection reagent, a complexation medium, and a matrix solution. In one embodiment, the matrix solution contains fibronectin and/or vitronectin or recombinant fibronectin and/or recombinant vitronectin. In one embodiment, one or more of the components of the kit are present as a plurality of aliquots. In one embodiment, the kit contains aliquots of nucleic acid transfection-reagent complexes. In another embodiment, the kit contains aliquots of nucleic acid transfection-reagent complexes that are provided in a solid form, for example, as frozen or freeze-dried

pellets. In yet another embodiment, the kit contains aliquots of medium, wherein each aliquot contains transfection reagent-nucleic acid complexes that are stabilized either by chemical treatment or by freezing.

Transfection, in general, and reprogramming, in particular, can be difficult and time-consuming techniques that can be repetitive and prone to error. However, these techniques are often performed manually due to the lack of automated transfection equipment. Certain embodiments are therefore directed to a system that can transfect, reprogram, and/or gene-edit cells *in vivo* in an automated or semi-automated manner.

It has now been discovered that the non-canonical nucleotide members of the 5-methylcytidine de-methylation pathway, when incorporated into synthetic RNA, can increase the efficiency with which the synthetic RNA can be translated into protein *in vivo*, and can decrease the toxicity of the synthetic RNA *in vivo*. These non-canonical nucleotides include, for example: 5-methylcytidine, 5-hydroxymethylcytidine, 5-formylcytidine, and 5-carboxycytidine (a.k.a. "cytidine-5-carboxylic acid"). Certain embodiments are therefore directed to a nucleic acid. In some embodiments, the nucleic acid is present *in vivo*. In one embodiment, the nucleic acid is a synthetic RNA molecule. In another embodiment, the nucleic acid comprises one or more non-canonical nucleotides. In one embodiment, the nucleic acid comprises one or more non-canonical nucleotide members of the 5-methylcytidine de-methylation pathway. In another embodiment, the nucleic acid comprises at least one of: 5-methylcytidine, 5-hydroxymethylcytidine, 5-formylcytidine, and 5-carboxycytidine or a derivative thereof. In a further embodiment, the nucleic acid comprises at least one of: pseudouridine, 5-methylpseudouridine, 5-hydroxyuridine, 5-methyluridine, 5-methylcytidine, 5-hydroxymethylcytidine, N4-methylcytidine, N4-acetylcytidine, and 7-deazaguanosine or a derivative thereof.

#### 20 5-methylcytidine De-Methylation Pathway



Certain embodiments are directed to a protein. Other embodiments are directed to a nucleic acid that encodes a protein. In one embodiment, the protein is a protein of interest. In another embodiment, the protein is selected from: a reprogramming protein and a gene-editing protein. In one embodiment, the nucleic acid is

a plasmid. In another embodiment, the nucleic acid is present in a virus or viral vector. In a further embodiment, the virus or viral vector is replication incompetent. In a still further embodiment, the virus or viral vector is replication competent. In one embodiment, the virus or viral vector includes at least one of: an adenovirus, a retrovirus, a lentivirus, a herpes virus, an adeno-associated virus or a natural or engineered variant thereof, and an engineered virus.

It has also been discovered that certain combinations of non-canonical nucleotides can be particularly effective at increasing the efficiency with which synthetic RNA can be translated into protein *in vivo*, and decreasing the toxicity of synthetic RNA *in vivo*, for example, the combinations: 5-methyluridine and 5-methylcytidine, 5-hydroxyuridine and 5-methylcytidine, 5-hydroxyuridine and 5-hydroxymethylcytidine, 5-methyluridine and 7-deazaguanosine, 5-methylcytidine and 7-deazaguanosine, 5-methyluridine, 5-methylcytidine, and 7-deazaguanosine, and 5-methyluridine, 5-hydroxymethylcytidine, and 7-deazaguanosine. Certain embodiments are therefore directed to a nucleic acid comprising at least two of: 5-methyluridine, 5-methylcytidine, 5-hydroxymethylcytidine, and 7-deazaguanosine or one or more derivatives thereof. Other embodiments are directed to a nucleic acid comprising at least three of: 5-methyluridine, 5-methylcytidine, 5-hydroxymethylcytidine, and 7-deazaguanosine or one or more derivatives thereof. Other embodiments are directed to a nucleic acid comprising all of: 5-methyluridine, 5-methylcytidine, 5-hydroxymethylcytidine, and 7-deazaguanosine or one or more derivatives thereof. In one embodiment, the nucleic acid comprises one or more 5-methyluridine residues, one or more 5-methylcytidine residues, and one or more 7-deazaguanosine residues or one or more 5-methyluridine residues, one or more 5-hydroxymethylcytidine residues, and one or more 7-deazaguanosine residues.

It has been further discovered that synthetic RNA molecules containing certain fractions of certain non-canonical nucleotides and combinations thereof can exhibit particularly high translation efficiency and low toxicity *in vivo*. Certain embodiments are therefore directed to a nucleic acid comprising at least one of: one or more uridine residues, one or more cytidine residues, and one or more guanosine residues, and comprising one or more non-canonical nucleotides. In one embodiment, between about 20% and about 80% of the uridine residues are 5-methyluridine residues. In another embodiment, between about 30% and about 50% of the uridine residues are 5-methyluridine residues. In a further embodiment, about 40% of the uridine residues are 5-methyluridine residues. In one embodiment, between about 60% and about 80% of the cytidine residues are 5-methylcytidine residues. In another embodiment, between about 80% and about 100% of the cytidine residues are 5-methylcytidine residues. In a further embodiment, about 100% of the cytidine residues are 5-methylcytidine residues. In a still further embodiment, between about 20% and about 100% of the cytidine residues are 5-hydroxymethylcytidine residues. In one embodiment, between about 20% and about 80% of the guanosine residues are 7-deazaguanosine residues. In another embodiment, between about 40% and about 60% of the guanosine residues are 7-deazaguanosine residues. In a further embodiment, about 50% of the guanosine residues are 7-deazaguanosine residues. In one embodiment,

between about 20% and about 80% or between about 30% and about 60% or about 40% of the cytidine residues are N4-methylcytidine and/or N4-acetylcytidine residues. In another embodiment, each cytidine residue is a 5-methylcytidine residue. In a further embodiment, about 100% of the cytidine residues are 5-methylcytidine residues and/or 5-hydroxymethylcytidine residues and/or N4-methylcytidine residues and/or N4-acetylcytidine residues and/or one or more derivatives thereof. In a still further embodiment, about 40% of the uridine residues are 5-methyluridine residues, between about 20% and about 100% of the cytidine residues are N4-methylcytidine and/or N4-acetylcytidine residues, and about 50% of the guanosine residues are 7-deazaguanosine residues. In one embodiment, about 40% of the uridine residues are 5-methyluridine residues and about 100% of the cytidine residues are 5-methylcytidine residues. In another embodiment, about 40% of the uridine residues are 5-methyluridine residues and about 50% of the guanosine residues are 7-deazaguanosine residues. In a further embodiment, about 100% of the cytidine residues are 5-methylcytidine residues and about 50% of the guanosine residues are 7-deazaguanosine residues. In a further embodiment, about 100% of the uridine residues are 5-hydroxyuridine residues. In one embodiment, about 40% of the uridine residues are 5-methyluridine residues, about 100% of the cytidine residues are 5-methylcytidine residues, and about 50% of the guanosine residues are 7-deazaguanosine residues. In another embodiment, about 40% of the uridine residues are 5-methyluridine residues, between about 20% and about 100% of the cytidine residues are 5-hydroxymethylcytidine residues, and about 50% of the guanosine residues are 7-deazaguanosine residues. In some embodiments, less than 100% of the cytidine residues are 5-methylcytidine residues. In other embodiments, less than 100% of the cytidine residues are 5-hydroxymethylcytidine residues. In one embodiment, each uridine residue in the synthetic RNA molecule is a pseudouridine residue or a 5-methylpseudouridine residue. In another embodiment, about 100% of the uridine residues are pseudouridine residues and/or 5-methylpseudouridine residues. In a further embodiment, about 100% of the uridine residues are pseudouridine residues and/or 5-methylpseudouridine residues, about 100% of the cytidine residues are 5-methylcytidine residues, and about 50% of the guanosine residues are 7-deazaguanosine residues.

Other non-canonical nucleotides that can be used in place of or in combination with 5-methyluridine include, but are not limited to: pseudouridine, 5-hydroxyuridine, and 5-methylpseudouridine (a.k.a. "1-methylpseudouridine", a.k.a. "N1-methylpseudouridine") or one or more derivatives thereof. Other non-canonical nucleotides that can be used in place of or in combination with 5-methylcytidine and/or 5-hydroxymethylcytidine include, but are not limited to: pseudoisocytidine, 5-methylpseudoisocytidine, 5-hydroxymethylcytidine, 5-formylcytidine, 5-carboxycytidine, N4-methylcytidine, N4-acetylcytidine or one or more derivatives thereof. In certain embodiments, for example, when performing only a single transfection, injection or delivery or when the cells, tissue, organ or patient being transfected, injected or delivered to are not particularly sensitive to transfection-associated toxicity or innate-immune signaling, the fractions of non-canonical nucleotides can be reduced. Reducing the fraction of non-canonical nucleotides can be beneficial,

in part, because reducing the fraction of non-canonical nucleotides can reduce the cost of the nucleic acid. In certain situations, for example, when minimal immunogenicity of the nucleic acid is desired, the fractions of non-canonical nucleotides can be increased.

Enzymes such as T7 RNA polymerase may preferentially incorporate canonical nucleotides in an *in vitro*-transcription reaction containing both canonical and non-canonical nucleotides. As a result, an *in vitro*-transcription reaction containing a certain fraction of a non-canonical nucleotide may yield RNA containing a different, often lower, fraction of the non-canonical nucleotide than the fraction at which the non-canonical nucleotide was present in the reaction. In certain embodiments, references to nucleotide incorporation fractions (for example, "50% 5-methyluridine") therefore can refer both to nucleic acids containing the stated fraction of the nucleotide, and to nucleic acids synthesized in a reaction containing the stated fraction of the nucleotide (or nucleotide derivative, for example, nucleotide-triphosphate), even though such a reaction may yield a nucleic acid containing a different fraction of the nucleotide than the fraction at which the non-canonical nucleotide was present in the reaction. In addition, different nucleotide sequences can encode the same protein by utilizing alternative codons. In certain embodiments, references to nucleotide incorporation fractions therefore can refer both to nucleic acids containing the stated fraction of the nucleotide, and to nucleic acids encoding the same protein as a different nucleic acid, wherein the different nucleic acid contains the stated fraction of the nucleotide.

The DNA sequence of a cell can be altered by contacting the cell with a gene-editing protein or by inducing the cell to express a gene-editing protein. However, previously disclosed gene-editing proteins suffer from low binding efficiency and excessive off-target activity, which can introduce undesired mutations in the DNA of the cell, severely limiting their use *in vivo*, for example in therapeutic and cosmetic applications, in which the introduction of undesired mutations in a patient's cells could lead to the development of cancer. It has now been discovered that gene-editing proteins that comprise the StsI endonuclease cleavage domain (SEQ ID NO: 1) can exhibit substantially lower off-target activity *in vivo* than previously disclosed gene-editing proteins, while maintaining a high level of on-target activity *in vivo*. Other novel engineered proteins have also been discovered that can exhibit high on-target activity *in vivo*, low off-target activity *in vivo*, small size, solubility, and other desirable characteristics when they are used as the nuclease domain of a gene-editing protein: StsI-HA (SEQ ID NO: 2), StsI-HA2 (SEQ ID NO: 3), StsI-UHA (SEQ ID NO: 4), StsI-UHA2 (SEQ ID NO: 5), StsI-HF (SEQ ID NO: 6), and StsI-UHF (SEQ ID NO: 7). StsI-HA, StsI-HA2 (high activity), StsI-UHA, and StsI-UHA2 (ultra-high activity) can exhibit higher on-target activity *in vivo* than both wild-type StsI and wild-type FokI, due in part to specific amino-acid substitutions within the N-terminal region at the 34 and 61 positions, while StsI-HF (high fidelity) and StsI-UHF (ultra-high fidelity) can exhibit lower off-target activity *in vivo* than both wild-type StsI and wild-type FokI, due in part to specific amino-acid substitutions within the C-terminal region at the 141 and 152 positions.

Certain embodiments are therefore directed to a protein. In some embodiments, the protein is present *in vivo*. In other embodiments, the protein comprises a nuclease domain. In one embodiment, the nuclease domain comprises one or more of: the cleavage domain of FokI endonuclease (SEQ ID NO: 53), the cleavage domain of StsI endonuclease (SEQ ID NO: 1), StsI-HA (SEQ ID NO: 2), StsI-HA2 (SEQ ID NO: 3), StsI-UHA (SEQ ID NO: 4), StsI-UHA2 (SEQ ID NO: 5), StsI-HF (SEQ ID NO: 6), and StsI-UHF (SEQ ID NO: 7) or a biologically active fragment or variant thereof.

It has also been discovered that engineered gene-editing proteins that comprise DNA-binding domains comprising certain novel repeat sequences can exhibit lower off-target activity *in vivo* than previously disclosed gene-editing proteins, while maintaining a high level of on-target activity *in vivo*. Certain of these engineered gene-editing proteins can provide several advantages over previously disclosed gene-editing proteins, including, for example, increased flexibility of the linker region connecting repeat sequences, which can result in increased binding efficiency. Certain embodiments are therefore directed to a protein comprising a plurality of repeat sequences. In one embodiment, at least one of the repeat sequences contains the amino-acid sequence: GabG, where "a" and "b" each represent any amino acid. In one embodiment, the protein is a gene-editing protein. In another embodiment, one or more of the repeat sequences are present in a DNA-binding domain. In a further embodiment, "a" and "b" are each independently selected from the group: H and G. In a still further embodiment, "a" and "b" are H and G, respectively. In one embodiment, the amino-acid sequence is present within about 5 amino acids of the C-terminus of the repeat sequence. In another embodiment, the amino-acid sequence is present at the C-terminus of the repeat sequence. In some embodiments, one or more G in the amino-acid sequence GabG is replaced with one or more amino acids other than G, for example A, H or GG. In one embodiment, the repeat sequence has a length of between about 32 and about 40 amino acids or between about 33 and about 39 amino acids or between about 34 and 38 amino acids or between about 35 and about 37 amino acids or about 36 amino acids or greater than about 32 amino acids or greater than about 33 amino acids or greater than about 34 amino acids or greater than about 35 amino acids. Other embodiments are directed to a protein comprising one or more transcription activator-like effector domains. In one embodiment, at least one of the transcription activator-like effector domains comprises a repeat sequence. Other embodiments are directed to a protein comprising a plurality of repeat sequences generated by inserting one or more amino acids between at least two of the repeat sequences of a transcription activator-like effector domain. In one embodiment, one or more amino acids is inserted about 1 or about 2 or about 3 or about 4 or about 5 amino acids from the C-terminus of at least one repeat sequence. Still other embodiments are directed to a protein comprising a plurality of repeat sequences, wherein about every other repeat sequence has a different length than the repeat sequence immediately preceding or following the repeat sequence. In one embodiment, every other repeat sequence is about 36 amino acids long. In another embodiment, every other repeat sequence is 36 amino acids long. Still other embodiments are directed to a protein comprising a plurality of repeat sequences, wherein the plurality of

repeat sequences comprises at least two repeat sequences that are each at least 36 amino acids long, and wherein at least two of the repeat sequences that are at least 36 amino acids long are separated by at least one repeat sequence that is less than 36 amino acids long. Some embodiments are directed to a protein that comprises one or more sequences selected from, for example, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, and SEQ ID NO: 60.

Other embodiments are directed to a protein that comprises a DNA-binding domain. In some embodiments, the DNA-binding domain comprises a plurality of repeat sequences. In one embodiment, the plurality of repeat sequences enables high-specificity recognition of a binding site in a target DNA molecule. In another embodiment, at least two of the repeat sequences have at least about 50%, or about 60%, or about 70%, or about 80%, or about 90%, or about 95%, or about 98%, or about 99% homology to each other. In a further embodiment, at least one of the repeat sequences comprises one or more regions capable of binding to a binding site in a target DNA molecule. In a still further embodiment, the binding site comprises a defined sequence of between about 1 to about 5 bases in length. In one embodiment, the DNA-binding domain comprises a zinc finger. In another embodiment, the DNA-binding domain comprises a transcription activator-like effector (TALE). In a further embodiment, the plurality of repeat sequences includes at least one repeat sequence having at least about 50% or about 60% or about 70% or about 80% or about 90% or about 95% or about 98%, or about 99% homology to a TALE. In a still further embodiment, the gene-editing protein comprises a clustered regularly interspaced short palindromic repeat (CRISPR)-associated protein. In one embodiment, the gene-editing protein comprises a nuclear-localization sequence. In another embodiment, the nuclear-localization sequence comprises the amino-acid sequence: PKKKRKV. In one embodiment, the gene-editing protein comprises a mitochondrial-localization sequence. In another embodiment, the mitochondrial-localization sequence comprises the amino-acid sequence: LGRVIPRKIASRSLM. In one embodiment, the gene-editing protein comprises a linker. In another embodiment, the linker connects a DNA-binding domain to a nuclease domain. In a further embodiment, the linker is between about 1 and about 10 amino acids long. In some embodiments, the linker is about 1, about 2, or about 3, or about 4, or about 5, or about 6, or about 7, or about 8, or about 9, or about 10 amino acids long. In one embodiment, the gene-editing protein is capable of generating a nick or a double-strand break in a target DNA molecule.

Certain embodiments are directed to a method for modifying the genome of a cell *in vivo*, the method comprising introducing into a cell *in vivo* a nucleic acid molecule encoding a non-naturally occurring fusion protein comprising an artificial transcription activator-like (TAL) effector repeat domain comprising one or more repeat units 36 amino acids in length and an endonuclease domain, wherein the repeat domain is engineered for recognition of a predetermined nucleotide sequence, and wherein the fusion protein recognizes the predetermined nucleotide sequence. In one embodiment, the cell is a eukaryotic cell. In another embodiment, the cell is an animal cell. In a further embodiment, the cell is a mammalian cell. In a still further embodiment, the cell is a human cell. In one embodiment, the cell is a plant cell. In another



embodiment, the cell is a prokaryotic cell. In some embodiments, the fusion protein introduces an endonucleolytic cleavage in a nucleic acid of the cell, whereby the genome of the cell is modified.

Certain embodiments are directed to a composition for altering the DNA sequence of a cell *in vivo* comprising a nucleic acid, wherein the nucleic acid encodes a gene-editing protein. Other embodiments are directed to a composition for altering the DNA sequence of a cell *in vivo* comprising a nucleic-acid mixture, wherein the nucleic-acid mixture comprises: a first nucleic acid that encodes a first gene-editing protein, and a second nucleic acid that encodes a second gene-editing protein. In one embodiment, the binding site of the first gene-editing protein and the binding site of the second gene-editing protein are present in the same target DNA molecule. In another embodiment, the binding site of the first gene-editing protein and the binding site of the second gene-editing protein are separated by less than about 50 bases, or less than about 40 bases, or less than about 30 bases or less than about 20 bases, or less than about 10 bases, or between about 10 bases and about 25 bases or about 15 bases. In one embodiment, the nuclease domain of the first gene-editing protein and the nuclease domain of the second gene-editing protein are capable of forming a dimer. In another embodiment, the dimer is capable of generating a nick or double-strand break in a target DNA molecule.

Certain embodiments are directed to a therapeutic composition. Other embodiments are directed to a cosmetic composition. In some embodiments, the composition comprises a repair template. In a further embodiment, the repair template is a single-stranded DNA molecule or a double-stranded DNA molecule.

Other embodiments are directed to an article of manufacture for synthesizing a protein or a nucleic acid encoding a protein. In one embodiment, the article is a nucleic acid. In another embodiment, the protein comprises a DNA-binding domain. In a further embodiment, the nucleic acid comprises a nucleotide sequence encoding a DNA-binding domain. In one embodiment, the protein comprises a nuclease domain. In another embodiment, the nucleic acid comprises a nucleotide sequence encoding a nuclease domain. In one embodiment, the protein comprises a plurality of repeat sequences. In another embodiment, the nucleic acid encodes a plurality of repeat sequences. In a further embodiment, the nuclease domain is selected from: FokI, StsI, StsI-HA, StsI-HA2, StsI-UHA, StsI-UHA2, StsI-HF, and StsI-UHF or a natural or engineered variant or biologically active fragment thereof. In one embodiment, the nucleic acid comprises an RNA-polymerase promoter. In another embodiment, the RNA-polymerase promoter is a T7 promoter or a SP6 promoter. In a further embodiment, the nucleic acid comprises a viral promoter. In one embodiment, the nucleic acid comprises an untranslated region. In another embodiment, the nucleic acid is an *in vitro*-transcription template.

Certain embodiments are directed to a method for inducing a cell to express a protein *in vivo*. Other embodiments are directed to a method for altering the DNA sequence of a cell *in vivo* comprising transfecting the cell *in vivo* with a gene-editing protein or inducing the cell to express a gene-editing protein *in vivo*. Still

other embodiments are directed to a method for reducing the expression of a protein of interest in a cell *in vivo*. In one embodiment, the cell is induced to express a gene-editing protein, wherein the gene-editing protein is capable of creating a nick or a double-strand break in a target DNA molecule. In another embodiment, the nick or double-strand break results in inactivation of a gene. Still other embodiments are directed to a method for generating an inactive, reduced-activity or dominant-negative form of a protein *in vivo*. In one embodiment, the protein is survivin. Still other embodiments are directed to a method for repairing one or more mutations in a cell *in vivo*. In one embodiment, the cell is contacted with a repair template. In another embodiment, the repair template is a DNA molecule. In a further embodiment, the repair template does not contain a binding site of the gene-editing protein. In a still further embodiment, the repair template encodes an amino-acid sequence that is encoded by a DNA sequence that comprises a binding site of the gene-editing protein.

Other embodiments are directed to a method for treating a patient comprising administering to the patient a therapeutically or cosmetically effective amount of a protein or a nucleic acid encoding a protein. In one embodiment, the treatment results in one or more of the patient's symptoms being ameliorated. Certain embodiments are directed to a method for treating a patient comprising: a. inducing a cell to express a protein of interest by transfecting the cell *in vivo* with a nucleic acid encoding the protein of interest and/or b. reprogramming the cell *in vivo*. In one embodiment, the cell is reprogrammed to a less differentiated state. In another embodiment, the cell is reprogrammed by transfecting the cell with one or more synthetic RNA molecules encoding one or more reprogramming proteins. In a further embodiment, the cell is differentiated. In a still further embodiment, the cell is differentiated into one of: a skin cell, a glucose-responsive insulin-producing cell, a hematopoietic cell, a cardiac cell, a retinal cell, a renal cell, a neural cell, a stromal cell, a fat cell, a bone cell, a muscle cell, an oocyte, and a sperm cell. Other embodiments are directed to a method for treating a patient comprising: a. inducing a cell to express a gene-editing protein by transfecting the cell *in vivo* with a nucleic acid encoding a gene-editing protein and/or b. reprogramming the cell *in vivo*.

Other embodiments are directed to a complexation medium. In one embodiment, the complexation medium has a pH greater than about 7, or greater than about 7.2, or greater than about 7.4, or greater than about 7.6, or greater than about 7.8, or greater than about 8.0, or greater than about 8.2, or greater than about 8.4, or greater than about 8.6, or greater than about 8.8, or greater than about 9.0. In another embodiment, the complexation medium comprises transferrin. In a further embodiment, the complexation medium comprises DMEM. In a still further embodiment, the complexation medium comprises DMEM/F12. Still other embodiments are directed to a method for forming nucleic-acid-transfection-reagent complexes. In one embodiment, the transfection reagent is incubated with a complexation medium. In another embodiment, the incubation occurs before a mixing step. In a further embodiment, the incubation step is between about 5 seconds and about 5 minutes or between about 10 seconds and about 2 minutes or between about 15 seconds and about 1 minute or between about 30 seconds and about 45 seconds. In one embodiment, the

transfection reagent is selected from Table 2. In another embodiment, the transfection reagent is a lipid or lipidoid. In a further embodiment, the transfection reagent comprises a cation. In a still further embodiment, the cation is a multivalent cation. In a still further embodiment, the transfection reagent is N1-[2-((1S)-1-[(3-aminopropyl)amino]-4-[di(3-amino-propyl)amino]butylcarboxamido)ethyl]-3,4-di[oleyloxy]-benzamide (a.k.a. MVL5) or a derivative thereof.

Certain embodiments are directed to a method for inducing a cell to express a protein by contacting the cell with a nucleic acid *in vivo*. In one embodiment, the cell is a mammalian cell. In another embodiment, the cell is a human cell or a rodent cell. Other embodiments are directed to a cell produced using one or more of the methods of the present invention. In one embodiment, the cell is present in a patient. In another embodiment, the cell is isolated from a patient. Other embodiments are directed to a screening library comprising a cell produced using one or more of the methods of the present invention. In one embodiment, the screening library is used for at least one of: toxicity screening, including: cardiotoxicity screening, neurotoxicity screening, and hepatotoxicity screening, efficacy screening, high-throughput screening, high-content screening, and other screening.

Other embodiments are directed to a kit containing a nucleic acid. In one embodiment, the kit contains a delivery reagent (a.k.a. "transfection reagent"). In another embodiment, the kit is a reprogramming kit. In a further embodiment, the kit is a gene-editing kit. Other embodiments are directed to a kit for producing nucleic acids. In one embodiment, the kit contains at least two of: pseudouridine-triphosphate, 5-methyluridine triphosphate, 5-methylcytidine triphosphate, 5-hydroxymethylcytidine triphosphate, N4-methylcytidine triphosphate, N4-acetylcytidine triphosphate, and 7-deazaguanosine triphosphate or one or more derivatives thereof. Other embodiments are directed to a therapeutic or cosmetic comprising a nucleic acid. In one embodiment, the therapeutic or cosmetic is a pharmaceutical composition. In another embodiment, the pharmaceutical composition is formulated. In a further embodiment, the formulation comprises an aqueous suspension of liposomes. Example liposome components are set forth in Table 2, and are given by way of example, and not by way of limitation. In one embodiment, the liposomes include one or more polyethylene glycol (PEG) chains. In another embodiment, the PEG is PEG2000. In a further embodiment, the liposomes include 1,2-distearoyl-sn-glycero-3-phosphoethanolamine (DSPE) or a derivative thereof. In one embodiment, the therapeutic comprises one or more ligands. In another embodiment, the therapeutic comprises at least one of: androgen, CD30 (TNFRSF8), a cell-penetrating peptide, CXCR, estrogen, epidermal growth factor, EGFR, HER2, folate, insulin, insulin-like growth factor-I, interleukin-13, integrin, progesterone, stromal-derived-factor-1, thrombin, vitamin D, and transferrin or a biologically active fragment or variant thereof. Still other embodiments are directed to a therapeutic or cosmetic comprising a cell generated using one or more of the methods of the present invention. In one embodiment, the therapeutic is administered to a patient for the treatment of at least one of: type 1 diabetes, heart disease, including ischemic and dilated cardiomyopathy, macular degeneration, Parkinson's disease, cystic fibrosis, sickle-cell anemia, thalassemia,

Fanconi anemia, severe combined immunodeficiency, hereditary sensory neuropathy, xeroderma pigmentosum, Huntington's disease, muscular dystrophy, amyotrophic lateral sclerosis, Alzheimer's disease, cancer, and infectious diseases including: hepatitis and HIV/AIDS.

Table 2. Illustrative Biocompatible Lipids

1	3 $\beta$ -[N-(N',N'-dimethylaminoethane)-carbamoyl]cholesterol (DC-Cholesterol)
2	1,2-dioleoyl-3-trimethylammonium-propane (DOTAP / 18:1 TAP)
3	N-(4-carboxybenzyl)-N,N-dimethyl-2,3-bis(oleoyloxy)propan-1-aminium (DOBAQ)
4	1,2-dimyristoyl-3-trimethylammonium-propane (14:0 TAP)
5	1,2-dipalmitoyl-3-trimethylammonium-propane (16:0 TAP)
6	1,2-stearoyl-3-trimethylammonium-propane (18:0 TAP)
7	1,2-dioleoyl-3-dimethylammonium-propane (DODAP / 18:1 DAP)
8	1,2-dimyristoyl-3-dimethylammonium-propane (14:0 DAP)
9	1,2-dipalmitoyl-3-dimethylammonium-propane (16:0 DAP)
10	1,2-distearoyl-3-dimethylammonium-propane (18:0 DAP)
11	dimethyldioctadecylammonium (18:0 DDAB)
12	1,2-dilauroyl-sn-glycero-3-ethylphosphocholine (12:0 EthylPC)
13	1,2-dimyristoyl-sn-glycero-3-ethylphosphocholine (14:0 EthylPC)
14	1,2-dimyristoleoyl-sn-glycero-3-ethylphosphocholine (14:1 EthylPC)
15	1,2-dipalmitoyl-sn-glycero-3-ethylphosphocholine (16:0 EthylPC)
16	1,2-distearoyl-sn-glycero-3-ethylphosphocholine (18:0 EthylPC)
17	1,2-dioleoyl-sn-glycero-3-ethylphosphocholine (18:1 EthylPC)
18	1-palmitoyl-2-oleoyl-sn-glycero-3-ethylphosphocholine (16:1-18:1 EthylPC)
19	1,2-di-O-octadecenyl-3-trimethylammonium propane (DOTMA)
20	N1-[2-((1S)-1-[(3-aminopropyl)amino]-4-[di(3-amino-propyl)amino]butylcarboxamido)ethyl]-3,4-di[oleoyloxy]-benzamide (MVL5)
21	2,3-dioleyloxy-N-[2-spermine carboxamide]ethyl-N,N-dimethyl-1-propanammonium trifluoroacetate (DOSPA)
22	1,3-di-oleoyloxy-2-(6-carboxy-spermyl)-propylamid (DOSPER)
23	N-[1-(2,3-dimyristyloxy)propyl]-N,N-dimethyl-N-(2-hydroxyethyl)ammonium bromide (DMRIE)
24	dioctadecyl amidoglycerol spermine (DOGS)
25	dioleoyl phosphatidyl ethanolamine (DOPE)

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In some embodiments, the present invention relates to one or more administration techniques described in US Patent Nos. 5,711,964; 5,891,468; 6,316,260; 6,413,544; 6,770,291; and 7,390,780, the entire contents of which are hereby incorporated by reference in their entireties.

Certain embodiments are directed to a nucleic acid comprising a 5'-cap structure selected from Cap 0, Cap 1, Cap 2, and Cap 3 or a derivative thereof. In one embodiment, the nucleic acid comprises one or more UTRs. In another embodiment, the one or more UTRs increase the stability of the nucleic acid. In a further

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embodiment, the one or more UTRs comprise an alpha-globin or beta-globin 5'-UTR. In a still further embodiment, the one or more UTRs comprise an alpha-globin or beta-globin 3'-UTR. In a still further embodiment, the synthetic RNA molecule comprises an alpha-globin or beta-globin 5'-UTR and an alpha-globin or beta-globin 3'-UTR. In one embodiment, the 5'-UTR comprises a Kozak sequence that is substantially similar to the Kozak consensus sequence. In another embodiment, the nucleic acid comprises a 3'-poly(A) tail. In a further embodiment, the 3'-poly(A) tail is between about 20nt and about 250nt or between about 120nt and about 150nt long. In a further embodiment, the 3'-poly(A) tail is about 20nt, or about 30nt, or about 40nt, or about 50nt, or about 60nt, or about 70nt, or about 80nt, or about 90nt, or about 100nt, or about 110nt, or about 120nt, or about 130nt, or about 140nt, or about 150nt, or about 160nt, or about 170nt, or about 180nt, or about 190nt, or about 200nt, or about 210nt, or about 220nt, or about 230nt, or about 240nt, or about 250nt long.

Other embodiments are directed to a method for reprogramming a cell *in vivo*. In one embodiment, the cell is reprogrammed by contacting the cell with one or more nucleic acids. In one embodiment, the cell is contacted with a plurality of nucleic acids encoding at least one of: Oct4 protein, Sox2 protein, Klf4 protein, c-Myc protein, Lin28 protein or a biologically active fragment, variant or derivative thereof. In another embodiment, the cell is contacted with a plurality of nucleic acids encoding a plurality of proteins including: Oct4 protein, Sox2 protein, Klf4 protein, and c-Myc protein or one or more biologically active fragments, variants or derivatives thereof. Still other embodiments are directed to a method for gene editing a cell *in vivo*. In one embodiment, the cell is gene-edited by contacting the cell with one or more nucleic acids.

Nucleic acids, including liposomal formulations containing nucleic acids, when delivered *in vivo*, can accumulate in the liver and/or spleen. It has now been discovered that nucleic acids encoding proteins can modulate protein expression in the liver and spleen, and that nucleic acids used in this manner can constitute potent therapeutics for the treatment of liver and spleen diseases. Certain embodiments are therefore directed to a method for treating liver and/or spleen disease by delivering to a patient a nucleic acid encoding a protein of interest. Other embodiments are directed to a therapeutic composition comprising a nucleic acid encoding a protein of interest, for the treatment of liver and/or spleen disease. Diseases and conditions of the liver and/or spleen that can be treated include, but are not limited to: hepatitis, alcohol-induced liver disease, drug-induced liver disease, Epstein Barr virus infection, adenovirus infection, cytomegalovirus infection, toxoplasmosis, Rocky Mountain spotted fever, non-alcoholic fatty liver disease, hemochromatosis, Wilson's Disease, Gilbert's Disease, and cancer of the liver and/or spleen.

Certain embodiments are directed to a method for inducing a cell *in vivo* to express a protein of interest comprising contacting a cell *in vivo* with a solution comprising albumin that is treated with an ion-exchange resin or charcoal and one or more nucleic acid molecules, wherein at least one of the one or more nucleic acid molecules encodes a protein of interest. In one embodiment, the method results in the cell expressing

the protein of interest. In another embodiment, the one or more nucleic acid molecules comprise a synthetic RNA molecule. In one embodiment, the cell is a skin cell. In another embodiment, the cell is a muscle cell. In yet another embodiment, the cell is a dermal fibroblast. In yet another embodiment, the cell is a myoblast. In one embodiment, the protein of interest is an extracellular matrix protein. In another embodiment, the protein of interest is selected from: elastin, collagen, laminin, fibronectin, vitronectin, lysyl oxidase, elastin binding protein, a growth factor, fibroblast growth factor, transforming growth factor beta, granulocyte colony-stimulating factor, a matrix metalloproteinase, an actin, fibrillin, microfibril-associated glycoprotein, a lysyl-oxidase-like protein, and platelet-derived growth factor. In one embodiment, the solution is delivered to the dermis. In another embodiment, the delivering is by injection. In yet another embodiment, the delivering is by injection using a microneedle array. In one embodiment, the solution further comprises a growth factor. In another embodiment, the growth factor is selected from: fibroblast growth factor and transforming growth factor beta. In yet another embodiment, the solution further comprises cholesterol.

Other embodiments are directed a method for inducing a cell *in vivo* to express a protein of interest comprising contacting a cell *in vivo* with a solution comprising cholesterol and one or more nucleic acid molecules, wherein at least one of the one or more nucleic acid molecules encodes a protein of interest. In one embodiment, the method results in the cell expressing the protein of interest. Still other embodiments are directed to a method for transfecting a cell *in vivo* with a nucleic acid molecule comprising contacting a cell *in vivo* with a solution comprising albumin that is treated with an ion-exchange resin or charcoal and a nucleic acid molecule. In one embodiment, the method results in the cell being transfected with the nucleic acid molecule. In another embodiment, the nucleic acid molecule is one of: a dsDNA molecule, a ssDNA molecule, a dsRNA molecule, a ssRNA molecule, a plasmid, an oligonucleotide, a synthetic RNA molecule, a miRNA molecule, an mRNA molecule, an siRNA molecule. Still other embodiments are directed to a method for treating a patient comprising delivering to a patient a composition comprising albumin that is treated with an ion-exchange resin or charcoal and one or more nucleic acid molecules, wherein at least one of the one or more nucleic acid molecules encodes a protein of interest. In one embodiment, the method results in the expression of the protein of interest in the patient. In another embodiment, the method results in the expression of the protein of interest in the dermis of the patient.

Certain embodiments are directed to a cosmetic composition comprising albumin that is treated with an ion-exchange resin or charcoal and a nucleic acid molecule. Other embodiments are directed to a cosmetic treatment article. In one embodiment, the cosmetic treatment article comprises a device configured to deliver a composition to a patient. In another embodiment, the nucleic acid molecule encodes elastin protein or collagen protein. Still other embodiments are directed to a solution for transfecting a cell *in vivo* comprising cholesterol or a cholesterol analog and one or more nucleic acid molecules. In one embodiment, the cholesterol or cholesterol analog is covalently bound to at least one of the one or more nucleic acid molecules. In another embodiment, the cholesterol analog is an oxysterol. In yet another embodiment, the

cholesterol analog includes one or more of: an A-ring substitution, a B-ring substitution, a D-ring substitution, a side-chain substitution, a cholestanoic acid, a cholestenoic acid, a polyunsaturated moiety, a deuterated moiety, a fluorinated moiety, a sulfonated moiety, a phosphorylated moiety, and a fluorescent moiety. In yet another embodiment, the method comprises treating the patient with one or more of: a dermal filler, a neurotoxin (by way of illustration sodium channel inhibitors (e.g., tetrodotoxin), potassium channel inhibitors (e.g., tetraethylammonium), chloride channel inhibitors (e.g., chlorotoxin and curare), calcium channel inhibitors (e.g., conotoxin), synaptic vesicle release inhibitors (e.g., botulinum toxin and tetanus toxin) and blood brain barrier inhibitor (e.g., aluminum and mercury)) and a repair-inducing treatment.

For instance, botulinum toxin type A has been approved by the U.S. Food and Drug Administration (FDA) for the treatment of essential blepharospasm, strabismus and hemifacial spasm in patients over the age of twelve, cervical dystonia, glabellar line (facial) wrinkles and for treating hyperhidrosis and botulinum toxin type B has been approved for the treatment of cervical dystonia. The present compositions may be combined with these toxins in the treatment of these diseases.

Further the combination of any one of the aforementioned toxins may be used in combination with the present compositions for various cosmetic procedures, including, without limitation, facial wrinkles, hyperkinetic skin lines, glabellar lines, crow's feet, marionette lines, skin disorders, nasolabial folds, blepharospasm, strabismus, hemifacial spasms and sweating disorders. Alternatively, the present compositions may be used to in these cosmetic procedures as a monotherapy.

Certain embodiments are directed to a combination therapy comprising one or more of the therapeutic or cosmetic compositions of the present invention and one or more adjuvant therapies or cosmetic treatments. In certain embodiments, one or more of the therapeutic or cosmetic compositions of the present invention are administered to a subject which is undergoing treatment with one or more adjuvant therapies or cosmetic treatments. Example adjuvant therapies and cosmetic treatments are set forth in Table 3 and Table 5 of U.S. Provisional Application No. 61/721,302, the contents of which are hereby incorporated by reference, and are given by way of example, and not by way of limitation.

*Table 3. Illustrative Adjuvant Therapies*

Therapy/Treatment Class	Disease/Condition	Example Therapy/Treatment
Acetylcholinesterase inhibitors	Myasthenia gravis, Glaucoma, Alzheimer's disease, Lewy body dementia, Postural tachycardia syndrome	Edrophonium
Angiotensin-converting-enzyme inhibitor	Hypertension, Congestive heart failure	Perindopril
Alkylating agents	Cancer	Cisplatin
Angiogenesis inhibitors	Cancer, Macular degeneration	Bevacizumab

Angiotensin II receptor antagonists	Hypertension, Diabetic nephropathy, Congestive heart failure	Valsartan
Antibiotics	Bacterial infection	Amoxicillin
Antidiabetic drugs	Diabetes	Metformin
Antimetabolites	Cancer, Infection	5-fluorouracil (5FU)
Antisense oligonucleotides	Cancer, Diabetes, Amyotrophic lateral sclerosis (ALS), Hypercholesterolemia	Mipomersen
Cytotoxic antibiotics	Cancer	Doxorubicin
Deep-brain stimulation	Chronic pain, Parkinson's disease, Tremor, Dystonia	N/A
Dopamine agonists	Parkinson's disease, Type II diabetes, Pituitary tumors	Bromocriptine
Entry/Fusion inhibitors	HIV/AIDS	Maraviroc
Glucagon-like peptide-1 agonists	Diabetes	Exenatide
Glucocorticoids	Asthma, Adrenal insufficiency, Inflammatory diseases, Immune diseases, Bacterial meningitis	Dexamethasone
Immunosuppressive drugs	Organ transplantation, Inflammatory diseases, Immune diseases	Azathioprine
Insulin/Insulin analogs	Diabetes	NPH insulin
Integrase inhibitors	HIV/AIDS	Raltegravir
MAO-B inhibitors	Parkinson's disease, Depression, Dementia	Selegiline
Maturation inhibitors	HIV/AIDS	Bevirimat
Nucleoside analog reverse-transcriptase inhibitors	HIV/AIDS, Hepatitis B	Lamivudine
Nucleotide analog reverse-transcriptase inhibitors	HIV/AIDS, Hepatitis B	Tenofovir
Non-nucleoside reverse-transcriptase inhibitors	HIV/AIDS	Rilpivirine
Pegylated interferon	Hepatitis B/C, Multiple sclerosis	Interferon beta-1a
Plant alkaloids/terpenoids	Cancer	Paclitaxel
Protease inhibitors	HIV/AIDS, Hepatitis C, Other viral infections	Telaprevir
Radiotherapy	Cancer	Brachytherapy
Renin inhibitors	Hypertension	Aliskiren
Statins	Hypercholesterolemia	Atorvastatin
Topoisomerase inhibitors	Cancer	Topotecan
Vasopressin receptor antagonist	Hyponatremia, Kidney disease	Tolvaptan
Dermal filler	Wrinkles, aged skin	Hyaluronic Acid
Botulinum toxin	Wrinkles, aged skin	botulinum toxin type A
Induction of skin repair	Acne scars, aged skin	Laser treatment, dermabrasion



Pharmaceutical preparations may additionally comprise delivery reagents (a.k.a. "transfection reagents") and/or excipients. Pharmaceutically acceptable delivery reagents, excipients, and methods of preparation and use thereof, including methods for preparing and administering pharmaceutical preparations to patients (a.k.a. "subjects") are well known in the art, and are set forth in numerous publications, including, for example,

5 in US Patent Appl. Pub. No. US 2008/0213377, the entirety of which is incorporated herein by reference.

For example, the present compositions can be in the form of pharmaceutically acceptable salts. Such salts include those listed in, for example, *J. Pharma. Sci.* 66, 2-19 (1977) and *The Handbook of Pharmaceutical Salts; Properties, Selection, and Use*. P. H. Stahl and C. G. Wermuth (eds.), Verlag, Zurich (Switzerland) 2002, which are hereby incorporated by reference in their entirety. Non-limiting examples of pharmaceutically

10 acceptable salts include: sulfate, citrate, acetate, oxalate, chloride, bromide, iodide, nitrate, bisulfate, phosphate, acid phosphate, isonicotinate, lactate, salicylate, acid citrate, tartrate, oleate, tannate, pantothenate, bitartrate, ascorbate, succinate, maleate, gentisinate, fumarate, gluconate, glucuronate, saccharate, formate, benzoate, glutamate, methanesulfonate, ethanesulfonate, benzenesulfonate, p-toluenesulfonate, camphorsulfonate, pamoate, phenylacetate, trifluoroacetate, acrylate, chlorobenzoate,

15 dinitrobenzoate, hydroxybenzoate, methoxybenzoate, methylbenzoate, o-acetoxybenzoate, naphthalene-2-benzoate, isobutyrate, phenylbutyrate,  $\alpha$ -hydroxybutyrate, butyne-1,4-dicarboxylate, hexyne-1,4-dicarboxylate, caprate, caprylate, cinnamate, glycollate, heptanoate, hippurate, malate, hydroxymaleate, malonate, mandelate, mesylate, nicotinate, phthalate, teraphthalate, propiolate, propionate, phenylpropionate, sebacate, suberate, p-bromobenzenesulfonate, chlorobenzenesulfonate, ethylsulfonate, 2-

20 hydroxyethylsulfonate, methylsulfonate, naphthalene-1-sulfonate, naphthalene-2-sulfonate, naphthalene-1,5-sulfonate, xylenesulfonate, tartarate salts, hydroxides of alkali metals such as sodium, potassium, and lithium; hydroxides of alkaline earth metal such as calcium and magnesium; hydroxides of other metals, such as aluminum and zinc; ammonia, and organic amines, such as unsubstituted or hydroxy-substituted mono-, di-, or tri-alkylamines, dicyclohexylamine; tributyl amine; pyridine; N-methyl, N-ethylamine; diethylamine;

25 triethylamine; mono-, bis-, or tris-(2-OH-lower alkylamines), such as mono-, bis-, or tris-(2-hydroxyethyl)amine, 2-hydroxy-tert-butylamine, or tris-(hydroxymethyl)methylamine, N,N-di-lower alkyl-N-(hydroxyl-lower alkyl)-amines, such as N,N-dimethyl-N-(2-hydroxyethyl)amine or tri-(2-hydroxyethyl)amine; N-methyl-D-glucamine; and amino acids such as arginine, lysine, and the like.

The present pharmaceutical compositions can comprises excipients, including liquids such as water and oils,

30 including those of petroleum, animal, vegetable, or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. The pharmaceutical excipients can be, for example, saline, gum acacia, gelatin, starch paste, talc, keratin, colloidal silica, urea and the like. In addition, auxiliary, stabilizing, thickening, lubricating, and coloring agents can be used. In one embodiment, the pharmaceutically acceptable excipients are sterile when administered to a subject. Suitable pharmaceutical excipients also include starch, glucose,

35 lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc,

sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. Any agent described herein, if desired, can also comprise minor amounts of wetting or emulsifying agents, or pH buffering agents.

In various embodiments, the compositions described herein can administered in an effective dose of, for example, from about 1 mg/kg to about 100 mg/kg, about 2.5 mg/kg to about 50 mg/kg, or about 5 mg/kg to about 25 mg/kg. The precise determination of what would be considered an effective dose may be based on factors individual to each patient, including their size, age, and type of disease. Dosages can be readily ascertained by those of ordinary skill in the art from this disclosure and the knowledge in the art. For example, doses may be determined with reference *Physicians' Desk Reference*, 66th Edition, PDR Network; 2012 Edition (December 27, 2011), the contents of which are incorporated by reference in its entirety.

The active compositions of the present invention may include classic pharmaceutical preparations. Administration of these compositions according to the present invention may be via any common route so long as the target tissue is available via that route. This includes oral, nasal, or buccal. Alternatively, administration may be by intradermal, subcutaneous, intramuscular, intraperitoneal or intravenous injection, or by direct injection into cancer tissue. The agents disclosed herein may also be administered by catheter systems. Such compositions would normally be administered as pharmaceutically acceptable compositions as described herein.

Upon formulation, solutions may be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations may easily be administered in a variety of dosage forms such as injectable solutions, drug release capsules and the like. For parenteral administration in an aqueous solution, for example, the solution generally is suitably buffered and the liquid diluent first rendered isotonic with, for example, sufficient saline or glucose. Such aqueous solutions may be used, for example, for intravenous, intramuscular, subcutaneous and intraperitoneal administration. Preferably, sterile aqueous media are employed as is known to those of skill in the art, particularly in light of the present disclosure.

Exemplary subjects or patients refers to any vertebrate including, without limitation, humans and other primates (e.g., chimpanzees and other apes and monkey species), farm animals (e.g., cattle, sheep, pigs, goats, and horses), domestic mammals (e.g., dogs and cats), laboratory animals (e.g., rodents such as mice, rats, and guinea pigs), and birds (e.g., domestic, wild and game birds such as chickens, turkeys and other gallinaceous birds, ducks, geese, and the like). In some embodiments, the subject is a mammal. In some embodiments, the subject is a human.

Administration of the compositions described herein may be, for example, by injection, topical administration, ophthalmic administration and intranasal administration. The injection may include injections such as, but not limited to, intradermal, subcutaneous and intramuscular. The injection, in some embodiments, may be linked to an electrical force (e.g. electroporation, including with devices that find use in electrochemotherapy (e.g.

- CLINIPORATOR, IGEA Srl, Carpi [MO], Italy)). The topical administration may be, but is not limited to, a cream, lotion, ointment, gel, spray, solution and the like. The topical administration may further include a penetration enhancer such as, but not limited to, surfactants, fatty acids, bile salts, chelating agents, non-chelating non-surfactants, polyoxyethylene-9-lauryl ether, polyoxyethylene-20-cetyl ether, fatty acids and/or salts in combination with bile acids and/or salts, sodium salt in combination with lauric acid, capric acid and UDCA, and the like. The topical administration may also include a fragrance, a colorant, a sunscreen, an antibacterial and/or a moisturizer. The compositions described herein may be administered to at least one site such as, but not limited to, forehead, scalp, hair follicles, hair, upper eyelids, lower eyelids, eyebrows, eyelashes, infraorbital area, periorbital areas, temple, nose, nose bridge, cheeks, tongue, nasolabial folds, lips, periocular areas, jaw line, ears, neck, breast, forearm, upper arm, palm, hand, finger, nails, back, abdomen, sides, buttocks, thigh, calf, feet, toes and the like.

### Sequences

SEQ ID NO	Description
1	Stsl
2	Stsl-HA
3	Stsl-HA2
4	Stsl-UHA
5	Stsl-UHA2
6	Stsl-HF
7	Stsl-UHF
8	Oct4
9	Sox2
10	Klf4
11	c-Myc
12	BIRC5_exon1
13	BIRC5_exon2
14	BIRC5_exon3
15	BIRC5_exon4
16	BIRC5-1.1-L
17	BIRC5-1.1-R
18	BIRC5-1.2-L
19	BIRC5-1.2-R
20	BIRC5-1.3-L
21	BIRC5-1.3-R
22	BIRC5-2.1-L
23	BIRC5-2.1-R
24	BIRC5-2.2-L
25	BIRC5-2.2-R
26	BIRC5-3.1-L

27	BIRC5-3.1-R
28	CDK1
29	CDK2
30	CDK3
31	CDK4
32	CDK5
33	CDK6
34	BIRC5
35	HIF1A
36	RRM2
37	KRAS
38	EGFR
39	MYC
40	PKN3
41	KIF11
42	APC
43	BRCA1
44	BRCA2
45	TP53
46	APP
47	HTT
48	IAPP
49	MAPT
50	PRNP
51	SNCA
52	SOD1
53	FokI
54	Repeat1
55	Repeat2
56	Repeat3
57	EO-GHGG-FokI
58	GHGG-FokI
59	EO-GHGG-StsI
60	GHGG-StsI
61	collagen alpha-1(I) chain preproprotein
62	collagen alpha-2(I) chain precursor
63	collagen alpha-1(II) chain isoform 1 precursor
64	collagen alpha-1(II) chain isoform 2 precursor
65	collagen alpha-1(III) chain preproprotein
66	collagen alpha-1(IV) chain preproprotein
67	collagen alpha-2(IV) chain preproprotein
68	collagen alpha-3(IV) chain precursor
69	collagen alpha-4(IV) chain precursor

70	collagen alpha-5(IV) chain isoform 1 precursor
71	collagen alpha-6(IV) chain isoform A precursor
72	collagen alpha-1(V) chain isoform 1 preproprotein
73	collagen alpha-2(V) chain preproprotein
74	collagen alpha-3(V) chain preproprotein
75	collagen alpha-1(VI) chain precursor
76	collagen alpha-2(VI) chain isoform 2C2 precursor
77	collagen alpha-3(VI) chain isoform 1 precursor
78	collagen alpha-1(VII) chain precursor
79	elastin isoform a precursor
80	elastin isoform b precursor
81	elastin isoform c precursor
82	elastin isoform d precursor
83	elastin isoform e precursor
84	elastin isoform f precursor
85	elastin isoform g precursor
86	elastin isoform h precursor
87	elastin isoform i precursor
88	elastin isoform j precursor
89	elastin isoform k precursor
90	elastin isoform l precursor
91	elastin isoform m precursor
92	protein-lysine 6-oxidase isoform 1 preproprotein
93	protein-lysine 6-oxidase isoform 2
94	telomerase reverse transcriptase isoform 1
95	telomerase reverse transcriptase isoform 2
96	fibronectin isoform 1 preproprotein
97	fibronectin isoform 3 preproprotein
98	fibronectin isoform 4 preproprotein
99	fibronectin isoform 5 preproprotein
100	fibronectin isoform 6 preproprotein
101	fibronectin isoform 7 preproprotein
102	vitronectin precursor
103	nidogen-1 precursor
104	laminin subunit alpha-1 precursor
105	insulin-like growth factor I isoform 1 preproprotein
106	fibroblast growth factor 1 isoform 1 precursor
107	fibroblast growth factor 2
108	transforming growth factor beta-1 precursor
109	transforming growth factor beta-2 isoform 1 precursor
110	transforming growth factor beta-2 isoform 2 precursor
111	actin, alpha skeletal muscle
112	actin, aortic smooth muscle

113	actin, cytoplasmic 1
114	actin, alpha cardiac muscle 1 proprotein
115	actin, cytoplasmic 2
116	actin, gamma-enteric smooth muscle isoform 1 precursor
117	actin, gamma-enteric smooth muscle isoform 2 precursor
118	granulocyte colony-stimulating factor isoform a precursor
119	granulocyte colony-stimulating factor isoform b precursor
120	granulocyte colony-stimulating factor isoform c precursor
121	granulocyte colony-stimulating factor isoform d precursor
122	platelet-derived growth factor subunit A isoform 1 preproprotein
123	platelet-derived growth factor subunit A isoform 2 preproprotein
124	platelet-derived growth factor subunit B isoform 1 preproprotein
125	platelet-derived growth factor subunit B isoform 2 preproprotein
126	platelet-derived growth factor C precursor
127	platelet-derived growth factor D isoform 1 precursor
128	platelet-derived growth factor D isoform 2 precursor
129	interstitial collagenase isoform 1 preproprotein
130	interstitial collagenase isoform 2
131	neutrophil collagenase preproprotein
132	stromelysin-2 preproprotein
133	macrophage metalloelastase preproprotein
134	fibrillin-1 precursor
135	fibrillin-2 precursor
136	lysyl oxidase homolog 1 preproprotein
137	lysyl oxidase homolog 2 precursor
138	lysyl oxidase homolog 3 isoform 1 precursor
139	lysyl oxidase homolog 3 isoform 2 precursor
140	lysyl oxidase homolog 3 isoform 3
141	lysyl oxidase homolog 4 precursor
142	microfibrillar-associated protein 2 isoform a precursor
143	microfibrillar-associated protein 2 isoform b precursor
144	microfibrillar-associated protein 5 precursor
145	disintegrin and metalloproteinase domain-containing protein 17 preprotein
146	desmoglein-2 preproprotein
147	DNA polymerase eta isoform 1
148	DNA polymerase eta isoform 2
149	DNA polymerase eta isoform 3
150	ferrochelatase, mitochondrial isoform a precursor
151	ferrochelatase, mitochondrial isoform b precursor
152	filaggrin
153	hyaluronan synthase 1 isoform 1
154	hyaluronan synthase 1 isoform 2
155	hyaluronan synthase 2

156	hyaluronan synthase 3 isoform a
157	hyaluronan synthase 3 isoform b
158	proopiomelanocortin
159	plakophilin-1 isoform 1a
160	plakophilin-1 isoform 1b
161	retinol dehydrogenase 10
162	mitochondrial brown fat uncoupling protein 1
163	tyrosinase precursor

This invention is further illustrated by the following non-limiting examples.

### EXAMPLES

#### *Example 1 RNA Synthesis*

- 5 RNA encoding green fluorescent protein or the human proteins Elastin, Tyrosinase, Melanocortin 1 receptor, Hyaluronan synthase 1, Hyaluronan synthase 2, Hyaluronan synthase 3, Collagen type III a1, Collagen type VII a1, Interleukin 10, P-selectin glycoprotein ligand-1, Alpha-(1,3)-fucosyltransferase Oct4, Sox2, Klf4, c-Myc-2 (T58A), and Lin28 or TALENs targeting the human genes XPA, CCR5, TERT, MYC, and BIRC5, and comprising various combinations of canonical and non-canonical nucleotides, was synthesized from DNA
- 10 templates using the T7 High Yield RNA Synthesis Kit and the Vaccinia Capping System kit with mRNA Cap 2'-O-Methyltransferase (all from New England Biolabs, Inc.), according to the manufacturer's instructions and the present inventors' previously disclosed inventions (U.S. Application No. 13/465,490 (now U.S. Patent No. 8,497,124), International Application No. PCT/US12/67966, U.S. Application No. 13/931,251, and International Application No. PCT/US13/68118, the contents of all of which are hereby incorporated by
- 15 reference in their entirety) (Table 4). The RNA was then diluted with nuclease-free water to between 100ng/ $\mu$ L and 1000ng/ $\mu$ L. For certain experiments, an RNase inhibitor (Superase-In, Life Technologies Corporation) was added at a concentration of 1 $\mu$ L/100 $\mu$ g of RNA. RNA solutions were stored at 4C. For reprogramming experiments, RNA encoding Oct4, Sox2, Klf4, c-Myc-2 (T58A), and Lin28 was mixed at a molar ratio of 3:1:1:1:1.

20 *Table 4. RNA Synthesis*

Template	Nucleotides	Reaction Volume/ $\mu$ L	ivT Yield/ $\mu$ g
hELN	A, 0.5 7dG, 0.4 5mU, 5mC	20	34.1
Oct4 (SEQ ID NO: 8)	A, 0.5 7dG, 0.4 5mU, 5mC	300	2752.0
Sox2 (SEQ ID NO: 9)	A, 0.5 7dG, 0.4 5mU, 5mC	100	965.0
Klf4 (SEQ ID NO: 10)	A, 0.5 7dG, 0.4 5mU, 5mC	100	1093.8
c-Myc-2 (T58A)	A, 0.5 7dG, 0.4 5mU, 5mC	100	1265.6
Lin28	A, 0.5 7dG, 0.4 5mU, 5mC	100	1197.8

ELN	A, G, U, 5hmC	20	67.6
GFP	A, 0.5 7dG, 0.4 5mU, 5mC	10	60.5
GFP	A, 0.5 7dG, 0.4 5mU, 5hmC	10	25.5
GFP	A, G, U, 5hmC	10	58.3
GFP	A, 0.5 7dG, U, 5hmC	10	47.3
GFP	A, 0.5 7dG, 0.4 5mU, 5cC	10	33.8
GFP	A, G, U, 5hmC	15	30.3
GFP	A, G, U, 5hmC	15	44.6
GFP	A, G, U, 5hmC	15	24.7
TYR	A, G, U, 5hmC	15	45.4
MC1R	A, G, U, 5hmC	15	47.5
TYR	A, G, U, C	20	67.0
TYR	A, G, psU, C	20	93.7
TYR	A, G, 5mU, C	20	85.7
TYR	A, G, U, 5mC	20	73.4
TYR	A, G, U, 5hmC	20	72.7
TYR	A, 0.5 7dG, U, C	20	62.7
TYR	A, G, psU, 5mC	20	116.3
TYR	A, G, psU, 5hmC	20	102.4
TYR	A, 0.5 7dG, psU, C	20	87.3
TYR	A, G, 0.4 5mU, 5mC	20	106.5
TYR	A, G, 0.4 5mU, 5hmC	20	85.0
TYR	A, 0.5 7dG, 0.4 5mU, C	20	70.9
TYR	A, 0.5 7dG, U, 5mC	20	88.5
TYR	A, 0.5 7dG, U, 5hmC	20	59.1
TYR	A, 0.5 7dG, psU, 5mC	20	7.8
TYR	A, 0.5 7dG, psU, 5hmC	20	98.0
TYR	A, 0.5 7dG, 0.4 5mU, 5mC	20	106.5
TYR	A, 0.5 7dG, 0.4 5mU, 5hmC	20	82.3
HAS1	A, G, 0.4 5mU, 5hmC	20	178.4
HAS2	A, G, 0.4 5mU, 5hmC	20	59.3
HAS3	A, G, 0.4 5mU, 5hmC	20	102.6
TYR	A, G, 0.4 5mU, 5hmC	100	377.3
COL3A1	A, G, 0.4 5mU, 5hmC	20	108.3
COL7A1	A, G, 0.4 5mU, 5hmC	20	94.6
IL10	A, G, psU, C	75	569.5
SELPLG	A, G, psU, C	75	542.6
FUT7	A, G, psU, C	75	564.5
Oct4 (SEQ ID NO: 8)	A, G, U, C	10	100.7
Oct4 (SEQ ID NO: 8)	A, G, U, 5mC	10	120.6
Oct4 (SEQ ID NO: 8)	A, G, U, 5mC	10	115.3
Oct4 (SEQ ID NO: 8)	A, G, U, 5hmC	10	101.4
Oct4 (SEQ ID NO: 8)	A, G, U, 5cC	10	50.8



Oct4 (SEQ ID NO: 8)	A, G, U, 5fC	10	84.0
Oct4 (SEQ ID NO: 8)	A, G, U, 5hmC	10	99.5
Sox2 (SEQ ID NO: 9)	A, G, U, 5hmC	10	84.0
Klf4 (SEQ ID NO: 10)	A, G, U, 5hmC	10	72.6
c-Myc-2 (T58A)	A, G, U, 5hmC	10	82.4
Lin28	A, G, U, 5hmC	10	83.1
Oct4 (SEQ ID NO: 8)	A, G, 0.4 5mU, 5hmC	10	78.9
Sox2 (SEQ ID NO: 9)	A, G, 0.4 5mU, 5hmC	10	91.9
Klf4 (SEQ ID NO: 10)	A, G, 0.4 5mU, 5hmC	10	91.2
c-Myc-2 (T58A)	A, G, 0.4 5mU, 5hmC	10	104.6
Lin28	A, G, 0.4 5mU, 5hmC	10	103.2
Oct4 (SEQ ID NO: 8)	A, G, 5hU, 5hmC	300	1925.5
Sox2 (SEQ ID NO: 9)	A, G, 5hU, 5hmC	100	641.8
Klf4 (SEQ ID NO: 10)	A, G, 5hU, 5hmC	100	739.0
c-Myc-2 (T58A)	A, G, 5hU, 5hmC	100	574.0
Lin28	A, G, 5hU, 5hmC	100	556.0

- "A" refers to adenosine-5'-triphosphate, "G" refers to guanosine-5'-triphosphate, "U" refers to uridine-5'-triphosphate, "C" refers to cytidine-5'-triphosphate, "5mC" refers to 5-methylcytidine-5'-triphosphate, "5hmC" refers to 5-hydroxymethylcytidine-5'-triphosphate, "5cC" refers to 5-carboxycytidine-5'-triphosphate, "5fC" refers to 5-formylcytidine-5'-triphosphate, "psU" refers to 5-pseudouridine-5'-triphosphate, "5mU" refers to 5-methyluridine-5'-triphosphate, "5hU" refers to the 5'-triphosphate of uridine with a methyl group bound to an oxygen atom bound to the 5C position of the uridine, and "7dG" refers to 7-deazaguanosine-5'-triphosphate.

#### Example 2 Transfection of Cells with Synthetic RNA

- For transfection in 6-well plates, 2µg RNA and 6µL transfection reagent (Lipofectamine RNAiMAX, Life Technologies Corporation) were first diluted separately in complexation medium (Opti-MEM, Life Technologies Corporation or DMEM/F12 + 10µg/mL insulin + 5.5µg/mL transferrin + 6.7ng/mL sodium selenite + 2µg/mL ethanolamine) to a total volume of 60µL each. Diluted RNA and transfection reagent were then mixed and incubated for 15min at room temperature, according to the transfection reagent-manufacturer's instructions. Complexes were then added to cells in culture. Between 12µL and 240µL of complexes were added to each well of a 6-well plate, which already contained 2mL of transfection medium per well. Plates were shaken gently to distribute the complexes throughout the well. Cells were incubated with complexes for 4 hours to overnight, before replacing the medium with fresh transfection medium (2mL/well). Volumes were scaled for transfection in 24-well and 96-well plates. Alternatively, between 0.5µg and 5µg of RNA and between 2-3µL of transfection reagent (Lipofectamine 2000, Life Technologies Corporation) per µg of RNA were first diluted separately in complexation medium (Opti-MEM, Life Technologies Corporation or DMEM/F12 + 10µg/mL insulin + 5.5µg/mL transferrin + 6.7ng/mL sodium

- selenite + 2µg/mL ethanolamine) to a total volume of between 5µL and 100µL each. Diluted RNA and transfection reagent were then mixed and incubated for 10min at room temperature. Complexes were then added to cells in culture. Between 10µL and 200µL of complexes were added to each well of a 6-well plate, which already contained 2mL of transfection medium per well. In certain experiments, DMEM + 10% FBS or
- 5 DMEM + 50% FBS was used in place of transfection medium. Plates were shaken gently to distribute the complexes throughout the well. Cells were incubated with complexes for 4 hours to overnight. In certain experiments, the medium was replaced with fresh transfection medium (2mL/well) 4h or 24h after transfection.

*Example 3 Toxicity of and Protein Translation from Synthetic RNA Containing Non-Canonical Nucleotides*

- Primary human fibroblasts were transfected according to Example 2, using RNA synthesized according to
- 10 Example 1. Cells were fixed and stained 20-24h after transfection using an antibody against Oct4. The relative toxicity of the RNA was determined by assessing cell density at the time of fixation.

*Example 4 Transfection Medium Formulation*

A cell-culture medium was developed to support efficient transfection of cells with nucleic acids and efficient reprogramming ("transfection medium"):

- 15 DMEM/F12 + 15mM HEPES + 2mM L-alanyl-L-glutamine + 10µg/mL insulin + 5.5µg/mL transferrin + 6.7ng/mL sodium selenite + 2µg/mL ethanolamine + 50µg/mL L-ascorbic acid 2-phosphate sesquimagnesium salt hydrate + 4µg/mL cholesterol + 1µM hydrocortisone + 25µg/mL polyoxyethylenesorbitan monooleate + 2µg/mL D-alpha-tocopherol acetate + 20ng/mL bFGF + 5mg/mL treated human serum albumin.

- 20 A variant of this medium was developed to support robust, long-term culture of a variety of cell types, including pluripotent stem cells ("maintenance medium"):

DMEM/F12 + 2mM L-alanyl-L-glutamine + 10µg/mL insulin + 5.5µg/mL transferrin + 6.7ng/mL sodium selenite + 2µg/mL ethanolamine + 50µg/mL L-ascorbic acid 2-phosphate sesquimagnesium salt hydrate + 20ng/mL bFGF + 2ng/mL TGF-β1.

- 25 Transfection medium, in which the treated human serum albumin was treated by addition of 32mM sodium octanoate, followed by heating at 60C for 4h, followed by treatment with ion-exchange resin (AG501-X8(D), Bio-Rad Laboratories, Inc.) for 6h at room temperature, followed by treatment with dextran-coated activated charcoal (C6241, Sigma-Aldrich Co. LLC.) overnight at room temperature, followed by centrifugation, filtering, adjustment to a 10% solution with nuclease-free water, followed by addition to the other components of the
- 30 medium, was used as the transfection medium in all Examples described herein, unless otherwise noted. For reprogramming experiments, cells were plated either on uncoated plates in DMEM + 10%-20% serum or on fibronectin and vitronectin-coated plates in transfection medium, unless otherwise noted. The transfection medium was not conditioned, unless otherwise noted. It is recognized that the formulation of the transfection

medium can be adjusted to meet the needs of the specific cell types being cultured. It is further recognized that treated human serum albumin can be replaced with other treated albumin, for example, treated bovine serum albumin, without negatively affecting the performance of the medium. It is further recognized that other glutamine sources can be used instead of or in addition to L-alanyl-L-glutamine, for example, L-glutamine, that other buffering systems can be used instead of or in addition to HEPES, for example, phosphate, bicarbonate, etc., that selenium can be provided in other forms instead of or in addition to sodium selenite, for example, selenous acid, that other antioxidants can be used instead of or in addition to L-ascorbic acid 2-phosphate sesquimagnesium salt hydrate and/or D-alpha-tocopherol acetate, for example, L-ascorbic acid, that other surfactants can be used instead of or in addition to polyoxyethylenesorbitan monooleate, for example, Pluronic F-68 and/or Pluronic F-127, that other basal media can be used instead of or in addition to DMEM/F12, for example, MEM, DMEM, etc., and that the components of the culture medium can be varied with time, for example, by using a medium without TGF- $\beta$  from day 0 to day 5, and then using a medium containing 2ng/mL TGF- $\beta$  after day 5, without negatively affecting the performance of the medium. It is further recognized that other ingredients can be added, for example, fatty acids, lysophosphatidic acid, lysosphingomyelin, sphingosine-1-phosphate, other sphingolipids, ROCK inhibitors, including Y-27632 and thiazovivin, members of the TGF- $\beta$ /NODAL family of proteins, IL-6, members of the Wnt family of proteins, etc., at appropriate concentrations, without negatively affecting the performance of the medium, and that ingredients that are known to promote or inhibit the growth of specific cell types and/or agonists and/or antagonists of proteins or other molecules that are known to promote or inhibit the growth of specific cell types can be added to the medium at appropriate concentrations when it is used with those cell types without negatively affecting the performance of the medium, for example, sphingosine-1-phosphate and pluripotent stem cells. The present invention relates equally to ingredients that are added as purified compounds, to ingredients that are added as parts of well-defined mixtures, to ingredients that are added as parts of complex or undefined mixtures, for example, animal or plant oils, and to ingredients that are added by biological processes, for example, conditioning. The concentrations of the components can be varied from the listed values within ranges that will be obvious to persons skilled in the art without negatively affecting the performance of the medium. An animal component-free version of the medium was produced by using recombinant versions of all protein ingredients, and non-animal-derived versions of all other components, including semi-synthetic plant-derived cholesterol (Avanti Polar Lipids, Inc.).

#### 30 *Example 5 Transfection Medium Formulation*

A medium was developed to support efficient transfection, reprogramming, and gene-editing of cells:

DMEM/F12 + 10 $\mu$ g/mL insulin + 5.5 $\mu$ g/mL transferrin + 6.7ng/mL sodium selenite + 20ng/mL bFGF + 5mg/mL treated human serum albumin.

Variants of this medium were also developed to provide improved performance when used with specific transfection reagents, specific nucleic acids, and specific cell types: DMEM/F12 + 10µg/mL insulin + 5.5µg/mL transferrin + 6.7ng/mL sodium selenite + 4.5µg/mL cholesterol + 20ng/mL bFGF + 5mg/mL treated human serum albumin, DMEM/F12 + 10µg/mL insulin + 5.5µg/mL transferrin + 6.7ng/mL sodium selenite +  
 5 1µM hydrocortisone + 20ng/mL bFGF + 5mg/mL treated human serum albumin, and DMEM/F12 + 10µg/mL insulin + 5.5µg/mL transferrin + 6.7ng/mL sodium selenite + 4.5µg/mL cholesterol + 1µM hydrocortisone + 20ng/mL bFGF + 5mg/mL treated human serum albumin.

Examples of additional components that were added to the cell-culture medium in certain experiments (listed with example concentrations) include: 15mM HEPES, 2mM L-alanyl-L-glutamine, 2µg/mL ethanolamine,  
 10 10µg/mL fatty acids, 10µg/mL cod liver oil fatty acids (methyl esters), 25µg/mL polyoxyethylenesorbitan monooleate, 2µg/mL D-alpha-tocopherol acetate, 1-50µg/mL L-ascorbic acid 2-phosphate sesquimagnesium salt hydrate, 200ng/mL B18R, and 0.1% Pluronic F-68.

For certain experiments in which the medium was conditioned, the following variant was used:

DMEM/F12 + 15mM HEPES + 2mM L-alanyl-L-glutamine + 10µg/mL insulin + 5.5µg/mL transferrin +  
 15 6.7ng/mL sodium selenite + 2µg/mL ethanolamine + 4.5µg/mL cholesterol + 10µg/mL cod liver oil fatty acids (methyl esters) + 25µg/mL polyoxyethylenesorbitan monooleate + 2µg/mL D-alpha-tocopherol acetate + 1µg/mL L-ascorbic acid 2-phosphate sesquimagnesium salt hydrate + 0.1% Pluronic F-68 + 20ng/mL bFGF + 5mg/mL treated human serum albumin.

For certain experiments in which the medium was not conditioned, the following variant was used.

20 DMEM/F12 + 15mM HEPES + 2mM L-alanyl-L-glutamine + 10µg/mL insulin + 5.5µg/mL transferrin + 6.7ng/mL sodium selenite + 2µg/mL ethanolamine + 4.5µg/mL cholesterol + 1µM hydrocortisone + 0-25µg/mL polyoxyethylenesorbitan monooleate + 2µg/mL D-alpha-tocopherol acetate + 50µg/mL L-ascorbic acid 2-phosphate sesquimagnesium salt hydrate + 20ng/mL bFGF + 5mg/mL treated human serum albumin.

For the preparation of the these variants, the treated human serum albumin was treated by addition of 32mM  
 25 sodium octanoate, followed by heating at 60C for 4h, followed by treatment with ion-exchange resin (AG501-X8(D)) for 6h at room temperature, followed by treatment with dextran-coated activated charcoal (C6241, Sigma-Aldrich Co. LLC.) overnight at room temperature, followed by centrifugation, filtering, adjustment to a 10% solution with nuclease-free water, followed by addition to the other components of the medium. For certain experiments in which the medium was conditioned, the medium was conditioned for 24h on irradiated  
 30 human neonatal fibroblast feeders. The cells were plated on fibronectin-coated plates or fibronectin and vitronectin-coated plates, unless otherwise noted.

The formulation of the medium can be adjusted to meet the needs of the specific cell types being cultured. Furthermore, in certain situations, treated human serum albumin can be replaced with other treated albumin,

for example, treated bovine serum albumin, other glutamine sources can be used instead of or in addition to L-alanyl-L-glutamine, for example, L-glutamine, other buffering systems can be used instead of or in addition to HEPES, for example, phosphate, bicarbonate, etc., selenium can be provided in other forms instead of or in addition to sodium selenite, for example, selenous acid, other antioxidants can be used instead of or in addition to L-ascorbic acid 2-phosphate sesquimagnesium salt hydrate and/or D-alpha-tocopherol acetate, for example, L-ascorbic acid, other surfactants can be used instead of or in addition to polyoxyethylenesorbitan monooleate and/or Pluronic F-68, for example, Pluronic F-127, other basal media can be used instead of or in addition to DMEM/F12, for example, MEM, DMEM, etc., and the components of the culture medium can be varied with time, for example, by using a medium without TGF- $\beta$  from day 0 to day 5, and then using a medium containing 2ng/mL TGF- $\beta$  after day 5. In certain situations, other ingredients can be added, for example, fatty acids, lysophosphatidic acid, lysosphingomyelin, sphingosine-1-phosphate, other sphingolipids, members of the TGF- $\beta$ /NODAL family of proteins, IL-6, members of the Wnt family of proteins, etc., at appropriate concentrations, and ingredients that are known to promote or inhibit the growth of specific cell types and/or agonists and/or antagonists of proteins or other molecules that are known to promote or inhibit the growth of specific cell types can be added to the medium at appropriate concentrations when it is used with those cell types, for example, sphingosine-1-phosphate and pluripotent stem cells. Ingredients can take the form of purified compounds, parts of well-defined mixtures, parts of complex or undefined mixtures, for example, animal or plant oils, and may be added by biological processes, for example, conditioning. The concentrations of the components can be varied from the listed values within ranges that will be obvious to persons skilled in the art.

#### *Example 6 Transfection of Cells with Synthetic RNA*

For transfection in 6-well plates, 2 $\mu$ g RNA and 6 $\mu$ L transfection reagent (Lipofectamine™ RNAiMAX, Life Technologies Corporation) were first diluted separately in complexation medium (Opti-MEM®, Life Technologies Corporation) to a total volume of 60 $\mu$ L each. Diluted RNA and transfection reagent were then mixed and incubated for 15min at room temperature, according to the transfection reagent-manufacturer's instructions. Complexes were then added to cells in culture. Between 30 $\mu$ L and 240 $\mu$ L of complexes were added to each well of a 6-well plate, which already contained 2mL of transfection medium per well. Plates were then shaken gently to distribute the complexes throughout the well. Cells were incubated with complexes for 2 hours to overnight, before replacing the medium with fresh transfection medium (2mL/well). Volumes were scaled for transfection in 24-well and 96-well plates. Cells were fixed and stained 20-24h after transfection using an antibody against Oct4. Nuclei were stained and counted to determine the relative toxicity of the RNA.

*Example 7 Analysis of the Ability of Untreated Human Serum Albumin Preparations to Support Nucleic Acid Transfection and RNA Reprogramming*

Primary human neonatal fibroblasts were cultured in medium with or without 5mg/mL HSA. Cohn Fraction V (A6784, Sigma-Aldrich Co. LLC.), and four different recombinant HSA preparations (A6608, A7736, A9731, and A9986, all from Sigma-Aldrich Co. LLC.) were screened. Cells were transfected according to Example 2, with RNA synthesized according to Example 1. While untransfected cells grew well in media containing any of the HSA preparations, in transfected wells, each of the HSA preparations yielded dramatically different cell morphologies and cell densities, and none resulted in morphological changes indicative of reprogramming.

*Example 8 Production of Octanoate-Treated Human Serum Albumin*

A 10% solution of HSA was pre-incubated with 22mM sodium chloride and 16mM sodium octanoate (Sigma-Aldrich Co. LLC), and was incubated at 37C for 3 hours before assembly of the complete medium.

*Example 9 Treatment of Human Serum Albumin Using Ion-Exchange Chromatography*

A 20% solution of recombinant HSA produced in *Pichia pastoris* (A7736, Sigma-Aldrich Co. LLC.) was prepared by dissolving 2g of HSA in 10mL of nuclease-free water with gentle agitation at room temperature. The HSA solution was then deionized by first adding 1g of mixed-bed deionizing resin (AG 501-X8(D), Bio-Rad Laboratories, Inc.), and rocking for 1h at room temperature. The HSA solution was then decanted into a tube containing 5g of fresh resin, and was rocked for 4h at room temperature. Finally, the deionized HSA solution was decanted, adjusted to a 10% total protein content with nuclease-free water, filter-sterilized using a 0.2µm PES-membrane filter, and stored at 4C.

*Example 10 Analysis of Transfection Efficiency and Viability of Cells Cultured in Media Containing Octanoate-Treated Human Serum Albumin*

Primary human neonatal fibroblasts were cultured in media containing recombinant HSA treated according to Example 8 and/or Example 9 or containing treated blood-derived HSA (Bio-Pure HSA, Biological Industries). Cells were transfected daily, according to Example 2, with RNA synthesized according to Example 1, beginning on day 0. Pictures were taken on day 3. Several small areas of cells undergoing morphological changes resembling mesenchymal to epithelial transition were observed in the wells containing octanoate, indicating an increased transfection efficiency. Many large areas of morphological changes resembling mesenchymal to epithelial transition were observed in the samples containing the treated blood-derived HSA. In both cases, the morphological changes were characteristic of reprogramming.

*Example 11 Reprogramming Human Fibroblasts Using Media Containing Octanoate-Treated Human Serum Albumin*

Primary human neonatal fibroblasts were plated in 6-well plates at a density of 5000 cells/well in fibroblast medium (DMEM + 10% fetal bovine serum). After 6 hours, the medium was replaced with transfection medium containing octanoate-treated HSA. The cells were transfected daily, according to Example 2, with RNA synthesized according to Example 1, beginning on day 0. By day 5, the well contained several areas of cells exhibiting morphology consistent with reprogramming. This experiment did not include the use of feeders or immunosuppressants.

*Example 12 Analysis of Transfection Efficiency and Viability of Cells Cultured in Media Containing Ion-Exchange-Resin-Treated Human Serum Albumin*

Primary human neonatal fibroblasts were transfected according to Example 2, with RNA synthesized according to Example 1, beginning on day 0. Pictures were taken on day 2. Cells in the well containing untreated HSA exhibited low viability compared to either the well containing treated blood-derived HSA or ion-exchange-resin-treated recombinant HSA.

*Example 13 Reprogramming Human Fibroblasts Using Ion-Exchange-Resin-Treated Human Serum Albumin*

Primary human neonatal fibroblasts were plated in 6-well plates on feeders at a density of 10,000 cells/well in fibroblast medium (DMEM + 10% fetal bovine serum). The cells were transfected daily according to Example 2, with RNA synthesized according to Example 1, beginning on day 0. A passage with a split ratio of 1:20 was performed on day 4. Pictures were taken on day 10. The well contained many large colonies of cells exhibiting morphology consistent with reprogramming. No colonies were observed in wells exposed to cell-culture media containing untreated HSA.

*Example 14 Reprogramming Human Fibroblasts without Using Feeders or Immunosuppressants*

Primary human fibroblasts were plated in 6-well plates at a density of 20,000 cells/well in fibroblast medium (DMEM + 10% fetal bovine serum). After 6 hours, the medium was replaced with transfection medium containing treated HSA and not containing immunosuppressants, and the cells were transfected daily according to Example 2, with RNA synthesized according to Example 1, except that the dose of RNA was reduced to 1µg/well and a total of 5 transfections were performed. Pictures were taken on day 7. Small colonies of cells exhibiting morphology consistent with reprogramming became visible as early as day 5. On day 7, the medium was replaced with DMEM/F12 + 20% Knockout™ Serum Replacement (Life Technologies Corporation) + 1X non-essential amino acids + 2mM L-glutamine, conditioned on irradiated mouse embryonic fibroblasts for 24 hours, and then supplemented with 20ng/mL bFGF and 10µM Y-27632. Large colonies with a reprogrammed morphology became visible as early as day 8. Colonies were picked on day 10, and plated in wells coated with basement membrane extract (Cultrex® Human BME Pathclear®, Trevigen Inc.). Cells

grew rapidly, and were passaged to establish lines. Established lines stained positive for the pluripotent stem-cell markers Oct4 and SSEA4. The entire protocol was repeated, and similar results were obtained.

*Example 15 Efficient, Rapid Derivation and Reprogramming of Cells from Human Skin Biopsy Tissue*

A full-thickness dermal punch biopsy was performed on a healthy, 31 year-old volunteer, according to an approved protocol. Briefly, an area of skin on the left, upper arm was anesthetized by topical application of 2.5% lidocaine. The field was disinfected with 70% isopropanol, and a full-thickness dermal biopsy was performed using a 1.5 mm-diameter punch. The tissue was rinsed in phosphate-buffered saline (PBS), and was placed in a 1.5mL tube containing 250 $\mu$ L of TrypLE™ Select CTS™ (Life Technologies Corporation), and incubated at 37C for 30min. The tissue was then transferred to a 1.5mL tube containing 250 $\mu$ L of DMEM/F12-CTS™ (Life Technologies Corporation) + 5mg/mL collagenase, and incubated at 37C for 2h. The epidermis was removed using forceps, and the tissue was mechanically dissociated. Cells were rinsed twice in DMEM/F12-CTS™ and were plated in fibronectin-coated wells of 24-well and 96-well plates. Phlebotomy was also performed on the same volunteer, and venous blood was collected in Vacutainer® SST™ tubes (Becton, Dickinson and Company). Serum was isolated according to the manufacturer's protocol. Isogenic plating medium was prepared by mixing DMEM/F12-CTS™ + 2mM L-alanyl-L-glutamine (Sigma-Aldrich Co. LLC.) + 20% human serum. Cells from the dermal tissue sample were plated either in transfection medium or in isogenic plating medium. After 2 days, the wells were rinsed, and the medium was replaced with transfection medium. Many cells with a fibroblast morphology attached and began to spread by day 2. Cells were transfected according to Example 2, with RNA synthesized according to Example 1, beginning on day 2, with all volumes scaled to accommodate the smaller wells. By day 5, areas of cells with morphologies consistent with reprogramming were observed.

*Example 16 Reprogramming Human Fibroblasts Using Synthetic RNA Containing Non-Canonical Nucleotides*

Primary human fibroblasts were plated in 6-well plates coated with recombinant human fibronectin and recombinant human vitronectin (each diluted in DMEM/F12 to a concentration of 1 $\mu$ g/mL, 1mL/well, incubated at room temperature for 1h) at a density of 20,000 cells/well in transfection medium. The following day, the cells were transfected as in Example 2, with RNA synthesized according to Example 1, except that the dose of RNA was 0.5 $\mu$ g/well on day 1, 0.5 $\mu$ g/well on day 2, and 2 $\mu$ g/well on day 3. Pictures were taken on day 4. Small colonies of cells exhibiting morphology consistent with reprogramming were visible on day 4.

*Example 17 Reprogramming Human Fibroblasts with a Non-Conditioned Transfection Medium*

Primary human fibroblasts were plated in 6-well plates coated with recombinant human fibronectin and recombinant human vitronectin (each diluted in DMEM/F12 to a concentration of 1 $\mu$ g/mL, 1mL/well, incubated at room temperature for 1h) at a density of 20,000 cells/well in transfection medium. The following



day, the cells were transfected as in Example 2, with RNA synthesized according to Example 1, except that the dose of RNA was 0.5µg/well on day 1, 0.5µg/well on day 2, 2µg/well on day 3, 2µg/well on day 4, and 4µg/well on day 5. Small colonies of cells exhibiting morphology consistent with reprogramming became visible as early as day 5. On day 7, the medium was replaced with DMEM/F12 + 20% Knockout™ Serum Replacement (Life Technologies Corporation) + 1X non-essential amino acids + 2mM L-glutamine, conditioned on irradiated mouse embryonic fibroblasts for 24 hours, and then supplemented with 20ng/mL bFGF and 10µM Y-27632. Large colonies with a reprogrammed morphology became visible as early as day 8. Colonies were picked on day 10, and plated in wells coated with basement membrane extract (Cultrex® Human BME Pathclear®, Trevigen Inc.). Cells grew rapidly, and were passaged to establish lines.

10 *Example 18 Reprogramming Human Fibroblasts Using Synthetic RNA Containing Non-Canonical Nucleotides*

Primary human neonatal fibroblasts were plated in 6-well plates coated with recombinant human fibronectin and recombinant human vitronectin (each diluted in DMEM/F12 to a concentration of 1µg/mL, 1mL/well, and incubated at room temperature for 1h) at a density of 10,000 cells/well in transfection medium. The following day, the cells were transfected as in Example 2, using RNA containing A, 0.5 7dG, 0.5 5mU, and 5mC, and an RNA dose of 0.5µg/well on day 1, 0.5µg/well on day 2, 2µg/well on day 3, 2µg/well on day 4, and 4µg/well on day 5. Small colonies of cells exhibiting morphology consistent with reprogramming became visible as early as day 5. The medium was replaced with maintenance medium on day 6. Cells were stained using an antibody against Oct4. Oct4-positive colonies of cells exhibiting a morphology consistent with reprogramming were visible throughout the well.

*Example 19 Feeder-Free, Passage-Free, Immunosuppressant-Free, Conditioning-Free Reprogramming of Primary Adult Human Fibroblasts Using Synthetic RNA*

Wells of a 6-well plate were coated with a mixture of recombinant human fibronectin and recombinant human vitronectin (1µg/mL in DMEM/F12, 1mL/well) for 1h at room temperature. Primary adult human fibroblasts were plated in the coated wells in transfection medium at a density of 10,000 cells/well. Cells were maintained at 37C, 5% CO<sub>2</sub>, and 5% O<sub>2</sub>. Beginning the following day, cells were transfected according to Example 2 daily for 5 days with RNA synthesized according to Example 1. The total amount of RNA transfected on each of the 5 days was 0.5µg, 0.5µg, 2µg, 2µg, and 4µg, respectively. Beginning with the fourth transfection, the medium was replaced twice a day. On the day following the final transfection, the medium was replaced with transfection medium, supplemented with 10µM Y-27632. Alternatively, the total amount of RNA transfected on each day was 0.25µg, 0, 0.5µg, 0.5µg, and 0.5µg, respectively or 0.25µg, 0, 0.25µg, 0.25µg, and 0.25µg, respectively. In certain experiments, transfection medium was changed only once per day, at the time of transfection. Compact colonies of cells with a reprogrammed morphology were visible in each transfected well by day 4.

*Example 20 Efficient, Rapid Derivation and Reprogramming of Cells from Adult Human Skin Biopsy Tissue*

A full-thickness dermal punch biopsy was performed on a healthy, 31 year-old volunteer, according to an approved protocol. Briefly, an area of skin on the left, upper arm was anesthetized by topical application of 2.5% lidocaine. The field was disinfected with 70% isopropanol, and a full-thickness dermal biopsy was performed using a 1.5 mm-diameter punch. The tissue was rinsed in phosphate-buffered saline (PBS), was placed in a 1.5mL tube containing 250 $\mu$ L of TrypLE Select CTS (Life Technologies Corporation), and was incubated at 37C for 30min. The tissue was then transferred to a 1.5mL tube containing 250 $\mu$ L of DMEM/F12-CTS (Life Technologies Corporation) + 5mg/mL collagenase, and was incubated at 37C for 2h. The epidermis was removed using forceps, and the tissue was mechanically dissociated. Cells were rinsed twice in DMEM/F12-CTS. Phlebotomy was also performed on the same volunteer, and venous blood was collected in Vacutainer SST tubes (Becton, Dickinson and Company). Serum was isolated according to the manufacturer's instructions. Isogenic plating medium was prepared by mixing DMEM/F12-CTS + 2mM L-alanyl-L-glutamine (Sigma-Aldrich Co. LLC.) + 20% human serum. Cells from the dermal tissue sample were plated in a fibronectin-coated well of a 6-well plate in isogenic plating medium. Many cells with a fibroblast morphology attached and began to spread by day 2. Cells were expanded and frozen in Synth-a-Freeze (Life Technologies Corporation).

Cells were passaged into 6-well plates at a density of 5,000 cells/well. The following day, the medium was replaced with transfection medium, and the cells were transfected as in Example 2, using RNA containing A, 0.5 7dG, 0.4 5mU, and 5mC, and an RNA dose of 0.5 $\mu$ g/well on day 1, 0.5 $\mu$ g/well on day 2, 2 $\mu$ g/well on day 3, 2 $\mu$ g/well on day 4, and 2 $\mu$ g/well on day 5. Certain wells received additional 2 $\mu$ g/well transfections on day 6 and day 7. In addition, certain wells received 2ng/mL TGF- $\beta$ 1 from day 4 onward. The medium was replaced with maintenance medium on day 6. Colonies of cells exhibiting morphology consistent with reprogramming became visible between day 5 and day 10. Colonies grew rapidly, and many exhibited a morphology similar to that of embryonic stem-cell colonies. Colonies were picked and plated in wells coated with recombinant human fibronectin and recombinant human vitronectin (each diluted in DMEM/F12 to a concentration of 1 $\mu$ g/mL, 1mL/well, incubated at room temperature for 1h). Cells grew rapidly, and were passaged to establish lines.

*Example 21 High-Efficiency Gene Editing by Repeated Transfection with RiboSlice*

Primary human fibroblasts were plated as in Example 19. The following day, the cells were transfected as in Example 2 with RNA synthesized according to Example 1. The following day cells in one of the wells were transfected a second time. Two days after the second transfection, the efficiency of gene editing was measured using a mutation-specific nuclease assay.

*Example 22 Transfection of Cells with Synthetic RNA Containing Non-Canonical Nucleotides and DNA Encoding a Repair Template*

For transfection in 6-well plates, 1µg RNA encoding gene-editing proteins targeting exon 16 of the human APP gene, 1µg single-stranded repair template DNA containing a PstI restriction site that was not present in the target cells, and 6µL transfection reagent (Lipofectamine RNAiMAX, Life Technologies Corporation) were first diluted separately in complexation medium (Opti-MEM, Life Technologies Corporation) to a total volume of 120µL. Diluted RNA, repair template, and transfection reagent were then mixed and incubated for 15min at room temperature, according to the transfection reagent-manufacturer's instructions. Complexes were added to cells in culture. Approximately 120µL of complexes were added to each well of a 6-well plate, which already contained 2mL of transfection medium per well. Plates were shaken gently to distribute the complexes throughout the well. Cells were incubated with complexes for 4 hours to overnight, before replacing the medium with fresh transfection medium (2mL/well). The next day, the medium was changed to DMEM + 10% FBS. Two days after transfection, genomic DNA was isolated and purified. A region within the APP gene was amplified by PCR, and the amplified product was digested with PstI and analyzed by gel electrophoresis.

*Example 23 in vivo RiboSlice Safety Study*

40 female NCr nu/nu mice were injected subcutaneously with  $5 \times 10^6$  MDA-MB-231 tumor cells in 50% Matrigel (BD Biosciences). Cell injection volume was 0.2mL/mouse. The age of the mice at the start of the study was 8 to 12 weeks. A pair match was conducted, and animals were divided into 4 groups of 10 animals each when the tumors reached an average size of 100-150mm<sup>3</sup>, and treatment was begun. Body weight was measured every day for the first 5 days, and then biweekly to the end of the study. Treatment consisted of RiboSlice BIRC5-1.2 complexed with a vehicle (Lipofectamine 2000, Life Technologies Corporation). To prepare the dosing solution for each group, 308µL of complexation buffer (Opti-MEM, Life Technologies Corporation) was pipetted into each of two sterile, RNase-free 1.5mL tubes. 22µL of RiboSlice BIRC5-1.2 (500ng/µL) was added to one of the two tubes, and the contents of the tube were mixed by pipetting. 22µL of vehicle was added to the second tube. The contents of the second tube were mixed, and then transferred to the first tube, and mixed with the contents of the first tube by pipetting to form complexes. Complexes were incubated at room temperature for 10min. During the incubation, syringes were loaded. Animals were injected either intravenously or intratumorally with a total dose of 1µg RNA/animal in 60µL total volume/animal. A total of 5 treatments were given, with injections performed every other day. Doses were not adjusted for body weight. Animals were followed for 17 days. No significant reduction in mean body weight was observed, demonstrating the *in vivo* safety of RiboSlice gene-editing RNA.

*Example 24 Screening of Reagents for Delivery of Nucleic Acids to Cells*

Delivery reagents including polyethyleneimine (PEI), various commercial lipid-based transfection reagents, a peptide-based transfection reagent (N-TER, Sigma-Aldrich Co. LLC.), and several lipid-based and sterol-based delivery reagents were screened for transfection efficiency and toxicity *in vitro*. Delivery reagents were  
5 complexed with RiboSlice BIRC5-1.2, and complexes were delivered to HeLa cells in culture. Toxicity was assessed by analyzing cell density 24h after transfection. Transfection efficiency was assessed by analyzing morphological changes. The tested reagents exhibited a wide range of toxicities and transfection efficiencies. Reagents containing a higher proportion of ester bonds exhibited lower toxicities than reagents containing a lower proportion of ester bonds or no ester bonds.

10 *Example 25 High-Concentration Liposomal RiboSlice*

High-Concentration Liposomal RiboSlice was prepared by mixing 1µg RNA at 500ng/µL with 3µL of complexation medium (Opti-MEM, Life Technologies Corporation), and 2.5µL of transfection reagent (Lipofectamine 2000, Life Technologies Corporation) per µg of RNA with 2.5µL of complexation medium. Diluted RNA and transfection reagent were then mixed and incubated for 10min at room temperature to form  
15 High-Concentration Liposomal RiboSlice. Alternatively, a transfection reagent containing DOSPA or DOSPER is used.

*Example 26 In Vivo RiboSlice Efficacy Study – Subcutaneous Glioma Model*

40 female NCr nu/nu mice were injected subcutaneously with  $1 \times 10^7$  U-251 tumor cells. Cell injection volume was 0.2mL/mouse. The age of the mice at the start of the study was 8 to 12 weeks. A pair match was  
20 conducted, and animals were divided into 4 groups of 10 animals each when the tumors reached an average size of 35-50mm<sup>3</sup>, and treatment was begun. Body weight was measured every day for the first 5 days, and then biweekly to the end of the study. Caliper measurements were made biweekly, and tumor size was calculated. Treatment consisted of RiboSlice BIRC5-2.1 complexed with a vehicle (Lipofectamine 2000, Life Technologies Corporation). To prepare the dosing solution, 294µL of complexation buffer (Opti-MEM, Life  
25 Technologies Corporation) was pipetted into a tube containing 196µL of RiboSlice BIRC5-1.2 (500ng/µL), and the contents of the tube were mixed by pipetting. 245µL of complexation buffer was pipetted into a tube containing 245µL of vehicle. The contents of the second tube were mixed, and then transferred to the first tube, and mixed with the contents of the first tube by pipetting to form complexes. Complexes were incubated at room temperature for 10min. During the incubation, syringes were loaded. Animals were injected  
30 intratumorally with a total dose of either 2µg or 5µg RNA/animal in either 20µL or 50µL total volume/animal. A total of 5 treatments were given, with injections performed every other day. Doses were not adjusted for body weight. Animals were followed for 25 days.

*Example 27 Liposome Formulation and Nucleic-Acid Encapsulation*

Liposomes are prepared using the following formulation: 3.2mg/mL N-(carbonyl-ethoxypolyethylene glycol 2000)-1,2-distearoyl-sn-glycero-3-phosphoethanolamine (MPEG2000-DSPE), 9.6mg/mL fully hydrogenated phosphatidylcholine, 3.2mg/mL cholesterol, 2mg/mL ammonium sulfate, and histidine as a buffer. pH is controlled using sodium hydroxide and isotonicity is maintained using sucrose. To form liposomes, lipids are mixed in an organic solvent, dried, hydrated with agitation, and sized by extrusion through a polycarbonate filter with a mean pore size of 800nm. Nucleic acids are encapsulated by combining 10 $\mu$ g of the liposome formulation per 1 $\mu$ g of nucleic acid and incubating at room temperature for 5 minutes.

*Example 28 Folate-Targeted Liposome Formulation*

Liposomes are prepared according to Example 62, except that 0.27mg/mL 1,2-distearoyl-sn-glycero-3-phosphoethanolamine-N-[folate(polyethylene glycol)-5000] (FA-MPEG5000-DSPE) is added to the lipid mixture.

*Example 29 Therapy Comprising Liposomal Protein-Encoding RNA*

Liposomes encapsulating synthetic RNA encoding a therapeutic protein, synthesized according to Example 1, are prepared according to Example 27 or Example 28. The liposomes are administered by injection or intravenous infusion.

*Example 30 Generation of elastin ivT-RNA template*

Total RNA was extracted from neonatal human dermal fibroblasts using the RNeasy mini kit (QIAGEN GmbH), according to the manufacturer's instructions. cDNA encoding human elastin was prepared using MonsterScript™ Reverse Transcriptase (Epicentre Biotechnologies) and the primer: AAAAAAACCGGTTCATTTTCTCTCCGGCCAC. An *in vitro* transcription (ivT) template was prepared from the cDNA by PCR amplification of the elastin coding sequence (CDS) using the primers: F: AAAAAAGCTAGCATGGCGGGTCTGACG, and R: AAAAAAACCGGTTTCATTTTCTCTCCGGCCAC. The PCR product was then purified using agarose gel electrophoresis and the QIAquick Gel Extraction Kit (QIAGEN GmbH) and was cloned into a vector containing the human beta globin (HBB) 5' and 3' untranslated regions and a strong Kozak sequence. The vector was amplified, purified, and linearized prior to RNA synthesis.

*Example 31 Synthesis of Elastin RNA*

RNA encoding human elastin was synthesized using the DNA template of Example 30 and the T7 High Yield RNA Synthesis Kit (New England Biolabs, Inc.), according to the manufacturer's instructions (Table 4). Samples of the RNA were analyzed by agarose gel electrophoresis to assess the quality of the RNA (FIG. 1).

The RNA was then diluted to 200ng/ $\mu$ L and an RNase inhibitor (Superase-In™, Life Technologies Corporation) was added at a concentration of 1 $\mu$ L/200 $\mu$ g of RNA. The RNA solution was stored at 4C.

*Example 32 Production of Octanoate-Treated Human Serum Albumin*

5 A 10% solution of HSA was pre-incubated with 16mM sodium octanoate (Sigma-Aldrich Co. LLC), and was incubated at 37C for 3 hours before assembly of the complete medium.

*Example 33 Formulation for in vivo delivery of nucleic acids*

The formulation for *in vivo* delivery of nucleic acids is prepared by combining RNA synthesized according to Example 31 and human serum albumin treated according to Examples 8, 9 and/or 32 in a suitable buffer (e.g., water, DMEM/F12, complexation medium, Opti-MEM, etc.).

10 *Example 34 Increasing elastin production in skin by transdermal injection via syringe of treated albumin and RNA encoding elastin*

The formulation of example 33 is loaded into an insulin syringe with a 28-gauge 0.5-inch needle and delivered to the dermis of a patient through the epidermis. Additional doses are administered as necessary.

15 *Example 35 Increasing elastin production in skin by intradermal injection via motorized microneedle array of treated albumin and RNA encoding elastin*

The formulation of example 33 is loaded into the chamber of a motorized microneedle array set to a penetration depth of approximately 0.1 mm. The microneedle array delivers the formulation to the dermis of a patient through the epidermis.

20 *Example 36 Increasing collagen production in skin by transdermal injection of treated albumin and RNA encoding collagen*

The formulation of example 33 is prepared using RNA encoding human collagen type I and/or type III. The formulation is delivered as in Example 34 or 35.

*Example 37 Increasing production of actin in skeletal muscle by intramuscular injection of treated albumin and RNA encoding actin*

25 The formulation of example 33 is prepared using RNA encoding skeletal alpha actin. The formulation is delivered to the patient via intramuscular injection.

*Example 38 Wound healing treatment*

The formulation of example 33 is prepared using RNA encoding basic fibroblast growth factor. The formulation is delivered as in Example 34 or 35.

*Example 39 Anti-scarring treatment*

The formulation of example 33 is prepared using RNA encoding collagenase. The formulation is delivered as in Example 34 or 35.

*Example 40 Generation of Tyrosinase ivT-RNA Template*

- 5 Total RNA was extracted from human epidermal melanocytes using the RNeasy mini kit (QIAGEN GmbH), according to the manufacturer's instructions. cDNA encoding human tyrosinase was prepared using MonsterScript™ Reverse Transcriptase (Epicentre Biotechnologies). An *in vitro* transcription (ivT) template was prepared from the cDNA by PCR amplification of the tyrosinase coding sequence (CDS). The PCR product was then purified using agarose gel electrophoresis and the QIAquick Gel Extraction Kit (QIAGEN
- 10 GmbH) and was cloned into a vector containing the human beta globin (HBB) 5' and 3' untranslated regions and a strong Kozak sequence. The vector was amplified, purified, and linearized prior to RNA synthesis.

*Example 41 Synthesis of Tyrosinase RNA*

- RNA encoding human tyrosinase was synthesized according to Example 1, using the DNA template of Example 40 and the T7 High Yield RNA Synthesis Kit (New England Biolabs, Inc.), according to the
- 15 manufacturer's instructions (Table 4). Samples of the RNA were analyzed by agarose gel electrophoresis to assess the quality of the RNA. The RNA was then diluted to 1 µg/µL. The RNA solution was stored at 4°C.

*Example 42 Production of Octanoate-Treated Human Serum Albumin*

A 10% solution of HSA was pre-incubated with 16mM sodium octanoate (Sigma-Aldrich Co. LLC), and was incubated at 37°C for 3 hours before assembly of the complete medium.

- 20 *Example 43 Increasing Melanin Production in Skin by Transdermal Injection via Syringe of RNA Encoding Tyrosinase*

The RNA of Example 41 was loaded into a syringe and delivered to the dermis of the ventral forearm of a healthy 33 year-old male patient over the course of approximately 30 seconds.

- 25 *Example 44 Increasing Melanin Production in Skin by Combined Delivery of RNA Encoding Tyrosinase and Electroporation*

- The area of skin treated in Example 43 was exposed to electrical pulses of between 10V and 155V and between approximately 10 milliseconds and approximately 1 second using a two-electrode array electrically connected to a capacitor. The patient reported a tingling sensation at all voltages and penetration depths. The treated area became darker after 24-48 hours (see **FIG. 16**). The experiment was repeated several times,
- 30 with similar results.

*Example 45 Increasing Melanin Production in Skin by Topical or Intradermal Application of RNA Encoding Tyrosinase*

The RNA of Example 41 or the liposomes of Example 29 are applied directly to the skin, with or without disruption of the stratum corneum or injected intradermally using a dose of one microgram or less per square centimeter. Optionally, an electric field is applied as in Example 44 or using a surface-contact patch to enhance delivery of the RNA.

*Example 46 Increasing Elastin Production in Skin by Transdermal Delivery of RNA Encoding Elastin*

RNA encoding elastin was prepared according to Example 1. The RNA is delivered as in Example 43, 44 or 45.

10 *Example 47 Increasing Collagen Production in Skin by Transdermal Delivery of RNA Encoding Collagen*

RNA encoding collagen was prepared according to Example 1. The RNA is delivered as in Example 43, 44 or 45.

*Example 48 Anemia Therapy Comprising Delivery of RNA Encoding Erythropoietin or Darbepoetin*

RNA encoding darbepoetin alfa was prepared according to Example 1. The RNA is delivered as in Example 43, 44 or 45.

*Example 49 Increasing Production of Actin in Skeletal Muscle by Intramuscular Delivery of RNA Encoding Actin*

RNA encoding actin is prepared according to Example 1. The RNA is delivered to the patient via intramuscular injection with or without the use of an electric field as in Example 43, 44 or 45.

20 *Example 50 Wound Healing Treatment*

RNA encoding basic fibroblast growth factor is prepared according to Example 1. The RNA is delivered as in Example 43, 44 or 45.

*Example 51 Anti-Scarring Treatment*

RNA encoding collagenase is prepared according to Example 1. The RNA is delivered as in Example 43, 44 or 45.

*Example 52 Production of Botulinum Toxin*

RNA encoding botulinum toxin is prepared according to Example 1. The RNA is delivered as in Example 43, 44 or 45.



*Example 53 Increasing Collagen Production in Skin Cells by Transfection with RNA Encoding Collagen I*

RNA comprising the coding sequence of the human COL1A1 gene was synthesized according to Example 1. Primary human dermal fibroblasts were plated in wells of a 24-well plate, and were transfected according to Example 2. Between 24 and 72 hours after transfection, the cells were fixed and stained using an antibody  
5 targeting collagen I. Many extracellular deposits of collagen were visible in the transfected wells (**FIG. 17**).

*Example 54 Increasing Collagen Production in Skin Cells by Transfection with RNA Encoding Collagen VII*

RNA comprising the coding sequence of the human COL7 gene was synthesized according to Example 1. Primary human dermal fibroblasts were plated in wells of a 24-well plate, and were transfected according to Example 2. Between 24 and 72 hours after transfection, the cells were fixed and stained using an antibody  
10 targeting collagen VII. Transfected cells exhibited high levels of collagen VII, compared to an un-transfected control (**FIG. 18**).

*Example 55 Increasing Collagen Production in Skin by Transdermal Injection via Syringe of RNA Encoding Collagen I or Collagen VII*

RNA comprising the coding sequence of the human COL1A1 gene or the human COL7 gene was  
15 synthesized according to Example 1. The RNA is loaded into a syringe and delivered to the dermis of a patient over the course of approximately 30 seconds or as in Example 43, 44 or 45.

*Example 56 Increasing Collagen Production in Skin by Combined Delivery of RNA Encoding Collagen I or Collagen VII and Electroporation*

The area of skin treated in Example 55 is exposed to electrical pulses of between 10V and 155V and  
20 between approximately 50 microseconds and approximately 1 second using a multi-electrode array electrically connected to a power source.

**EQUIVALENTS**

Those skilled in the art will recognize, or be able to ascertain, using no more than routine experimentation, numerous equivalents to the specific embodiments described specifically herein. Such equivalents are  
25 intended to be encompassed in the scope of the following claims.

**INCORPORATION BY REFERENCE**

All patents and publications referenced herein are hereby incorporated by reference in their entireties.

**THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:**

1. An *in vivo* method for treating a dystrophic epidermolysis bullosa patient comprising delivering a synthetic RNA encoding collagen type VII to the patient's keratinocytes by injection to the epidermis, thereby resulting in the amelioration of one or more of the dystrophic epidermolysis bullosa patient's symptoms.
2. The method of claim 1, wherein the synthetic RNA comprises a non-canonical nucleotide selected from the group consisting of 5-methyluridine, 5-hydroxyuridine, pseudouridine, 5-methylpseudouridine, 5-hydroxypseudouridine, 5-methylcytidine, and 5-hydroxycytidine.
3. The method of claim 1 or claim 2, wherein the synthetic RNA comprises 5-hydroxymethylcytidine.
4. The method of any one of claims 1 to 3, wherein the synthetic RNA comprises 5-methyluridine at about 40% of the uridine residues.
5. The method of any one of claims 1 to 4, wherein the collagen type VII is collagen type VII (A1).
6. The method of any one of claims 1 to 5, wherein the synthetic RNA encodes the amino acid sequence of SEQ ID NO: 78.
7. The method of any one of claims 1 to 6, further resulting in increased expression of collagen type VII within between about 24 and about 72 hours of delivery.
8. The method of any one of claims 1 to 7, wherein the synthetic RNA encodes the coding sequence of a human COL7 gene.
9. An *in vivo* method for treating epidermolysis bullosa, comprising delivering a synthetic RNA encoding a gene-editing protein that targets a COL7 gene to a patient in need thereof and inducing a single-strand or double-strand break in the COL7 gene of the patient's keratinocytes, thereby eliminating a mutation that is at least partially responsible for a disease phenotype, wherein: the synthetic RNA is delivered to the patient's keratinocytes by injection to the epidermis and the gene-editing protein comprises a DNA-binding domain and a nuclease domain.
10. The method of claim 9, wherein the synthetic RNA comprises a non-canonical nucleotide selected from the group consisting of 5-methyluridine, 5-hydroxyuridine, pseudouridine, 5-methylpseudouridine, 5-hydroxypseudouridine, 5-methylcytidine, and 5-hydroxycytidine.

11. The method of claim 9 or claim 10, further comprising delivering a repair template to the patient.
12. The method of claim 11, wherein the repair template is a single-stranded DNA molecule or a double-stranded DNA molecule.
13. The method of claim 11, wherein the repair template does not contain a binding site of the gene-editing protein.
14. The method of claim 13, wherein the repair template encodes an amino-acid sequence that is encoded by a DNA sequence that comprises a binding site of the gene-editing protein.
15. The method of any one of claims 9 to 14, wherein the gene-editing protein targets a nucleic acid sequence that encodes the amino acid sequence of SEQ ID NO: 78.
16. The method of any one of claims 9 to 15, wherein the gene-editing protein is selected from the group consisting of a nuclease, a transcription activator-like effector nuclease (TALEN), a zinc-finger nuclease, a meganuclease, a nickase, and a clustered regularly interspaced short palindromic repeat (CRISPR)-associated protein.
17. The method of any one of claims 9 to 16, further resulting in editing of the COL7 gene.
18. An *in vivo* method for treating dystrophic epidermolysis bullosa, comprising  
delivering a synthetic RNA encoding a gene-editing protein that targets a COL7 gene to a patient in need thereof and  
delivering a COL7 repair template to the patient, thereby editing the COL7 gene, wherein:  
the synthetic RNA and repair template are delivered to the patient's keratinocytes by injection to the epidermis and  
the gene-editing protein comprises a DNA-binding domain and a nuclease domain and causes a double-strand break in the COL7 gene of the patient's keratinocytes.
19. The method of claim 18, wherein the gene-editing protein corrects or eliminates, either alone or in combination with one or more other molecules or gene-editing proteins, a mutation that is at least partially responsible for a disease phenotype.
20. The method of claim 18 or 19, wherein the COL7 repair template is a single-stranded DNA molecule or a double-stranded DNA molecule.
21. The method of any one of claims 18 to 20, wherein the COL7 repair template does not contain a binding site of the gene-editing protein.

22. The method of any one of claims 18 to 21, wherein the gene-editing protein targets a nucleic acid sequence that encodes the amino acid sequence of SEQ ID NO: 78.
23. The method of any one of claims 18 to 22, wherein the gene-editing protein is selected from the group consisting of a nuclease, a transcription activator-like effector nuclease (TALEN), a zinc-finger nuclease, a meganuclease, a nickase, and a clustered regularly interspaced short palindromic repeat (CRISPR)-associated protein.
24. The method of any one of claims 18 to 23, wherein the synthetic RNA molecule further comprises one or more of a 5'-cap, a 5'-cap 1 structure, and a 3'-poly(A) tail.

FIG. 1

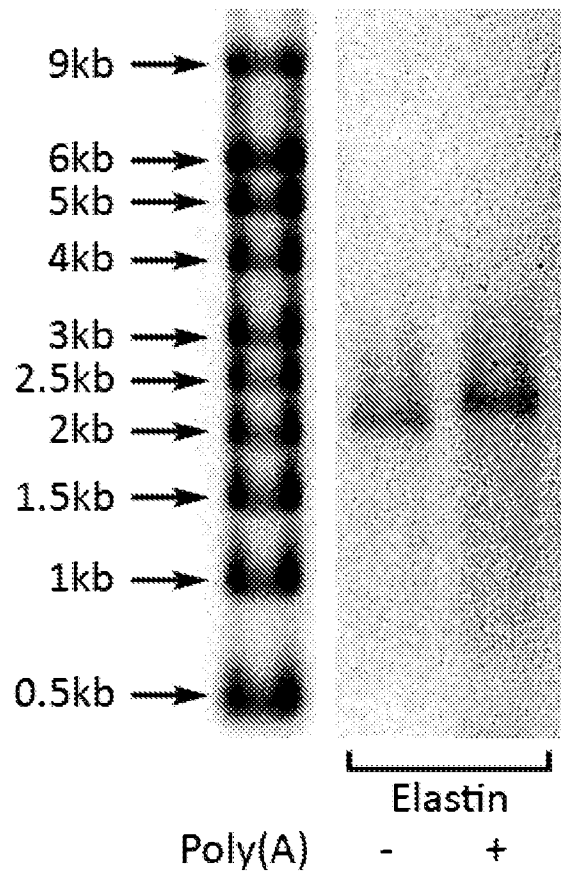


FIG. 2

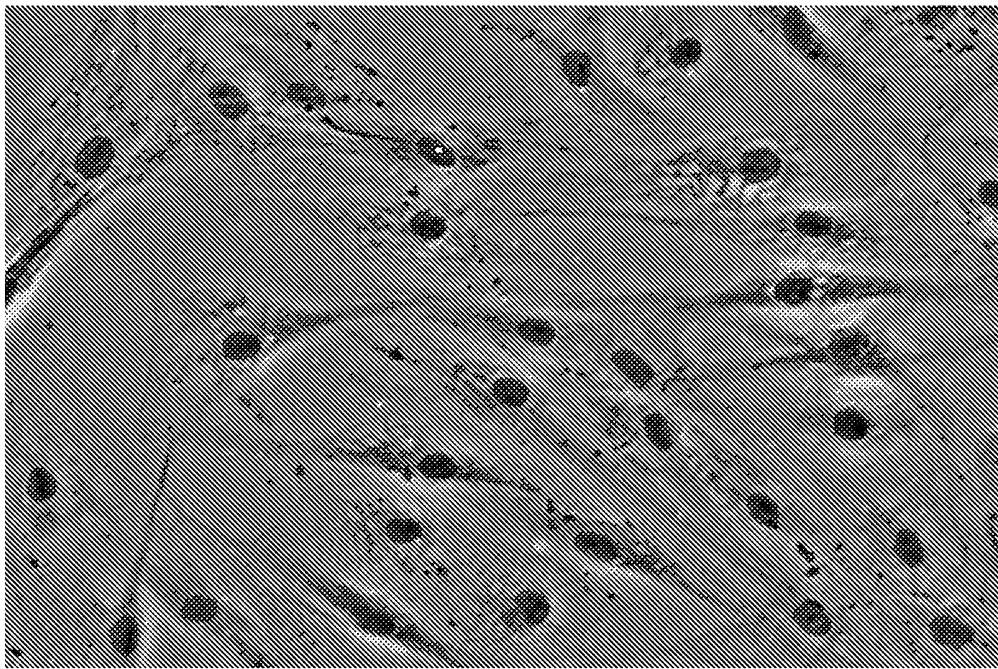


FIG. 3

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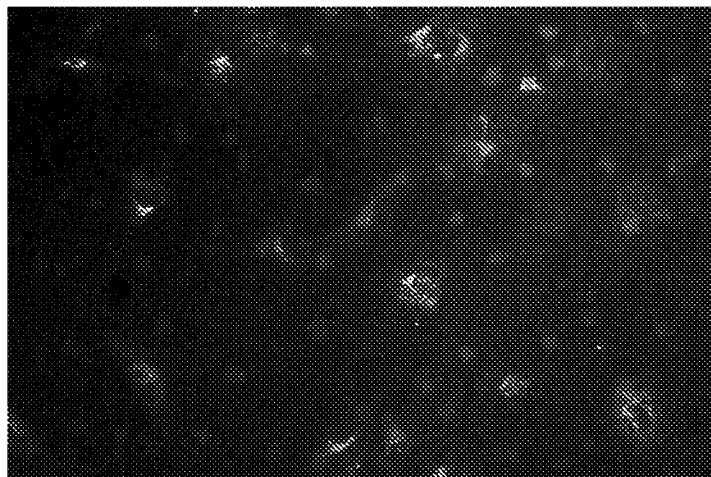
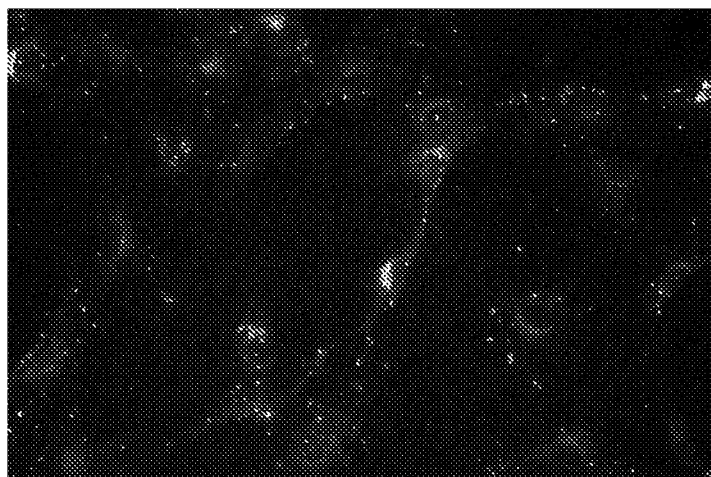
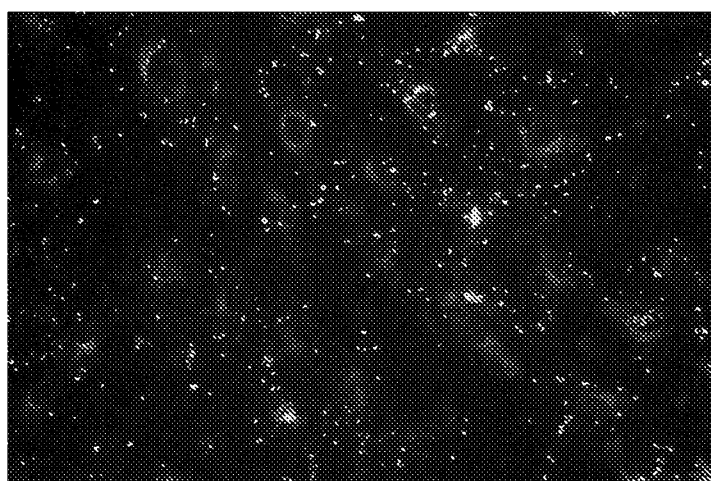
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FIG. 4

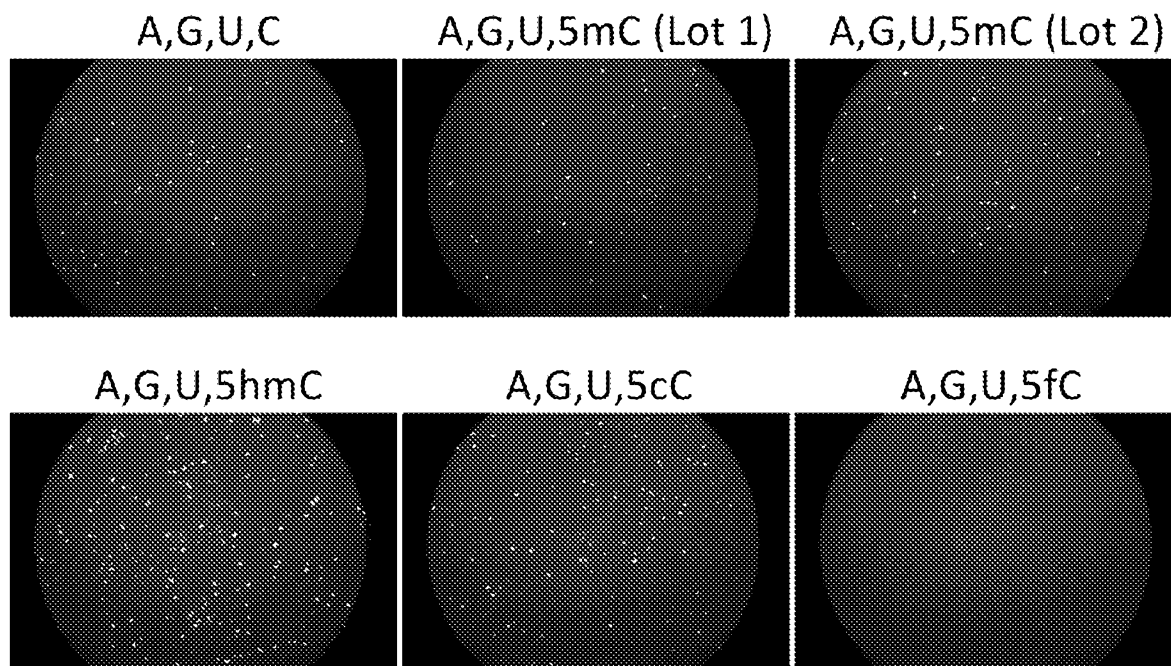


FIG. 5

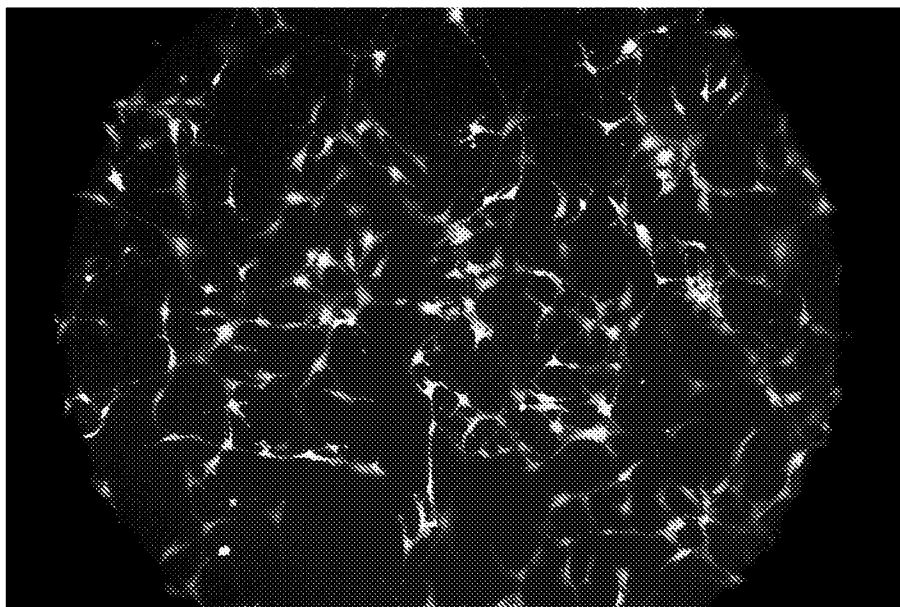


FIG. 6

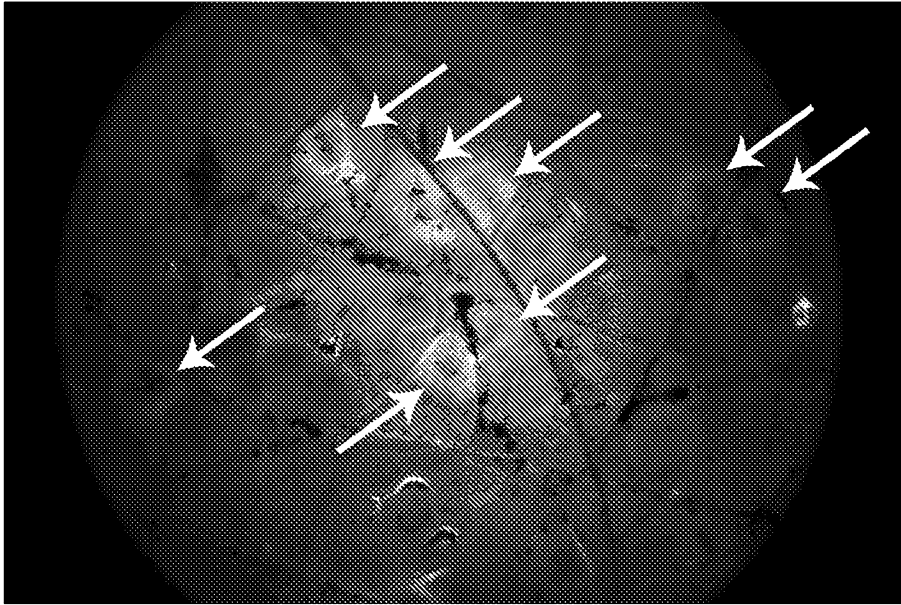


FIG. 7

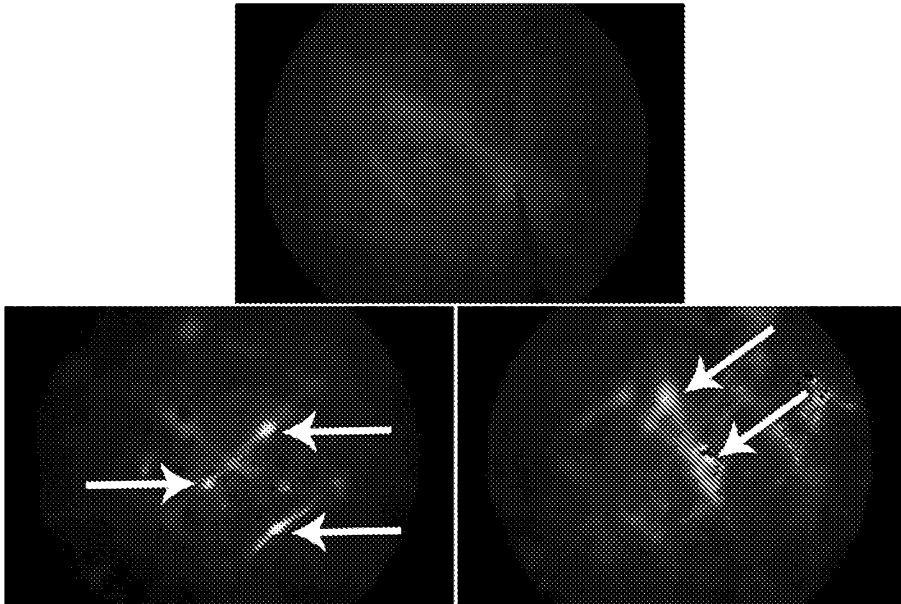




FIG. 8

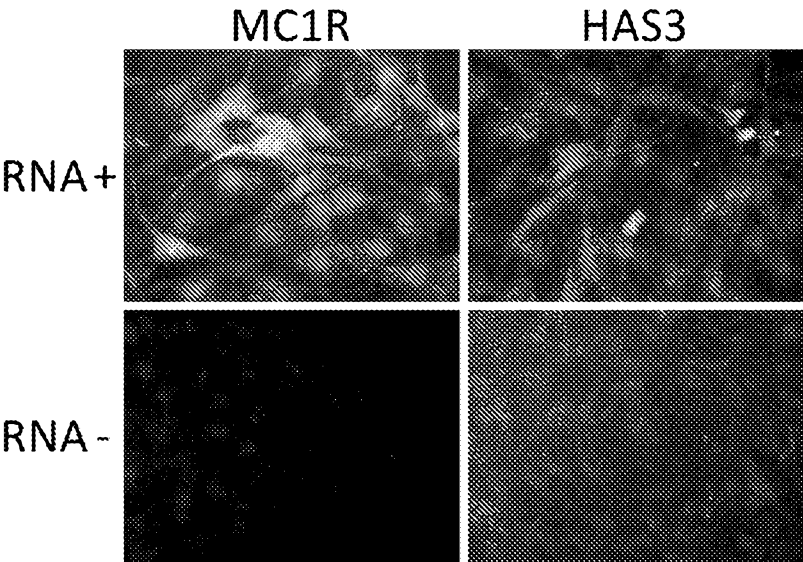


FIG. 9

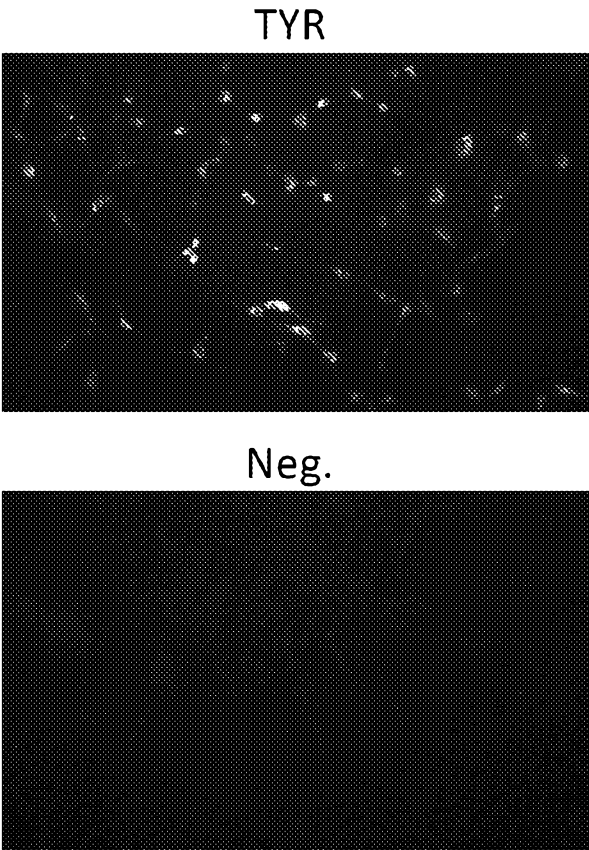


FIG. 10

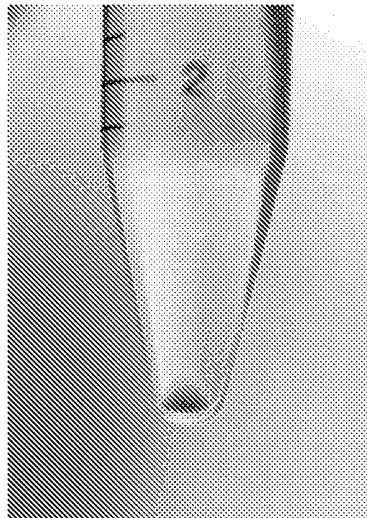


FIG. 11

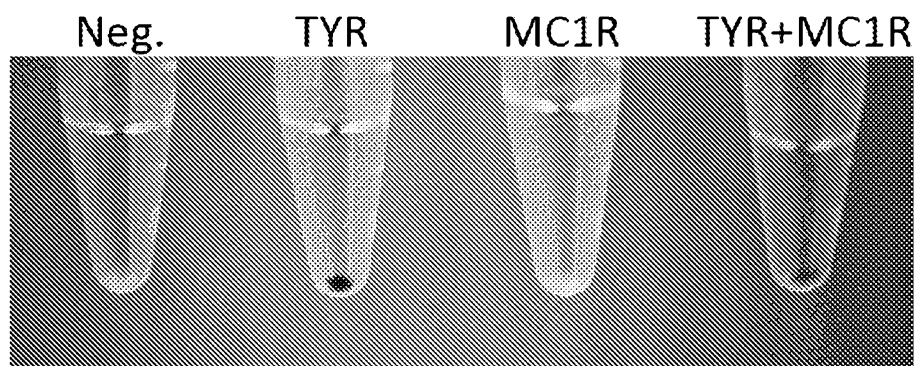


FIG. 12

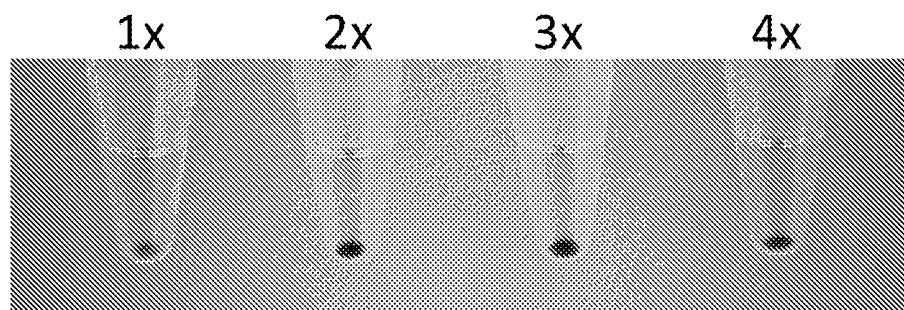


FIG. 13

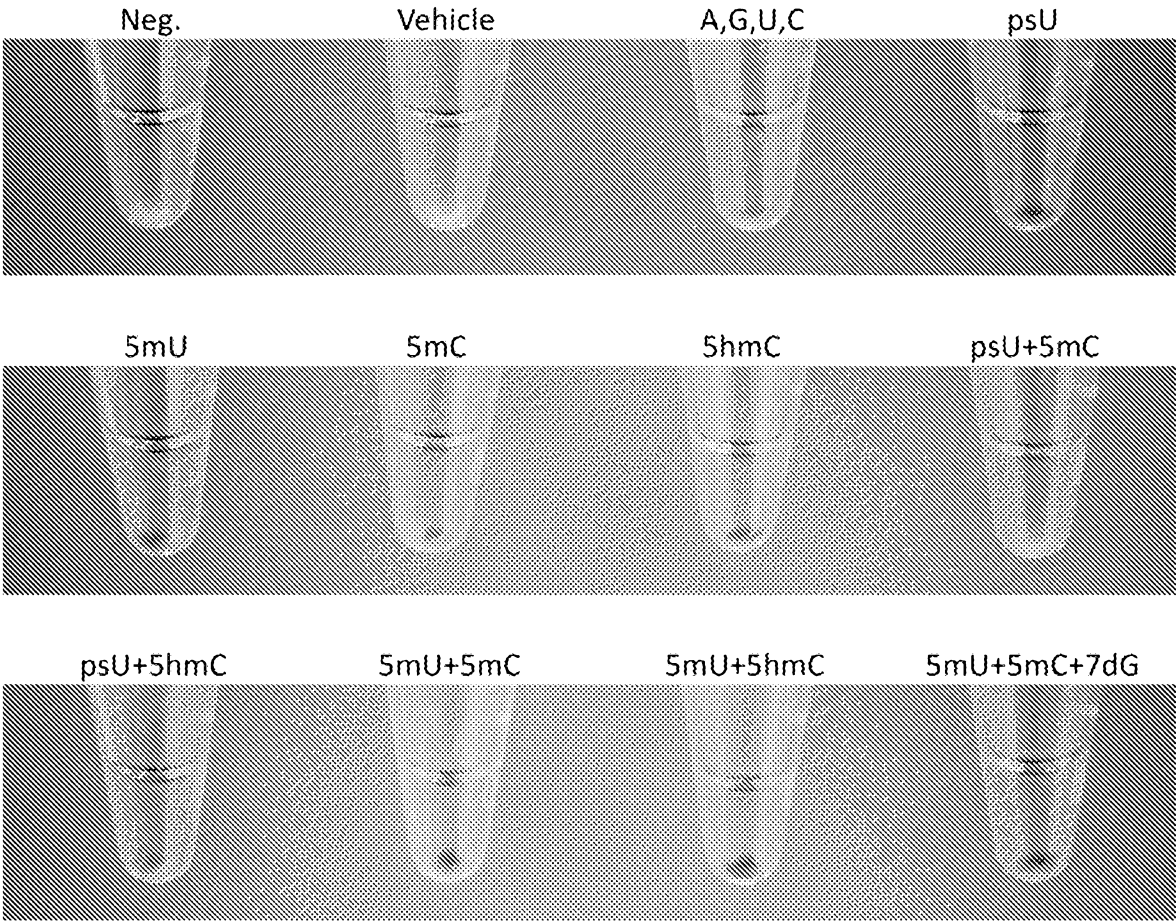


FIG. 14

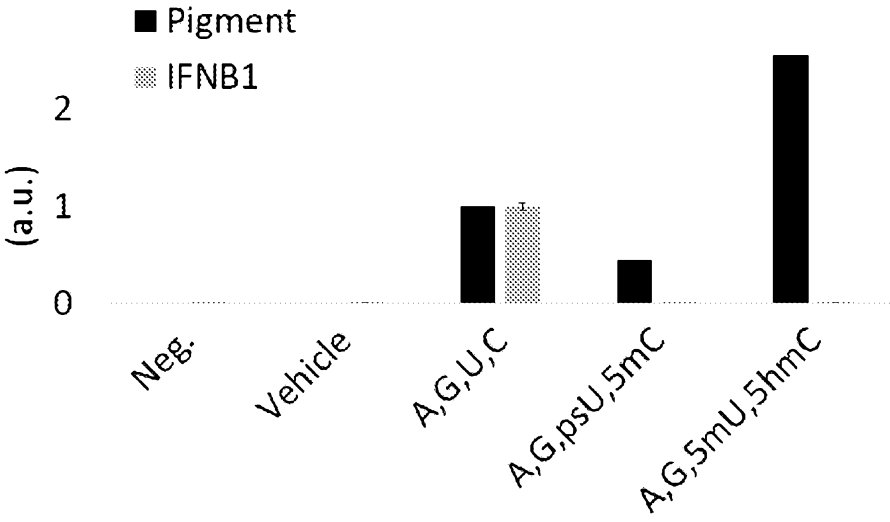


FIG. 15

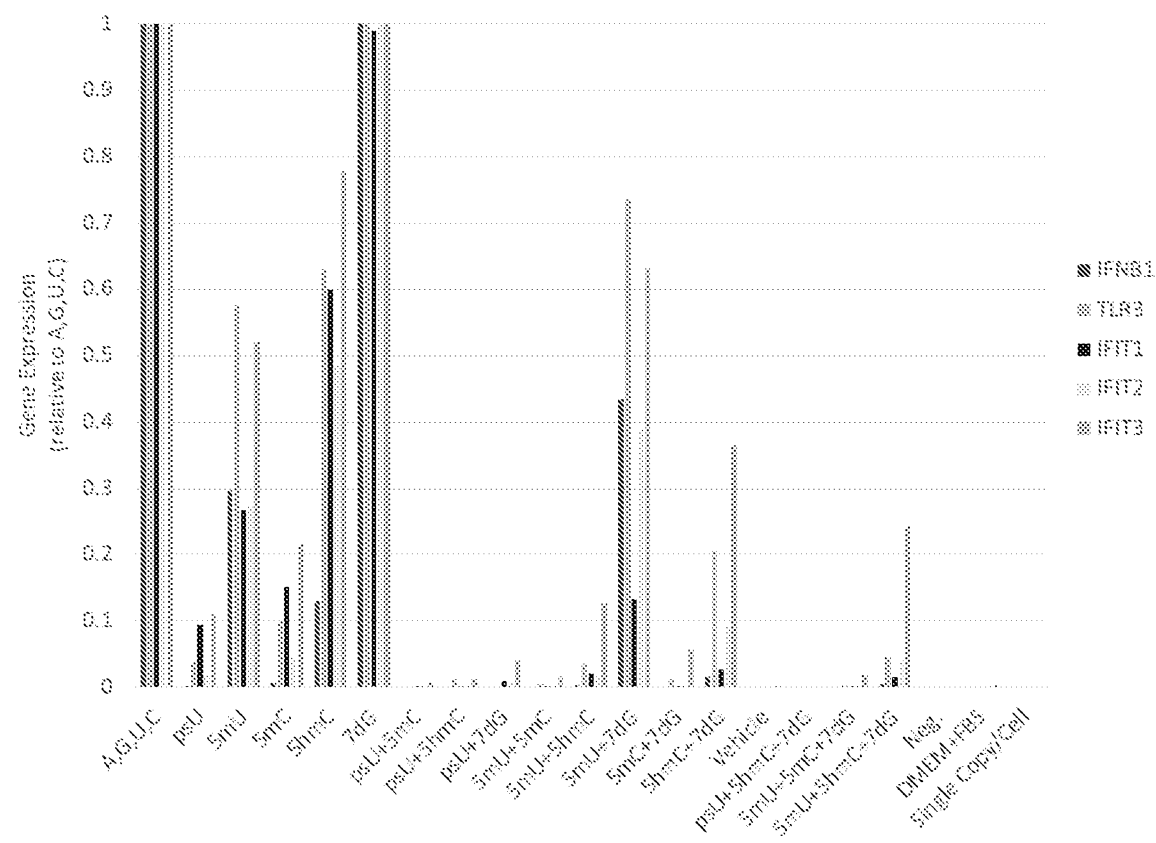


FIG. 16

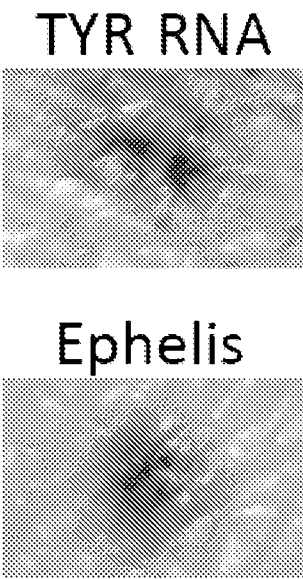


FIG. 17

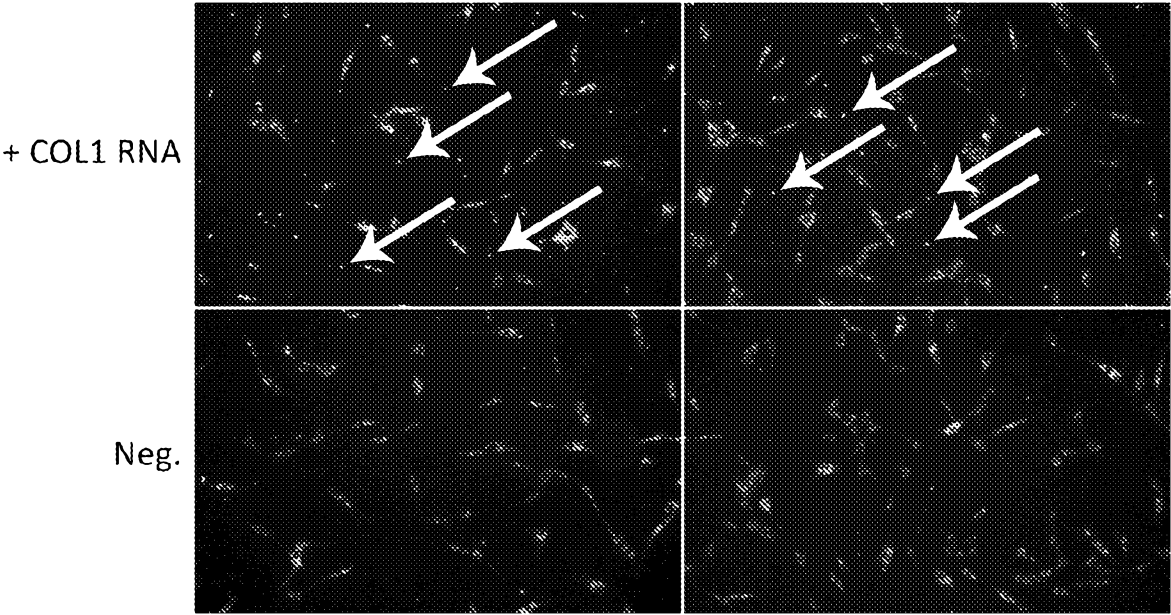
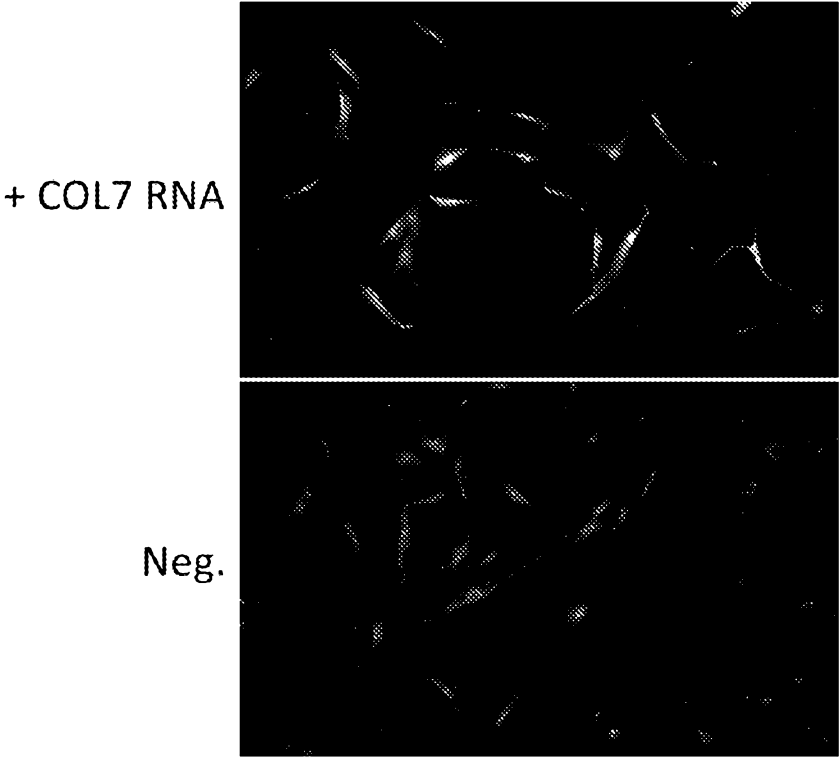


FIG. 18



FAB-008PC-SequenceListing  
SEQUENCE LISTING

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Rohde, Christopher

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Ser	His	Thr	Asp	Ala	Met	Gly	Arg	Tyr	Leu	Arg	Gln	Phe	Thr	Glu	Arg
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Ser His Thr Asp Ala Met Gly Arg Tyr Leu Arg Gln Phe Thr Glu Arg  
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Lys Glu Glu Ile Lys Pro Thr Trp Trp Asp Ile Ala Pro Glu His Leu  
115 120 125

Asp Asn Thr Tyr Phe Ala Tyr Val Ser Gly Ser Phe Ser Gly Asn Tyr  
130 135 140

Lys Glu Gln Leu Gln Lys Phe Arg Gln Asp Thr Asn His Leu Gly Gly  
145 150 155 160

Ala Leu Glu Phe Val Lys Leu Leu Leu Leu Ala Asn Asn Tyr Lys Thr  
165 170 175

Gln Lys Met Ser Lys Lys Glu Val Lys Lys Ser Ile Leu Asp Tyr Asn  
180 185 190

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Ile Ser Tyr  
195

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<212> PRT  
<213> Homo sapiens

<400> 3

Val Leu Glu Lys Ser Asp Ile Glu Lys Phe Lys Asn Gln Leu Arg Thr  
1 5 10 15

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

Ser Lys Pro Lys Thr Ser Asn Val Glu Asn Thr Glu Phe Glu Ala Ile  
35 40 45

Ser Thr Lys Ile Phe Thr Asp Glu Leu Gly Phe Ser Gly Lys His Leu  
50 55 60

Gly Gly Ser Asn Lys Pro Asp Gly Leu Leu Trp Asp Asp Asp Cys Ala  
65 70 75 80

Ile Ile Leu Asp Ser Lys Ala Tyr Ser Glu Gly Phe Pro Leu Thr Ala  
85 90 95

Ser His Thr Asp Ala Met Gly Arg Tyr Leu Arg Gln Phe Thr Glu Arg  
100 105 110

Lys Glu Glu Ile Lys Pro Thr Trp Trp Asp Ile Ala Pro Glu His Leu  
115 120 125

Asp Asn Thr Tyr Phe Ala Tyr Val Ser Gly Ser Phe Ser Gly Asn Tyr  
130 135 140

Lys Glu Gln Leu Gln Lys Phe Arg Gln Asp Thr Asn His Leu Gly Gly  
145 150 155 160

Ala Leu Glu Phe Val Lys Leu Leu Leu Leu Ala Asn Asn Tyr Lys Thr  
165 170 175

Gln Lys Met Ser Lys Lys Glu Val Lys Lys Ser Ile Leu Asp Tyr Asn  
180 185 190

Ile Ser Tyr  
195

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<213> Homo sapiens



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<400> 4

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

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<210> 5

<211> 191

<212> PRT

<213> Homo sapiens

<400> 5

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

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Ser Lys Pro Val Glu Asn Thr Glu Phe Glu Ala Ile Ser Thr Lys Ile  
35 40 45

Phe Thr Asp Glu Leu Gly Phe Ser Gly Glu His Leu Gly Gly Ser Asn  
50 55 60

Lys Pro Asp Gly Leu Leu Trp Asp Asp Asp Cys Ala Ile Ile Leu Asp  
65 70 75 80

Ser Lys Ala Tyr Ser Glu Gly Phe Pro Leu Thr Ala Ser His Thr Asp  
85 90 95

Ala Met Gly Arg Tyr Leu Arg Gln Phe Thr Glu Arg Lys Glu Glu Ile  
100 105 110

Lys Pro Thr Trp Trp Asp Ile Ala Pro Glu His Leu Asp Asn Thr Tyr  
115 120 125

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

Gln Lys Phe Arg Gln Asp Thr Asn His Leu Gly Gly Ala Leu Glu Phe  
145 150 155 160

Val Lys Leu Leu Leu Leu Ala Asn Asn Tyr Lys Thr Gln Lys Met Ser  
165 170 175

Lys Lys Glu Val Lys Lys Ser Ile Leu Asp Tyr Asn Ile Ser Tyr  
180 185 190

<210> 6  
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<213> Homo sapiens  
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Val Leu Glu Lys Ser Asp Ile Glu Lys Phe Lys Asn Gln Leu Arg Thr  
1 5 10 15

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

Ser Lys Lys Lys Thr Ser Asn Val Glu Asn Thr Glu Phe Glu Ala Ile  
35 40 45

Ser Thr Lys Ile Phe Thr Asp Glu Leu Gly Phe Ser Gly Lys His Leu  
50 55 60

Gly Gly Ser Asn Lys Pro Asp Gly Leu Leu Trp Asp Asp Asp Cys Ala  
65 70 75 80

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Ile Ile Leu Asp Ser Lys Ala Tyr Ser Glu Gly Phe Pro Leu Thr Ala  
85 90 95

Ser His Thr Asp Ala Met Gly Arg Tyr Leu Arg Gln Phe Thr Glu Arg  
100 105 110

Lys Glu Glu Ile Lys Pro Thr Trp Trp Asp Ile Ala Pro Glu His Leu  
115 120 125

Asp Asn Thr Tyr Phe Ala Tyr Val Ser Gly Ser Phe Ser Gly Asp Tyr  
130 135 140

Lys Glu Gln Leu Gln Lys Phe Arg Gln Asp Thr Asn His Leu Gly Gly  
145 150 155 160

Ala Leu Glu Phe Val Lys Leu Leu Leu Leu Ala Asn Asn Tyr Lys Thr  
165 170 175

Gln Lys Met Ser Lys Lys Glu Val Lys Lys Ser Ile Leu Asp Tyr Asn  
180 185 190

Ile Ser Tyr  
195

<210> 7  
<211> 195  
<212> PRT  
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<400> 7

Val Leu Glu Lys Ser Asp Ile Glu Lys Phe Lys Asn Gln Leu Arg Thr  
1 5 10 15

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

Ser Lys Lys Lys Thr Ser Asn Val Glu Asn Thr Glu Phe Glu Ala Ile  
35 40 45

Ser Thr Lys Ile Phe Thr Asp Glu Leu Gly Phe Ser Gly Lys His Leu  
50 55 60

Gly Gly Ser Asn Lys Pro Asp Gly Leu Leu Trp Asp Asp Asp Cys Ala  
65 70 75 80

Ile Ile Leu Asp Ser Lys Ala Tyr Ser Glu Gly Phe Pro Leu Thr Ala  
85 90 95

Ser His Thr Asp Ala Met Gly Arg Tyr Leu Arg Gln Phe Thr Glu Arg  
100 105 110

Lys Glu Glu Ile Lys Pro Thr Trp Trp Asp Ile Ala Pro Glu His Leu  
Page 6

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115

120

125

Asp Asn Thr Tyr Phe Ala Tyr Val Ser Gly Ser Phe Ser Gly Asp Tyr  
 130 135 140

Lys Glu Gln Leu Gln Lys Phe Arg Gln Asn Thr Asn His Leu Gly Gly  
 145 150 155 160

Ala Leu Glu Phe Val Lys Leu Leu Leu Leu Ala Asn Asn Tyr Lys Thr  
 165 170 175

Gln Lys Met Ser Lys Lys Glu Val Lys Lys Ser Ile Leu Asp Tyr Asn  
 180 185 190

Ile Ser Tyr  
 195

<210> 8  
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 <213> Homo sapiens

<400> 8

Met Ala Gly His Leu Ala Ser Asp Phe Ala Phe Ser Pro Pro Pro Gly  
 1 5 10 15

Gly Gly Gly Asp Gly Pro Gly Gly Pro Glu Pro Gly Trp Val Asp Pro  
 20 25 30

Arg Thr Trp Leu Ser Phe Gln Gly Pro Pro Gly Gly Pro Gly Ile Gly  
 35 40 45

Pro Gly Val Gly Pro Gly Ser Glu Val Trp Gly Ile Pro Pro Cys Pro  
 50 55 60

Pro Pro Tyr Glu Phe Cys Gly Gly Met Ala Tyr Cys Gly Pro Gln Val  
 65 70 75 80

Gly Val Gly Leu Val Pro Gln Gly Gly Leu Glu Thr Ser Gln Pro Glu  
 85 90 95

Gly Glu Ala Gly Val Gly Val Glu Ser Asn Ser Asp Gly Ala Ser Pro  
 100 105 110

Glu Pro Cys Thr Val Thr Pro Gly Ala Val Lys Leu Glu Lys Glu Lys  
 115 120 125

Leu Glu Gln Asn Pro Glu Glu Ser Gln Asp Ile Lys Ala Leu Gln Lys  
 130 135 140

Glu Leu Glu Gln Phe Ala Lys Leu Leu Lys Gln Lys Arg Ile Thr Leu  
 145 150 155 160

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Gly Tyr Thr Gln Ala Asp Val Gly Leu Thr Leu Gly Val Leu Phe Gly  
 165 170 175  
 Lys Val Phe Ser Gln Thr Thr Ile Cys Arg Phe Glu Ala Leu Gln Leu  
 180 185 190  
 Ser Phe Lys Asn Met Cys Lys Leu Arg Pro Leu Leu Gln Lys Trp Val  
 195 200 205  
 Glu Glu Ala Asp Asn Asn Glu Asn Leu Gln Glu Ile Cys Lys Ala Glu  
 210 215 220  
 Thr Leu Val Gln Ala Arg Lys Arg Lys Arg Thr Ser Ile Glu Asn Arg  
 225 230 235 240  
 Val Arg Gly Asn Leu Glu Asn Leu Phe Leu Gln Cys Pro Lys Pro Thr  
 245 250 255  
 Leu Gln Gln Ile Ser His Ile Ala Gln Gln Leu Gly Leu Glu Lys Asp  
 260 265 270  
 Val Val Arg Val Trp Phe Cys Asn Arg Arg Gln Lys Gly Lys Arg Ser  
 275 280 285  
 Ser Ser Asp Tyr Ala Gln Arg Glu Asp Phe Glu Ala Ala Gly Ser Pro  
 290 295 300  
 Phe Ser Gly Gly Pro Val Ser Phe Pro Leu Ala Pro Gly Pro His Phe  
 305 310 315 320  
 Gly Thr Pro Gly Tyr Gly Ser Pro His Phe Thr Ala Leu Tyr Ser Ser  
 325 330 335  
 Val Pro Phe Pro Glu Gly Glu Ala Phe Pro Pro Val Ser Val Thr Thr  
 340 345 350  
 Leu Gly Ser Pro Met His Ser Asn  
 355 360  
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 Met Tyr Asn Met Met Glu Thr Glu Leu Lys Pro Pro Gly Pro Gln Gln  
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 Thr ser Gly Gly Gly Gly Gly Asn Ser Thr Ala Ala Ala Ala Gly Gly  
 20 25 30

# FAB-008PC-SequenceListing

Asn Gln Lys Asn Ser Pro Asp Arg Val Lys Arg Pro Met Asn Ala Phe  
 35 40 45  
 Met Val Trp Ser Arg Gly Gln Arg Arg Lys Met Ala Gln Glu Asn Pro  
 50 55 60  
 Lys Met His Asn Ser Glu Ile Ser Lys Arg Leu Gly Ala Glu Trp Lys  
 65 70 75 80  
 Leu Leu Ser Glu Thr Glu Lys Arg Pro Phe Ile Asp Glu Ala Lys Arg  
 85 90 95  
 Leu Arg Ala Leu His Met Lys Glu His Pro Asp Tyr Lys Tyr Arg Pro  
 100 105 110  
 Arg Arg Lys Thr Lys Thr Leu Met Lys Lys Asp Lys Tyr Thr Leu Pro  
 115 120 125  
 Gly Gly Leu Leu Ala Pro Gly Gly Asn Ser Met Ala Ser Gly Val Gly  
 130 135 140  
 Val Gly Ala Gly Leu Gly Ala Gly Val Asn Gln Arg Met Asp Ser Tyr  
 145 150 155 160  
 Ala His Met Asn Gly Trp Ser Asn Gly Ser Tyr Ser Met Met Gln Asp  
 165 170 175  
 Gln Leu Gly Tyr Pro Gln His Pro Gly Leu Asn Ala His Gly Ala Ala  
 180 185 190  
 Gln Met Gln Pro Met His Arg Tyr Asp Val Ser Ala Leu Gln Tyr Asn  
 195 200 205  
 Ser Met Thr Ser Ser Gln Thr Tyr Met Asn Gly Ser Pro Thr Tyr Ser  
 210 215 220  
 Met Ser Tyr Ser Gln Gln Gly Thr Pro Gly Met Ala Leu Gly Ser Met  
 225 230 235 240  
 Gly Ser Val Val Lys Ser Glu Ala Ser Ser Ser Pro Pro Val Val Thr  
 245 250 255  
 Ser Ser Ser His Ser Arg Ala Pro Cys Gln Ala Gly Asp Leu Arg Asp  
 260 265 270  
 Met Ile Ser Met Tyr Leu Pro Gly Ala Glu Val Pro Glu Pro Ala Ala  
 275 280 285  
 Pro Ser Arg Leu His Met Ser Gln His Tyr Gln Ser Gly Pro Val Pro  
 290 295 300

# FAB-008PC-SequenceListing

Gly Thr Ala Ile Asn Gly Thr Leu Pro Leu Ser His Met  
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<212> PRT  
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Leu Pro Ser Phe Ser Thr Phe Ala Ser Gly Pro Ala Gly Arg Glu Lys  
20 25 30

Thr Leu Arg Gln Ala Gly Ala Pro Asn Asn Arg Trp Arg Glu Glu Leu  
35 40 45

Ser His Met Lys Arg Leu Pro Pro Val Leu Pro Gly Arg Pro Tyr Asp  
50 55 60

Leu Ala Ala Ala Thr Val Ala Thr Asp Leu Glu Ser Gly Gly Ala Gly  
65 70 75 80

Ala Ala Cys Gly Gly Ser Asn Leu Ala Pro Leu Pro Arg Arg Glu Thr  
85 90 95

Glu Glu Phe Asn Asp Leu Leu Asp Leu Asp Phe Ile Leu Ser Asn Ser  
100 105 110

Leu Thr His Pro Pro Glu Ser Val Ala Ala Thr Val Ser Ser Ser Ala  
115 120 125

Ser Ala Ser Ser Ser Ser Ser Pro Ser Ser Ser Gly Pro Ala Ser Ala  
130 135 140

Pro Ser Thr Cys Ser Phe Thr Tyr Pro Ile Arg Ala Gly Asn Asp Pro  
145 150 155 160

Gly Val Ala Pro Gly Gly Thr Gly Gly Gly Leu Leu Tyr Gly Arg Glu  
165 170 175

Ser Ala Pro Pro Pro Thr Ala Pro Phe Asn Leu Ala Asp Ile Asn Asp  
180 185 190

Val Ser Pro Ser Gly Gly Phe Val Ala Glu Leu Leu Arg Pro Glu Leu  
195 200 205

Asp Pro Val Tyr Ile Pro Pro Gln Gln Pro Gln Pro Pro Gly Gly Gly  
210 215 220

# FAB-008PC-SequenceListing

Leu Met Gly Lys Phe Val Leu Lys Ala Ser Leu Ser Ala Pro Gly Ser  
 225 230 235 240  
 Glu Tyr Gly Ser Pro Ser Val Ile Ser Val Ser Lys Gly Ser Pro Asp  
 245 250 255  
 Gly Ser His Pro Val Val Val Ala Pro Tyr Asn Gly Gly Pro Pro Arg  
 260 265 270  
 Thr Cys Pro Lys Ile Lys Gln Glu Ala Val Ser Ser Cys Thr His Leu  
 275 280 285  
 Gly Ala Gly Pro Pro Leu Ser Asn Gly His Arg Pro Ala Ala His Asp  
 290 295 300  
 Phe Pro Leu Gly Arg Gln Leu Pro Ser Arg Thr Thr Pro Thr Leu Gly  
 305 310 315 320  
 Leu Glu Glu Val Leu Ser Ser Arg Asp Cys His Pro Ala Leu Pro Leu  
 325 330 335  
 Pro Pro Gly Phe His Pro His Pro Gly Pro Asn Tyr Pro Ser Phe Leu  
 340 345 350  
 Pro Asp Gln Met Gln Pro Gln Val Pro Pro Leu His Tyr Gln Glu Leu  
 355 360 365  
 Met Pro Pro Gly Ser Cys Met Pro Glu Glu Pro Lys Pro Lys Arg Gly  
 370 375 380  
 Arg Arg Ser Trp Pro Arg Lys Arg Thr Ala Thr His Thr Cys Asp Tyr  
 385 390 395 400  
 Ala Gly Cys Gly Lys Thr Tyr Thr Lys Ser Ser His Leu Lys Ala His  
 405 410 415  
 Leu Arg Thr His Thr Gly Glu Lys Pro Tyr His Cys Asp Trp Asp Gly  
 420 425 430  
 Cys Gly Trp Lys Phe Ala Arg Ser Asp Glu Leu Thr Arg His Tyr Arg  
 435 440 445  
 Lys His Thr Gly His Arg Pro Phe Gln Cys Gln Lys Cys Asp Arg Ala  
 450 455 460  
 Phe Ser Arg Ser Asp His Leu Ala Leu His Met Lys Arg His Phe  
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 <211> 454  
 <212> PRT  
 <213> Homo sapiens



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Pro Leu Asn Val Ser Phe Thr Asn Arg Asn Tyr Asp Leu Asp Tyr Asp
      20      25      30

Ser Val Gln Pro Tyr Phe Tyr Cys Asp Glu Glu Glu Asn Phe Tyr Gln
      35      40      45

Gln Gln Gln Gln Ser Glu Leu Gln Pro Pro Ala Pro Ser Glu Asp Ile
      50      55      60

Trp Lys Lys Phe Glu Leu Leu Pro Thr Pro Pro Leu Ser Pro Ser Arg
65      70      75      80

Arg Ser Gly Leu Cys Ser Pro Ser Tyr Val Ala Val Thr Pro Phe Ser
      85      90      95

Leu Arg Gly Asp Asn Asp Gly Gly Gly Gly Ser Phe Ser Thr Ala Asp
      100      105      110

Gln Leu Glu Met Val Thr Glu Leu Leu Gly Gly Asp Met Val Asn Gln
      115      120      125

Ser Phe Ile Cys Asp Pro Asp Asp Glu Thr Phe Ile Lys Asn Ile Ile
      130      135      140

Ile Gln Asp Cys Met Trp Ser Gly Phe Ser Ala Ala Ala Lys Leu Val
145      150      155      160

Ser Glu Lys Leu Ala Ser Tyr Gln Ala Ala Arg Lys Asp Ser Gly Ser
      165      170      175

Pro Asn Pro Ala Arg Gly His Ser Val Cys Ser Thr Ser Ser Leu Tyr
      180      185      190

Leu Gln Asp Leu Ser Ala Ala Ala Ser Glu Cys Ile Asp Pro Ser Val
      195      200      205

Val Phe Pro Tyr Pro Leu Asn Asp Ser Ser Ser Pro Lys Ser Cys Ala
      210      215      220

Ser Gln Asp Ser Ser Ala Phe Ser Pro Ser Ser Asp Ser Leu Leu Ser
225      230      235      240

Ser Thr Glu Ser Ser Pro Gln Gly Ser Pro Glu Pro Leu Val Leu His
      245      250      255

Glu Glu Thr Pro Pro Thr Thr Ser Ser Asp Ser Glu Glu Glu Gln Glu

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260

265

270

Asp Glu Glu Glu Ile Asp Val Val Ser Val Glu Lys Arg Gln Ala Pro  
275 280 285

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

Pro Pro His Ser Pro Leu Val Leu Lys Arg Cys His Val Ser Thr His  
305 310 315 320

Gln His Asn Tyr Ala Ala Pro Pro Ser Thr Arg Lys Asp Tyr Pro Ala  
325 330 335

Ala Lys Arg Val Lys Leu Asp Ser Val Arg Val Leu Arg Gln Ile Ser  
340 345 350

Asn Asn Arg Lys Cys Thr Ser Pro Arg Ser Ser Asp Thr Glu Glu Asn  
355 360 365

Val Lys Arg Arg Thr His Asn Val Leu Glu Arg Gln Arg Arg Asn Glu  
370 375 380

Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp Gln Ile Pro Glu Leu Glu  
385 390 395 400

Asn Asn Glu Lys Ala Pro Lys Val Val Ile Leu Lys Lys Ala Thr Ala  
405 410 415

Tyr Ile Leu Ser Val Gln Ala Glu Glu Gln Lys Leu Ile Ser Glu Glu  
420 425 430

Asp Leu Leu Arg Lys Arg Arg Glu Gln Leu Lys His Lys Leu Glu Gln  
435 440 445

Leu Arg Asn Ser Cys Ala  
450

<210> 12  
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<212> DNA  
<213> Homo sapiens

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ccctgcctgg cagccctttc tcaaggacca ccgcattctt acattcaaga actggcctt 120  
cttgaggggc tgcgcctgca cccggagcg ggtgagactg cccggcctcc tgggggtcccc 180  
cagccccgcc t 191

<210> 13  
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<212> DNA  
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 ccactgcccc actgagaacg agccagactt ggcccagtgt ttcttctgct tcaaggagct 120  
 ggaaggctgg gagccagatg acgaccccat gtaagtcttc tctggccagc ctcgatgggc 180  
 tttgttttga 190

<210> 14  
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 <212> DNA  
 <213> Homo sapiens

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 cgtccggttg cgctttcctt tctgtcaaga agcagtttga agaattaacc cttggtgaat 120  
 ttttgaaact ggacagagaa agagccaaga acaaaattgt atgtattggg aataagaact 180  
 gctcaaacc tgttcaat 198

<210> 15  
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 <212> DNA  
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 gaagaaagaa tttgaggaaa ctgcggagaa agtgcgccgt gccatcgagc agctggctgc 120  
 catggattga ggcctctggc cggagctgcc tgggtcccaga gtggctgcac 170

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 <212> DNA  
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<400> 17  
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<210> 18  
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 <212> DNA  
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<400> 18  
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## FAB-008PC-SequenceListing

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		20
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		20
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	tggccgaggc	tggcttcac
		20
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		20
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	tcgtcatctg	gctcccagcc
		20
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<400> 26  
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 <212> DNA  
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<400> 27  
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<210> 28  
 <211> 297  
 <212> PRT  
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<400> 28  
 Met Glu Asp Tyr Thr Lys Ile Glu Lys Ile Gly Glu Gly Thr Tyr Gly  
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 Val Val Tyr Lys Gly Arg His Lys Thr Thr Gly Gln Val Val Ala Met  
 20 25 30  
 Lys Lys Ile Arg Leu Glu Ser Glu Glu Glu Gly Val Pro Ser Thr Ala  
 35 40 45  
 Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Arg His Pro Asn Ile Val  
 50 55 60  
 Ser Leu Gln Asp Val Leu Met Gln Asp Ser Arg Leu Tyr Leu Ile Phe  
 65 70 75 80  
 Glu Phe Leu Ser Met Asp Leu Lys Lys Tyr Leu Asp Ser Ile Pro Pro  
 85 90 95  
 Gly Gln Tyr Met Asp Ser Ser Leu Val Lys Ser Tyr Leu Tyr Gln Ile  
 100 105 110  
 Leu Gln Gly Ile Val Phe Cys His Ser Arg Arg Val Leu His Arg Asp  
 115 120 125  
 Leu Lys Pro Gln Asn Leu Leu Ile Asp Asp Lys Gly Thr Ile Lys Leu  
 130 135 140  
 Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Ile Pro Ile Arg Val Tyr  
 145 150 155 160  
 Thr His Glu Val Val Thr Leu Trp Tyr Arg Ser Pro Glu Val Leu Leu  
 165 170 175  
 Gly Ser Ala Arg Tyr Ser Thr Pro Val Asp Ile Trp Ser Ile Gly Thr  
 180 185 190

# FAB-008PC-SequenceListing

Ile Phe Ala Glu Leu Ala Thr Lys Lys Pro Leu Phe His Gly Asp Ser  
195 200 205

Glu Ile Asp Gln Leu Phe Arg Ile Phe Arg Ala Leu Gly Thr Pro Asn  
210 215 220

Asn Glu Val Trp Pro Glu Val Glu Ser Leu Gln Asp Tyr Lys Asn Thr  
225 230 235 240

Phe Pro Lys Trp Lys Pro Gly Ser Leu Ala Ser His Val Lys Asn Leu  
245 250 255

Asp Glu Asn Gly Leu Asp Leu Leu Ser Lys Met Leu Ile Tyr Asp Pro  
260 265 270

Ala Lys Arg Ile Ser Gly Lys Met Ala Leu Asn His Pro Tyr Phe Asn  
275 280 285

Asp Leu Asp Asn Gln Ile Lys Lys Met  
290 295

<210> 29  
<211> 298  
<212> PRT  
<213> Homo sapiens  
<400> 29

Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly  
1 5 10 15

Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu  
20 25 30

Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala  
35 40 45

Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val  
50 55 60

Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe  
65 70 75 80

Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu  
85 90 95

Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu  
100 105 110

Gln Gly Leu Ala Phe Cys His Ser His Arg Val Leu His Arg Asp Leu  
115 120 125

Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu Gly Ala Ile Lys Leu Ala

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130

135

140

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

His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly  
165 170 175

Cys Lys Tyr Tyr Ser Thr Ala Val Asp Ile Trp Ser Leu Gly Cys Ile  
180 185 190

Phe Ala Glu Met Val Thr Arg Arg Ala Leu Phe Pro Gly Asp Ser Glu  
195 200 205

Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr Leu Gly Thr Pro Asp Glu  
210 215 220

Val Val Trp Pro Gly Val Thr Ser Met Pro Asp Tyr Lys Pro Ser Phe  
225 230 235 240

Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys Val Val Pro Pro Leu Asp  
245 250 255

Glu Asp Gly Arg Ser Leu Leu Ser Gln Met Leu His Tyr Asp Pro Asn  
260 265 270

Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala His Pro Phe Phe Gln Asp  
275 280 285

Val Thr Lys Pro Val Pro His Leu Arg Leu  
290 295

<210> 30  
<211> 305  
<212> PRT  
<213> Homo sapiens

<400> 30

Met Asp Met Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly  
1 5 10 15

Val Val Tyr Lys Ala Lys Asn Arg Glu Thr Gly Gln Leu Val Ala Leu  
20 25 30

Lys Lys Ile Arg Leu Asp Leu Glu Met Glu Gly Val Pro Ser Thr Ala  
35 40 45

Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Lys His Pro Asn Ile Val  
50 55 60

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

# FAB-008PC-SequenceListing

Glu Phe Leu Ser Gln Asp Leu Lys Lys Tyr Met Asp Ser Thr Pro Gly  
 85 90 95  
 Ser Glu Leu Pro Leu His Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu  
 100 105 110  
 Gln Gly Val Ser Phe Cys His Ser His Arg Val Ile His Arg Asp Leu  
 115 120 125  
 Lys Pro Gln Asn Leu Leu Ile Asn Glu Leu Gly Ala Ile Lys Leu Ala  
 130 135 140  
 Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Leu Arg Thr Tyr Thr  
 145 150 155 160  
 His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly  
 165 170 175  
 Ser Lys Phe Tyr Thr Thr Ala Val Asp Ile Trp Ser Ile Gly Cys Ile  
 180 185 190  
 Phe Ala Glu Met Val Thr Arg Lys Ala Leu Phe Pro Gly Asp Ser Glu  
 195 200 205  
 Ile Asp Gln Leu Phe Arg Ile Phe Arg Met Leu Gly Thr Pro Ser Glu  
 210 215 220  
 Asp Thr Trp Pro Gly Val Thr Gln Leu Pro Asp Tyr Lys Gly Ser Phe  
 225 230 235 240  
 Pro Lys Trp Thr Arg Lys Gly Leu Glu Glu Ile Val Pro Asn Leu Glu  
 245 250 255  
 Pro Glu Gly Arg Asp Leu Leu Met Gln Leu Leu Gln Tyr Asp Pro Ser  
 260 265 270  
 Gln Arg Ile Thr Ala Lys Thr Ala Leu Ala His Pro Tyr Phe Ser Ser  
 275 280 285  
 Pro Glu Pro Ser Pro Ala Ala Arg Gln Tyr Val Leu Gln Arg Phe Arg  
 290 295 300

His  
305

<210> 31  
 <211> 303  
 <212> PRT  
 <213> Homo sapiens

<400> 31



# FAB-008PC-SequenceListing

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala  
 1 5 10 15  
 Tyr Gly Thr Val Tyr Lys Ala Arg Asp Pro His Ser Gly His Phe Val  
 20 25 30  
 Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly  
 35 40 45  
 Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu  
 50 55 60  
 Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr  
 65 70 75 80  
 Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val  
 85 90 95  
 Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu  
 100 105 110  
 Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu  
 115 120 125  
 Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu  
 130 135 140  
 Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly  
 145 150 155 160  
 Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val  
 165 170 175  
 Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala  
 180 185 190  
 Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe  
 195 200 205  
 Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly  
 210 215 220  
 Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg  
 225 230 235 240  
 Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro  
 245 250 255  
 Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu  
 260 265 270

FAB-008PC-SequenceListing

Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg  
275 280 285

Ala Leu Gln His Ser Tyr Leu His Lys Asp Glu Gly Asn Pro Glu  
290 295 300

<210> 32  
<211> 292  
<212> PRT  
<213> Homo sapiens  
<400> 32

Met Gln Lys Tyr Glu Lys Leu Glu Lys Ile Gly Glu Gly Thr Tyr Gly  
1 5 10 15

Thr Val Phe Lys Ala Lys Asn Arg Glu Thr His Glu Ile Val Ala Leu  
20 25 30

Lys Arg Val Arg Leu Asp Asp Asp Glu Gly Val Pro Ser Ser Ala  
35 40 45

Leu Arg Glu Ile Cys Leu Leu Lys Glu Leu Lys His Lys Asn Ile Val  
50 55 60

Arg Leu His Asp Val Leu His Ser Asp Lys Lys Leu Thr Leu Val Phe  
65 70 75 80

Glu Phe Cys Asp Gln Asp Leu Lys Lys Tyr Phe Asp Ser Cys Asn Gly  
85 90 95

Asp Leu Asp Pro Glu Ile Val Lys Ser Phe Leu Phe Gln Leu Leu Lys  
100 105 110

Gly Leu Gly Phe Cys His Ser Arg Asn Val Leu His Arg Asp Leu Lys  
115 120 125

Pro Gln Asn Leu Leu Ile Asn Arg Asn Gly Glu Leu Lys Leu Ala Asp  
130 135 140

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

Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Val Leu Phe Gly Ala  
165 170 175

Lys Leu Tyr Ser Thr Ser Ile Asp Met Trp Ser Ala Gly Cys Ile Phe  
180 185 190

Ala Glu Leu Ala Asn Ala Gly Arg Pro Leu Phe Pro Gly Asn Asp Val  
195 200 205

# FAB-008PC-SequenceListing

Asp Asp Gln Leu Lys Arg Ile Phe Arg Leu Leu Gly Thr Pro Thr Glu  
210 215 220

Glu Gln Trp Pro Ser Met Thr Lys Leu Pro Asp Tyr Lys Pro Tyr Pro  
225 230 235 240

Met Tyr Pro Ala Thr Thr Ser Leu Val Asn Val Val Pro Lys Leu Asn  
245 250 255

Ala Thr Gly Arg Asp Leu Leu Gln Asn Leu Leu Lys Cys Asn Pro Val  
260 265 270

Gln Arg Ile Ser Ala Glu Glu Ala Leu Gln His Pro Tyr Phe Ser Asp  
275 280 285

Phe Cys Pro Pro  
290

<210> 33  
<211> 326  
<212> PRT  
<213> Homo sapiens

<400> 33

Met Glu Lys Asp Gly Leu Cys Arg Ala Asp Gln Gln Tyr Glu Cys Val  
1 5 10 15

Ala Glu Ile Gly Glu Gly Ala Tyr Gly Lys Val Phe Lys Ala Arg Asp  
20 25 30

Leu Lys Asn Gly Gly Arg Phe Val Ala Leu Lys Arg Val Arg Val Gln  
35 40 45

Thr Gly Glu Glu Gly Met Pro Leu Ser Thr Ile Arg Glu Val Ala Val  
50 55 60

Leu Arg His Leu Glu Thr Phe Glu His Pro Asn Val Val Arg Leu Phe  
65 70 75 80

Asp Val Cys Thr Val Ser Arg Thr Asp Arg Glu Thr Lys Leu Thr Leu  
85 90 95

Val Phe Glu His Val Asp Gln Asp Leu Thr Thr Tyr Leu Asp Lys Val  
100 105 110

Pro Glu Pro Gly Val Pro Thr Glu Thr Ile Lys Asp Met Met Phe Gln  
115 120 125

Leu Leu Arg Gly Leu Asp Phe Leu His Ser His Arg Val Val His Arg  
130 135 140

Asp Leu Lys Pro Gln Asn Ile Leu Val Thr Ser Ser Gly Gln Ile Lys

FAB-008PC-SequenceListing

145 150 155 160

Leu Ala Asp Phe Gly Leu Ala Arg Ile Tyr Ser Phe Gln Met Ala Leu  
165 170 175

Thr Ser Val Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu  
180 185 190

Gln Ser Ser Tyr Ala Thr Pro Val Asp Leu Trp Ser Val Gly Cys Ile  
195 200 205

Phe Ala Glu Met Phe Arg Arg Lys Pro Leu Phe Arg Gly Ser Ser Asp  
210 215 220

Val Asp Gln Leu Gly Lys Ile Leu Asp Val Ile Gly Leu Pro Gly Glu  
225 230 235 240

Glu Asp Trp Pro Arg Asp Val Ala Leu Pro Arg Gln Ala Phe His Ser  
245 250 255

Lys Ser Ala Gln Pro Ile Glu Lys Phe Val Thr Asp Ile Asp Glu Leu  
260 265 270

Gly Lys Asp Leu Leu Leu Lys Cys Leu Thr Phe Asn Pro Ala Lys Arg  
275 280 285

Ile Ser Ala Tyr Ser Ala Leu Ser His Pro Tyr Phe Gln Asp Leu Glu  
290 295 300

Arg Cys Lys Glu Asn Leu Asp Ser His Leu Pro Pro Ser Gln Asn Thr  
305 310 315 320

Ser Glu Leu Asn Thr Ala  
325

<210> 34  
<211> 142  
<212> PRT  
<213> Homo sapiens

<400> 34

Met Gly Ala Pro Thr Leu Pro Pro Ala Trp Gln Pro Phe Leu Lys Asp  
1 5 10 15

His Arg Ile Ser Thr Phe Lys Asn Trp Pro Phe Leu Glu Gly Cys Ala  
20 25 30

Cys Thr Pro Glu Arg Met Ala Glu Ala Gly Phe Ile His Cys Pro Thr  
35 40 45

Glu Asn Glu Pro Asp Leu Ala Gln Cys Phe Phe Cys Phe Lys Glu Leu  
50 55 60

FAB-008PC-SequenceListing

Glu Gly Trp Glu Pro Asp Asp Asp Pro Ile Glu Glu His Lys Lys His  
65 70 75 80

Ser Ser Gly Cys Ala Phe Leu Ser Val Lys Lys Gln Phe Glu Glu Leu  
85 90 95

Thr Leu Gly Glu Phe Leu Lys Leu Asp Arg Glu Arg Ala Lys Asn Lys  
100 105 110

Ile Ala Lys Glu Thr Asn Asn Lys Lys Lys Glu Phe Glu Glu Thr Ala  
115 120 125

Glu Lys Val Arg Arg Ala Ile Glu Gln Leu Ala Ala Met Asp  
130 135 140

<210> 35  
<211> 826  
<212> PRT  
<213> Homo sapiens

<400> 35

Met Glu Gly Ala Gly Gly Ala Asn Asp Lys Lys Lys Ile Ser Ser Glu  
1 5 10 15

Arg Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys  
20 25 30

Glu Ser Glu Val Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His  
35 40 45

Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile  
50 55 60

Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile  
65 70 75 80

Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu  
85 90 95

Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile  
100 105 110

Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr  
115 120 125

Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met  
130 135 140

Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu  
145 150 155 160

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Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr  
165 170 175

Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu  
180 185 190

His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro  
195 200 205

Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys  
210 215 220

Glu Pro Ile Pro His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys  
225 230 235 240

Thr Phe Leu Ser Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp  
245 250 255

Glu Arg Ile Thr Glu Leu Met Gly Tyr Glu Pro Glu Glu Leu Leu Gly  
260 265 270

Arg Ser Ile Tyr Glu Tyr Tyr His Ala Leu Asp Ser Asp His Leu Thr  
275 280 285

Lys Thr His His Asp Met Phe Thr Lys Gly Gln Val Thr Thr Gly Gln  
290 295 300

Tyr Arg Met Leu Ala Lys Arg Gly Gly Tyr Val Trp Val Glu Thr Gln  
305 310 315 320

Ala Thr Val Ile Tyr Asn Thr Lys Asn Ser Gln Pro Gln Cys Ile Val  
325 330 335

Cys Val Asn Tyr Val Val Ser Gly Ile Ile Gln His Asp Leu Ile Phe  
340 345 350

Ser Leu Gln Gln Thr Glu Cys Val Leu Lys Pro Val Glu Ser Ser Asp  
355 360 365

Met Lys Met Thr Gln Leu Phe Thr Lys Val Glu Ser Glu Asp Thr Ser  
370 375 380

Ser Leu Phe Asp Lys Leu Lys Lys Glu Pro Asp Ala Leu Thr Leu Leu  
385 390 395 400

Ala Pro Ala Ala Gly Asp Thr Ile Ile Ser Leu Asp Phe Gly Ser Asn  
405 410 415

Asp Thr Glu Thr Asp Asp Gln Gln Leu Glu Glu Val Pro Leu Tyr Asn  
420 425 430

# FAB-008PC-SequenceListing

Asp Val Met Leu Pro Ser Pro Asn Glu Lys Leu Gln Asn Ile Asn Leu  
 435 440 445  
 Ala Met Ser Pro Leu Pro Thr Ala Glu Thr Pro Lys Pro Leu Arg Ser  
 450 455 460  
 Ser Ala Asp Pro Ala Leu Asn Gln Glu Val Ala Leu Lys Leu Glu Pro  
 465 470 475 480  
 Asn Pro Glu Ser Leu Glu Leu Ser Phe Thr Met Pro Gln Ile Gln Asp  
 485 490 495  
 Gln Thr Pro Ser Pro Ser Asp Gly Ser Thr Arg Gln Ser Ser Pro Glu  
 500 505 510  
 Pro Asn Ser Pro Ser Glu Tyr Cys Phe Tyr Val Asp Ser Asp Met Val  
 515 520 525  
 Asn Glu Phe Lys Leu Glu Leu Val Glu Lys Leu Phe Ala Glu Asp Thr  
 530 535 540  
 Glu Ala Lys Asn Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp Leu Glu  
 545 550 555 560  
 Met Leu Ala Pro Tyr Ile Pro Met Asp Asp Asp Phe Gln Leu Arg Ser  
 565 570 575  
 Phe Asp Gln Leu Ser Pro Leu Glu Ser Ser Ser Ala Ser Pro Glu Ser  
 580 585 590  
 Ala Ser Pro Gln Ser Thr Val Thr Val Phe Gln Gln Thr Gln Ile Gln  
 595 600 605  
 Glu Pro Thr Ala Asn Ala Thr Thr Thr Thr Ala Thr Thr Asp Glu Leu  
 610 615 620  
 Lys Thr Val Thr Lys Asp Arg Met Glu Asp Ile Lys Ile Leu Ile Ala  
 625 630 635 640  
 Ser Pro Ser Pro Thr His Ile His Lys Glu Thr Thr Ser Ala Thr Ser  
 645 650 655  
 Ser Pro Tyr Arg Asp Thr Gln Ser Arg Thr Ala Ser Pro Asn Arg Ala  
 660 665 670  
 Gly Lys Gly Val Ile Glu Gln Thr Glu Lys Ser His Pro Arg Ser Pro  
 675 680 685  
 Asn Val Leu Ser Val Ala Leu Ser Gln Arg Thr Thr Val Pro Glu Glu  
 690 695 700

FAB-008PC-SequenceListing

Glu Leu Asn Pro Lys Ile Leu Ala Leu Gln Asn Ala Gln Arg Lys Arg  
 705 710 715 720  
 Lys Met Glu His Asp Gly Ser Leu Phe Gln Ala Val Gly Ile Gly Thr  
 725 730 735  
 Leu Leu Gln Gln Pro Asp Asp His Ala Ala Thr Thr Ser Leu Ser Trp  
 740 745 750  
 Lys Arg Val Lys Gly Cys Lys Ser Ser Glu Gln Asn Gly Met Glu Gln  
 755 760 765  
 Lys Thr Ile Ile Leu Ile Pro Ser Asp Leu Ala Cys Arg Leu Leu Gly  
 770 775 780  
 Gln Ser Met Asp Glu Ser Gly Leu Pro Gln Leu Thr Ser Tyr Asp Cys  
 785 790 795 800  
 Glu Val Asn Ala Pro Ile Gln Gly Ser Arg Asn Leu Leu Gln Gly Glu  
 805 810 815  
 Glu Leu Leu Arg Ala Leu Asp Gln Val Asn  
 820 825  
 <210> 36  
 <211> 449  
 <212> PRT  
 <213> Homo sapiens  
 <400> 36  
 Met Gly Arg Val Gly Gly Met Ala Gln Pro Met Gly Arg Ala Gly Ala  
 1 5 10 15  
 Pro Lys Pro Met Gly Arg Ala Gly Ser Ala Arg Arg Gly Arg Phe Lys  
 20 25 30  
 Gly Cys Trp Ser Glu Gly Ser Pro Val His Pro Val Pro Ala Val Leu  
 35 40 45  
 Ser Trp Leu Leu Ala Leu Leu Arg Cys Ala Ser Thr Met Leu Ser Leu  
 50 55 60  
 Arg Val Pro Leu Ala Pro Ile Thr Asp Pro Gln Gln Leu Gln Leu Ser  
 65 70 75 80  
 Pro Leu Lys Gly Leu Ser Leu Val Asp Lys Glu Asn Thr Pro Pro Ala  
 85 90 95  
 Leu Ser Gly Thr Arg Val Leu Ala Ser Lys Thr Ala Arg Arg Ile Phe  
 100 105 110



FAB-008PC-SequenceListing

Gln Glu Pro Thr Glu Pro Lys Thr Lys Ala Ala Ala Pro Gly Val Glu  
115 120 125

Asp Glu Pro Leu Leu Arg Glu Asn Pro Arg Arg Phe Val Ile Phe Pro  
130 135 140

Ile Glu Tyr His Asp Ile Trp Gln Met Tyr Lys Lys Ala Glu Ala Ser  
145 150 155 160

Phe Trp Thr Ala Glu Glu Val Asp Leu Ser Lys Asp Ile Gln His Trp  
165 170 175

Glu Ser Leu Lys Pro Glu Glu Arg Tyr Phe Ile Ser His Val Leu Ala  
180 185 190

Phe Phe Ala Ala Ser Asp Gly Ile Val Asn Glu Asn Leu Val Glu Arg  
195 200 205

Phe Ser Gln Glu Val Gln Ile Thr Glu Ala Arg Cys Phe Tyr Gly Phe  
210 215 220

Gln Ile Ala Met Glu Asn Ile His Ser Glu Met Tyr Ser Leu Leu Ile  
225 230 235 240

Asp Thr Tyr Ile Lys Asp Pro Lys Glu Arg Glu Phe Leu Phe Asn Ala  
245 250 255

Ile Glu Thr Met Pro Cys Val Lys Lys Lys Ala Asp Trp Ala Leu Arg  
260 265 270

Trp Ile Gly Asp Lys Glu Ala Thr Tyr Gly Glu Arg Val Val Ala Phe  
275 280 285

Ala Ala Val Glu Gly Ile Phe Phe Ser Gly Ser Phe Ala Ser Ile Phe  
290 295 300

Trp Leu Lys Lys Arg Gly Leu Met Pro Gly Leu Thr Phe Ser Asn Glu  
305 310 315 320

Leu Ile Ser Arg Asp Glu Gly Leu His Cys Asp Phe Ala Cys Leu Met  
325 330 335

Phe Lys His Leu Val His Lys Pro Ser Glu Glu Arg Val Arg Glu Ile  
340 345 350

Ile Ile Asn Ala Val Arg Ile Glu Gln Glu Phe Leu Thr Glu Ala Leu  
355 360 365

Pro Val Lys Leu Ile Gly Met Asn Cys Thr Leu Met Lys Gln Tyr Ile  
370 375 380

# FAB-008PC-SequenceListing

Glu Phe Val Ala Asp Arg Leu Met Leu Glu Leu Gly Phe Ser Lys Val  
385 390 395 400

Phe Arg Val Glu Asn Pro Phe Asp Phe Met Glu Asn Ile Ser Leu Glu  
405 410 415

Gly Lys Thr Asn Phe Phe Glu Lys Arg Val Gly Glu Tyr Gln Arg Met  
420 425 430

Gly Val Met Ser Ser Pro Thr Glu Asn Ser Phe Thr Leu Asp Ala Asp  
435 440 445

Phe

<210> 37  
<211> 188  
<212> PRT  
<213> Homo sapiens

<400> 37

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys  
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr  
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly  
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr  
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys  
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His His Tyr  
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Glu Asp Val Pro Met Val  
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Pro Ser Arg Thr Val Asp Thr Lys  
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Phe Ile Glu Thr  
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Asp Asp Ala Phe Tyr Thr Leu Val  
145 150 155 160

Arg Glu Ile Arg Lys His Lys Glu Lys Met Ser Lys Asp Gly Lys Lys

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165

170

175

Lys Lys Lys Lys Ser Lys Thr Lys Cys Val Ile Met  
180 185

<210> 38  
<211> 1210  
<212> PRT  
<213> Homo sapiens  
<400> 38

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

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln  
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe  
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn  
50 55 60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys  
65 70 75 80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val  
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr  
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn  
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu  
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu  
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met  
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro  
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln  
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg  
210 215 220

# FAB-008PC-SequenceListing

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys  
 225 230 235 240  
 Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp  
 245 250 255  
 Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro  
 260 265 270  
 Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly  
 275 280 285  
 Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His  
 290 295 300  
 Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu  
 305 310 315 320  
 Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val  
 325 330 335  
 Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn  
 340 345 350  
 Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp  
 355 360 365  
 Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr  
 370 375 380  
 Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu  
 385 390 395 400  
 Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp  
 405 410 415  
 Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln  
 420 425 430  
 His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu  
 435 440 445  
 Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser  
 450 455 460  
 Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu  
 465 470 475 480  
 Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu  
 485 490 495

FAB-008PC-SequenceListing

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro  
 500 505 510  
 Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn  
 515 520 525  
 Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly  
 530 535 540  
 Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro  
 545 550 555 560  
 Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro  
 565 570 575  
 Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val  
 580 585 590  
 Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp  
 595 600 605  
 Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys  
 610 615 620  
 Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly  
 625 630 635 640  
 Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu  
 645 650 655  
 Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His  
 660 665 670  
 Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu  
 675 680 685  
 Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu  
 690 695 700  
 Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser  
 705 710 715 720  
 Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu  
 725 730 735  
 Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser  
 740 745 750  
 Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser  
 755 760 765

FAB-008PC-SequenceListing

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser  
 770 775 780  
 Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp  
 785 790 795 800  
 Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn  
 805 810 815  
 Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg  
 820 825 830  
 Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro  
 835 840 845  
 Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala  
 850 855 860  
 Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp  
 865 870 875 880  
 Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp  
 885 890 895  
 Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser  
 900 905 910  
 Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu  
 915 920 925  
 Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr  
 930 935 940  
 Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys  
 945 950 955 960  
 Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln  
 965 970 975  
 Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro  
 980 985 990  
 Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp  
 995 1000 1005  
 Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe  
 1010 1015 1020  
 Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu  
 1025 1030 1035

FAB-008PC-SequenceListing

Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn  
1040 1045 1050

Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg  
1055 1060 1065

Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp  
1070 1075 1080

Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro  
1085 1090 1095

Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln  
1100 1105 1110

Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro  
1115 1120 1125

His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln  
1130 1135 1140

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala  
1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln  
1160 1165 1170

Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys  
1175 1180 1185

Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro Gln  
1190 1195 1200

Ser Ser Glu Phe Ile Gly Ala  
1205 1210

<210> 39  
<211> 454  
<212> PRT  
<213> Homo sapiens

<400> 39

Met Asp Phe Phe Arg Val Val Glu Asn Gln Gln Pro Pro Ala Thr Met  
1 5 10 15

Pro Leu Asn Val Ser Phe Thr Asn Arg Asn Tyr Asp Leu Asp Tyr Asp  
20 25 30

Ser Val Gln Pro Tyr Phe Tyr Cys Asp Glu Glu Glu Asn Phe Tyr Gln  
35 40 45

# FAB-008PC-SequenceListing

Gln Gln Gln Gln Ser Glu Leu Gln Pro Pro Ala Pro Ser Glu Asp Ile  
 50 55 60  
 Trp Lys Lys Phe Glu Leu Leu Pro Thr Pro Pro Leu Ser Pro Ser Arg  
 65 70 75 80  
 Arg Ser Gly Leu Cys Ser Pro Ser Tyr Val Ala Val Thr Pro Phe Ser  
 85 90 95  
 Leu Arg Gly Asp Asn Asp Gly Gly Gly Gly Ser Phe Ser Thr Ala Asp  
 100 105 110  
 Gln Leu Glu Met Val Thr Glu Leu Leu Gly Gly Asp Met Val Asn Gln  
 115 120 125  
 Ser Phe Ile Cys Asp Pro Asp Asp Glu Thr Phe Ile Lys Asn Ile Ile  
 130 135 140  
 Ile Gln Asp Cys Met Trp Ser Gly Phe Ser Ala Ala Ala Lys Leu Val  
 145 150 155 160  
 Ser Glu Lys Leu Ala Ser Tyr Gln Ala Ala Arg Lys Asp Ser Gly Ser  
 165 170 175  
 Pro Asn Pro Ala Arg Gly His Ser Val Cys Ser Thr Ser Ser Leu Tyr  
 180 185 190  
 Leu Gln Asp Leu Ser Ala Ala Ala Ser Glu Cys Ile Asp Pro Ser Val  
 195 200 205  
 Val Phe Pro Tyr Pro Leu Asn Asp Ser Ser Ser Pro Lys Ser Cys Ala  
 210 215 220  
 Ser Gln Asp Ser Ser Ala Phe Ser Pro Ser Ser Asp Ser Leu Leu Ser  
 225 230 235 240  
 Ser Thr Glu Ser Ser Pro Gln Gly Ser Pro Glu Pro Leu Val Leu His  
 245 250 255  
 Glu Glu Thr Pro Pro Thr Thr Ser Ser Asp Ser Glu Glu Glu Gln Glu  
 260 265 270  
 Asp Glu Glu Glu Ile Asp Val Val Ser Val Glu Lys Arg Gln Ala Pro  
 275 280 285  
 Gly Lys Arg Ser Glu Ser Gly Ser Pro Ser Ala Gly Gly His Ser Lys  
 290 295 300  
 Pro Pro His Ser Pro Leu Val Leu Lys Arg Cys His Val Ser Thr His  
 305 310 315 320



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Gln His Asn Tyr Ala Ala Pro Pro Ser Thr Arg Lys Asp Tyr Pro Ala  
325 330 335

Ala Lys Arg Val Lys Leu Asp Ser Val Arg Val Leu Arg Gln Ile Ser  
340 345 350

Asn Asn Arg Lys Cys Thr Ser Pro Arg Ser Ser Asp Thr Glu Glu Asn  
355 360 365

Val Lys Arg Arg Thr His Asn Val Leu Glu Arg Gln Arg Arg Asn Glu  
370 375 380

Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp Gln Ile Pro Glu Leu Glu  
385 390 395 400

Asn Asn Glu Lys Ala Pro Lys Val Val Ile Leu Lys Lys Ala Thr Ala  
405 410 415

Tyr Ile Leu Ser Val Gln Ala Glu Glu Gln Lys Leu Ile Ser Glu Glu  
420 425 430

Asp Leu Leu Arg Lys Arg Arg Glu Gln Leu Lys His Lys Leu Glu Gln  
435 440 445

Leu Arg Asn Ser Cys Ala  
450

<210> 40  
<211> 889  
<212> PRT  
<213> Homo sapiens

<400> 40

Met Glu Glu Gly Ala Pro Arg Gln Pro Gly Pro Ser Gln Trp Pro Pro  
1 5 10 15

Glu Asp Glu Lys Glu Val Ile Arg Arg Ala Ile Gln Lys Glu Leu Lys  
20 25 30

Ile Lys Glu Gly Val Glu Asn Leu Arg Arg Val Ala Thr Asp Arg Arg  
35 40 45

His Leu Gly His Val Gln Gln Leu Leu Arg Ser Ser Asn Arg Arg Leu  
50 55 60

Glu Gln Leu His Gly Glu Leu Arg Glu Leu His Ala Arg Ile Leu Leu  
65 70 75 80

Pro Gly Pro Gly Pro Gly Pro Ala Glu Pro Val Ala Ser Gly Pro Arg  
85 90 95

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Pro Trp Ala Glu Gln Leu Arg Ala Arg His Leu Glu Ala Leu Arg Arg  
100 105 110

Gln Leu His Val Glu Leu Lys Val Lys Gln Gly Ala Glu Asn Met Thr  
115 120 125

His Thr Cys Ala Ser Gly Thr Pro Lys Glu Arg Lys Leu Leu Ala Ala  
130 135 140

Ala Gln Gln Met Leu Arg Asp Ser Gln Leu Lys Val Ala Leu Leu Arg  
145 150 155 160

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

Glu Leu Leu Ala Glu Glu Leu Gln His Arg Leu His Val Glu Ala Ala  
180 185 190

Val Ala Glu Gly Ala Lys Asn Val Val Lys Leu Leu Ser Ser Arg Arg  
195 200 205

Thr Gln Asp Arg Lys Ala Leu Ala Glu Ala Gln Ala Gln Leu Gln Glu  
210 215 220

Ser Ser Gln Lys Leu Asp Leu Leu Arg Leu Ala Leu Glu Gln Leu Leu  
225 230 235 240

Glu Gln Leu Pro Pro Ala His Pro Leu Arg Ser Arg Val Thr Arg Glu  
245 250 255

Leu Arg Ala Ala Val Pro Gly Tyr Pro Gln Pro Ser Gly Thr Pro Val  
260 265 270

Lys Pro Thr Ala Leu Thr Gly Thr Leu Gln Val Arg Leu Leu Gly Cys  
275 280 285

Glu Gln Leu Leu Thr Ala Val Pro Gly Arg Ser Pro Ala Ala Ala Leu  
290 295 300

Ala Ser Ser Pro Ser Glu Gly Trp Leu Arg Thr Lys Ala Lys His Gln  
305 310 315 320

Arg Gly Arg Gly Glu Leu Ala Ser Glu Val Leu Ala Val Leu Lys Val  
325 330 335

Asp Asn Arg Val Val Gly Gln Thr Gly Trp Gly Gln Val Ala Glu Gln  
340 345 350

Ser Trp Asp Gln Thr Phe Val Ile Pro Leu Glu Arg Ala Arg Glu Leu  
355 360 365

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Glu Ile Gly Val His Trp Arg Asp Trp Arg Gln Leu Cys Gly Val Ala  
370 375 380

Phe Leu Arg Leu Glu Asp Phe Leu Asp Asn Ala Cys His Gln Leu Ser  
385 390 400

Leu Ser Leu Val Pro Gln Gly Leu Leu Phe Ala Gln Val Thr Phe Cys  
405 410 415

Asp Pro Val Ile Glu Arg Arg Pro Arg Leu Gln Arg Gln Glu Arg Ile  
420 425 430

Phe Ser Lys Arg Arg Gly Gln Asp Phe Leu Arg Ala Ser Gln Met Asn  
435 440 445

Leu Gly Met Ala Ala Trp Gly Arg Leu Val Met Asn Leu Leu Pro Pro  
450 455 460

Cys Ser Ser Pro Ser Thr Ile Ser Pro Pro Lys Gly Cys Pro Arg Thr  
465 470 475 480

Pro Thr Thr Leu Arg Glu Ala Ser Asp Pro Ala Thr Pro Ser Asn Phe  
485 490 495

Leu Pro Lys Lys Thr Pro Leu Gly Glu Glu Met Thr Pro Pro Pro Lys  
500 505 510

Pro Pro Arg Leu Tyr Leu Pro Gln Glu Pro Thr Ser Glu Glu Thr Pro  
515 520 525

Arg Thr Lys Arg Pro His Met Glu Pro Arg Thr Arg Arg Gly Pro Ser  
530 535 540

Pro Pro Ala Ser Pro Thr Arg Lys Pro Pro Arg Leu Gln Asp Phe Arg  
545 550 555 560

Cys Leu Ala Val Leu Gly Arg Gly His Phe Gly Lys Val Leu Leu Val  
565 570 575

Gln Phe Lys Gly Thr Gly Lys Tyr Tyr Ala Ile Lys Ala Leu Lys Lys  
580 585 590

Gln Glu Val Leu Ser Arg Asp Glu Ile Glu Ser Leu Tyr Cys Glu Lys  
595 600 605

Arg Ile Leu Glu Ala Val Gly Cys Thr Gly His Pro Phe Leu Leu Ser  
610 615 620

Leu Leu Ala Cys Phe Gln Thr Ser Ser His Ala Cys Phe Val Thr Glu  
625 630 635 640

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Phe Val Pro Gly Gly Asp Leu Met Met Gln Ile His Glu Asp Val Phe  
 645 650 655  
 Pro Glu Pro Gln Ala Arg Phe Tyr Val Ala Cys Val Val Leu Gly Leu  
 660 665 670  
 Gln Phe Leu His Glu Lys Lys Ile Ile Tyr Arg Asp Leu Lys Leu Asp  
 675 680 685  
 Asn Leu Leu Leu Asp Ala Gln Gly Phe Leu Lys Ile Ala Asp Phe Gly  
 690 695 700  
 Leu Cys Lys Glu Gly Ile Gly Phe Gly Asp Arg Thr Ser Thr Phe Cys  
 705 710 715 720  
 Gly Thr Pro Glu Phe Leu Ala Pro Glu Val Leu Thr Gln Glu Ala Tyr  
 725 730 735  
 Thr Arg Ala Val Asp Trp Trp Gly Leu Gly Val Leu Leu Tyr Glu Met  
 740 745 750  
 Leu Val Gly Glu Cys Pro Phe Pro Gly Asp Thr Glu Glu Glu Val Phe  
 755 760 765  
 Asp Cys Ile Val Asn Met Asp Ala Pro Tyr Pro Gly Phe Leu Ser Val  
 770 775 780  
 Gln Gly Leu Glu Phe Ile Gln Lys Leu Leu Gln Lys Cys Pro Glu Lys  
 785 790 795 800  
 Arg Leu Gly Ala Gly Glu Gln Asp Ala Glu Glu Ile Lys Val Gln Pro  
 805 810 815  
 Phe Phe Arg Thr Thr Asn Trp Gln Ala Leu Leu Ala Arg Thr Ile Gln  
 820 825 830  
 Pro Pro Phe Val Pro Thr Leu Cys Gly Pro Ala Asp Leu Arg Tyr Phe  
 835 840 845  
 Glu Gly Glu Phe Thr Gly Leu Pro Pro Ala Leu Thr Pro Pro Ala Pro  
 850 855 860  
 His Ser Leu Leu Thr Ala Arg Gln Gln Ala Ala Phe Arg Asp Phe Asp  
 865 870 875 880  
 Phe Val Ser Glu Arg Phe Leu Glu Pro  
 885

<210> 41  
 <211> 1056  
 <212> PRT  
 <213> Homo sapiens

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<400> 41

Met Ala Ser Gln Pro Asn Ser Ser Ala Lys Lys Lys Glu Glu Lys Gly  
1 5 10 15

Lys Asn Ile Gln Val Val Val Arg Cys Arg Pro Phe Asn Leu Ala Glu  
20 25 30

Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys Asp Pro Val Arg Lys  
35 40 45

Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser Ser Arg Lys  
50 55 60

Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser Thr Lys Gln Ile Asp  
65 70 75 80

Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp Glu Val Ile Met Gly  
85 90 95

Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln Thr Gly Thr Gly Lys Thr  
100 105 110

Phe Thr Met Glu Gly Glu Arg Ser Pro Asn Glu Glu Tyr Thr Trp Glu  
115 120 125

Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg Thr Leu His Gln Ile Phe  
130 135 140

Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe Ser Val Lys Val Ser Leu  
145 150 155 160

Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp Leu Leu Asn Pro Ser Ser  
165 170 175

Asp Val Ser Glu Arg Leu Gln Met Phe Asp Asp Pro Arg Asn Lys Arg  
180 185 190

Gly Val Ile Ile Lys Gly Leu Glu Glu Ile Thr Val His Asn Lys Asp  
195 200 205

Glu Val Tyr Gln Ile Leu Glu Lys Gly Ala Ala Lys Arg Thr Thr Ala  
210 215 220

Ala Thr Leu Met Asn Ala Tyr Ser Ser Arg Ser His Ser Val Phe Ser  
225 230 235 240

Val Thr Ile His Met Lys Glu Thr Thr Ile Asp Gly Glu Glu Leu Val  
245 250 255

Lys Ile Gly Lys Leu Asn Leu Val Asp Leu Ala Gly Ser Glu Asn Ile

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260

265

270

Gly Arg Ser Gly Ala Val Asp Lys Arg Ala Arg Glu Ala Gly Asn Ile  
275 280 285

Asn Gln Ser Leu Leu Thr Leu Gly Arg Val Ile Thr Ala Leu Val Glu  
290 295 300

Arg Thr Pro His Val Pro Tyr Arg Glu Ser Lys Leu Thr Arg Ile Leu  
305 310 315 320

Gln Asp Ser Leu Gly Gly Arg Thr Arg Thr Ser Ile Ile Ala Thr Ile  
325 330 335

Ser Pro Ala Ser Leu Asn Leu Glu Glu Thr Leu Ser Thr Leu Glu Tyr  
340 345 350

Ala His Arg Ala Lys Asn Ile Leu Asn Lys Pro Glu Val Asn Gln Lys  
355 360 365

Leu Thr Lys Lys Ala Leu Ile Lys Glu Tyr Thr Glu Glu Ile Glu Arg  
370 375 380

Leu Lys Arg Asp Leu Ala Ala Ala Arg Glu Lys Asn Gly Val Tyr Ile  
385 390 395 400

Ser Glu Glu Asn Phe Arg Val Met Ser Gly Lys Leu Thr Val Gln Glu  
405 410 415

Glu Gln Ile Val Glu Leu Ile Glu Lys Ile Gly Ala Val Glu Glu Glu  
420 425 430

Leu Asn Arg Val Thr Glu Leu Phe Met Asp Asn Lys Asn Glu Leu Asp  
435 440 445

Gln Cys Lys Ser Asp Leu Gln Asn Lys Thr Gln Glu Leu Glu Thr Thr  
450 455 460

Gln Lys His Leu Gln Glu Thr Lys Leu Gln Leu Val Lys Glu Glu Tyr  
465 470 475 480

Ile Thr Ser Ala Leu Glu Ser Thr Glu Glu Lys Leu His Asp Ala Ala  
485 490 495

Ser Lys Leu Leu Asn Thr Val Glu Glu Thr Thr Lys Asp Val Ser Gly  
500 505 510

Leu His Ser Lys Leu Asp Arg Lys Lys Ala Val Asp Gln His Asn Ala  
515 520 525

Glu Ala Gln Asp Ile Phe Gly Lys Asn Leu Asn Ser Leu Phe Asn Asn

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530

535

540

Met Glu Glu Leu Ile Lys Asp Gly Ser Ser Lys Gln Lys Ala Met Leu  
 545 550 555 560

Glu Val His Lys Thr Leu Phe Gly Asn Leu Leu Ser Ser Ser Val Ser  
 565 570 575

Ala Leu Asp Thr Ile Thr Thr Val Ala Leu Gly Ser Leu Thr Ser Ile  
 580 585 590

Pro Glu Asn Val Ser Thr His Val Ser Gln Ile Phe Asn Met Ile Leu  
 595 600 605

Lys Glu Gln Ser Leu Ala Ala Glu Ser Lys Thr Val Leu Gln Glu Leu  
 610 615 620

Ile Asn Val Leu Lys Thr Asp Leu Leu Ser Ser Leu Glu Met Ile Leu  
 625 630 635 640

Ser Pro Thr Val Val Ser Ile Leu Lys Ile Asn Ser Gln Leu Lys His  
 645 650 655

Ile Phe Lys Thr Ser Leu Thr Val Ala Asp Lys Ile Glu Asp Gln Lys  
 660 665 670

Lys Glu Leu Asp Gly Phe Leu Ser Ile Leu Cys Asn Asn Leu His Glu  
 675 680 685

Leu Gln Glu Asn Thr Ile Cys Ser Leu Val Glu Ser Gln Lys Gln Cys  
 690 695 700

Gly Asn Leu Thr Glu Asp Leu Lys Thr Ile Lys Gln Thr His Ser Gln  
 705 710 715 720

Glu Leu Cys Lys Leu Met Asn Leu Trp Thr Glu Arg Phe Cys Ala Leu  
 725 730 735

Glu Glu Lys Cys Glu Asn Ile Gln Lys Pro Leu Ser Ser Val Gln Glu  
 740 745 750

Asn Ile Gln Gln Lys Ser Lys Asp Ile Val Asn Lys Met Thr Phe His  
 755 760 765

Ser Gln Lys Phe Cys Ala Asp Ser Asp Gly Phe Ser Gln Glu Leu Arg  
 770 775 780

Asn Phe Asn Gln Glu Gly Thr Lys Leu Val Glu Glu Ser Val Lys His  
 785 790 795 800

Ser Asp Lys Leu Asn Gly Asn Leu Glu Lys Ile Ser Gln Glu Thr Glu  
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805

810

815

Gln Arg Cys Glu Ser Leu Asn Thr Arg Thr Val Tyr Phe Ser Glu Gln  
820 825 830

Trp Val Ser Ser Leu Asn Glu Arg Glu Gln Glu Leu His Asn Leu Leu  
835 840 845

Glu Val Val Ser Gln Cys Cys Glu Ala Ser Ser Ser Asp Ile Thr Glu  
850 855 860

Lys Ser Asp Gly Arg Lys Ala Ala His Glu Lys Gln His Asn Ile Phe  
865 870 875 880

Leu Asp Gln Met Thr Ile Asp Glu Asp Lys Leu Ile Ala Gln Asn Leu  
885 890 895

Glu Leu Asn Glu Thr Ile Lys Ile Gly Leu Thr Lys Leu Asn Cys Phe  
900 905 910

Leu Glu Gln Asp Leu Lys Leu Asp Ile Pro Thr Gly Thr Thr Pro Gln  
915 920 925

Arg Lys Ser Tyr Leu Tyr Pro Ser Thr Leu Val Arg Thr Glu Pro Arg  
930 935 940

Glu His Leu Leu Asp Gln Leu Lys Arg Lys Gln Pro Glu Leu Leu Met  
945 950 955 960

Met Leu Asn Cys Ser Glu Asn Asn Lys Glu Glu Thr Ile Pro Asp Val  
965 970 975

Asp Val Glu Glu Ala Val Leu Gly Gln Tyr Thr Glu Glu Pro Leu Ser  
980 985 990

Gln Glu Pro Ser Val Asp Ala Gly Val Asp Cys Ser Ser Ile Gly Gly  
995 1000 1005

Val Pro Phe Phe Gln His Lys Lys Ser His Gly Lys Asp Lys Glu  
1010 1015 1020

Asn Arg Gly Ile Asn Thr Leu Glu Arg Ser Lys Val Glu Glu Thr  
1025 1030 1035

Thr Glu His Leu Val Thr Lys Ser Arg Leu Pro Leu Arg Ala Gln  
1040 1045 1050

Ile Asn Leu  
1055

<210> 42



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<211> 2825  
 <212> PRT  
 <213> Homo sapiens

<400> 42

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Met Tyr Ala Ser Leu Gly Ser Gly Pro Val Ala Pro Leu Pro Ala Ser
1      5      10      15

Val Pro Pro Ser Val Leu Gly Ser Trp Ser Thr Gly Gly Ser Arg Ser
20      25      30

Cys Val Arg Gln Glu Thr Lys Ser Pro Gly Gly Ala Arg Thr Ser Gly
35      40      45

His Trp Ala Ser Val Trp Gln Glu Val Leu Lys Gln Leu Gln Gly Ser
50      55      60

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

Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser Asn Phe Pro Gly Val Lys
85      90      95

Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr Gly Ser Arg Glu Gly Ser
100     105     110

Val Ser Ser Arg Ser Gly Glu Cys Ser Pro Val Pro Met Gly Ser Phe
115     120     125

Pro Arg Arg Gly Phe Val Asn Gly Ser Arg Glu Ser Thr Gly Tyr Leu
130     135     140

Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu Leu Ala Asp Leu Asp Lys
145     150     155     160

Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala Gln Leu Gln Asn Leu Thr
165     170     175

Lys Arg Ile Asp Ser Leu Pro Leu Thr Glu Asn Phe Ser Leu Gln Thr
180     185     190

Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu Ala Arg Gln Ile Arg Val
195     200     205

Ala Met Glu Glu Gln Leu Gly Thr Cys Gln Asp Met Glu Lys Arg Ala
210     215     220

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

Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala Thr Ser
245     250     255
    
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Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr Ala Ser  
 260 265 270  
 Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu Thr Ser  
 275 280 285  
 His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser Met Leu  
 290 295 300  
 Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala Met Ser  
 305 310 315 320  
 Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys Leu Pro  
 325 330 335  
 Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val Leu Leu  
 340 345 350  
 Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser Ala Ala  
 355 360 365  
 Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly Arg Arg  
 370 375 380  
 Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr Cys Glu  
 385 390 395 400  
 Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp Gln Asp  
 405 410 415  
 Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro Ala Val  
 420 425 430  
 Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His Ala Met  
 435 440 445  
 Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln Val Asp  
 450 455 460  
 Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr Leu Arg  
 465 470 475 480  
 Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp Val Ala  
 485 490 495  
 Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala Leu Val  
 500 505 510  
 Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile Ala Ser  
 515 520 525

# FAB-008PC-SequenceListing

Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys Lys Thr  
 530 535 540  
 Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala Leu Glu  
 545 550 555 560  
 Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu Trp Asn  
 565 570 575  
 Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala Val Asp  
 580 585 590  
 Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln Thr  
 595 600 605  
 Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg Asn Val  
 610 615 620  
 Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu Arg Glu  
 625 630 635 640  
 Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His Ser Leu  
 645 650 655  
 Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala Arg  
 660 665 670  
 Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val Ser Met  
 675 680 685  
 Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met Gly Ser  
 690 695 700  
 Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr Lys  
 705 710 715 720  
 Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu His Val  
 725 730 735  
 Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His Leu Ser  
 740 745 750  
 Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser His Arg  
 755 760 765  
 Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val Phe Asp  
 770 775 780  
 Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly Asn  
 785 790 795 800

# FAB-008PC-SequenceListing

Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser Ser  
 805 810 815  
 Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp Arg  
 820 825 830  
 Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His Pro Ala  
 835 840 845  
 Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser Thr  
 850 855 860  
 Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala Ile His  
 865 870 875 880  
 Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu His Cys  
 885 890 895  
 Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala His Thr  
 900 905 910  
 His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn Arg Thr  
 915 920 925  
 Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser Asn Asp  
 930 935 940  
 Ser Leu Asn Ser Val Ser Ser Ser Asp Gly Tyr Gly Lys Arg Gly Gln  
 945 950 955 960  
 Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser Lys Phe  
 965 970 975  
 Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile His Ser  
 980 985 990  
 Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro Ile Asn  
 995 1000 1005  
 Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg Gln  
 1010 1015 1020  
 Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile  
 1025 1030 1035  
 Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln  
 1040 1045 1050  
 Ser Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His  
 1055 1060 1065

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Leu	Lys 1070	Phe	Gln	Pro	His	Phe 1075	Gly	Gln	Gln	Glu	Cys 1080	Val	Ser	Pro
Tyr	Arg 1085	Ser	Arg	Gly	Ala	Asn 1090	Gly	Ser	Glu	Thr	Asn 1095	Arg	Val	Gly
Ser	Asn 1100	His	Gly	Ile	Asn	Gln 1105	Asn	Val	Ser	Gln	Ser 1110	Leu	Cys	Gln
Glu	Asp 1115	Asp	Tyr	Glu	Asp	Asp 1120	Lys	Pro	Thr	Asn	Tyr 1125	Ser	Glu	Arg
Tyr	Ser 1130	Glu	Glu	Glu	Gln	His 1135	Glu	Glu	Glu	Glu	Arg 1140	Pro	Thr	Asn
Tyr	Ser 1145	Ile	Lys	Tyr	Asn	Glu 1150	Glu	Lys	Arg	His	Val 1155	Asp	Gln	Pro
Ile	Asp 1160	Tyr	Ser	Leu	Lys	Tyr 1165	Ala	Thr	Asp	Ile	Pro 1170	Ser	Ser	Gln
Lys	Gln 1175	Ser	Phe	Ser	Phe	Ser 1180	Lys	Ser	Ser	Ser	Gly 1185	Gln	Ser	Ser
Lys	Thr 1190	Glu	His	Met	Ser	Ser 1195	Ser	Ser	Glu	Asn	Thr 1200	Ser	Thr	Pro
Ser	Ser 1205	Asn	Ala	Lys	Arg	Gln 1210	Asn	Gln	Leu	His	Pro 1215	Ser	Ser	Ala
Gln	Ser 1220	Arg	Ser	Gly	Gln	Pro 1225	Gln	Lys	Ala	Ala	Thr 1230	Cys	Lys	Val
Ser	Ser 1235	Ile	Asn	Gln	Glu	Thr 1240	Ile	Gln	Thr	Tyr	Cys 1245	Val	Glu	Asp
Thr	Pro 1250	Ile	Cys	Phe	Ser	Arg 1255	Cys	Ser	Ser	Leu	Ser 1260	Ser	Leu	Ser
Ser	Ala 1265	Glu	Asp	Glu	Ile	Gly 1270	Cys	Asn	Gln	Thr	Thr 1275	Gln	Glu	Ala
Asp	Ser 1280	Ala	Asn	Thr	Leu	Gln 1285	Ile	Ala	Glu	Ile	Lys 1290	Glu	Lys	Ile
Gly	Thr 1295	Arg	Ser	Ala	Glu	Asp 1300	Pro	Val	Ser	Glu	Val 1305	Pro	Ala	Val
Ser	Gln 1310	His	Pro	Arg	Thr	Lys 1315	Ser	Ser	Arg	Leu	Gln 1320	Gly	Ser	Ser

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Leu	Ser	Ser	Glu	Ser	Ala	Arg	His	Lys	Ala	Val	Glu	Phe	Ser	Ser
	1325					1330					1335			
Gly	Ala	Lys	Ser	Pro	Ser	Lys	Ser	Gly	Ala	Gln	Thr	Pro	Lys	Ser
	1340					1345					1350			
Pro	Pro	Glu	His	Tyr	Val	Gln	Glu	Thr	Pro	Leu	Met	Phe	Ser	Arg
	1355					1360					1365			
Cys	Thr	Ser	Val	Ser	Ser	Leu	Asp	Ser	Phe	Glu	Ser	Arg	Ser	Ile
	1370					1375					1380			
Ala	Ser	Ser	Val	Gln	Ser	Glu	Pro	Cys	Ser	Gly	Met	Val	Ser	Gly
	1385					1390					1395			
Ile	Ile	Ser	Pro	Ser	Asp	Leu	Pro	Asp	Ser	Pro	Gly	Gln	Thr	Met
	1400					1405					1410			
Pro	Pro	Ser	Arg	Ser	Lys	Thr	Pro	Pro	Pro	Pro	Pro	Gln	Thr	Ala
	1415					1420					1425			
Gln	Thr	Lys	Arg	Glu	Val	Pro	Lys	Asn	Lys	Ala	Pro	Thr	Ala	Glu
	1430					1435					1440			
Lys	Arg	Glu	Ser	Gly	Pro	Lys	Gln	Ala	Ala	Val	Asn	Ala	Ala	Val
	1445					1450					1455			
Gln	Arg	Val	Gln	Val	Leu	Pro	Asp	Ala	Asp	Thr	Leu	Leu	His	Phe
	1460					1465					1470			
Ala	Thr	Glu	Ser	Thr	Pro	Asp	Gly	Phe	Ser	Cys	Ser	Ser	Ser	Leu
	1475					1480					1485			
Ser	Ala	Leu	Ser	Leu	Asp	Glu	Pro	Phe	Ile	Gln	Lys	Asp	Val	Glu
	1490					1495					1500			
Leu	Arg	Ile	Met	Pro	Pro	Val	Gln	Glu	Asn	Asp	Asn	Gly	Asn	Glu
	1505					1510					1515			
Thr	Glu	Ser	Glu	Gln	Pro	Lys	Glu	Ser	Asn	Glu	Asn	Gln	Glu	Lys
	1520					1525					1530			
Glu	Ala	Glu	Lys	Thr	Ile	Asp	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Asp
	1535					1540					1545			
Ser	Asp	Asp	Asp	Asp	Ile	Glu	Ile	Leu	Glu	Glu	Cys	Ile	Ile	Ser
	1550					1555					1560			
Ala	Met	Pro	Thr	Lys	Ser	Ser	Arg	Lys	Ala	Lys	Lys	Pro	Ala	Gln
	1565					1570					1575			

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Thr	Ala	Ser	Lys	Leu	Pro	Pro	Pro	Val	Ala	Arg	Lys	Pro	Ser	Gln
	1580					1585					1590			
Leu	Pro	Val	Tyr	Lys	Leu	Leu	Pro	Ser	Gln	Asn	Arg	Leu	Gln	Pro
	1595					1600					1605			
Gln	Lys	His	Val	Ser	Phe	Thr	Pro	Gly	Asp	Asp	Met	Pro	Arg	Val
	1610					1615					1620			
Tyr	Cys	Val	Glu	Gly	Thr	Pro	Ile	Asn	Phe	Ser	Thr	Ala	Thr	Ser
	1625					1630					1635			
Leu	Ser	Asp	Leu	Thr	Ile	Glu	Ser	Pro	Pro	Asn	Glu	Leu	Ala	Ala
	1640					1645					1650			
Gly	Glu	Gly	Val	Arg	Gly	Gly	Ala	Gln	Ser	Gly	Glu	Phe	Glu	Lys
	1655					1660					1665			
Arg	Asp	Thr	Ile	Pro	Thr	Glu	Gly	Arg	Ser	Thr	Asp	Glu	Ala	Gln
	1670					1675					1680			
Gly	Gly	Lys	Thr	Ser	Ser	Val	Thr	Ile	Pro	Glu	Leu	Asp	Asp	Asn
	1685					1690					1695			
Lys	Ala	Glu	Glu	Gly	Asp	Ile	Leu	Ala	Glu	Cys	Ile	Asn	Ser	Ala
	1700					1705					1710			
Met	Pro	Lys	Gly	Lys	Ser	His	Lys	Pro	Phe	Arg	Val	Lys	Lys	Ile
	1715					1720					1725			
Met	Asp	Gln	Val	Gln	Gln	Ala	Ser	Ala	Ser	Ser	Ser	Ala	Pro	Asn
	1730					1735					1740			
Lys	Asn	Gln	Leu	Asp	Gly	Lys	Lys	Lys	Lys	Pro	Thr	Ser	Pro	Val
	1745					1750					1755			
Lys	Pro	Ile	Pro	Gln	Asn	Thr	Glu	Tyr	Arg	Thr	Arg	Val	Arg	Lys
	1760					1765					1770			
Asn	Ala	Asp	Ser	Lys	Asn	Asn	Leu	Asn	Ala	Glu	Arg	Val	Phe	Ser
	1775					1780					1785			
Asp	Asn	Lys	Asp	Ser	Lys	Lys	Gln	Asn	Leu	Lys	Asn	Asn	Ser	Lys
	1790					1795					1800			
Val	Phe	Asn	Asp	Lys	Leu	Pro	Asn	Asn	Glu	Asp	Arg	Val	Arg	Gly
	1805					1810					1815			
Ser	Phe	Ala	Phe	Asp	Ser	Pro	His	His	Tyr	Thr	Pro	Ile	Glu	Gly
	1820					1825					1830			

# FAB-008PC-SequenceListing

Thr	Pro	Tyr	Cys	Phe	Ser	Arg	Asn	Asp	Ser	Leu	Ser	Ser	Leu	Asp
	1835					1840					1845			
Phe	Asp	Asp	Asp	Asp	Val	Asp	Leu	Ser	Arg	Glu	Lys	Ala	Glu	Leu
	1850					1855					1860			
Arg	Lys	Ala	Lys	Glu	Asn	Lys	Glu	Ser	Glu	Ala	Lys	Val	Thr	Ser
	1865					1870					1875			
His	Thr	Glu	Leu	Thr	Ser	Asn	Gln	Gln	Ser	Ala	Asn	Lys	Thr	Gln
	1880					1885					1890			
Ala	Ile	Ala	Lys	Gln	Pro	Ile	Asn	Arg	Gly	Gln	Pro	Lys	Pro	Ile
	1895					1900					1905			
Leu	Gln	Lys	Gln	Ser	Thr	Phe	Pro	Gln	Ser	Ser	Lys	Asp	Ile	Pro
	1910					1915					1920			
Asp	Arg	Gly	Ala	Ala	Thr	Asp	Glu	Lys	Leu	Gln	Asn	Phe	Ala	Ile
	1925					1930					1935			
Glu	Asn	Thr	Pro	Val	Cys	Phe	Ser	His	Asn	Ser	Ser	Leu	Ser	Ser
	1940					1945					1950			
Leu	Ser	Asp	Ile	Asp	Gln	Glu	Asn	Asn	Asn	Lys	Glu	Asn	Glu	Pro
	1955					1960					1965			
Ile	Lys	Glu	Thr	Glu	Pro	Pro	Asp	Ser	Gln	Gly	Glu	Pro	Ser	Lys
	1970					1975					1980			
Pro	Gln	Ala	Ser	Gly	Tyr	Ala	Pro	Lys	Ser	Phe	His	Val	Glu	Asp
	1985					1990					1995			
Thr	Pro	Val	Cys	Phe	Ser	Arg	Asn	Ser	Ser	Leu	Ser	Ser	Leu	Ser
	2000					2005					2010			
Ile	Asp	Ser	Glu	Asp	Asp	Leu	Leu	Gln	Glu	Cys	Ile	Ser	Ser	Ala
	2015					2020					2025			
Met	Pro	Lys	Lys	Lys	Lys	Pro	Ser	Arg	Leu	Lys	Gly	Asp	Asn	Glu
	2030					2035					2040			
Lys	His	Ser	Pro	Arg	Asn	Met	Gly	Gly	Ile	Leu	Gly	Glu	Asp	Leu
	2045					2050					2055			
Thr	Leu	Asp	Leu	Lys	Asp	Ile	Gln	Arg	Pro	Asp	Ser	Glu	His	Gly
	2060					2065					2070			
Leu	Ser	Pro	Asp	Ser	Glu	Asn	Phe	Asp	Trp	Lys	Ala	Ile	Gln	Glu
	2075					2080					2085			



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Gly	Ala	Asn	Ser	Ile	Val	Ser	Ser	Leu	His	Gln	Ala	Ala	Ala	Ala
2090						2095					2100			
Ala	Cys	Leu	Ser	Arg	Gln	Ala	Ser	Ser	Asp	Ser	Asp	Ser	Ile	Leu
2105						2110					2115			
Ser	Leu	Lys	Ser	Gly	Ile	Ser	Leu	Gly	Ser	Pro	Phe	His	Leu	Thr
2120						2125					2130			
Pro	Asp	Gln	Glu	Glu	Lys	Pro	Phe	Thr	Ser	Asn	Lys	Gly	Pro	Arg
2135						2140					2145			
Ile	Leu	Lys	Pro	Gly	Glu	Lys	Ser	Thr	Leu	Glu	Thr	Lys	Lys	Ile
2150						2155					2160			
Glu	Ser	Glu	Ser	Lys	Gly	Ile	Lys	Gly	Gly	Lys	Lys	Val	Tyr	Lys
2165						2170					2175			
Ser	Leu	Ile	Thr	Gly	Lys	Val	Arg	Ser	Asn	Ser	Glu	Ile	Ser	Gly
2180						2185					2190			
Gln	Met	Lys	Gln	Pro	Leu	Gln	Ala	Asn	Met	Pro	Ser	Ile	Ser	Arg
2195						2200					2205			
Gly	Arg	Thr	Met	Ile	His	Ile	Pro	Gly	Val	Arg	Asn	Ser	Ser	Ser
2210						2215					2220			
Ser	Thr	Ser	Pro	Val	Ser	Lys	Lys	Gly	Pro	Pro	Leu	Lys	Thr	Pro
2225						2230					2235			
Ala	Ser	Lys	Ser	Pro	Ser	Glu	Gly	Gln	Thr	Ala	Thr	Thr	Ser	Pro
2240						2245					2250			
Arg	Gly	Ala	Lys	Pro	Ser	Val	Lys	Ser	Glu	Leu	Ser	Pro	Val	Ala
2255						2260					2265			
Arg	Gln	Thr	Ser	Gln	Ile	Gly	Gly	Ser	Ser	Lys	Ala	Pro	Ser	Arg
2270						2275					2280			
Ser	Gly	Ser	Arg	Asp	Ser	Thr	Pro	Ser	Arg	Pro	Ala	Gln	Gln	Pro
2285						2290					2295			
Leu	Ser	Arg	Pro	Ile	Gln	Ser	Pro	Gly	Arg	Asn	Ser	Ile	Ser	Pro
2300						2305					2310			
Gly	Arg	Asn	Gly	Ile	Ser	Pro	Pro	Asn	Lys	Leu	Ser	Gln	Leu	Pro
2315						2320					2325			
Arg	Thr	Ser	Ser	Pro	Ser	Thr	Ala	Ser	Thr	Lys	Ser	Ser	Gly	Ser
2330						2335					2340			

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Gly	Lys	Met	Ser	Tyr	Thr	Ser	Pro	Gly	Arg	Gln	Met	Ser	Gln	Gln
	2345					2350					2355			
Asn	Leu	Thr	Lys	Gln	Thr	Gly	Leu	Ser	Lys	Asn	Ala	Ser	Ser	Ile
	2360					2365					2370			
Pro	Arg	Ser	Glu	Ser	Ala	Ser	Lys	Gly	Leu	Asn	Gln	Met	Asn	Asn
	2375					2380					2385			
Gly	Asn	Gly	Ala	Asn	Lys	Lys	Val	Glu	Leu	Ser	Arg	Met	Ser	Ser
	2390					2395					2400			
Thr	Lys	Ser	Ser	Gly	Ser	Glu	Ser	Asp	Arg	Ser	Glu	Arg	Pro	Val
	2405					2410					2415			
Leu	Val	Arg	Gln	Ser	Thr	Phe	Ile	Lys	Glu	Ala	Pro	Ser	Pro	Thr
	2420					2425					2430			
Leu	Arg	Arg	Lys	Leu	Glu	Glu	Ser	Ala	Ser	Phe	Glu	Ser	Leu	Ser
	2435					2440					2445			
Pro	Ser	Ser	Arg	Pro	Ala	Ser	Pro	Thr	Arg	Ser	Gln	Ala	Gln	Thr
	2450					2455					2460			
Pro	Val	Leu	Ser	Pro	Ser	Leu	Pro	Asp	Met	Ser	Leu	Ser	Thr	His
	2465					2470					2475			
Ser	Ser	Val	Gln	Ala	Gly	Gly	Trp	Arg	Lys	Leu	Pro	Pro	Asn	Leu
	2480					2485					2490			
Ser	Pro	Thr	Ile	Glu	Tyr	Asn	Asp	Gly	Arg	Pro	Ala	Lys	Arg	His
	2495					2500					2505			
Asp	Ile	Ala	Arg	Ser	His	Ser	Glu	Ser	Pro	Ser	Arg	Leu	Pro	Ile
	2510					2515					2520			
Asn	Arg	Ser	Gly	Thr	Trp	Lys	Arg	Glu	His	Ser	Lys	His	Ser	Ser
	2525					2530					2535			
Ser	Leu	Pro	Arg	Val	Ser	Thr	Trp	Arg	Arg	Thr	Gly	Ser	Ser	Ser
	2540					2545					2550			
Ser	Ile	Leu	Ser	Ala	Ser	Ser	Glu	Ser	Ser	Glu	Lys	Ala	Lys	Ser
	2555					2560					2565			
Glu	Asp	Glu	Lys	His	Val	Asn	Ser	Ile	Ser	Gly	Thr	Lys	Gln	Ser
	2570					2575					2580			
Lys	Glu	Asn	Gln	Val	Ser	Ala	Lys	Gly	Thr	Trp	Arg	Lys	Ile	Lys
	2585					2590					2595			

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Glu	Asn	Glu	Phe	Ser	Pro	Thr	Asn	Ser	Thr	Ser	Gln	Thr	Val	Ser
	2600					2605					2610			
Ser	Gly	Ala	Thr	Asn	Gly	Ala	Glu	Ser	Lys	Thr	Leu	Ile	Tyr	Gln
	2615					2620					2625			
Met	Ala	Pro	Ala	Val	Ser	Lys	Thr	Glu	Asp	Val	Trp	Val	Arg	Ile
	2630					2635					2640			
Glu	Asp	Cys	Pro	Ile	Asn	Asn	Pro	Arg	Ser	Gly	Arg	Ser	Pro	Thr
	2645					2650					2655			
Gly	Asn	Thr	Pro	Pro	Val	Ile	Asp	Ser	Val	Ser	Glu	Lys	Ala	Asn
	2660					2665					2670			
Pro	Asn	Ile	Lys	Asp	Ser	Lys	Asp	Asn	Gln	Ala	Lys	Gln	Asn	Val
	2675					2680					2685			
Gly	Asn	Gly	Ser	Val	Pro	Met	Arg	Thr	Val	Gly	Leu	Glu	Asn	Arg
	2690					2695					2700			
Leu	Asn	Ser	Phe	Ile	Gln	Val	Asp	Ala	Pro	Asp	Gln	Lys	Gly	Thr
	2705					2710					2715			
Glu	Ile	Lys	Pro	Gly	Gln	Asn	Asn	Pro	Val	Pro	Val	Ser	Glu	Thr
	2720					2725					2730			
Asn	Glu	Ser	Ser	Ile	Val	Glu	Arg	Thr	Pro	Phe	Ser	Ser	Ser	Ser
	2735					2740					2745			
Ser	Ser	Lys	His	Ser	Ser	Pro	Ser	Gly	Thr	Val	Ala	Ala	Arg	Val
	2750					2755					2760			
Thr	Pro	Phe	Asn	Tyr	Asn	Pro	Ser	Pro	Arg	Lys	Ser	Ser	Ala	Asp
	2765					2770					2775			
Ser	Thr	Ser	Ala	Arg	Pro	Ser	Gln	Ile	Pro	Thr	Pro	Val	Asn	Asn
	2780					2785					2790			
Asn	Thr	Lys	Lys	Arg	Asp	Ser	Lys	Thr	Asp	Ser	Thr	Glu	Ser	Ser
	2795					2800					2805			
Gly	Thr	Gln	Ser	Pro	Lys	Arg	His	Ser	Gly	Ser	Tyr	Leu	Val	Thr
	2810					2815					2820			
Ser	Val													
	2825													

<210> 43  
<211> 1863

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<212> PRT  
 <213> Homo sapiens  
 <400> 43

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Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn
1      5      10      15

Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys
      20      25      30

Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met
      35      40      45

Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys
      50      55      60

Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser
65      70      75      80

Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp
      85      90      95

Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn
      100      105      110

Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met
      115      120      125

Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn
      130      135      140

Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly
145      150      155      160

Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr
      165      170      175

Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn
      180      185      190

Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr
      195      200      205

Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala
      210      215      220

Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln
225      230      235      240

Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg
      245      250      255
    
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His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu  
260 265 270

Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser  
275 280 285

Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe  
290 295 300

Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg  
305 310 315 320

Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr  
325 330 335

Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu  
340 345 350

Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu  
355 360 365

Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu  
370 375 380

Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp  
385 390 395 400

Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu  
405 410 415

Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu  
420 425 430

Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His  
435 440 445

Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr  
450 455 460

Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn  
465 470 475 480

Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg  
485 490 495

Pro Leu Thr Asn Lys Leu Lys Arg Lys Arg Arg Pro Thr Ser Gly Leu  
500 505 510

His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr  
515 520 525

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Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln  
530 535 540

Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp  
545 550 555 560

Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys  
565 570 575

Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser  
580 585 590

Asn Met Glu Leu Glu Leu Asn Ile His Asn Ser Lys Ala Pro Lys Lys  
595 600 605

Asn Arg Leu Arg Arg Lys Ser Ser Thr Arg His Ile His Ala Leu Glu  
610 615 620

Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln  
625 630 635 640

Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Lys Tyr Asn  
645 650 655

Gln Met Pro Val Arg His Ser Arg Asn Leu Gln Leu Met Glu Gly Lys  
660 665 670

Glu Pro Ala Thr Gly Ala Lys Lys Ser Asn Lys Pro Asn Glu Gln Thr  
675 680 685

Ser Lys Arg His Asp Ser Asp Thr Phe Pro Glu Leu Lys Leu Thr Asn  
690 695 700

Ala Pro Gly Ser Phe Thr Lys Cys Ser Asn Thr Ser Glu Leu Lys Glu  
705 710 715 720

Phe Val Asn Pro Ser Leu Pro Arg Glu Glu Lys Glu Glu Lys Leu Glu  
725 730 735

Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu  
740 745 750

Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ser  
755 760 765

Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser  
770 775 780

Leu Leu Glu Val Ser Thr Leu Gly Lys Ala Lys Thr Glu Pro Asn Lys  
785 790 795 800

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Cys Val Ser Gln Cys Ala Ala Phe Glu Asn Pro Lys Gly Leu Ile His  
 805 810 815  
 Gly Cys Ser Lys Asp Asn Arg Asn Asp Thr Glu Gly Phe Lys Tyr Pro  
 820 825 830  
 Leu Gly His Glu Val Asn His Ser Arg Glu Thr Ser Ile Glu Met Glu  
 835 840 845  
 Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser  
 850 855 860  
 Lys Arg Gln Ser Phe Ala Pro Phe Ser Asn Pro Gly Asn Ala Glu Glu  
 865 870 875 880  
 Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser  
 885 890 895  
 Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys  
 900 905 910  
 Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly  
 915 920 925  
 Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys  
 930 935 940  
 Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly  
 945 950 955 960  
 Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn  
 965 970 975  
 Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr  
 980 985 990  
 Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met  
 995 1000 1005  
 Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val  
 1010 1015 1020  
 Ser Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Glu  
 1025 1030 1035  
 Ala Ser Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu  
 1040 1045 1050  
 Val Gly Ser Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile  
 1055 1060 1065

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Gln	Ala	Glu	Leu	Gly	Arg	Asn	Arg	Gly	Pro	Lys	Leu	Asn	Ala	Met
	1070					1075					1080			
Leu	Arg	Leu	Gly	Val	Leu	Gln	Pro	Glu	Val	Tyr	Lys	Gln	Ser	Leu
	1085					1090					1095			
Pro	Gly	Ser	Asn	Cys	Lys	His	Pro	Glu	Ile	Lys	Lys	Gln	Glu	Tyr
	1100					1105					1110			
Glu	Glu	Val	Val	Gln	Thr	Val	Asn	Thr	Asp	Phe	Ser	Pro	Tyr	Leu
	1115					1120					1125			
Ile	Ser	Asp	Asn	Leu	Glu	Gln	Pro	Met	Gly	Ser	Ser	His	Ala	Ser
	1130					1135					1140			
Gln	Val	Cys	Ser	Glu	Thr	Pro	Asp	Asp	Leu	Leu	Asp	Asp	Gly	Glu
	1145					1150					1155			
Ile	Lys	Glu	Asp	Thr	Ser	Phe	Ala	Glu	Asn	Asp	Ile	Lys	Glu	Ser
	1160					1165					1170			
Ser	Ala	Val	Phe	Ser	Lys	Ser	Val	Gln	Lys	Gly	Glu	Leu	Ser	Arg
	1175					1180					1185			
Ser	Pro	Ser	Pro	Phe	Thr	His	Thr	His	Leu	Ala	Gln	Gly	Tyr	Arg
	1190					1195					1200			
Arg	Gly	Ala	Lys	Lys	Leu	Glu	Ser	Ser	Glu	Glu	Asn	Leu	Ser	Ser
	1205					1210					1215			
Glu	Asp	Glu	Glu	Leu	Pro	Cys	Phe	Gln	His	Leu	Leu	Phe	Gly	Lys
	1220					1225					1230			
Val	Asn	Asn	Ile	Pro	Ser	Gln	Ser	Thr	Arg	His	Ser	Thr	Val	Ala
	1235					1240					1245			
Thr	Glu	Cys	Leu	Ser	Lys	Asn	Thr	Glu	Glu	Asn	Leu	Leu	Ser	Leu
	1250					1255					1260			
Lys	Asn	Ser	Leu	Asn	Asp	Cys	Ser	Asn	Gln	Val	Ile	Leu	Ala	Lys
	1265					1270					1275			
Ala	Ser	Gln	Glu	His	His	Leu	Ser	Glu	Glu	Thr	Lys	Cys	Ser	Ala
	1280					1285					1290			
Ser	Leu	Phe	Ser	Ser	Gln	Cys	Ser	Glu	Leu	Glu	Asp	Leu	Thr	Ala
	1295					1300					1305			
Asn	Thr	Asn	Thr	Gln	Asp	Pro	Phe	Leu	Ile	Gly	Ser	Ser	Lys	Gln
	1310					1315					1320			



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Met	Arg	His	Gln	Ser	Glu	Ser	Gln	Gly	Val	Gly	Leu	Ser	Asp	Lys
	1325					1330					1335			
Glu	Leu	Val	Ser	Asp	Asp	Glu	Glu	Arg	Gly	Thr	Gly	Leu	Glu	Glu
	1340					1345					1350			
Asn	Asn	Gln	Glu	Glu	Gln	Ser	Met	Asp	Ser	Asn	Leu	Gly	Glu	Ala
	1355					1360					1365			
Ala	Ser	Gly	Cys	Glu	Ser	Glu	Thr	Ser	Val	Ser	Glu	Asp	Cys	Ser
	1370					1375					1380			
Gly	Leu	Ser	Ser	Gln	Ser	Asp	Ile	Leu	Thr	Thr	Gln	Gln	Arg	Asp
	1385					1390					1395			
Thr	Met	Gln	His	Asn	Leu	Ile	Lys	Leu	Gln	Gln	Glu	Met	Ala	Glu
	1400					1405					1410			
Leu	Glu	Ala	Val	Leu	Glu	Gln	His	Gly	Ser	Gln	Pro	Ser	Asn	Ser
	1415					1420					1425			
Tyr	Pro	Ser	Ile	Ile	Ser	Asp	Ser	Ser	Ala	Leu	Glu	Asp	Leu	Arg
	1430					1435					1440			
Asn	Pro	Glu	Gln	Ser	Thr	Ser	Glu	Lys	Ala	Val	Leu	Thr	Ser	Gln
	1445					1450					1455			
Lys	Ser	Ser	Glu	Tyr	Pro	Ile	Ser	Gln	Asn	Pro	Glu	Gly	Leu	Ser
	1460					1465					1470			
Ala	Asp	Lys	Phe	Glu	Val	Ser	Ala	Asp	Ser	Ser	Thr	Ser	Lys	Asn
	1475					1480					1485			
Lys	Glu	Pro	Gly	Val	Glu	Arg	Ser	Ser	Pro	Ser	Lys	Cys	Pro	Ser
	1490					1495					1500			
Leu	Asp	Asp	Arg	Trp	Tyr	Met	His	Ser	Cys	Ser	Gly	Ser	Leu	Gln
	1505					1510					1515			
Asn	Arg	Asn	Tyr	Pro	Ser	Gln	Glu	Glu	Leu	Ile	Lys	Val	Val	Asp
	1520					1525					1530			
Val	Glu	Glu	Gln	Gln	Leu	Glu	Glu	Ser	Gly	Pro	His	Asp	Leu	Thr
	1535					1540					1545			
Glu	Thr	Ser	Tyr	Leu	Pro	Arg	Gln	Asp	Leu	Glu	Gly	Thr	Pro	Tyr
	1550					1555					1560			
Leu	Glu	Ser	Gly	Ile	Ser	Leu	Phe	Ser	Asp	Asp	Pro	Glu	Ser	Asp
	1565					1570					1575			

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Pro	Ser	Glu	Asp	Arg	Ala	Pro	Glu	Ser	Ala	Arg	Val	Gly	Asn	Ile
	1580					1585					1590			
Pro	Ser	Ser	Thr	Ser	Ala	Leu	Lys	Val	Pro	Gln	Leu	Lys	Val	Ala
	1595					1600					1605			
Glu	Ser	Ala	Gln	Ser	Pro	Ala	Ala	Ala	His	Thr	Thr	Asp	Thr	Ala
	1610					1615					1620			
Gly	Tyr	Asn	Ala	Met	Glu	Glu	Ser	Val	Ser	Arg	Glu	Lys	Pro	Glu
	1625					1630					1635			
Leu	Thr	Ala	Ser	Thr	Glu	Arg	Val	Asn	Lys	Arg	Met	Ser	Met	Val
	1640					1645					1650			
Val	Ser	Gly	Leu	Thr	Pro	Glu	Glu	Phe	Met	Leu	Val	Tyr	Lys	Phe
	1655					1660					1665			
Ala	Arg	Lys	His	His	Ile	Thr	Leu	Thr	Asn	Leu	Ile	Thr	Glu	Glu
	1670					1675					1680			
Thr	Thr	His	Val	Val	Met	Lys	Thr	Asp	Ala	Glu	Phe	Val	Cys	Glu
	1685					1690					1695			
Arg	Thr	Leu	Lys	Tyr	Phe	Leu	Gly	Ile	Ala	Gly	Gly	Lys	Trp	Val
	1700					1705					1710			
Val	Ser	Tyr	Phe	Trp	Val	Thr	Gln	Ser	Ile	Lys	Glu	Arg	Lys	Met
	1715					1720					1725			
Leu	Asn	Glu	His	Asp	Phe	Glu	Val	Arg	Gly	Asp	Val	Val	Asn	Gly
	1730					1735					1740			
Arg	Asn	His	Gln	Gly	Pro	Lys	Arg	Ala	Arg	Glu	Ser	Gln	Asp	Arg
	1745					1750					1755			
Lys	Ile	Phe	Arg	Gly	Leu	Glu	Ile	Cys	Cys	Tyr	Gly	Pro	Phe	Thr
	1760					1765					1770			
Asn	Met	Pro	Thr	Asp	Gln	Leu	Glu	Trp	Met	Val	Gln	Leu	Cys	Gly
	1775					1780					1785			
Ala	Ser	Val	Val	Lys	Glu	Leu	Ser	Ser	Phe	Thr	Leu	Gly	Thr	Gly
	1790					1795					1800			
Val	His	Pro	Ile	Val	Val	Val	Gln	Pro	Asp	Ala	Trp	Thr	Glu	Asp
	1805					1810					1815			
Asn	Gly	Phe	His	Ala	Ile	Gly	Gln	Met	Cys	Glu	Ala	Pro	Val	Val
	1820					1825					1830			

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Thr Arg Glu Trp Val Leu Asp Ser Val Ala Leu Tyr Gln Cys Gln  
1835 1840 1845

Glu Leu Asp Thr Tyr Leu Ile Pro Gln Ile Pro His Ser His Tyr  
1850 1855 1860

<210> 44  
<211> 3418  
<212> PRT  
<213> Homo sapiens

<400> 44

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys  
1 5 10 15

Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe  
20 25 30

Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu  
35 40 45

Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr  
50 55 60

Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile  
65 70 75 80

Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys  
85 90 95

Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser  
100 105 110

Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp  
115 120 125

Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val  
130 135 140

Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val  
145 150 155 160

Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr  
165 170 175

Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met  
180 185 190

Ser Trp Ser Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val  
195 200 205

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Leu Ile Val Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp  
210 215 220

Thr Thr Ala Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu  
225 230 235 240

Lys Lys Asn Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr  
245 250 255

Asn Gln Arg Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn  
260 265 270

Ser Phe Lys Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro  
275 280 285

Asn Val Leu Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu  
290 295 300

Glu Asp Ser Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu  
305 310 315 320

Gln Lys Val Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala  
325 330 335

Asn Ala Asp Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr  
340 345 350

Ser Phe Val Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser  
355 360 365

Asn Val Ala Asn Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser  
370 375 380

Lys Glu Val Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu  
385 390 395 400

Ser Gly Leu Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile  
405 410 415

Ser Ser Cys Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu  
420 425 430

Asn Lys Arg Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg  
435 440 445

Ile Ser Ser Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val  
450 455 460

Val Asn Lys Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys  
465 470 475 480

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Ile Leu Ala Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser  
485 490 495

Ser Phe Gln Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro  
500 505 510

Lys Glu Thr Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn  
515 520 525

Phe Lys Lys Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr  
530 535 540

Val Cys Ser Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn  
545 550 555 560

Gly Ser Trp Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn  
565 570 575

Ala Gly Leu Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr  
580 585 590

Ala Ile His Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp  
595 600 605

Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala  
610 615 620

Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His  
625 630 635 640

Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr  
645 650 655

Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg  
660 665 670

Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr  
675 680 685

Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro  
690 695 700

Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp  
705 710 715 720

Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala  
725 730 735

Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp  
740 745 750

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Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr  
 755 760 765  
 Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met  
 770 775 780  
 Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly  
 785 790 795 800  
 Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu  
 805 810 815  
 Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu  
 820 825 830  
 Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys  
 835 840 845  
 Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln  
 850 855 860  
 Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu  
 865 870 875 880  
 Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn  
 885 890 895  
 Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr  
 900 905 910  
 Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val  
 915 920 925  
 Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys  
 930 935 940  
 Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys  
 945 950 955 960  
 Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser  
 965 970 975  
 Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys  
 980 985 990  
 Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser  
 995 1000 1005  
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn  
 1010 1015 1020

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Ile	Lys	Lys	Ser	Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr
1025						1030					1035			
Pro	Thr	Ser	Leu	Ala	Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu
1040						1045					1050			
Asp	Asn	Gln	Lys	Lys	Leu	Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val
1055						1060					1065			
Ser	Ala	His	Leu	Gln	Ser	Ser	Val	Val	Val	Ser	Asp	Cys	Lys	Asn
1070						1075					1080			
Ser	His	Ile	Thr	Pro	Gln	Met	Leu	Phe	Ser	Lys	Gln	Asp	Phe	Asn
1085						1090					1095			
Ser	Asn	His	Asn	Leu	Thr	Pro	Ser	Gln	Lys	Ala	Glu	Ile	Thr	Glu
1100						1105					1110			
Leu	Ser	Thr	Ile	Leu	Glu	Glu	Ser	Gly	Ser	Gln	Phe	Glu	Phe	Thr
1115						1120					1125			
Gln	Phe	Arg	Lys	Pro	Ser	Tyr	Ile	Leu	Gln	Lys	Ser	Thr	Phe	Glu
1130						1135					1140			
Val	Pro	Glu	Asn	Gln	Met	Thr	Ile	Leu	Lys	Thr	Thr	Ser	Glu	Glu
1145						1150					1155			
Cys	Arg	Asp	Ala	Asp	Leu	His	Val	Ile	Met	Asn	Ala	Pro	Ser	Ile
1160						1165					1170			
Gly	Gln	Val	Asp	Ser	Ser	Lys	Gln	Phe	Glu	Gly	Thr	Val	Glu	Ile
1175						1180					1185			
Lys	Arg	Lys	Phe	Ala	Gly	Leu	Leu	Lys	Asn	Asp	Cys	Asn	Lys	Ser
1190						1195					1200			
Ala	Ser	Gly	Tyr	Leu	Thr	Asp	Glu	Asn	Glu	Val	Gly	Phe	Arg	Gly
1205						1210					1215			
Phe	Tyr	Ser	Ala	His	Gly	Thr	Lys	Leu	Asn	Val	Ser	Thr	Glu	Ala
1220						1225					1230			
Leu	Gln	Lys	Ala	Val	Lys	Leu	Phe	Ser	Asp	Ile	Glu	Asn	Ile	Ser
1235						1240					1245			
Glu	Glu	Thr	Ser	Ala	Glu	Val	His	Pro	Ile	Ser	Leu	Ser	Ser	Ser
1250						1255					1260			
Lys	Cys	His	Asp	Ser	Val	Val	Ser	Met	Phe	Lys	Ile	Glu	Asn	His
1265						1270					1275			

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Asn	Asp	Lys	Thr	Val	Ser	Glu	Lys	Asn	Asn	Lys	Cys	Gln	Leu	Ile
	1280					1285					1290			
Leu	Gln	Asn	Asn	Ile	Glu	Met	Thr	Thr	Gly	Thr	Phe	Val	Glu	Glu
	1295					1300					1305			
Ile	Thr	Glu	Asn	Tyr	Lys	Arg	Asn	Thr	Glu	Asn	Glu	Asp	Asn	Lys
	1310					1315					1320			
Tyr	Thr	Ala	Ala	Ser	Arg	Asn	Ser	His	Asn	Leu	Glu	Phe	Asp	Gly
	1325					1330					1335			
Ser	Asp	Ser	Ser	Lys	Asn	Asp	Thr	Val	Cys	Ile	His	Lys	Asp	Glu
	1340					1345					1350			
Thr	Asp	Leu	Leu	Phe	Thr	Asp	Gln	His	Asn	Ile	Cys	Leu	Lys	Leu
	1355					1360					1365			
Ser	Gly	Gln	Phe	Met	Lys	Glu	Gly	Asn	Thr	Gln	Ile	Lys	Glu	Asp
	1370					1375					1380			
Leu	Ser	Asp	Leu	Thr	Phe	Leu	Glu	Val	Ala	Lys	Ala	Gln	Glu	Ala
	1385					1390					1395			
Cys	His	Gly	Asn	Thr	Ser	Asn	Lys	Glu	Gln	Leu	Thr	Ala	Thr	Lys
	1400					1405					1410			
Thr	Glu	Gln	Asn	Ile	Lys	Asp	Phe	Glu	Thr	Ser	Asp	Thr	Phe	Phe
	1415					1420					1425			
Gln	Thr	Ala	Ser	Gly	Lys	Asn	Ile	Ser	Val	Ala	Lys	Glu	Ser	Phe
	1430					1435					1440			
Asn	Lys	Ile	Val	Asn	Phe	Phe	Asp	Gln	Lys	Pro	Glu	Glu	Leu	His
	1445					1450					1455			
Asn	Phe	Ser	Leu	Asn	Ser	Glu	Leu	His	Ser	Asp	Ile	Arg	Lys	Asn
	1460					1465					1470			
Lys	Met	Asp	Ile	Leu	Ser	Tyr	Glu	Glu	Thr	Asp	Ile	Val	Lys	His
	1475					1480					1485			
Lys	Ile	Leu	Lys	Glu	Ser	Val	Pro	Val	Gly	Thr	Gly	Asn	Gln	Leu
	1490					1495					1500			
Val	Thr	Phe	Gln	Gly	Gln	Pro	Glu	Arg	Asp	Glu	Lys	Ile	Lys	Glu
	1505					1510					1515			
Pro	Thr	Leu	Leu	Gly	Phe	His	Thr	Ala	Ser	Gly	Lys	Lys	Val	Lys
	1520					1525					1530			



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Ile	Ala	Lys	Glu	Ser	Leu	Asp	Lys	Val	Lys	Asn	Leu	Phe	Asp	Glu
	1535					1540					1545			
Lys	Glu	Gln	Gly	Thr	Ser	Glu	Ile	Thr	Ser	Phe	Ser	His	Gln	Trp
	1550					1555					1560			
Ala	Lys	Thr	Leu	Lys	Tyr	Arg	Glu	Ala	Cys	Lys	Asp	Leu	Glu	Leu
	1565					1570					1575			
Ala	Cys	Glu	Thr	Ile	Glu	Ile	Thr	Ala	Ala	Pro	Lys	Cys	Lys	Glu
	1580					1585					1590			
Met	Gln	Asn	Ser	Leu	Asn	Asn	Asp	Lys	Asn	Leu	Val	Ser	Ile	Glu
	1595					1600					1605			
Thr	Val	Val	Pro	Pro	Lys	Leu	Leu	Ser	Asp	Asn	Leu	Cys	Arg	Gln
	1610					1615					1620			
Thr	Glu	Asn	Leu	Lys	Thr	Ser	Lys	Ser	Ile	Phe	Leu	Lys	Val	Lys
	1625					1630					1635			
Val	His	Glu	Asn	Val	Glu	Lys	Glu	Thr	Ala	Lys	Ser	Pro	Ala	Thr
	1640					1645					1650			
Cys	Tyr	Thr	Asn	Gln	Ser	Pro	Tyr	Ser	Val	Ile	Glu	Asn	Ser	Ala
	1655					1660					1665			
Leu	Ala	Phe	Tyr	Thr	Ser	Cys	Ser	Arg	Lys	Thr	Ser	Val	Ser	Gln
	1670					1675					1680			
Thr	Ser	Leu	Leu	Glu	Ala	Lys	Lys	Trp	Leu	Arg	Glu	Gly	Ile	Phe
	1685					1690					1695			
Asp	Gly	Gln	Pro	Glu	Arg	Ile	Asn	Thr	Ala	Asp	Tyr	Val	Gly	Asn
	1700					1705					1710			
Tyr	Leu	Tyr	Glu	Asn	Asn	Ser	Asn	Ser	Thr	Ile	Ala	Glu	Asn	Asp
	1715					1720					1725			
Lys	Asn	His	Leu	Ser	Glu	Lys	Gln	Asp	Thr	Tyr	Leu	Ser	Asn	Ser
	1730					1735					1740			
Ser	Met	Ser	Asn	Ser	Tyr	Ser	Tyr	His	Ser	Asp	Glu	Val	Tyr	Asn
	1745					1750					1755			
Asp	Ser	Gly	Tyr	Leu	Ser	Lys	Asn	Lys	Leu	Asp	Ser	Gly	Ile	Glu
	1760					1765					1770			
Pro	Val	Leu	Lys	Asn	Val	Glu	Asp	Gln	Lys	Asn	Thr	Ser	Phe	Ser
	1775					1780					1785			

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Lys	Val	Ile	Ser	Asn	Val	Lys	Asp	Ala	Asn	Ala	Tyr	Pro	Gln	Thr
1790						1795					1800			
Val	Asn	Glu	Asp	Ile	Cys	Val	Glu	Glu	Leu	Val	Thr	Ser	Ser	Ser
1805						1810					1815			
Pro	Cys	Lys	Asn	Lys	Asn	Ala	Ala	Ile	Lys	Leu	Ser	Ile	Ser	Asn
1820						1825					1830			
Ser	Asn	Asn	Phe	Glu	Val	Gly	Pro	Pro	Ala	Phe	Arg	Ile	Ala	Ser
1835						1840					1845			
Gly	Lys	Ile	Val	Cys	Val	Ser	His	Glu	Thr	Ile	Lys	Lys	Val	Lys
1850						1855					1860			
Asp	Ile	Phe	Thr	Asp	Ser	Phe	Ser	Lys	Val	Ile	Lys	Glu	Asn	Asn
1865						1870					1875			
Glu	Asn	Lys	Ser	Lys	Ile	Cys	Gln	Thr	Lys	Ile	Met	Ala	Gly	Cys
1880						1885					1890			
Tyr	Glu	Ala	Leu	Asp	Asp	Ser	Glu	Asp	Ile	Leu	His	Asn	Ser	Leu
1895						1900					1905			
Asp	Asn	Asp	Glu	Cys	Ser	Thr	His	Ser	His	Lys	Val	Phe	Ala	Asp
1910						1915					1920			
Ile	Gln	Ser	Glu	Glu	Ile	Leu	Gln	His	Asn	Gln	Asn	Met	Ser	Gly
1925						1930					1935			
Leu	Glu	Lys	Val	Ser	Lys	Ile	Ser	Pro	Cys	Asp	Val	Ser	Leu	Glu
1940						1945					1950			
Thr	Ser	Asp	Ile	Cys	Lys	Cys	Ser	Ile	Gly	Lys	Leu	His	Lys	Ser
1955						1960					1965			
Val	Ser	Ser	Ala	Asn	Thr	Cys	Gly	Ile	Phe	Ser	Thr	Ala	Ser	Gly
1970						1975					1980			
Lys	Ser	Val	Gln	Val	Ser	Asp	Ala	Ser	Leu	Gln	Asn	Ala	Arg	Gln
1985						1990					1995			
Val	Phe	Ser	Glu	Ile	Glu	Asp	Ser	Thr	Lys	Gln	Val	Phe	Ser	Lys
2000						2005					2010			
Val	Leu	Phe	Lys	Ser	Asn	Glu	His	Ser	Asp	Gln	Leu	Thr	Arg	Glu
2015						2020					2025			
Glu	Asn	Thr	Ala	Ile	Arg	Thr	Pro	Glu	His	Leu	Ile	Ser	Gln	Lys
2030						2035					2040			

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Gly	Phe	Ser	Tyr	Asn	Val	Val	Asn	Ser	Ser	Ala	Phe	Ser	Gly	Phe
	2045					2050					2055			
Ser	Thr	Ala	Ser	Gly	Lys	Gln	Val	Ser	Ile	Leu	Glu	Ser	Ser	Leu
	2060					2065					2070			
His	Lys	Val	Lys	Gly	Val	Leu	Glu	Glu	Phe	Asp	Leu	Ile	Arg	Thr
	2075					2080					2085			
Glu	His	Ser	Leu	His	Tyr	Ser	Pro	Thr	Ser	Arg	Gln	Asn	Val	Ser
	2090					2095					2100			
Lys	Ile	Leu	Pro	Arg	Val	Asp	Lys	Arg	Asn	Pro	Glu	His	Cys	Val
	2105					2110					2115			
Asn	Ser	Glu	Met	Glu	Lys	Thr	Cys	Ser	Lys	Glu	Phe	Lys	Leu	Ser
	2120					2125					2130			
Asn	Asn	Leu	Asn	Val	Glu	Gly	Gly	Ser	Ser	Glu	Asn	Asn	His	Ser
	2135					2140					2145			
Ile	Lys	Val	Ser	Pro	Tyr	Leu	Ser	Gln	Phe	Gln	Gln	Asp	Lys	Gln
	2150					2155					2160			
Gln	Leu	Val	Leu	Gly	Thr	Lys	Val	Ser	Leu	Val	Glu	Asn	Ile	His
	2165					2170					2175			
Val	Leu	Gly	Lys	Glu	Gln	Ala	Ser	Pro	Lys	Asn	Val	Lys	Met	Glu
	2180					2185					2190			
Ile	Gly	Lys	Thr	Glu	Thr	Phe	Ser	Asp	Val	Pro	Val	Lys	Thr	Asn
	2195					2200					2205			
Ile	Glu	Val	Cys	Ser	Thr	Tyr	Ser	Lys	Asp	Ser	Glu	Asn	Tyr	Phe
	2210					2215					2220			
Glu	Thr	Glu	Ala	Val	Glu	Ile	Ala	Lys	Ala	Phe	Met	Glu	Asp	Asp
	2225					2230					2235			
Glu	Leu	Thr	Asp	Ser	Lys	Leu	Pro	Ser	His	Ala	Thr	His	Ser	Leu
	2240					2245					2250			
Phe	Thr	Cys	Pro	Glu	Asn	Glu	Glu	Met	Val	Leu	Ser	Asn	Ser	Arg
	2255					2260					2265			
Ile	Gly	Lys	Arg	Arg	Gly	Glu	Pro	Leu	Ile	Leu	Val	Gly	Glu	Pro
	2270					2275					2280			
Ser	Ile	Lys	Arg	Asn	Leu	Leu	Asn	Glu	Phe	Asp	Arg	Ile	Ile	Glu
	2285					2290					2295			

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Asn	Gln	Glu	Lys	Ser	Leu	Lys	Ala	Ser	Lys	Ser	Thr	Pro	Asp	Gly
	2300					2305					2310			
Thr	Ile	Lys	Asp	Arg	Arg	Leu	Phe	Met	His	His	Val	Ser	Leu	Glu
	2315					2320					2325			
Pro	Ile	Thr	Cys	Val	Pro	Phe	Arg	Thr	Thr	Lys	Glu	Arg	Gln	Glu
	2330					2335					2340			
Ile	Gln	Asn	Pro	Asn	Phe	Thr	Ala	Pro	Gly	Gln	Glu	Phe	Leu	Ser
	2345					2350					2355			
Lys	Ser	His	Leu	Tyr	Glu	His	Leu	Thr	Leu	Glu	Lys	Ser	Ser	Ser
	2360					2365					2370			
Asn	Leu	Ala	Val	Ser	Gly	His	Pro	Phe	Tyr	Gln	Val	Ser	Ala	Thr
	2375					2380					2385			
Arg	Asn	Glu	Lys	Met	Arg	His	Leu	Ile	Thr	Thr	Gly	Arg	Pro	Thr
	2390					2395					2400			
Lys	Val	Phe	Val	Pro	Pro	Phe	Lys	Thr	Lys	Ser	His	Phe	His	Arg
	2405					2410					2415			
Val	Glu	Gln	Cys	Val	Arg	Asn	Ile	Asn	Leu	Glu	Glu	Asn	Arg	Gln
	2420					2425					2430			
Lys	Gln	Asn	Ile	Asp	Gly	His	Gly	Ser	Asp	Asp	Ser	Lys	Asn	Lys
	2435					2440					2445			
Ile	Asn	Asp	Asn	Glu	Ile	His	Gln	Phe	Asn	Lys	Asn	Asn	Ser	Asn
	2450					2455					2460			
Gln	Ala	Ala	Ala	Val	Thr	Phe	Thr	Lys	Cys	Glu	Glu	Glu	Pro	Leu
	2465					2470					2475			
Asp	Leu	Ile	Thr	Ser	Leu	Gln	Asn	Ala	Arg	Asp	Ile	Gln	Asp	Met
	2480					2485					2490			
Arg	Ile	Lys	Lys	Lys	Gln	Arg	Gln	Arg	Val	Phe	Pro	Gln	Pro	Gly
	2495					2500					2505			
Ser	Leu	Tyr	Leu	Ala	Lys	Thr	Ser	Thr	Leu	Pro	Arg	Ile	Ser	Leu
	2510					2515					2520			
Lys	Ala	Ala	Val	Gly	Gly	Gln	Val	Pro	Ser	Ala	Cys	Ser	His	Lys
	2525					2530					2535			
Gln	Leu	Tyr	Thr	Tyr	Gly	Val	Ser	Lys	His	Cys	Ile	Lys	Ile	Asn
	2540					2545					2550			

## FAB-008PC-SequenceListing

Ser	Lys	Asn	Ala	Glu	Ser	Phe	Gln	Phe	His	Thr	Glu	Asp	Tyr	Phe
	2555					2560					2565			
Gly	Lys	Glu	Ser	Leu	Trp	Thr	Gly	Lys	Gly	Ile	Gln	Leu	Ala	Asp
	2570					2575					2580			
Gly	Gly	Trp	Leu	Ile	Pro	Ser	Asn	Asp	Gly	Lys	Ala	Gly	Lys	Glu
	2585					2590					2595			
Glu	Phe	Tyr	Arg	Ala	Leu	Cys	Asp	Thr	Pro	Gly	Val	Asp	Pro	Lys
	2600					2605					2610			
Leu	Ile	Ser	Arg	Ile	Trp	Val	Tyr	Asn	His	Tyr	Arg	Trp	Ile	Ile
	2615					2620					2625			
Trp	Lys	Leu	Ala	Ala	Met	Glu	Cys	Ala	Phe	Pro	Lys	Glu	Phe	Ala
	2630					2635					2640			
Asn	Arg	Cys	Leu	Ser	Pro	Glu	Arg	Val	Leu	Leu	Gln	Leu	Lys	Tyr
	2645					2650					2655			
Arg	Tyr	Asp	Thr	Glu	Ile	Asp	Arg	Ser	Arg	Arg	Ser	Ala	Ile	Lys
	2660					2665					2670			
Lys	Ile	Met	Glu	Arg	Asp	Asp	Thr	Ala	Ala	Lys	Thr	Leu	Val	Leu
	2675					2680					2685			
Cys	Val	Ser	Asp	Ile	Ile	Ser	Leu	Ser	Ala	Asn	Ile	Ser	Glu	Thr
	2690					2695					2700			
Ser	Ser	Asn	Lys	Thr	Ser	Ser	Ala	Asp	Thr	Gln	Lys	Val	Ala	Ile
	2705					2710					2715			
Ile	Glu	Leu	Thr	Asp	Gly	Trp	Tyr	Ala	Val	Lys	Ala	Gln	Leu	Asp
	2720					2725					2730			
Pro	Pro	Leu	Leu	Ala	Val	Leu	Lys	Asn	Gly	Arg	Leu	Thr	Val	Gly
	2735					2740					2745			
Gln	Lys	Ile	Ile	Leu	His	Gly	Ala	Glu	Leu	Val	Gly	Ser	Pro	Asp
	2750					2755					2760			
Ala	Cys	Thr	Pro	Leu	Glu	Ala	Pro	Glu	Ser	Leu	Met	Leu	Lys	Ile
	2765					2770					2775			
Ser	Ala	Asn	Ser	Thr	Arg	Pro	Ala	Arg	Trp	Tyr	Thr	Lys	Leu	Gly
	2780					2785					2790			
Phe	Phe	Pro	Asp	Pro	Arg	Pro	Phe	Pro	Leu	Pro	Leu	Ser	Ser	Leu
	2795					2800					2805			

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Phe	Ser	Asp	Gly	Gly	Asn	Val	Gly	Cys	Val	Asp	Val	Ile	Ile	Gln
	2810					2815					2820			
Arg	Ala	Tyr	Pro	Ile	Gln	Trp	Met	Glu	Lys	Thr	Ser	Ser	Gly	Leu
	2825					2830					2835			
Tyr	Ile	Phe	Arg	Asn	Glu	Arg	Glu	Glu	Glu	Lys	Glu	Ala	Ala	Lys
	2840					2845					2850			
Tyr	Val	Glu	Ala	Gln	Gln	Lys	Arg	Leu	Glu	Ala	Leu	Phe	Thr	Lys
	2855					2860					2865			
Ile	Gln	Glu	Glu	Phe	Glu	Glu	His	Glu	Glu	Asn	Thr	Thr	Lys	Pro
	2870					2875					2880			
Tyr	Leu	Pro	Ser	Arg	Ala	Leu	Thr	Arg	Gln	Gln	Val	Arg	Ala	Leu
	2885					2890					2895			
Gln	Asp	Gly	Ala	Glu	Leu	Tyr	Glu	Ala	Val	Lys	Asn	Ala	Ala	Asp
	2900					2905					2910			
Pro	Ala	Tyr	Leu	Glu	Gly	Tyr	Phe	Ser	Glu	Glu	Gln	Leu	Arg	Ala
	2915					2920					2925			
Leu	Asn	Asn	His	Arg	Gln	Met	Leu	Asn	Asp	Lys	Lys	Gln	Ala	Gln
	2930					2935					2940			
Ile	Gln	Leu	Glu	Ile	Arg	Lys	Ala	Met	Glu	Ser	Ala	Glu	Gln	Lys
	2945					2950					2955			
Glu	Gln	Gly	Leu	Ser	Arg	Asp	Val	Thr	Thr	Val	Trp	Lys	Leu	Arg
	2960					2965					2970			
Ile	Val	Ser	Tyr	Ser	Lys	Lys	Glu	Lys	Asp	Ser	Val	Ile	Leu	Ser
	2975					2980					2985			
Ile	Trp	Arg	Pro	Ser	Ser	Asp	Leu	Tyr	Ser	Leu	Leu	Thr	Glu	Gly
	2990					2995					3000			
Lys	Arg	Tyr	Arg	Ile	Tyr	His	Leu	Ala	Thr	Ser	Lys	Ser	Lys	Ser
	3005					3010					3015			
Lys	Ser	Glu	Arg	Ala	Asn	Ile	Gln	Leu	Ala	Ala	Thr	Lys	Lys	Thr
	3020					3025					3030			
Gln	Tyr	Gln	Gln	Leu	Pro	Val	Ser	Asp	Glu	Ile	Leu	Phe	Gln	Ile
	3035					3040					3045			
Tyr	Gln	Pro	Arg	Glu	Pro	Leu	His	Phe	Ser	Lys	Phe	Leu	Asp	Pro
	3050					3055					3060			

## FAB-008PC-SequenceListing

Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile Gly Phe Val  
 3065 3070 3075  
 Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val Tyr Leu  
 3080 3085 3090  
 Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile Asp  
 3095 3100 3105  
 Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser  
 3110 3115 3120  
 Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu  
 3125 3130 3135  
 Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly  
 3140 3145 3150  
 His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn  
 3155 3160 3165  
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile  
 3170 3175 3180  
 Leu His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys  
 3185 3190 3195  
 Thr Ser Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn  
 3200 3205 3210  
 Lys Leu Leu Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser  
 3215 3220 3225  
 Pro Leu Ser Leu Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro  
 3230 3235 3240  
 Val Ser Ala Gln Met Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu  
 3245 3250 3255  
 Ile Asp Asp Gln Lys Asn Cys Lys Lys Arg Arg Ala Leu Asp Phe  
 3260 3265 3270  
 Leu Ser Arg Leu Pro Leu Pro Pro Pro Val Ser Pro Ile Cys Thr  
 3275 3280 3285  
 Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln Pro Pro Arg Ser  
 3290 3295 3300  
 Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys Glu Leu Asn  
 3305 3310 3315

# FAB-008PC-SequenceListing

Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile Ser Leu  
3320 3325 3330

Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile Asn  
3335 3340 3345

Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile  
3350 3355 3360

Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp  
3365 3370 3375

Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu  
3380 3385 3390

Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys  
3395 3400 3405

Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile  
3410 3415

<210> 45  
<211> 393  
<212> PRT  
<213> Homo sapiens  
<400> 45

Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln  
1 5 10 15

Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu  
20 25 30

Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp  
35 40 45

Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro  
50 55 60

Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Ala Pro  
65 70 75 80

Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser  
85 90 95

Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly  
100 105 110

Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro  
115 120 125

Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln  
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130

135

140

Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met  
 145 150 155 160

Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys  
 165 170 175

Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln  
 180 185 190

His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp  
 195 200 205

Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu  
 210 215 220

Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser  
 225 230 235 240

Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr  
 245 250 255

Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val  
 260 265 270

Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn  
 275 280 285

Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr  
 290 295 300

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys  
 305 310 315 320

Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu  
 325 330 335

Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp  
 340 345 350

Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His  
 355 360 365

Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met  
 370 375 380

Phe Lys Thr Glu Gly Pro Asp Ser Asp  
 385 390

&lt;210&gt; 46

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<211> 770  
<212> PRT  
<213> Homo sapiens

<400> 46

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

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20      25      30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35      40      45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50      55      60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65      70      75      80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85      90      95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100     105     110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115     120     125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130     135     140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145     150     155     160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165     170     175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180     185     190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195     200     205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210     215     220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225     230     235     240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245     250     255

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Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
 260 265 270  
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
 275 280 285  
 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
 290 295 300  
 Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
 305 310 315 320  
 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
 325 330 335  
 Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr  
 340 345 350  
 Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala  
 355 360 365  
 Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp  
 370 375 380  
 Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala  
 385 390 395 400  
 Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala  
 405 410 415  
 Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile  
 420 425 430  
 Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn  
 435 440 445  
 Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met  
 450 455 460  
 Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu  
 465 470 475 480  
 Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys  
 485 490 495  
 Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe  
 500 505 510  
 Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser  
 515 520 525

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Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser  
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met  
755 760 765

Gln Asn  
770

<210> 47  
<211> 3144

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<212> PRT  
 <213> Homo sapiens  
 <400> 47

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Met Ala Thr Leu Glu Lys Leu Met Lys Ala Phe Glu Ser Leu Lys Ser
1      5      10     15

Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
20     25     30

Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro
35     40     45

Pro Pro Pro Gln Leu Pro Gln Pro Pro Pro Gln Ala Gln Pro Leu Leu
50     55     60

Pro Gln Pro Gln Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly Pro
65     70     75     80

Ala Val Ala Glu Glu Pro Leu His Arg Pro Lys Lys Glu Leu Ser Ala
85     90     95

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

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

Ile Ala Met Glu Leu Phe Leu Leu Cys Ser Asp Asp Ala Glu Ser Asp
130    135    140

Val Arg Met Val Ala Asp Glu Cys Leu Asn Lys Val Ile Lys Ala Leu
145    150    155    160

Met Asp Ser Asn Leu Pro Arg Leu Gln Leu Glu Leu Tyr Lys Glu Ile
165    170    175

Lys Lys Asn Gly Ala Pro Arg Ser Leu Arg Ala Ala Leu Trp Arg Phe
180    185    190

Ala Glu Leu Ala His Leu Val Arg Pro Gln Lys Cys Arg Pro Tyr Leu
195    200    205

Val Asn Leu Leu Pro Cys Leu Thr Arg Thr Ser Lys Arg Pro Glu Glu
210    215    220

Ser Val Gln Glu Thr Leu Ala Ala Ala Val Pro Lys Ile Met Ala Ser
225    230    235    240

Phe Gly Asn Phe Ala Asn Asp Asn Glu Ile Lys Val Leu Leu Lys Ala
245    250    255
  
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Phe Ile Ala Asn<sub>260</sub> Leu Lys Ser Ser<sub>265</sub> Pro Thr Ile Arg Arg<sub>270</sub> Thr Ala  
 Ala Gly Ser<sub>275</sub> Ala Val Ser Ile Cys<sub>280</sub> Gln His Ser Arg Arg<sub>285</sub> Thr Gln Tyr  
 Phe Tyr<sub>290</sub> Ser Trp Leu Leu Asn<sub>295</sub> Val Leu Leu Gly Leu<sub>300</sub> Leu Val Pro Val  
 Glu<sub>305</sub> Asp Glu His Ser Thr<sub>310</sub> Leu Leu Ile Leu Gly<sub>315</sub> Val Leu Leu Thr Leu<sub>320</sub>  
 Arg Tyr Leu Val Pro<sub>325</sub> Leu Leu Gln Gln Gln<sub>330</sub> Val Lys Asp Thr Ser<sub>335</sub> Leu  
 Lys Gly Ser Phe<sub>340</sub> Gly Val Thr Arg Lys<sub>345</sub> Glu Met Glu Val Ser<sub>350</sub> Pro Ser  
 Ala Glu Gln<sub>355</sub> Leu Val Gln Val Tyr<sub>360</sub> Glu Leu Thr Leu His<sub>365</sub> His Thr Gln  
 His Gln<sub>370</sub> Asp His Asn Val Val<sub>375</sub> Thr Gly Ala Leu Glu<sub>380</sub> Leu Leu Gln Gln  
 Leu<sub>385</sub> Phe Arg Thr Pro Pro<sub>390</sub> Pro Glu Leu Leu Gln<sub>395</sub> Thr Leu Thr Ala Val<sub>400</sub>  
 Gly Gly Ile Gly Gln<sub>405</sub> Leu Thr Ala Ala Lys<sub>410</sub> Glu Glu Ser Gly Gly<sub>415</sub> Arg  
 Ser Arg Ser Gly<sub>420</sub> Ser Ile Val Glu Leu<sub>425</sub> Ile Ala Gly Gly Gly<sub>430</sub> Ser Ser  
 Cys Ser Pro<sub>435</sub> Val Leu Ser Arg Lys<sub>440</sub> Gln Lys Gly Lys Val<sub>445</sub> Leu Leu Gly  
 Glu Glu<sub>450</sub> Glu Ala Leu Glu Asp<sub>455</sub> Asp Ser Glu Ser Arg<sub>460</sub> Ser Asp Val Ser  
 Ser<sub>465</sub> Ser Ala Leu Thr Ala<sub>470</sub> Ser Val Lys Asp Glu<sub>475</sub> Ile Ser Gly Glu Leu<sub>480</sub>  
 Ala Ala Ser Ser Gly<sub>485</sub> Val Ser Thr Pro Gly<sub>490</sub> Ser Ala Gly His Asp<sub>495</sub> Ile  
 Ile Thr Glu Gln<sub>500</sub> Pro Arg Ser Gln His<sub>505</sub> Thr Leu Gln Ala Asp<sub>510</sub> Ser Val  
 Asp Leu Ala<sub>515</sub> Ser Cys Asp Leu Thr<sub>520</sub> Ser Ser Ala Thr Asp<sub>525</sub> Gly Asp Glu

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Glu Asp Ile Leu Ser His Ser Ser Ser Gln Val Ser Ala Val Pro Ser  
 530 535 540  
 Asp Pro Ala Met Asp Leu Asn Asp Gly Thr Gln Ala Ser Ser Pro Ile  
 545 550 555 560  
 Ser Asp Ser Ser Gln Thr Thr Thr Glu Gly Pro Asp Ser Ala Val Thr  
 565 570 575  
 Pro Ser Asp Ser Ser Glu Ile Val Leu Asp Gly Thr Asp Asn Gln Tyr  
 580 585 590  
 Leu Gly Leu Gln Ile Gly Gln Pro Gln Asp Glu Asp Glu Glu Ala Thr  
 595 600 605  
 Gly Ile Leu Pro Asp Glu Ala Ser Glu Ala Phe Arg Asn Ser Ser Met  
 610 615 620  
 Ala Leu Gln Gln Ala His Leu Leu Lys Asn Met Ser His Cys Arg Gln  
 625 630 635 640  
 Pro Ser Asp Ser Ser Val Asp Lys Phe Val Leu Arg Asp Glu Ala Thr  
 645 650 655  
 Glu Pro Gly Asp Gln Glu Asn Lys Pro Cys Arg Ile Lys Gly Asp Ile  
 660 665 670  
 Gly Gln Ser Thr Asp Asp Asp Ser Ala Pro Leu Val His Cys Val Arg  
 675 680 685  
 Leu Leu Ser Ala Ser Phe Leu Leu Thr Gly Gly Lys Asn Val Leu Val  
 690 695 700  
 Pro Asp Arg Asp Val Arg Val Ser Val Lys Ala Leu Ala Leu Ser Cys  
 705 710 715 720  
 Val Gly Ala Ala Val Ala Leu His Pro Glu Ser Phe Phe Ser Lys Leu  
 725 730 735  
 Tyr Lys Val Pro Leu Asp Thr Thr Glu Tyr Pro Glu Glu Gln Tyr Val  
 740 745 750  
 Ser Asp Ile Leu Asn Tyr Ile Asp His Gly Asp Pro Gln Val Arg Gly  
 755 760 765  
 Ala Thr Ala Ile Leu Cys Gly Thr Leu Ile Cys Ser Ile Leu Ser Arg  
 770 775 780  
 Ser Arg Phe His Val Gly Asp Trp Met Gly Thr Ile Arg Thr Leu Thr  
 785 790 795 800

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Gly Asn Thr Phe Ser<sub>805</sub> Leu Ala Asp Cys Ile<sub>810</sub> Pro Leu Leu Arg Lys<sub>815</sub> Thr

Leu Lys Asp Glu<sub>820</sub> Ser Ser Val Thr Cys<sub>825</sub> Lys Leu Ala Cys Thr<sub>830</sub> Ala Val

Arg Asn Cys<sub>835</sub> Val Met Ser Leu Cys<sub>840</sub> Ser Ser Ser Tyr Ser<sub>845</sub> Glu Leu Gly

Leu Gln<sub>850</sub> Leu Ile Ile Asp Val<sub>855</sub> Leu Thr Leu Arg Asn<sub>860</sub> Ser Ser Tyr Trp

Leu Val Arg Thr Glu<sub>865</sub> Leu<sub>870</sub> Leu Glu Thr Leu Ala<sub>875</sub> Glu Ile Asp Phe Arg<sub>880</sub>

Leu Val Ser Phe<sub>885</sub> Leu Glu Ala Lys Ala Glu<sub>890</sub> Asn Leu His Arg Gly<sub>895</sub> Ala

His His Tyr Thr<sub>900</sub> Gly Leu Leu Lys Leu<sub>905</sub> Gln Glu Arg Val Leu<sub>910</sub> Asn Asn

Val Val Ile<sub>915</sub> His Leu Leu Gly Asp<sub>920</sub> Glu Asp Pro Arg Val<sub>925</sub> Arg His Val

Ala Ala<sub>930</sub> Ala Ser Leu Ile Arg<sub>935</sub> Leu Val Pro Lys Leu<sub>940</sub> Phe Tyr Lys Cys

Asp<sub>945</sub> Gln Gly Gln Ala Asp<sub>950</sub> Pro Val Val Ala Val<sub>955</sub> Ala Arg Asp Gln Ser<sub>960</sub>

Ser Val Tyr Leu Lys<sub>965</sub> Leu Leu Met His Glu<sub>970</sub> Thr Gln Pro Pro Ser<sub>975</sub> His

Phe Ser Val Ser<sub>980</sub> Thr Ile Thr Arg Ile<sub>985</sub> Tyr Arg Gly Tyr Asn<sub>990</sub> Leu Leu

Pro Ser Ile<sub>995</sub> Thr Asp Val Thr Met<sub>1000</sub> Glu Asn Asn Leu Ser<sub>1005</sub> Arg Val Ile

Ala Ala<sub>1010</sub> Val Ser His Glu Leu<sub>1015</sub> Ile Thr Ser Thr Thr<sub>1020</sub> Arg Ala Leu

Thr Phe<sub>1025</sub> Gly Cys Cys Glu Ala<sub>1030</sub> Leu Cys Leu Leu Ser<sub>1035</sub> Thr Ala Phe

Pro Val<sub>1040</sub> Cys Ile Trp Ser Leu<sub>1045</sub> Gly Trp His Cys Gly<sub>1050</sub> Val Pro Pro

Leu Ser<sub>1055</sub> Ala Ser Asp Glu Ser<sub>1060</sub> Arg Lys Ser Cys Thr<sub>1065</sub> Val Gly Met



# FAB-008PC-SequenceListing

Ala	Thr	Met	Ile	Leu	Thr	Leu	Leu	Ser	Ser	Ala	Trp	Phe	Pro	Leu
	1070					1075					1080			
Asp	Leu	Ser	Ala	His	Gln	Asp	Ala	Leu	Ile	Leu	Ala	Gly	Asn	Leu
	1085					1090					1095			
Leu	Ala	Ala	Ser	Ala	Pro	Lys	Ser	Leu	Arg	Ser	Ser	Trp	Ala	Ser
	1100					1105					1110			
Glu	Glu	Glu	Ala	Asn	Pro	Ala	Ala	Thr	Lys	Gln	Glu	Glu	Val	Trp
	1115					1120					1125			
Pro	Ala	Leu	Gly	Asp	Arg	Ala	Leu	Val	Pro	Met	Val	Glu	Gln	Leu
	1130					1135					1140			
Phe	Ser	His	Leu	Leu	Lys	Val	Ile	Asn	Ile	Cys	Ala	His	Val	Leu
	1145					1150					1155			
Asp	Asp	Val	Ala	Pro	Gly	Pro	Ala	Ile	Lys	Ala	Ala	Leu	Pro	Ser
	1160					1165					1170			
Leu	Thr	Asn	Pro	Pro	Ser	Leu	Ser	Pro	Ile	Arg	Arg	Lys	Gly	Lys
	1175					1180					1185			
Glu	Lys	Glu	Pro	Gly	Glu	Gln	Ala	Ser	Val	Pro	Leu	Ser	Pro	Lys
	1190					1195					1200			
Lys	Gly	Ser	Glu	Ala	Ser	Ala	Ala	Ser	Arg	Gln	Ser	Asp	Thr	Ser
	1205					1210					1215			
Gly	Pro	Val	Thr	Thr	Ser	Lys	Ser	Ser	Ser	Leu	Gly	Ser	Phe	Tyr
	1220					1225					1230			
His	Leu	Pro	Ser	Tyr	Leu	Lys	Leu	His	Asp	Val	Leu	Lys	Ala	Thr
	1235					1240					1245			
His	Ala	Asn	Tyr	Lys	Val	Thr	Leu	Asp	Leu	Gln	Asn	Ser	Thr	Glu
	1250					1255					1260			
Lys	Phe	Gly	Gly	Phe	Leu	Arg	Ser	Ala	Leu	Asp	Val	Leu	Ser	Gln
	1265					1270					1275			
Ile	Leu	Glu	Leu	Ala	Thr	Leu	Gln	Asp	Ile	Gly	Lys	Cys	Val	Glu
	1280					1285					1290			
Glu	Ile	Leu	Gly	Tyr	Leu	Lys	Ser	Cys	Phe	Ser	Arg	Glu	Pro	Met
	1295					1300					1305			
Met	Ala	Thr	Val	Cys	Val	Gln	Gln	Leu	Leu	Lys	Thr	Leu	Phe	Gly
	1310					1315					1320			

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Thr	Asn 1325	Leu	Ala	Ser	Gln	Phe 1330	Asp	Gly	Leu	Ser	Ser 1335	Asn	Pro	Ser
Lys	Ser 1340	Gln	Gly	Arg	Ala	Gln 1345	Arg	Leu	Gly	Ser	Ser 1350	Ser	Val	Arg
Pro	Gly 1355	Leu	Tyr	His	Tyr	Cys 1360	Phe	Met	Ala	Pro	Tyr 1365	Thr	His	Phe
Thr	Gln 1370	Ala	Leu	Ala	Asp	Ala 1375	Ser	Leu	Arg	Asn	Met 1380	Val	Gln	Ala
Glu	Gln 1385	Glu	Asn	Asp	Thr	Ser 1390	Gly	Trp	Phe	Asp	Val 1395	Leu	Gln	Lys
Val	Ser 1400	Thr	Gln	Leu	Lys	Thr 1405	Asn	Leu	Thr	Ser	Val 1410	Thr	Lys	Asn
Arg	Ala 1415	Asp	Lys	Asn	Ala	Ile 1420	His	Asn	His	Ile	Arg 1425	Leu	Phe	Glu
Pro	Leu 1430	Val	Ile	Lys	Ala	Leu 1435	Lys	Gln	Tyr	Thr	Thr 1440	Thr	Thr	Cys
Val	Gln 1445	Leu	Gln	Lys	Gln	Val 1450	Leu	Asp	Leu	Leu	Ala 1455	Gln	Leu	Val
Gln	Leu 1460	Arg	Val	Asn	Tyr	Cys 1465	Leu	Leu	Asp	Ser	Asp 1470	Gln	Val	Phe
Ile	Gly 1475	Phe	Val	Leu	Lys	Gln 1480	Phe	Glu	Tyr	Ile	Glu 1485	Val	Gly	Gln
Phe	Arg 1490	Glu	Ser	Glu	Ala	Ile 1495	Ile	Pro	Asn	Ile	Phe 1500	Phe	Phe	Leu
Val	Leu 1505	Leu	Ser	Tyr	Glu	Arg 1510	Tyr	His	Ser	Lys	Gln 1515	Ile	Ile	Gly
Ile	Pro 1520	Lys	Ile	Ile	Gln	Leu 1525	Cys	Asp	Gly	Ile	Met 1530	Ala	Ser	Gly
Arg	Lys 1535	Ala	Val	Thr	His	Ala 1540	Ile	Pro	Ala	Leu	Gln 1545	Pro	Ile	Val
His	Asp 1550	Leu	Phe	Val	Leu	Arg 1555	Gly	Thr	Asn	Lys	Ala 1560	Asp	Ala	Gly
Lys	Glu 1565	Leu	Glu	Thr	Gln	Lys 1570	Glu	Val	Val	Val	Ser 1575	Met	Leu	Leu

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Arg	Leu	Ile	Gln	Tyr	His	Gln	Val	Leu	Glu	Met	Phe	Ile	Leu	Val
	1580					1585					1590			
Leu	Gln	Gln	Cys	His	Lys	Glu	Asn	Glu	Asp	Lys	Trp	Lys	Arg	Leu
	1595					1600					1605			
Ser	Arg	Gln	Ile	Ala	Asp	Ile	Ile	Leu	Pro	Met	Leu	Ala	Lys	Gln
	1610					1615					1620			
Gln	Met	His	Ile	Asp	Ser	His	Glu	Ala	Leu	Gly	Val	Leu	Asn	Thr
	1625					1630					1635			
Leu	Phe	Glu	Ile	Leu	Ala	Pro	Ser	Ser	Leu	Arg	Pro	Val	Asp	Met
	1640					1645					1650			
Leu	Leu	Arg	Ser	Met	Phe	Val	Thr	Pro	Asn	Thr	Met	Ala	Ser	Val
	1655					1660					1665			
Ser	Thr	Val	Gln	Leu	Trp	Ile	Ser	Gly	Ile	Leu	Ala	Ile	Leu	Arg
	1670					1675					1680			
Val	Leu	Ile	Ser	Gln	Ser	Thr	Glu	Asp	Ile	Val	Leu	Ser	Arg	Ile
	1685					1690					1695			
Gln	Glu	Leu	Ser	Phe	Ser	Pro	Tyr	Leu	Ile	Ser	Cys	Thr	Val	Ile
	1700					1705					1710			
Asn	Arg	Leu	Arg	Asp	Gly	Asp	Ser	Thr	Ser	Thr	Leu	Glu	Glu	His
	1715					1720					1725			
Ser	Glu	Gly	Lys	Gln	Ile	Lys	Asn	Leu	Pro	Glu	Glu	Thr	Phe	Ser
	1730					1735					1740			
Arg	Phe	Leu	Leu	Gln	Leu	Val	Gly	Ile	Leu	Leu	Glu	Asp	Ile	Val
	1745					1750					1755			
Thr	Lys	Gln	Leu	Lys	Val	Glu	Met	Ser	Glu	Gln	Gln	His	Thr	Phe
	1760					1765					1770			
Tyr	Cys	Gln	Glu	Leu	Gly	Thr	Leu	Leu	Met	Cys	Leu	Ile	His	Ile
	1775					1780					1785			
Phe	Lys	Ser	Gly	Met	Phe	Arg	Arg	Ile	Thr	Ala	Ala	Ala	Thr	Arg
	1790					1795					1800			
Leu	Phe	Arg	Ser	Asp	Gly	Cys	Gly	Gly	Ser	Phe	Tyr	Thr	Leu	Asp
	1805					1810					1815			
Ser	Leu	Asn	Leu	Arg	Ala	Arg	Ser	Met	Ile	Thr	Thr	His	Pro	Ala
	1820					1825					1830			

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Leu Val 1835	Leu Leu Trp Cys	Gln 1840	Ile Leu Leu Leu Val 1845	Asn His Thr
Asp Tyr 1850	Arg Trp Trp Ala	Glu 1855	Val Gln Gln Thr Pro 1860	Lys Arg His
Ser Leu 1865	Ser Ser Thr Lys	Leu 1870	Leu Ser Pro Gln Met 1875	Ser Gly Glu
Glu Glu 1880	Asp Ser Asp Leu	Ala 1885	Ala Lys Leu Gly Met 1890	Cys Asn Arg
Glu Ile 1895	Val Arg Arg Gly	Ala 1900	Leu Ile Leu Phe Cys 1905	Asp Tyr Val
Cys Gln 1910	Asn Leu His Asp	Ser 1915	Glu His Leu Thr Trp 1920	Leu Ile Val
Asn His 1925	Ile Gln Asp Leu	Ile 1930	Ser Leu Ser His Glu 1935	Pro Pro Val
Gln Asp 1940	Phe Ile Ser Ala	Val 1945	His Arg Asn Ser Ala 1950	Ala Ser Gly
Leu Phe 1955	Ile Gln Ala Ile	Gln 1960	Ser Arg Cys Glu Asn 1965	Leu Ser Thr
Pro Thr 1970	Met Leu Lys Lys	Thr 1975	Leu Gln Cys Leu Glu 1980	Gly Ile His
Leu Ser 1985	Gln Ser Gly Ala	Val 1990	Leu Thr Leu Tyr Val 1995	Asp Arg Leu
Leu Cys 2000	Thr Pro Phe Arg	Val 2005	Leu Ala Arg Met Val 2010	Asp Ile Leu
Ala Cys 2015	Arg Arg Val Glu	Met 2020	Leu Leu Ala Ala Asn 2025	Leu Gln Ser
Ser Met 2030	Ala Gln Leu Pro	Met 2035	Glu Glu Leu Asn Arg 2040	Ile Gln Glu
Tyr Leu 2045	Gln Ser Ser Gly	Leu 2050	Ala Gln Arg His Gln 2055	Arg Leu Tyr
Ser Leu 2060	Leu Asp Arg Phe	Arg 2065	Leu Ser Thr Met Gln 2070	Asp Ser Leu
Ser Pro 2075	Ser Pro Pro Val	Ser 2080	Ser His Pro Leu Asp 2085	Gly Asp Gly

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His	Val	Ser	Leu	Glu	Thr	Val	Ser	Pro	Asp	Lys	Asp	Trp	Tyr	Val
	2090					2095					2100			
His	Leu	Val	Lys	Ser	Gln	Cys	Trp	Thr	Arg	Ser	Asp	Ser	Ala	Leu
	2105					2110					2115			
Leu	Glu	Gly	Ala	Glu	Leu	Val	Asn	Arg	Ile	Pro	Ala	Glu	Asp	Met
	2120					2125					2130			
Asn	Ala	Phe	Met	Met	Asn	Ser	Glu	Phe	Asn	Leu	Ser	Leu	Leu	Ala
	2135					2140					2145			
Pro	Cys	Leu	Ser	Leu	Gly	Met	Ser	Glu	Ile	Ser	Gly	Gly	Gln	Lys
	2150					2155					2160			
Ser	Ala	Leu	Phe	Glu	Ala	Ala	Arg	Glu	Val	Thr	Leu	Ala	Arg	Val
	2165					2170					2175			
Ser	Gly	Thr	Val	Gln	Gln	Leu	Pro	Ala	Val	His	His	Val	Phe	Gln
	2180					2185					2190			
Pro	Glu	Leu	Pro	Ala	Glu	Pro	Ala	Ala	Tyr	Trp	Ser	Lys	Leu	Asn
	2195					2200					2205			
Asp	Leu	Phe	Gly	Asp	Ala	Ala	Leu	Tyr	Gln	Ser	Leu	Pro	Thr	Leu
	2210					2215					2220			
Ala	Arg	Ala	Leu	Ala	Gln	Tyr	Leu	Val	Val	Val	Ser	Lys	Leu	Pro
	2225					2230					2235			
Ser	His	Leu	His	Leu	Pro	Pro	Glu	Lys	Glu	Lys	Asp	Ile	Val	Lys
	2240					2245					2250			
Phe	Val	Val	Ala	Thr	Leu	Glu	Ala	Leu	Ser	Trp	His	Leu	Ile	His
	2255					2260					2265			
Glu	Gln	Ile	Pro	Leu	Ser	Leu	Asp	Leu	Gln	Ala	Gly	Leu	Asp	Cys
	2270					2275					2280			
Cys	Cys	Leu	Ala	Leu	Gln	Leu	Pro	Gly	Leu	Trp	Ser	Val	Val	Ser
	2285					2290					2295			
Ser	Thr	Glu	Phe	Val	Thr	His	Ala	Cys	Ser	Leu	Ile	Tyr	Cys	Val
	2300					2305					2310			
His	Phe	Ile	Leu	Glu	Ala	Val	Ala	Val	Gln	Pro	Gly	Glu	Gln	Leu
	2315					2320					2325			
Leu	Ser	Pro	Glu	Arg	Arg	Thr	Asn	Thr	Pro	Lys	Ala	Ile	Ser	Glu
	2330					2335					2340			

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Glu	Glu	Glu	Glu	Val	Asp	Pro	Asn	Thr	Gln	Asn	Pro	Lys	Tyr	Ile
	2345					2350					2355			
Thr	Ala	Ala	Cys	Glu	Met	Val	Ala	Glu	Met	Val	Glu	Ser	Leu	Gln
	2360					2365					2370			
Ser	Val	Leu	Ala	Leu	Gly	His	Lys	Arg	Asn	Ser	Gly	Val	Pro	Ala
	2375					2380					2385			
Phe	Leu	Thr	Pro	Leu	Leu	Arg	Asn	Ile	Ile	Ile	Ser	Leu	Ala	Arg
	2390					2395					2400			
Leu	Pro	Leu	Val	Asn	Ser	Tyr	Thr	Arg	Val	Pro	Pro	Leu	Val	Trp
	2405					2410					2415			
Lys	Leu	Gly	Trp	Ser	Pro	Lys	Pro	Gly	Gly	Asp	Phe	Gly	Thr	Ala
	2420					2425					2430			
Phe	Pro	Glu	Ile	Pro	Val	Glu	Phe	Leu	Gln	Glu	Lys	Glu	Val	Phe
	2435					2440					2445			
Lys	Glu	Phe	Ile	Tyr	Arg	Ile	Asn	Thr	Leu	Gly	Trp	Thr	Ser	Arg
	2450					2455					2460			
Thr	Gln	Phe	Glu	Glu	Thr	Trp	Ala	Thr	Leu	Leu	Gly	Val	Leu	Val
	2465					2470					2475			
Thr	Gln	Pro	Leu	Val	Met	Glu	Gln	Glu	Glu	Ser	Pro	Pro	Glu	Glu
	2480					2485					2490			
Asp	Thr	Glu	Arg	Thr	Gln	Ile	Asn	Val	Leu	Ala	Val	Gln	Ala	Ile
	2495					2500					2505			
Thr	Ser	Leu	Val	Leu	Ser	Ala	Met	Thr	Val	Pro	Val	Ala	Gly	Asn
	2510					2515					2520			
Pro	Ala	Val	Ser	Cys	Leu	Glu	Gln	Gln	Pro	Arg	Asn	Lys	Pro	Leu
	2525					2530					2535			
Lys	Ala	Leu	Asp	Thr	Arg	Phe	Gly	Arg	Lys	Leu	Ser	Ile	Ile	Arg
	2540					2545					2550			
Gly	Ile	Val	Glu	Gln	Glu	Ile	Gln	Ala	Met	Val	Ser	Lys	Arg	Glu
	2555					2560					2565			
Asn	Ile	Ala	Thr	His	His	Leu	Tyr	Gln	Ala	Trp	Asp	Pro	Val	Pro
	2570					2575					2580			
Ser	Leu	Ser	Pro	Ala	Thr	Thr	Gly	Ala	Leu	Ile	Ser	His	Glu	Lys
	2585					2590					2595			

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Leu	Leu	Leu	Gln	Ile	Asn	Pro	Glu	Arg	Glu	Leu	Gly	Ser	Met	Ser
	2600					2605					2610			
Tyr	Lys	Leu	Gly	Gln	Val	Ser	Ile	His	Ser	Val	Trp	Leu	Gly	Asn
	2615					2620					2625			
Ser	Ile	Thr	Pro	Leu	Arg	Glu	Glu	Glu	Trp	Asp	Glu	Glu	Glu	Glu
	2630					2635					2640			
Glu	Glu	Ala	Asp	Ala	Pro	Ala	Pro	Ser	Ser	Pro	Pro	Thr	Ser	Pro
	2645					2650					2655			
Val	Asn	Ser	Arg	Lys	His	Arg	Ala	Gly	Val	Asp	Ile	His	Ser	Cys
	2660					2665					2670			
Ser	Gln	Phe	Leu	Leu	Glu	Leu	Tyr	Ser	Arg	Trp	Ile	Leu	Pro	Ser
	2675					2680					2685			
Ser	Ser	Ala	Arg	Arg	Thr	Pro	Ala	Ile	Leu	Ile	Ser	Glu	Val	Val
	2690					2695					2700			
Arg	Ser	Leu	Leu	Val	Val	Ser	Asp	Leu	Phe	Thr	Glu	Arg	Asn	Gln
	2705					2710					2715			
Phe	Glu	Leu	Met	Tyr	Val	Thr	Leu	Thr	Glu	Leu	Arg	Arg	Val	His
	2720					2725					2730			
Pro	Ser	Glu	Asp	Glu	Ile	Leu	Ala	Gln	Tyr	Leu	Val	Pro	Ala	Thr
	2735					2740					2745			
Cys	Lys	Ala	Ala	Ala	Val	Leu	Gly	Met	Asp	Lys	Ala	Val	Ala	Glu
	2750					2755					2760			
Pro	Val	Ser	Arg	Leu	Leu	Glu	Ser	Thr	Leu	Arg	Ser	Ser	His	Leu
	2765					2770					2775			
Pro	Ser	Arg	Val	Gly	Ala	Leu	His	Gly	Val	Leu	Tyr	Val	Leu	Glu
	2780					2785					2790			
Cys	Asp	Leu	Leu	Asp	Asp	Thr	Ala	Lys	Gln	Leu	Ile	Pro	Val	Ile
	2795					2800					2805			
Ser	Asp	Tyr	Leu	Leu	Ser	Asn	Leu	Lys	Gly	Ile	Ala	His	Cys	Val
	2810					2815					2820			
Asn	Ile	His	Ser	Gln	Gln	His	Val	Leu	Val	Met	Cys	Ala	Thr	Ala
	2825					2830					2835			
Phe	Tyr	Leu	Ile	Glu	Asn	Tyr	Pro	Leu	Asp	Val	Gly	Pro	Glu	Phe
	2840					2845					2850			

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Ser	Ala	Ser	Ile	Ile	Gln	Met	Cys	Gly	Val	Met	Leu	Ser	Gly	Ser
	2855					2860					2865			
Glu	Glu	Ser	Thr	Pro	Ser	Ile	Ile	Tyr	His	Cys	Ala	Leu	Arg	Gly
	2870					2875					2880			
Leu	Glu	Arg	Leu	Leu	Leu	Ser	Glu	Gln	Leu	Ser	Arg	Leu	Asp	Ala
	2885					2890					2895			
Glu	Ser	Leu	Val	Lys	Leu	Ser	Val	Asp	Arg	Val	Asn	Val	His	Ser
	2900					2905					2910			
Pro	His	Arg	Ala	Met	Ala	Ala	Leu	Gly	Leu	Met	Leu	Thr	Cys	Met
	2915					2920					2925			
Tyr	Thr	Gly	Lys	Glu	Lys	Val	Ser	Pro	Gly	Arg	Thr	Ser	Asp	Pro
	2930					2935					2940			
Asn	Pro	Ala	Ala	Pro	Asp	Ser	Glu	Ser	Val	Ile	Val	Ala	Met	Glu
	2945					2950					2955			
Arg	Val	Ser	Val	Leu	Phe	Asp	Arg	Ile	Arg	Lys	Gly	Phe	Pro	Cys
	2960					2965					2970			
Glu	Ala	Arg	Val	Val	Ala	Arg	Ile	Leu	Pro	Gln	Phe	Leu	Asp	Asp
	2975					2980					2985			
Phe	Phe	Pro	Pro	Gln	Asp	Ile	Met	Asn	Lys	Val	Ile	Gly	Glu	Phe
	2990					2995					3000			
Leu	Ser	Asn	Gln	Gln	Pro	Tyr	Pro	Gln	Phe	Met	Ala	Thr	Val	Val
	3005					3010					3015			
Tyr	Lys	Val	Phe	Gln	Thr	Leu	His	Ser	Thr	Gly	Gln	Ser	Ser	Met
	3020					3025					3030			
Val	Arg	Asp	Trp	Val	Met	Leu	Ser	Leu	Ser	Asn	Phe	Thr	Gln	Arg
	3035					3040					3045			
Ala	Pro	Val	Ala	Met	Ala	Thr	Trp	Ser	Leu	Ser	Cys	Phe	Phe	Val
	3050					3055					3060			
Ser	Ala	Ser	Thr	Ser	Pro	Trp	Val	Ala	Ala	Ile	Leu	Pro	His	Val
	3065					3070					3075			
Ile	Ser	Arg	Met	Gly	Lys	Leu	Glu	Gln	Val	Asp	Val	Asn	Leu	Phe
	3080					3085					3090			
Cys	Leu	Val	Ala	Thr	Asp	Phe	Tyr	Arg	His	Gln	Ile	Glu	Glu	Glu
	3095					3100					3105			



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Leu Asp Arg Arg Ala Phe Gln Ser Val Leu Glu Val Val Ala Ala  
3110 3115 3120

Pro Gly Ser Pro Tyr His Arg Leu Leu Thr Cys Leu Arg Asn Val  
3125 3130 3135

His Lys Val Thr Thr Cys  
3140

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<211> 89  
<212> PRT  
<213> Homo sapiens  
<400> 48

Met Gly Ile Leu Lys Leu Gln Val Phe Leu Ile Val Leu Ser Val Ala  
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Leu Asn His Leu Lys Ala Thr Pro Ile Glu Ser His Gln Val Glu Lys  
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Arg Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe  
35 40 45

Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr Asn  
50 55 60

Val Gly Ser Asn Thr Tyr Gly Lys Arg Asn Ala Val Glu Val Leu Lys  
65 70 75 80

Arg Glu Pro Leu Asn Tyr Leu Pro Leu  
85

<210> 49  
<211> 776  
<212> PRT  
<213> Homo sapiens  
<400> 49

Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly  
1 5 10 15

Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His  
20 25 30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu  
35 40 45

Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser  
50 55 60

Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val  
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65		70		75		80
Asp	Glu	Gly	Ala	Pro	Gly	Lys
				85		
					Gln	Ala
					90	
					Ala	Ala
					Gln	Pro
					His	Thr
					95	Glu
Ile	Pro	Glu	Gly	Thr	Thr	Ala
			100			
					Glu	Glu
					105	
					Ala	Gly
					Ile	Gly
					110	Asp
					Thr	Pro
Ser	Leu	Glu	Asp	Glu	Ala	Ala
		115				
					Gly	His
					120	Val
					Thr	Gln
					Glu	Pro
					125	Glu
					Pro	Glu
					Ser	
Gly	Lys	Val	Val	Gln	Glu	Gly
	130					
					Gly	Phe
					135	
					Leu	Arg
					Glu	Pro
					140	Gly
					Pro	Pro
					Gly	Pro
					Pro	Gly
Leu	Ser	His	Gln	Leu	Met	Ser
					150	
					Gly	Met
					155	Pro
					Gly	Ala
					Pro	Leu
					Leu	Pro
					160	
Glu	Gly	Pro	Arg	Glu	Ala	Thr
				165		
					Arg	Gln
					170	Pro
					Ser	Gly
					Thr	Gly
					175	Pro
					Glu	
Asp	Thr	Glu	Gly	Gly	Arg	His
			180			
					Ala	Pro
					185	Glu
					Leu	Leu
					Lys	His
					190	Gln
					Leu	
Leu	Gly	Asp	Leu	His	Gln	Glu
		195				
					Gly	Pro
					200	Pro
					Leu	Lys
					Gly	Ala
					205	Gly
					Gly	Gly
Lys	Glu	Arg	Pro	Gly	Ser	Lys
	210					
					Glu	Glu
					215	Val
					Asp	Glu
					220	Asp
					Arg	Asp
					Val	
Asp	Glu	Ser	Ser	Pro	Gln	Asp
					230	
					Ser	Pro
					235	Pro
					Lys	Ala
					Ser	Pro
					Ala	Ala
					240	
Gln	Asp	Gly	Arg	Pro	Pro	Gln
					Thr	Ala
					250	Ala
					Arg	Glu
					Ala	Thr
					255	Ser
					Ile	
Pro	Gly	Phe	Pro	Ala	Glu	Gly
			260			
					Ala	Ile
					265	Pro
					Leu	Pro
					Val	Asp
					270	Phe
					Leu	
Ser	Lys	Val	Ser	Thr	Glu	Ile
		275				
					Pro	Ala
					280	Ser
					Glu	Pro
					Asp	Gly
					285	Pro
					Ser	
Val	Gly	Arg	Ala	Lys	Gly	Gln
	290					
					Asp	Ala
					295	Pro
					Leu	Glu
					300	Phe
					Thr	Phe
					His	
Val	Glu	Ile	Thr	Pro	Asn	Val
	305					
					Gln	Lys
					310	Glu
					Gln	Ala
					315	His
					Ser	Glu
					320	Glu
His	Leu	Gly	Arg	Ala	Ala	Phe
				325		
					Pro	Gly
					330	Ala
					Pro	Gly
					Glu	Gly
					335	Pro
					Glu	
Ala	Arg	Gly	Pro	Ser	Leu	Gly
					Glu	Asp
					Thr	Lys
					Glu	Ala
					Asp	Leu
					Pro	

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340

345

350

Glu Pro Ser Glu Lys Gln Pro Ala Ala Ala Pro Arg Gly Lys Pro Val  
355 360 365

Ser Arg Val Pro Gln Leu Lys Ala Arg Met Val Ser Lys Ser Lys Asp  
370 375 380

Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Thr Ser Thr Arg Ser Ser  
385 390 395 400

Ala Lys Thr Leu Lys Asn Arg Pro Cys Leu Ser Pro Lys His Pro Thr  
405 410 415

Pro Gly Ser Ser Asp Pro Leu Ile Gln Pro Ser Ser Pro Ala Val Cys  
420 425 430

Pro Glu Pro Pro Ser Ser Pro Lys Tyr Val Ser Ser Val Thr Ser Arg  
435 440 445

Thr Gly Ser Ser Gly Ala Lys Glu Met Lys Leu Lys Gly Ala Asp Gly  
450 455 460

Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro Gly Gln Lys  
465 470 475 480

Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro Pro Ala Pro  
485 490 495

Lys Thr Pro Pro Ser Ser Ala Thr Lys Gln Val Gln Arg Arg Pro Pro  
500 505 510

Pro Ala Gly Pro Arg Ser Glu Arg Gly Glu Pro Pro Lys Ser Gly Asp  
515 520 525

Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser Arg  
530 535 540

Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys Lys  
545 550 555 560

Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys Ser  
565 570 575

Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val Lys  
580 585 590

Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly Gly  
595 600 605

Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln Ser  
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## FAB-008PC-SequenceListing

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Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly Ser  
 625 630 635 640

Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser Lys  
 645 650 655

Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln Val  
 660 665 670

Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser Lys  
 675 680 685

Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn Lys  
 690 695 700

Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala Lys  
 705 710 715 720

Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser Gly  
 725 730 735

Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser Ile  
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Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val Ser  
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Ala Ser Leu Ala Lys Gln Gly Leu  
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Thr Gly Gly Ser Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg  
 35 40 45

Tyr Pro Pro Gln Gly Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly  
 50 55 60

Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly  
 65 70 75 80

FAB-008PC-SequenceListing

Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Gly Gly Gly Thr His  
85 90 95

Ser Gln Trp Asn Lys Pro Ser Lys Pro Lys Thr Asn Met Lys His Met  
100 105 110

Ala Gly Ala Ala Ala Ala Gly Ala Val Val Gly Gly Leu Gly Gly Tyr  
115 120 125

Met Leu Gly Ser Ala Met Ser Arg Pro Ile Ile His Phe Gly Ser Asp  
130 135 140

Tyr Glu Asp Arg Tyr Tyr Arg Glu Asn Met His Arg Tyr Pro Asn Gln  
145 150 155 160

Val Tyr Tyr Arg Pro Met Asp Glu Tyr Ser Asn Gln Asn Asn Phe Val  
165 170 175

His Asp Cys Val Asn Ile Thr Ile Lys Gln His Thr Val Thr Thr Thr  
180 185 190

Thr Lys Gly Glu Asn Phe Thr Glu Thr Asp Val Lys Met Met Glu Arg  
195 200 205

Val Val Glu Gln Met Cys Ile Thr Gln Tyr Glu Arg Glu Ser Gln Ala  
210 215 220

Tyr Tyr Gln Arg Gly Ser Ser Met Val Leu Phe Ser Ser Pro Pro Val  
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Ile Leu Leu Ile Ser Phe Leu Ile Phe Leu Ile Val Gly  
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Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val  
35 40 45

Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr  
50 55 60

FAB-008PC-SequenceListing

Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys  
65 70 75 80

Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys  
85 90 95

Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile  
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Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro  
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Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala  
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<400> 52

Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val  
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20 25 30

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val  
35 40 45

Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr  
50 55 60

Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys  
65 70 75 80

Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys  
85 90 95

Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile  
100 105 110

Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro  
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Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala  
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FAB-008PC-SequenceListing

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Gln Leu Val Lys Ser Glu Leu Glu Glu Lys Lys Ser Glu Leu Arg His  
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Lys Leu Lys Tyr Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala  
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Arg Asn Ser Thr Gln Asp Arg Ile Leu Glu Met Lys Val Met Glu Phe  
35 40 45  
Phe Met Lys Val Tyr Gly Tyr Arg Gly Lys His Leu Gly Gly Ser Arg  
50 55 60  
Lys Pro Asp Gly Ala Ile Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly  
65 70 75 80  
Val Ile Val Asp Thr Lys Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile  
85 90 95  
Gly Gln Ala Asp Glu Met Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg  
100 105 110  
Asn Lys His Ile Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser  
115 120 125  
Val Thr Glu Phe Lys Phe Leu Phe Val Ser Gly His Phe Lys Gly Asn  
130 135 140  
Tyr Lys Ala Gln Leu Thr Arg Leu Asn His Ile Thr Asn Cys Asn Gly  
145 150 155 160  
Ala Val Leu Ser Val Glu Glu Leu Leu Ile Gly Gly Glu Met Ile Lys  
165 170 175  
Ala Gly Thr Leu Thr Leu Glu Glu Val Arg Arg Lys Phe Asn Asn Gly  
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Glu Ile Asn Phe  
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FAB-008PC-SequenceListing

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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
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His Gly Gly Gly  
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<212> PRT  
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Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
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Gly His Gly Gly  
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Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
1 5 10 15

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
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His Gly Ser Gly  
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FAB-008PC-SequenceListing

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20 25 30

Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr  
35 40 45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val  
50 55 60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His  
65 70 75 80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val  
85 90 95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala  
100 105 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala  
115 120 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp  
130 135 140

Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val  
145 150 155 160

FAB-008PC-SequenceListing

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn  
 165 170 175  
 Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
 180 185 190  
 Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
 195 200 205  
 Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
 210 215 220  
 Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
 225 230 235 240  
 Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala  
 245 250 255  
 Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu  
 260 265 270  
 Pro Val Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val  
 275 280 285  
 Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val  
 290 295 300  
 Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu  
 305 310 315 320  
 Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu  
 325 330 335  
 Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly  
 340 345 350  
 Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
 355 360 365  
 Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
 370 375 380  
 His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly  
 385 390 395 400  
 Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys  
 405 410 415  
 Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala  
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FAB-008PC-SequenceListing

Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu  
435 440 445

Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala  
450 455 460

Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg  
465 470 475 480

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

Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu  
500 505 510

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr  
515 520 525

Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala  
530 535 540

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala Gly His  
545 550 555 560

Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly  
565 570 575

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys  
580 585 590

Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
595 600 605

Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
610 615 620

Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala  
625 630 635 640

Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg  
645 650 655

Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val  
660 665 670

Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val  
675 680 685

Gln Arg Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly Leu Thr  
690 695 700

# FAB-008PC-SequenceListing

Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala  
 705 710 715 720  
 Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly  
 725 730 735  
 Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
 740 745 750  
 Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
 755 760 765  
 Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
 770 775 780  
 Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
 785 790 795 800  
 Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala  
 805 810 815  
 Ser Xaa Xaa Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu  
 820 825 830  
 Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val  
 835 840 845  
 Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys  
 850 855 860  
 Gly Leu Pro His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile  
 865 870 875 880  
 Pro Glu Arg Thr Ser His Arg Val Ala Gly Ser Gln Leu Val Lys Ser  
 885 890 895  
 Glu Leu Glu Glu Lys Lys Ser Glu Leu Arg His Lys Leu Lys Tyr Val  
 900 905 910  
 Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser Thr Gln  
 915 920 925  
 Asp Arg Ile Leu Glu Met Lys Val Met Glu Phe Phe Met Lys Val Tyr  
 930 935 940  
 Gly Tyr Arg Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ala  
 945 950 955 960  
 Ile Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly Val Ile Val Asp Thr  
 965 970 975

# FAB-008PC-SequenceListing

Lys Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala Asp Glu  
980 985 990

Met Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn Lys His Ile Asn  
995 1000 1005

Pro Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser Val Thr Glu Phe  
1010 1015 1020

Lys Phe Leu Phe Val Ser Gly His Phe Lys Gly Asn Tyr Lys Ala  
1025 1030 1035

Gln Leu Thr Arg Leu Asn His Ile Thr Asn Cys Asn Gly Ala Val  
1040 1045 1050

Leu Ser Val Glu Glu Leu Leu Ile Gly Gly Glu Met Ile Lys Ala  
1055 1060 1065

Gly Thr Leu Thr Leu Glu Glu Val Arg Arg Lys Phe Asn Asn Gly  
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Glu Ile Asn Phe Arg Ser  
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FAB-008PC-SequenceListing

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Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val  
20 25 30

Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr  
35 40 45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val  
50 55 60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His  
65 70 75 80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val  
85 90 95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala  
100 105 110

Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala  
115 120 125

Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp  
130 135 140

Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val  
145 150 155 160

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn  
165 170 175

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
180 185 190

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
195 200 205

Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
210 215 220

Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
225 230 235 240

Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala  
245 250 255

Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg  
260 265 270



FAB-008PC-SequenceListing

Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu  
275 280 285

Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu  
290 295 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly  
305 310 315 320

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
325 330 335

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
340 345 350

Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
355 360 365

Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
370 375 380

Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala  
385 390 395 400

Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg  
405 410 415

Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu  
420 425 430

Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu  
435 440 445

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly  
450 455 460

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
465 470 475 480

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
485 490 495

Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
500 505 510

Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
515 520 525

Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala  
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## FAB-008PC-SequenceListing

Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg  
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Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu  
 565 570 575

Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu  
 580 585 590

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly  
 595 600 605

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
 610 615 620

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
 625 630 635 640

Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
 645 650 655

Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
 660 665 670

Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala  
 675 680 685

Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg  
 690 695 700

Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu  
 705 710 715 720

Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu  
 725 730 735

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly  
 740 745 750

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
 755 760 765

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
 770 775 780

Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
 785 790 795 800

Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
 805 810 815

FAB-008PC-SequenceListing

Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala  
820 825 830

Ile Ala Ser Xaa Xaa Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala  
835 840 845

Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His  
850 855 860

Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val  
865 870 875 880

Lys Lys Gly Leu Pro His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg  
885 890 895

Arg Ile Pro Glu Arg Thr Ser His Arg Val Ala Gly Ser Gln Leu Val  
900 905 910

Lys Ser Glu Leu Glu Glu Lys Lys Ser Glu Leu Arg His Lys Leu Lys  
915 920 925

Tyr Val Pro His Glu Tyr Ile Glu Leu Ile Glu Ile Ala Arg Asn Ser  
930 935 940

Thr Gln Asp Arg Ile Leu Glu Met Lys Val Met Glu Phe Phe Met Lys  
945 950 955 960

Val Tyr Gly Tyr Arg Gly Lys His Leu Gly Gly Ser Arg Lys Pro Asp  
965 970 975

Gly Ala Ile Tyr Thr Val Gly Ser Pro Ile Asp Tyr Gly Val Ile Val  
980 985 990

Asp Thr Lys Ala Tyr Ser Gly Gly Tyr Asn Leu Pro Ile Gly Gln Ala  
995 1000 1005

Asp Glu Met Gln Arg Tyr Val Glu Glu Asn Gln Thr Arg Asn Lys  
1010 1015 1020

His Ile Asn Pro Asn Glu Trp Trp Lys Val Tyr Pro Ser Ser Val  
1025 1030 1035

Thr Glu Phe Lys Phe Leu Phe Val Ser Gly His Phe Lys Gly Asn  
1040 1045 1050

Tyr Lys Ala Gln Leu Thr Arg Leu Asn His Ile Thr Asn Cys Asn  
1055 1060 1065

Gly Ala Val Leu Ser Val Glu Glu Leu Leu Ile Gly Gly Glu Met  
1070 1075 1080

FAB-008PC-SequenceListing

Ile Lys Ala Gly Thr Leu Thr Leu Glu Glu Val Arg Arg Lys Phe  
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# FAB-008PC-SequenceListing

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Gly Ile His Gly Val Pro Ala Ala Val Asp Leu Arg Thr Leu Gly Tyr  
 35 40 45

Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val  
 50 55 60

Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His  
 65 70 75 80

Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val  
 85 90 95

Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala  
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105

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Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala  
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Leu Leu Thr Val Ala Gly Glu Leu Arg Gly Pro Pro Leu Gln Leu Asp  
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Thr Gly Gln Leu Leu Lys Ile Ala Lys Arg Gly Gly Val Thr Ala Val  
 145 150 155 160

Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn  
 165 170 175

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
 195 200 205

Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
 210 215 220

Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
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Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala  
 245 250 255

Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu  
 260 265 270

Pro Val Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val  
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Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val  
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Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu  
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Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu  
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Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly  
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Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala

## FAB-008PC-SequenceListing

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Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys  
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Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala  
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Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu  
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Pro Val Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala  
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Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg  
 465 470 475 480

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

Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu  
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Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly Leu Thr  
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Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala  
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Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala Gly His  
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Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly  
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Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys  
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Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
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Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
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Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala  
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Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg

FAB-008PC-SequenceListing

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650

655

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Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val  
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Gln Arg Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly Leu Thr  
690 695 700

Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala  
705 710 715 720

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala His Gly  
725 730 735

Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys  
740 745 750

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
755 760 765

Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
770 775 780

Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
785 790 795 800

Leu Cys Gln Ala His Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala  
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Ser Xaa Xaa Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala Gln Leu  
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Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val  
835 840 845

Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val Lys Lys  
850 855 860

Gly Leu Pro His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg Arg Ile  
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Pro Glu Arg Thr Ser His Arg Val Ala Gly Ser Val Leu Glu Lys Ser  
885 890 895

Asp Ile Glu Lys Phe Lys Asn Gln Leu Arg Thr Glu Leu Thr Asn Ile  
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Asp His Ser Tyr Leu Lys Gly Ile Asp Ile Ala Ser Lys Lys Lys Thr



915

920

925

Ser Asn Val Glu Asn Thr Glu Phe Glu Ala Ile Ser Thr Lys Ile Phe  
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Thr Asp Glu Leu Gly Phe Ser Gly Lys His Leu Gly Gly Ser Asn Lys  
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Pro Asp Gly Leu Leu Trp Asp Asp Asp Cys Ala Ile Ile Leu Asp Ser  
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Lys Ala Tyr Ser Glu Gly Phe Pro Leu Thr Ala Ser His Thr Asp Ala  
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Met Gly Arg Tyr Leu Arg Gln Phe Thr Glu Arg Lys Glu Glu Ile Lys  
 995 1000 1005

Pro Thr Trp Trp Asp Ile Ala Pro Glu His Leu Asp Asn Thr Tyr  
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Phe Ala Tyr Val Ser Gly Ser Phe Ser Gly Asn Tyr Lys Glu Gln  
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Leu Gln Lys Phe Arg Gln Asp Thr Asn His Leu Gly Gly Ala Leu  
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Glu Phe Val Lys Leu Leu Leu Leu Ala Asn Asn Tyr Lys Thr Gln  
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Ile Ser Tyr  
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Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val Arg Ser Thr Val  
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Ala Gln His His Glu Ala Leu Val Gly His Gly Phe Thr His Ala His  
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Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly Thr Val Ala Val  
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Lys Tyr Gln Asp Met Ile Ala Ala Leu Pro Glu Ala Thr His Glu Ala  
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Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg Ala Leu Glu Ala  
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Glu Ala Val His Ala Trp Arg Asn Ala Leu Thr Gly Ala Pro Leu Asn  
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Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Ala  
195 200 205

Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala Ile Ala Ser Xaa  
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FAB-008PC-SequenceListing

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 Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg  
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 Leu Leu Pro Val Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu  
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 Gln Val Val Ala Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu  
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FAB-008PC-SequenceListing

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Ile Ala Ser Xaa Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg  
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FAB-008PC-SequenceListing

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Xaa Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val  
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Leu Cys Gln Ala Gly His Gly Gly Leu Thr Pro Glu Gln Val Val Ala  
820 825 830

Ile Ala Ser Xaa Xaa Gly Gly Arg Pro Ala Leu Glu Ser Ile Val Ala  
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Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His  
850 855 860

Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Leu Asp Ala Val  
865 870 875 880

Lys Lys Gly Leu Pro His Ala Pro Ala Leu Ile Lys Arg Thr Asn Arg  
885 890 895

Arg Ile Pro Glu Arg Thr Ser His Arg Val Ala Gly Ser Val Leu Glu  
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Lys Ser Asp Ile Glu Lys Phe Lys Asn Gln Leu Arg Thr Glu Leu Thr  
915 920 925

Asn Ile Asp His Ser Tyr Leu Lys Gly Ile Asp Ile Ala Ser Lys Lys  
930 935 940

Lys Thr Ser Asn Val Glu Asn Thr Glu Phe Glu Ala Ile Ser Thr Lys  
945 950 955 960

Ile Phe Thr Asp Glu Leu Gly Phe Ser Gly Lys His Leu Gly Gly Ser  
965 970 975

Asn Lys Pro Asp Gly Leu Leu Trp Asp Asp Asp Cys Ala Ile Ile Leu  
980 985 990

Asp Ser Lys Ala Tyr Ser Glu Gly Phe Pro Leu Thr Ala Ser His Thr  
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Asp Ala Met Gly Arg Tyr Leu Arg Gln Phe Thr Glu Arg Lys Glu  
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Glu Ile Lys Pro Thr Trp Trp Asp Ile Ala Pro Glu His Leu Asp  
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# FAB-008PC-SequenceListing

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Gly Ala Leu Glu Phe Val Lys Leu Leu Leu Leu Ala Asn Asn Tyr  
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Asp Tyr Asn Ile Ser Tyr  
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Glu Asp Ile Pro Pro Ile Thr Cys Val Gln Asn Gly Leu Arg Tyr His  
35 40 45

Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Arg Ile Cys Val Cys Asp  
50 55 60

Asn Gly Lys Val Leu Cys Asp Asp Val Ile Cys Asp Glu Thr Lys Asn  
65 70 75 80

Cys Pro Gly Ala Glu Val Pro Glu Gly Glu Cys Cys Pro Val Cys Pro  
85 90 95

Asp Gly Ser Glu Ser Pro Thr Asp Gln Glu Thr Thr Gly Val Glu Gly  
100 105 110

Pro Lys Gly Asp Thr Gly Pro Arg Gly Pro Arg Gly Pro Ala Gly Pro  
115 120 125

Pro Gly Arg Asp Gly Ile Pro Gly Gln Pro Gly Leu Pro Gly Pro Pro  
130 135 140

Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala  
145 150 155 160

FAB-008PC-SequenceListing

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Pro Gly Ala<sub>195</sub> Pro Gly Pro Gln Gly<sub>200</sub> Phe Gln Gly Pro<sub>205</sub> Gly Glu Pro

Gly Glu<sub>210</sub> Pro Gly Ala Ser Gly<sub>215</sub> Pro Met Gly Pro Arg<sub>220</sub> Gly Pro Pro Gly

Pro<sub>225</sub> Pro Gly Lys Asn Gly<sub>230</sub> Asp Asp Gly Glu Ala<sub>235</sub> Gly Lys Pro Gly Arg<sub>240</sub>

Pro Gly Glu Arg Gly<sub>245</sub> Pro Pro Gly Pro Gln Gly Ala Arg Gly Leu<sub>255</sub> Pro

Gly Thr Ala Gly<sub>260</sub> Leu Pro Gly Met Lys<sub>265</sub> Gly His Arg Gly Phe<sub>270</sub> Ser Gly

Leu Asp Gly<sub>275</sub> Ala Lys Gly Asp Ala<sub>280</sub> Gly Pro Ala Gly<sub>285</sub> Pro Lys Gly Glu

Pro Gly<sub>290</sub> Ser Pro Gly Glu Asn<sub>295</sub> Gly Ala Pro Gly Gln<sub>300</sub> Met Gly Pro Arg

Gly<sub>305</sub> Leu Pro Gly Glu Arg<sub>310</sub> Gly Arg Pro Gly Ala<sub>315</sub> Pro Gly Pro Ala Gly<sub>320</sub>

Ala Arg Gly Asn<sub>325</sub> Asp Gly Ala Thr Gly Ala<sub>330</sub> Ala Gly Pro Pro Gly<sub>335</sub> Pro

Thr Gly Pro Ala<sub>340</sub> Gly Pro Pro Gly Phe<sub>345</sub> Pro Gly Ala Val Gly<sub>350</sub> Ala Lys

Gly Glu Ala<sub>355</sub> Gly Pro Gln Gly Pro<sub>360</sub> Arg Gly Ser Glu Gly<sub>365</sub> Pro Gln Gly

Val Arg<sub>370</sub> Gly Glu Pro Gly Pro<sub>375</sub> Pro Gly Pro Ala Gly<sub>380</sub> Ala Ala Gly Pro

Ala<sub>385</sub> Gly Asn Pro Gly Ala<sub>390</sub> Asp Gly Gln Pro Gly<sub>395</sub> Ala Lys Gly Ala Asn<sub>400</sub>

Gly Ala Pro Gly Ile<sub>405</sub> Ala Gly Ala Pro Gly<sub>410</sub> Phe Pro Gly Ala Arg<sub>415</sub> Gly

Pro Ser Gly Pro<sub>420</sub> Gln Gly Pro Gly Gly<sub>425</sub> Pro Pro Gly Pro Lys<sub>430</sub> Gly Asn



FAB-008PC-SequenceListing

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

Glu Glu Gly Lys Arg Gly Ala Arg Gly Glu Pro Gly Pro Thr Gly Leu  
465 470 475 480

Pro Gly Pro Pro Gly Glu Arg Gly Gly Pro Gly Ser Arg Gly Phe Pro  
485 490 495

Gly Ala Asp Gly Val Ala Gly Pro Lys Gly Pro Ala Gly Glu Arg Gly  
500 505 510

Ser Pro Gly Pro Ala Gly Pro Lys Gly Ser Pro Gly Glu Ala Gly Arg  
515 520 525

Pro Gly Glu Ala Gly Leu Pro Gly Ala Lys Gly Leu Thr Gly Ser Pro  
530 535 540

Gly Ser Pro Gly Pro Asp Gly Lys Thr Gly Pro Pro Gly Pro Ala Gly  
545 550 555 560

Gln Asp Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Ala Arg Gly Gln  
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Ala Gly Val Met Gly Phe Pro Gly Pro Lys Gly Ala Ala Gly Glu Pro  
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Gly Lys Ala Gly Glu Arg Gly Val Pro Gly Pro Pro Gly Ala Val Gly  
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Pro Ala Gly Lys Asp Gly Glu Ala Gly Ala Gln Gly Pro Pro Gly Pro  
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Ala Gly Pro Ala Gly Glu Arg Gly Glu Gln Gly Pro Ala Gly Ser Pro  
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Gly Phe Gln Gly Leu Pro Gly Pro Ala Gly Pro Pro Gly Glu Ala Gly  
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Lys Pro Gly Glu Gln Gly Val Pro Gly Asp Leu Gly Ala Pro Gly Pro  
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Gly Pro Pro Gly Pro Ala Gly Pro Arg Gly Ala Asn Gly Ala Pro Gly  
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# FAB-008PC-SequenceListing

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FAB-008PC-SequenceListing

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Thr Gly Pro Ala Gly Pro Pro Gly Ala Pro Gly Ala Pro Gly Ala  
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Pro Gly Pro Val Gly Pro Ala Gly Lys Ser Gly Asp Arg Gly Glu  
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Thr Gly Pro Ala Gly Pro Ala Gly Pro Val Gly Pro Val Gly Ala  
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Arg Gly Pro Ala Gly Pro Gln Gly Pro Arg Gly Asp Lys Gly Glu  
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Thr Gly Glu Gln Gly Asp Arg Gly Ile Lys Gly His Arg Gly Phe  
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Ser Gly Leu Gln Gly Pro Pro Gly Pro Pro Gly Ser Pro Gly Glu  
1115 1120 1125

Gln Gly Pro Ser Gly Ala Ser Gly Pro Ala Gly Pro Arg Gly Pro  
1130 1135 1140

Pro Gly Ser Ala Gly Ala Pro Gly Lys Asp Gly Leu Asn Gly Leu  
1145 1150 1155

Pro Gly Pro Ile Gly Pro Pro Gly Pro Arg Gly Arg Thr Gly Asp  
1160 1165 1170

Ala Gly Pro Val Gly Pro Pro Gly Pro Pro Gly Pro Gly Pro  
1175 1180 1185

Pro Gly Pro Pro Ser Ala Gly Phe Asp Phe Ser Phe Leu Pro Gln  
1190 1195 1200

Pro Pro Gln Glu Lys Ala His Asp Gly Gly Arg Tyr Tyr Arg Ala  
1205 1210 1215

Asp Asp Ala Asn Val Val Arg Asp Arg Asp Leu Glu Val Asp Thr  
1220 1225 1230

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Thr	Leu	Lys	Ser	Leu	Ser	Gln	Gln	Ile	Glu	Asn	Ile	Arg	Ser	Pro
	1235					1240					1245			
Glu	Gly	Ser	Arg	Lys	Asn	Pro	Ala	Arg	Thr	Cys	Arg	Asp	Leu	Lys
	1250					1255					1260			
Met	Cys	His	Ser	Asp	Trp	Lys	Ser	Gly	Glu	Tyr	Trp	Ile	Asp	Pro
	1265					1270					1275			
Asn	Gln	Gly	Cys	Asn	Leu	Asp	Ala	Ile	Lys	Val	Phe	Cys	Asn	Met
	1280					1285					1290			
Glu	Thr	Gly	Glu	Thr	Cys	Val	Tyr	Pro	Thr	Gln	Pro	Ser	Val	Ala
	1295					1300					1305			
Gln	Lys	Asn	Trp	Tyr	Ile	Ser	Lys	Asn	Pro	Lys	Asp	Lys	Arg	His
	1310					1315					1320			
Val	Trp	Phe	Gly	Glu	Ser	Met	Thr	Asp	Gly	Phe	Gln	Phe	Glu	Tyr
	1325					1330					1335			
Gly	Gly	Gln	Gly	Ser	Asp	Pro	Ala	Asp	Val	Ala	Ile	Gln	Leu	Thr
	1340					1345					1350			
Phe	Leu	Arg	Leu	Met	Ser	Thr	Glu	Ala	Ser	Gln	Asn	Ile	Thr	Tyr
	1355					1360					1365			
His	Cys	Lys	Asn	Ser	Val	Ala	Tyr	Met	Asp	Gln	Gln	Thr	Gly	Asn
	1370					1375					1380			
Leu	Lys	Lys	Ala	Leu	Leu	Leu	Gln	Gly	Ser	Asn	Glu	Ile	Glu	Ile
	1385					1390					1395			
Arg	Ala	Glu	Gly	Asn	Ser	Arg	Phe	Thr	Tyr	Ser	Val	Thr	Val	Asp
	1400					1405					1410			
Gly	Cys	Thr	Ser	His	Thr	Gly	Ala	Trp	Gly	Lys	Thr	Val	Ile	Glu
	1415					1420					1425			
Tyr	Lys	Thr	Thr	Lys	Thr	Ser	Arg	Leu	Pro	Ile	Ile	Asp	Val	Ala
	1430					1435					1440			
Pro	Leu	Asp	Val	Gly	Ala	Pro	Asp	Gln	Glu	Phe	Gly	Phe	Asp	Val
	1445					1450					1455			
Gly	Pro	Val	Cys	Phe	Leu									
	1460													

<210> 62  
 <211> 1366  
 <212> PRT

## FAB-008PC-SequenceListing

&lt;213&gt; Homo sapiens

&lt;400&gt; 62

Met Leu Ser Phe Val Asp Thr Arg Thr Leu Leu Leu Leu Ala Val Thr  
 1 5 10 15  
 Leu Cys Leu Ala Thr Cys Gln Ser Leu Gln Glu Glu Thr Val Arg Lys  
 20 25 30  
 Gly Pro Ala Gly Asp Arg Gly Pro Arg Gly Glu Arg Gly Pro Pro Gly  
 35 40 45  
 Pro Pro Gly Arg Asp Gly Glu Asp Gly Pro Thr Gly Pro Pro Gly Pro  
 50 55 60  
 Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala Ala Gln  
 65 70 75 80  
 Tyr Asp Gly Lys Gly Val Gly Leu Gly Pro Gly Pro Met Gly Leu Met  
 85 90 95  
 Gly Pro Arg Gly Pro Pro Gly Ala Ala Gly Ala Pro Gly Pro Gln Gly  
 100 105 110  
 Phe Gln Gly Pro Ala Gly Glu Pro Gly Glu Pro Gly Gln Thr Gly Pro  
 115 120 125  
 Ala Gly Ala Arg Gly Pro Ala Gly Pro Pro Gly Lys Ala Gly Glu Asp  
 130 135 140  
 Gly His Pro Gly Lys Pro Gly Arg Pro Gly Glu Arg Gly Val Val Gly  
 145 150 155 160  
 Pro Gln Gly Ala Arg Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Phe  
 165 170 175  
 Lys Gly Ile Arg Gly His Asn Gly Leu Asp Gly Leu Lys Gly Gln Pro  
 180 185 190  
 Gly Ala Pro Gly Val Lys Gly Glu Pro Gly Ala Pro Gly Glu Asn Gly  
 195 200 205  
 Thr Pro Gly Gln Thr Gly Ala Arg Gly Leu Pro Gly Glu Arg Gly Arg  
 210 215 220  
 Val Gly Ala Pro Gly Pro Ala Gly Ala Arg Gly Ser Asp Gly Ser Val  
 225 230 235 240  
 Gly Pro Val Gly Pro Ala Gly Pro Ile Gly Ser Ala Gly Pro Pro Gly  
 245 250 255

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Phe Pro Gly Ala Pro Gly Pro Lys Gly Glu Ile Gly Ala Val Gly Asn  
 260 265 270  
 Ala Gly Pro Ala Gly Pro Ala Gly Pro Arg Gly Glu Val Gly Leu Pro  
 275 280 285  
 Gly Leu Ser Gly Pro Val Gly Pro Pro Gly Asn Pro Gly Ala Asn Gly  
 290 295 300  
 Leu Thr Gly Ala Lys Gly Ala Ala Gly Leu Pro Gly Val Ala Gly Ala  
 305 310 315 320  
 Pro Gly Leu Pro Gly Pro Arg Gly Ile Pro Gly Pro Val Gly Ala Ala  
 325 330 335  
 Gly Ala Thr Gly Ala Arg Gly Leu Val Gly Glu Pro Gly Pro Ala Gly  
 340 345 350  
 Ser Lys Gly Glu Ser Gly Asn Lys Gly Glu Pro Gly Ser Ala Gly Pro  
 355 360 365  
 Gln Gly Pro Pro Gly Pro Ser Gly Glu Glu Gly Lys Arg Gly Pro Asn  
 370 375 380  
 Gly Glu Ala Gly Ser Ala Gly Pro Pro Gly Pro Pro Gly Leu Arg Gly  
 385 390 395 400  
 Ser Pro Gly Ser Arg Gly Leu Pro Gly Ala Asp Gly Arg Ala Gly Val  
 405 410 415  
 Met Gly Pro Pro Gly Ser Arg Gly Ala Ser Gly Pro Ala Gly Val Arg  
 420 425 430  
 Gly Pro Asn Gly Asp Ala Gly Arg Pro Gly Glu Pro Gly Leu Met Gly  
 435 440 445  
 Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly Lys  
 450 455 460  
 Glu Gly Pro Val Gly Leu Pro Gly Ile Asp Gly Arg Pro Gly Pro Ile  
 465 470 475 480  
 Gly Pro Ala Gly Ala Arg Gly Glu Pro Gly Asn Ile Gly Phe Pro Gly  
 485 490 495  
 Pro Lys Gly Pro Thr Gly Asp Pro Gly Lys Asn Gly Asp Lys Gly His  
 500 505 510  
 Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn  
 515 520 525

## FAB-008PC-SequenceListing

Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Gly Lys Gly  
 530 535 540

Glu Gln Gly Pro Pro Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro  
 545 550 555 560

Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His  
 565 570 575

Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly  
 580 585 590

Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly Pro Ile Gly Ser  
 595 600 605

Arg Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro  
 610 615 620

Gly Val Val Gly Ala Val Gly Thr Ala Gly Pro Ser Gly Pro Ser Gly  
 625 630 635 640

Leu Pro Gly Glu Arg Gly Ala Ala Gly Ile Pro Gly Gly Lys Gly Glu  
 645 650 655

Lys Gly Glu Pro Gly Leu Arg Gly Glu Ile Gly Asn Pro Gly Arg Asp  
 660 665 670

Gly Ala Arg Gly Ala Pro Gly Ala Val Gly Ala Pro Gly Pro Ala Gly  
 675 680 685

Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro  
 690 695 700

Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Val Gly Pro Ala  
 705 710 715 720

Gly Pro Asn Gly Phe Ala Gly Pro Ala Gly Ala Ala Gly Gln Pro Gly  
 725 730 735

Ala Lys Gly Glu Arg Gly Ala Lys Gly Pro Lys Gly Glu Asn Gly Val  
 740 745 750

Val Gly Pro Thr Gly Pro Val Gly Ala Ala Gly Pro Ala Gly Pro Asn  
 755 760 765

Gly Pro Pro Gly Pro Ala Gly Ser Arg Gly Asp Gly Gly Pro Pro Gly  
 770 775 780

Met Thr Gly Phe Pro Gly Ala Ala Gly Arg Thr Gly Pro Pro Gly Pro  
 785 790 795 800

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Ser Gly Ile Ser Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Lys Glu  
805 810 815

Gly Leu Arg Gly Pro Arg Gly Asp Gln Gly Pro Val Gly Arg Thr Gly  
820 825 830

Glu Val Gly Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro  
835 840 845

Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln  
850 855 860

Gly Leu Leu Gly Ala Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg Gly  
865 870 875 880

Glu Arg Gly Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro  
885 890 895

Leu Gly Ile Ala Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Ala Val  
900 905 910

Gly Ser Pro Gly Val Asn Gly Ala Pro Gly Glu Ala Gly Arg Asp Gly  
915 920 925

Asn Pro Gly Asn Asp Gly Pro Pro Gly Arg Asp Gly Gln Pro Gly His  
930 935 940

Lys Gly Glu Arg Gly Tyr Pro Gly Asn Ile Gly Pro Val Gly Ala Ala  
945 950 955 960

Gly Ala Pro Gly Pro His Gly Pro Val Gly Pro Ala Gly Lys His Gly  
965 970 975

Asn Arg Gly Glu Thr Gly Pro Ser Gly Pro Val Gly Pro Ala Gly Ala  
980 985 990

Val Gly Pro Arg Gly Pro Ser Gly Pro Gln Gly Ile Arg Gly Asp Lys  
995 1000 1005

Gly Glu Pro Gly Glu Lys Gly Pro Arg Gly Leu Pro Gly Leu Lys  
1010 1015 1020

Gly His Asn Gly Leu Gln Gly Leu Pro Gly Ile Ala Gly His His  
1025 1030 1035

Gly Asp Gln Gly Ala Pro Gly Ser Val Gly Pro Ala Gly Pro Arg  
1040 1045 1050

Gly Pro Ala Gly Pro Ser Gly Pro Ala Gly Lys Asp Gly Arg Thr  
1055 1060 1065



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Gly	His	Pro	Gly	Thr	Val	Gly	Pro	Ala	Gly	Ile	Arg	Gly	Pro	Gln
	1070					1075					1080			
Gly	His	Gln	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro
	1085					1090					1095			
Gly	Pro	Pro	Gly	Val	Ser	Gly	Gly	Gly	Tyr	Asp	Phe	Gly	Tyr	Asp
	1100					1105					1110			
Gly	Asp	Phe	Tyr	Arg	Ala	Asp	Gln	Pro	Arg	Ser	Ala	Pro	Ser	Leu
	1115					1120					1125			
Arg	Pro	Lys	Asp	Tyr	Glu	Val	Asp	Ala	Thr	Leu	Lys	Ser	Leu	Asn
	1130					1135					1140			
Asn	Gln	Ile	Glu	Thr	Leu	Leu	Thr	Pro	Glu	Gly	Ser	Arg	Lys	Asn
	1145					1150					1155			
Pro	Ala	Arg	Thr	Cys	Arg	Asp	Leu	Arg	Leu	Ser	His	Pro	Glu	Trp
	1160					1165					1170			
Ser	Ser	Gly	Tyr	Tyr	Trp	Ile	Asp	Pro	Asn	Gln	Gly	Cys	Thr	Met
	1175					1180					1185			
Asp	Ala	Ile	Lys	Val	Tyr	Cys	Asp	Phe	Ser	Thr	Gly	Glu	Thr	Cys
	1190					1195					1200			
Ile	Arg	Ala	Gln	Pro	Glu	Asn	Ile	Pro	Ala	Lys	Asn	Trp	Tyr	Arg
	1205					1210					1215			
Ser	Ser	Lys	Asp	Lys	Lys	His	Val	Trp	Leu	Gly	Glu	Thr	Ile	Asn
	1220					1225					1230			
Ala	Gly	Ser	Gln	Phe	Glu	Tyr	Asn	Val	Glu	Gly	Val	Thr	Ser	Lys
	1235					1240					1245			
Glu	Met	Ala	Thr	Gln	Leu	Ala	Phe	Met	Arg	Leu	Leu	Ala	Asn	Tyr
	1250					1255					1260			
Ala	Ser	Gln	Asn	Ile	Thr	Tyr	His	Cys	Lys	Asn	Ser	Ile	Ala	Tyr
	1265					1270					1275			
Met	Asp	Glu	Glu	Thr	Gly	Asn	Leu	Lys	Lys	Ala	Val	Ile	Leu	Gln
	1280					1285					1290			
Gly	Ser	Asn	Asp	Val	Glu	Leu	Val	Ala	Glu	Gly	Asn	Ser	Arg	Phe
	1295					1300					1305			
Thr	Tyr	Thr	Val	Leu	Val	Asp	Gly	Cys	Ser	Lys	Lys	Thr	Asn	Glu
	1310					1315					1320			

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Trp Gly Lys Thr Ile Ile Glu Tyr Lys Thr Asn Lys Pro Ser Arg  
1325 1330 1335

Leu Pro Phe Leu Asp Ile Ala Pro Leu Asp Ile Gly Gly Ala Asp  
1340 1345 1350

Gln Glu Phe Phe Val Asp Ile Gly Pro Val Cys Phe Lys  
1355 1360 1365

<210> 63  
<211> 1487  
<212> PRT  
<213> Homo sapiens

<400> 63

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

Val Ala Ala Val Leu Arg Cys Gln Gly Gln Asp Val Gln Glu Ala Gly  
20 25 30

Ser Cys Val Gln Asp Gly Gln Arg Tyr Asn Asp Lys Asp Val Trp Lys  
35 40 45

Pro Glu Pro Cys Arg Ile Cys Val Cys Asp Thr Gly Thr Val Leu Cys  
50 55 60

Asp Asp Ile Ile Cys Glu Asp Val Lys Asp Cys Leu Ser Pro Glu Ile  
65 70 75 80

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

Ser Gly Gln Pro Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Asp Ile  
100 105 110

Lys Asp Ile Val Gly Pro Lys Gly Pro Pro Gly Pro Gln Gly Pro Ala  
115 120 125

Gly Glu Gln Gly Pro Arg Gly Asp Arg Gly Asp Lys Gly Glu Lys Gly  
130 135 140

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

Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly  
165 170 175

Gly Asn Phe Ala Ala Gln Met Ala Gly Gly Phe Asp Glu Lys Ala Gly  
180 185 190

Gly Ala Gln Leu Gly Val Met Gln Gly Pro Met Gly Pro Met Gly Pro

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195

200

205

Arg Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Pro Gln Gly Phe Gln  
 210 215 220

Gly Asn Pro Gly Glu Pro Gly Glu Pro Gly Val Ser Gly Pro Met Gly  
 225 230 235 240

Pro Arg Gly Pro Pro Gly Pro Pro Gly Lys Pro Gly Asp Asp Gly Glu  
 245 250 255

Ala Gly Lys Pro Gly Lys Ala Gly Glu Arg Gly Pro Pro Gly Pro Gln  
 260 265 270

Gly Ala Arg Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Val Lys Gly  
 275 280 285

His Arg Gly Tyr Pro Gly Leu Asp Gly Ala Lys Gly Glu Ala Gly Ala  
 290 295 300

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

Gly Pro Met Gly Pro Arg Gly Leu Pro Gly Glu Arg Gly Arg Thr Gly  
 325 330 335

Pro Ala Gly Ala Ala Gly Ala Arg Gly Asn Asp Gly Gln Pro Gly Pro  
 340 345 350

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

Gly Ala Pro Gly Ala Lys Gly Glu Ala Gly Pro Thr Gly Ala Arg Gly  
 370 375 380

Pro Glu Gly Ala Gln Gly Pro Arg Gly Glu Pro Gly Thr Pro Gly Ser  
 385 390 395 400

Pro Gly Pro Ala Gly Ala Ser Gly Asn Pro Gly Thr Asp Gly Ile Pro  
 405 410 415

Gly Ala Lys Gly Ser Ala Gly Ala Pro Gly Ile Ala Gly Ala Pro Gly  
 420 425 430

Phe Pro Gly Pro Arg Gly Pro Pro Gly Pro Gln Gly Ala Thr Gly Pro  
 435 440 445

Leu Gly Pro Lys Gly Gln Thr Gly Glu Pro Gly Ile Ala Gly Phe Lys  
 450 455 460

Gly Glu Gln Gly Pro Lys Gly Glu Pro Gly Pro Ala Gly Pro Gln Gly  
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465                      470                      475                      480

Ala Pro Gly Pro Ala Gly Glu Glu Gly Lys Arg Gly Ala Arg Gly Glu  
                                  485                                   490                                   495

Pro Gly Gly Val Gly Pro Ile Gly Pro Pro Gly Glu Arg Gly Ala Pro  
                                  500                                   505                                   510

Gly Asn Arg Gly Phe Pro Gly Gln Asp Gly Leu Ala Gly Pro Lys Gly  
                                  515                                   520                                   525

Ala Pro Gly Glu Arg Gly Pro Ser Gly Leu Ala Gly Pro Lys Gly Ala  
                                  530                                   535                                   540

Asn Gly Asp Pro Gly Arg Pro Gly Glu Pro Gly Leu Pro Gly Ala Arg  
 545                                   550                                   555                                   560

Gly Leu Thr Gly Arg Pro Gly Asp Ala Gly Pro Gln Gly Lys Val Gly  
                                  565                                   570                                   575

Pro Ser Gly Ala Pro Gly Glu Asp Gly Arg Pro Gly Pro Pro Gly Pro  
                                  580                                   585                                   590

Gln Gly Ala Arg Gly Gln Pro Gly Val Met Gly Phe Pro Gly Pro Lys  
                                  595                                   600                                   605

Gly Ala Asn Gly Glu Pro Gly Lys Ala Gly Glu Lys Gly Leu Pro Gly  
                                  610                                   615                                   620

Ala Pro Gly Leu Arg Gly Leu Pro Gly Lys Asp Gly Glu Thr Gly Ala  
 625                                   630                                   635                                   640

Ala Gly Pro Pro Gly Pro Ala Gly Pro Ala Gly Glu Arg Gly Glu Gln  
                                  645                                   650                                   655

Gly Ala Pro Gly Pro Ser Gly Phe Gln Gly Leu Pro Gly Pro Pro Gly  
                                  660                                   665                                   670

Pro Pro Gly Glu Gly Gly Lys Pro Gly Asp Gln Gly Val Pro Gly Glu  
                                  675                                   680                                   685

Ala Gly Ala Pro Gly Leu Val Gly Pro Arg Gly Glu Arg Gly Phe Pro  
                                  690                                   695                                   700

Gly Glu Arg Gly Ser Pro Gly Ala Gln Gly Leu Gln Gly Pro Arg Gly  
 705                                   710                                   715                                   720

Leu Pro Gly Thr Pro Gly Thr Asp Gly Pro Lys Gly Ala Ser Gly Pro  
                                  725                                   730                                   735

Ala Gly Pro Pro Gly Ala Gln Gly Pro Pro Gly Leu Gln Gly Met Pro

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740

745

750

Gly Glu Arg Gly Ala Ala Gly Ile Ala Gly Pro Lys Gly Asp Arg Gly  
755 760 765

Asp Val Gly Glu Lys Gly Pro Glu Gly Ala Pro Gly Lys Asp Gly Gly  
770 775 780

Arg Gly Leu Thr Gly Pro Ile Gly Pro Pro Gly Pro Ala Gly Ala Asn  
785 790 795 800

Gly Glu Lys Gly Glu Val Gly Pro Pro Gly Pro Ala Gly Ser Ala Gly  
805 810 815

Ala Arg Gly Ala Pro Gly Glu Arg Gly Glu Thr Gly Pro Pro Gly Pro  
820 825 830

Ala Gly Phe Ala Gly Pro Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys  
835 840 845

Gly Glu Gln Gly Glu Ala Gly Gln Lys Gly Asp Ala Gly Ala Pro Gly  
850 855 860

Pro Gln Gly Pro Ser Gly Ala Pro Gly Pro Gln Gly Pro Thr Gly Val  
865 870 875 880

Thr Gly Pro Lys Gly Ala Arg Gly Ala Gln Gly Pro Pro Gly Ala Thr  
885 890 895

Gly Phe Pro Gly Ala Ala Gly Arg Val Gly Pro Pro Gly Ser Asn Gly  
900 905 910

Asn Pro Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Lys Asp Gly Pro  
915 920 925

Lys Gly Ala Arg Gly Asp Ser Gly Pro Pro Gly Arg Ala Gly Glu Pro  
930 935 940

Gly Leu Gln Gly Pro Ala Gly Pro Pro Gly Glu Lys Gly Glu Pro Gly  
945 950 955 960

Asp Asp Gly Pro Ser Gly Ala Glu Gly Pro Pro Gly Pro Gln Gly Leu  
965 970 975

Ala Gly Gln Arg Gly Ile Val Gly Leu Pro Gly Gln Arg Gly Glu Arg  
980 985 990

Gly Phe Pro Gly Leu Pro Gly Pro Ser Gly Glu Pro Gly Lys Gln Gly  
995 1000 1005

Ala Pro Gly Ala Ser Gly Asp Arg Gly Pro Pro Gly Pro Val Gly

## FAB-008PC-SequenceListing

1010	1015	1020													
Pro	Pro	Gly	Leu	Thr	Gly	Pro	Ala	Gly	Glu	Pro	Gly	Arg	Glu	Gly	
1025						1030					1035				
Ser	Pro	Gly	Ala	Asp	Gly	Pro	Pro	Gly	Arg	Asp	Gly	Ala	Ala	Gly	
1040						1045					1050				
Val	Lys	Gly	Asp	Arg	Gly	Glu	Thr	Gly	Ala	Val	Gly	Ala	Pro	Gly	
1055						1060					1065				
Ala	Pro	Gly	Pro	Pro	Gly	Ser	Pro	Gly	Pro	Ala	Gly	Pro	Thr	Gly	
1070						1075					1080				
Lys	Gln	Gly	Asp	Arg	Gly	Glu	Ala	Gly	Ala	Gln	Gly	Pro	Met	Gly	
1085						1090					1095				
Pro	Ser	Gly	Pro	Ala	Gly	Ala	Arg	Gly	Ile	Gln	Gly	Pro	Gln	Gly	
1100						1105					1110				
Pro	Arg	Gly	Asp	Lys	Gly	Glu	Ala	Gly	Glu	Pro	Gly	Glu	Arg	Gly	
1115						1120					1125				
Leu	Lys	Gly	His	Arg	Gly	Phe	Thr	Gly	Leu	Gln	Gly	Leu	Pro	Gly	
1130						1135					1140				
Pro	Pro	Gly	Pro	Ser	Gly	Asp	Gln	Gly	Ala	Ser	Gly	Pro	Ala	Gly	
1145						1150					1155				
Pro	Ser	Gly	Pro	Arg	Gly	Pro	Pro	Gly	Pro	Val	Gly	Pro	Ser	Gly	
1160						1165					1170				
Lys	Asp	Gly	Ala	Asn	Gly	Ile	Pro	Gly	Pro	Ile	Gly	Pro	Pro	Gly	
1175						1180					1185				
Pro	Arg	Gly	Arg	Ser	Gly	Glu	Thr	Gly	Pro	Ala	Gly	Pro	Pro	Gly	
1190						1195					1200				
Asn	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Gly	Ile	
1205						1210					1215				
Asp	Met	Ser	Ala	Phe	Ala	Gly	Leu	Gly	Pro	Arg	Glu	Lys	Gly	Pro	
1220						1225					1230				
Asp	Pro	Leu	Gln	Tyr	Met	Arg	Ala	Asp	Gln	Ala	Ala	Gly	Gly	Leu	
1235						1240					1245				
Arg	Gln	His	Asp	Ala	Glu	Val	Asp	Ala	Thr	Leu	Lys	Ser	Leu	Asn	
1250						1255					1260				
Asn	Gln	Ile	Glu	Ser	Ile	Arg	Ser	Pro	Glu	Gly	Ser	Arg	Lys	Asn	

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1265

1270

1275

Pro Ala Arg Thr Cys Arg Asp Leu Lys Leu Cys His Pro Glu Trp  
1280 1285 1290

Lys Ser Gly Asp Tyr Trp Ile Asp Pro Asn Gln Gly Cys Thr Leu  
1295 1300 1305

Asp Ala Met Lys Val Phe Cys Asn Met Glu Thr Gly Glu Thr Cys  
1310 1315 1320

Val Tyr Pro Asn Pro Ala Asn Val Pro Lys Lys Asn Trp Trp Ser  
1325 1330 1335

Ser Lys Ser Lys Glu Lys Lys His Ile Trp Phe Gly Glu Thr Ile  
1340 1345 1350

Asn Gly Gly Phe His Phe Ser Tyr Gly Asp Asp Asn Leu Ala Pro  
1355 1360 1365

Asn Thr Ala Asn Val Gln Met Thr Phe Leu Arg Leu Leu Ser Thr  
1370 1375 1380

Glu Gly Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Ile Ala  
1385 1390 1395

Tyr Leu Asp Glu Ala Ala Gly Asn Leu Lys Lys Ala Leu Leu Ile  
1400 1405 1410

Gln Gly Ser Asn Asp Val Glu Ile Arg Ala Glu Gly Asn Ser Arg  
1415 1420 1425

Phe Thr Tyr Thr Ala Leu Lys Asp Gly Cys Thr Lys His Thr Gly  
1430 1435 1440

Lys Trp Gly Lys Thr Val Ile Glu Tyr Arg Ser Gln Lys Thr Ser  
1445 1450 1455

Arg Leu Pro Ile Ile Asp Ile Ala Pro Met Asp Ile Gly Gly Pro  
1460 1465 1470

Glu Gln Glu Phe Gly Val Asp Ile Gly Pro Val Cys Phe Leu  
1475 1480 1485

<210> 64  
<211> 1418  
<212> PRT  
<213> Homo sapiens

<400> 64

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

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Val Ala Ala Val Leu Arg Cys Gln Gly Gln Asp Val Arg Gln Pro Gly  
 20 25 30  
 Pro Lys Gly Gln Lys Gly Glu Pro Gly Asp Ile Lys Asp Ile Val Gly  
 35 40 45  
 Pro Lys Gly Pro Pro Gly Pro Gln Gly Pro Ala Gly Glu Gln Gly Pro  
 50 55 60  
 Arg Gly Asp Arg Gly Asp Lys Gly Glu Lys Gly Ala Pro Gly Pro Arg  
 65 70 75 80  
 Gly Arg Asp Gly Glu Pro Gly Thr Pro Gly Asn Pro Gly Pro Pro Gly  
 85 90 95  
 Pro Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala Ala  
 100 105 110  
 Gln Met Ala Gly Gly Phe Asp Glu Lys Ala Gly Gly Ala Gln Leu Gly  
 115 120 125  
 Val Met Gln Gly Pro Met Gly Pro Met Gly Pro Arg Gly Pro Pro Gly  
 130 135 140  
 Pro Ala Gly Ala Pro Gly Pro Gln Gly Phe Gln Gly Asn Pro Gly Glu  
 145 150 155 160  
 Pro Gly Glu Pro Gly Val Ser Gly Pro Met Gly Pro Arg Gly Pro Pro  
 165 170 175  
 Gly Pro Pro Gly Lys Pro Gly Asp Asp Gly Glu Ala Gly Lys Pro Gly  
 180 185 190  
 Lys Ala Gly Glu Arg Gly Pro Pro Gly Pro Gln Gly Ala Arg Gly Phe  
 195 200 205  
 Pro Gly Thr Pro Gly Leu Pro Gly Val Lys Gly His Arg Gly Tyr Pro  
 210 215 220  
 Gly Leu Asp Gly Ala Lys Gly Glu Ala Gly Ala Pro Gly Val Lys Gly  
 225 230 235 240  
 Glu Ser Gly Ser Pro Gly Glu Asn Gly Ser Pro Gly Pro Met Gly Pro  
 245 250 255  
 Arg Gly Leu Pro Gly Glu Arg Gly Arg Thr Gly Pro Ala Gly Ala Ala  
 260 265 270  
 Gly Ala Arg Gly Asn Asp Gly Gln Pro Gly Pro Ala Gly Pro Pro Gly  
 275 280 285



# FAB-008PC-SequenceListing

Pro Val Gly Pro Ala Gly Gly Pro Gly Phe Pro Gly Ala Pro Gly Ala  
 290 295 300  
 Lys Gly Glu Ala Gly Pro Thr Gly Ala Arg Gly Pro Glu Gly Ala Gln  
 305 310 315 320  
 Gly Pro Arg Gly Glu Pro Gly Thr Pro Gly Ser Pro Gly Pro Ala Gly  
 325 330 335  
 Ala Ser Gly Asn Pro Gly Thr Asp Gly Ile Pro Gly Ala Lys Gly Ser  
 340 345 350  
 Ala Gly Ala Pro Gly Ile Ala Gly Ala Pro Gly Phe Pro Gly Pro Arg  
 355 360 365  
 Gly Pro Pro Gly Pro Gln Gly Ala Thr Gly Pro Leu Gly Pro Lys Gly  
 370 375 380  
 Gln Thr Gly Glu Pro Gly Ile Ala Gly Phe Lys Gly Glu Gln Gly Pro  
 385 390 395 400  
 Lys Gly Glu Pro Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Pro Ala  
 405 410 415  
 Gly Glu Glu Gly Lys Arg Gly Ala Arg Gly Glu Pro Gly Gly Val Gly  
 420 425 430  
 Pro Ile Gly Pro Pro Gly Glu Arg Gly Ala Pro Gly Asn Arg Gly Phe  
 435 440 445  
 Pro Gly Gln Asp Gly Leu Ala Gly Pro Lys Gly Ala Pro Gly Glu Arg  
 450 455 460  
 Gly Pro Ser Gly Leu Ala Gly Pro Lys Gly Ala Asn Gly Asp Pro Gly  
 465 470 475 480  
 Arg Pro Gly Glu Pro Gly Leu Pro Gly Ala Arg Gly Leu Thr Gly Arg  
 485 490 495  
 Pro Gly Asp Ala Gly Pro Gln Gly Lys Val Gly Pro Ser Gly Ala Pro  
 500 505 510  
 Gly Glu Asp Gly Arg Pro Gly Pro Gly Pro Gln Gly Ala Arg Gly  
 515 520 525  
 Gln Pro Gly Val Met Gly Phe Pro Gly Pro Lys Gly Ala Asn Gly Glu  
 530 535 540  
 Pro Gly Lys Ala Gly Glu Lys Gly Leu Pro Gly Ala Pro Gly Leu Arg  
 545 550 555 560

# FAB-008PC-SequenceListing

Gly Leu Pro Gly Lys Asp Gly Glu Thr Gly Ala Ala Gly Pro Pro Gly  
 565 570 575  
 Pro Ala Gly Pro Ala Gly Glu Arg Gly Glu Gln Gly Ala Pro Gly Pro  
 580 585 590  
 Ser Gly Phe Gln Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Glu Gly  
 595 600 605  
 Gly Lys Pro Gly Asp Gln Gly Val Pro Gly Glu Ala Gly Ala Pro Gly  
 610 615 620  
 Leu Val Gly Pro Arg Gly Glu Arg Gly Phe Pro Gly Glu Arg Gly Ser  
 625 630 635 640  
 Pro Gly Ala Gln Gly Leu Gln Gly Pro Arg Gly Leu Pro Gly Thr Pro  
 645 650 655  
 Gly Thr Asp Gly Pro Lys Gly Ala Ser Gly Pro Ala Gly Pro Pro Gly  
 660 665 670  
 Ala Gln Gly Pro Pro Gly Leu Gln Gly Met Pro Gly Glu Arg Gly Ala  
 675 680 685  
 Ala Gly Ile Ala Gly Pro Lys Gly Asp Arg Gly Asp Val Gly Glu Lys  
 690 695 700  
 Gly Pro Glu Gly Ala Pro Gly Lys Asp Gly Gly Arg Gly Leu Thr Gly  
 705 710 715 720  
 Pro Ile Gly Pro Pro Gly Pro Ala Gly Ala Asn Gly Glu Lys Gly Glu  
 725 730 735  
 Val Gly Pro Pro Gly Pro Ala Gly Ser Ala Gly Ala Arg Gly Ala Pro  
 740 745 750  
 Gly Glu Arg Gly Glu Thr Gly Pro Pro Gly Pro Ala Gly Phe Ala Gly  
 755 760 765  
 Pro Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys Gly Glu Gln Gly Glu  
 770 775 780  
 Ala Gly Gln Lys Gly Asp Ala Gly Ala Pro Gly Pro Gln Gly Pro Ser  
 785 790 795 800  
 Gly Ala Pro Gly Pro Gln Gly Pro Thr Gly Val Thr Gly Pro Lys Gly  
 805 810 815  
 Ala Arg Gly Ala Gln Gly Pro Pro Gly Ala Thr Gly Phe Pro Gly Ala  
 820 825 830

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Ala Gly Arg Val Gly Pro Pro Gly Ser Asn Gly Asn Pro Gly Pro Pro  
835 840 845

Gly Pro Pro Gly Pro Ser Gly Lys Asp Gly Pro Lys Gly Ala Arg Gly  
850 855 860

Asp Ser Gly Pro Pro Gly Arg Ala Gly Glu Pro Gly Leu Gln Gly Pro  
865 870 875 880

Ala Gly Pro Pro Gly Glu Lys Gly Glu Pro Gly Asp Asp Gly Pro Ser  
885 890 895

Gly Ala Glu Gly Pro Pro Gly Pro Gln Gly Leu Ala Gly Gln Arg Gly  
900 905 910

Ile Val Gly Leu Pro Gly Gln Arg Gly Glu Arg Gly Phe Pro Gly Leu  
915 920 925

Pro Gly Pro Ser Gly Glu Pro Gly Lys Gln Gly Ala Pro Gly Ala Ser  
930 935 940

Gly Asp Arg Gly Pro Pro Gly Pro Val Gly Pro Pro Gly Leu Thr Gly  
945 950 955 960

Pro Ala Gly Glu Pro Gly Arg Glu Gly Ser Pro Gly Ala Asp Gly Pro  
965 970 975

Pro Gly Arg Asp Gly Ala Ala Gly Val Lys Gly Asp Arg Gly Glu Thr  
980 985 990

Gly Ala Val Gly Ala Pro Gly Ala Pro Gly Pro Pro Gly Ser Pro Gly  
995 1000 1005

Pro Ala Gly Pro Thr Gly Lys Gln Gly Asp Arg Gly Glu Ala Gly  
1010 1015 1020

Ala Gln Gly Pro Met Gly Pro Ser Gly Pro Ala Gly Ala Arg Gly  
1025 1030 1035

Ile Gln Gly Pro Gln Gly Pro Arg Gly Asp Lys Gly Glu Ala Gly  
1040 1045 1050

Glu Pro Gly Glu Arg Gly Leu Lys Gly His Arg Gly Phe Thr Gly  
1055 1060 1065

Leu Gln Gly Leu Pro Gly Pro Pro Gly Pro Ser Gly Asp Gln Gly  
1070 1075 1080

Ala Ser Gly Pro Ala Gly Pro Ser Gly Pro Arg Gly Pro Pro Gly  
1085 1090 1095

FAB-008PC-SequenceListing

Pro	Val	Gly	Pro	Ser	Gly	Lys	Asp	Gly	Ala	Asn	Gly	Ile	Pro	Gly
	1100					1105					1110			
Pro	Ile	Gly	Pro	Pro	Gly	Pro	Arg	Gly	Arg	Ser	Gly	Glu	Thr	Gly
	1115					1120					1125			
Pro	Ala	Gly	Pro	Pro	Gly	Asn	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly
	1130					1135					1140			
Pro	Pro	Gly	Pro	Gly	Ile	Asp	Met	Ser	Ala	Phe	Ala	Gly	Leu	Gly
	1145					1150					1155			
Pro	Arg	Glu	Lys	Gly	Pro	Asp	Pro	Leu	Gln	Tyr	Met	Arg	Ala	Asp
	1160					1165					1170			
Gln	Ala	Ala	Gly	Gly	Leu	Arg	Gln	His	Asp	Ala	Glu	Val	Asp	Ala
	1175					1180					1185			
Thr	Leu	Lys	Ser	Leu	Asn	Asn	Gln	Ile	Glu	Ser	Ile	Arg	Ser	Pro
	1190					1195					1200			
Glu	Gly	Ser	Arg	Lys	Asn	Pro	Ala	Arg	Thr	Cys	Arg	Asp	Leu	Lys
	1205					1210					1215			
Leu	Cys	His	Pro	Glu	Trp	Lys	Ser	Gly	Asp	Tyr	Trp	Ile	Asp	Pro
	1220					1225					1230			
Asn	Gln	Gly	Cys	Thr	Leu	Asp	Ala	Met	Lys	Val	Phe	Cys	Asn	Met
	1235					1240					1245			
Glu	Thr	Gly	Glu	Thr	Cys	Val	Tyr	Pro	Asn	Pro	Ala	Asn	Val	Pro
	1250					1255					1260			
Lys	Lys	Asn	Trp	Trp	Ser	Ser	Lys	Ser	Lys	Glu	Lys	Lys	His	Ile
	1265					1270					1275			
Trp	Phe	Gly	Glu	Thr	Ile	Asn	Gly	Gly	Phe	His	Phe	Ser	Tyr	Gly
	1280					1285					1290			
Asp	Asp	Asn	Leu	Ala	Pro	Asn	Thr	Ala	Asn	Val	Gln	Met	Thr	Phe
	1295					1300					1305			
Leu	Arg	Leu	Leu	Ser	Thr	Glu	Gly	Ser	Gln	Asn	Ile	Thr	Tyr	His
	1310					1315					1320			
Cys	Lys	Asn	Ser	Ile	Ala	Tyr	Leu	Asp	Glu	Ala	Ala	Gly	Asn	Leu
	1325					1330					1335			
Lys	Lys	Ala	Leu	Leu	Ile	Gln	Gly	Ser	Asn	Asp	Val	Glu	Ile	Arg
	1340					1345					1350			

# FAB-008PC-SequenceListing

Ala Glu Gly Asn Ser Arg Phe Thr Tyr Thr Ala Leu Lys Asp Gly  
1355 1360 1365

Cys Thr Lys His Thr Gly Lys Trp Gly Lys Thr Val Ile Glu Tyr  
1370 1375 1380

Arg Ser Gln Lys Thr Ser Arg Leu Pro Ile Ile Asp Ile Ala Pro  
1385 1390 1395

Met Asp Ile Gly Gly Pro Glu Gln Glu Phe Gly Val Asp Ile Gly  
1400 1405 1410

Pro Val Cys Phe Leu  
1415

<210> 65  
<211> 1466  
<212> PRT  
<213> Homo sapiens

<400> 65

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

His Pro Thr Ile Ile Leu Ala Gln Gln Glu Ala Val Glu Gly Gly Cys  
20 25 30

Ser His Leu Gly Gln Ser Tyr Ala Asp Arg Asp Val Trp Lys Pro Glu  
35 40 45

Pro Cys Gln Ile Cys Val Cys Asp Ser Gly Ser Val Leu Cys Asp Asp  
50 55 60

Ile Ile Cys Asp Asp Gln Glu Leu Asp Cys Pro Asn Pro Glu Ile Pro  
65 70 75 80

Phe Gly Glu Cys Cys Ala Val Cys Pro Gln Pro Pro Thr Ala Pro Thr  
85 90 95

Arg Pro Pro Asn Gly Gln Gly Pro Gln Gly Pro Lys Gly Asp Pro Gly  
100 105 110

Pro Pro Gly Ile Pro Gly Arg Asn Gly Asp Pro Gly Ile Pro Gly Gln  
115 120 125

Pro Gly Ser Pro Gly Ser Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys  
130 135 140

Pro Thr Gly Pro Gln Asn Tyr Ser Pro Gln Tyr Asp Ser Tyr Asp Val  
145 150 155 160

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Lys Ser Gly Val Ala Val Gly Gly Leu Ala Gly Tyr Pro Gly Pro Ala  
 165 170 175  
 Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Thr Ser Gly His Pro Gly  
 180 185 190  
 Ser Pro Gly Ser Pro Gly Tyr Gln Gly Pro Pro Gly Glu Pro Gly Gln  
 195 200 205  
 Ala Gly Pro Ser Gly Pro Pro Gly Pro Pro Gly Ala Ile Gly Pro Ser  
 210 215 220  
 Gly Pro Ala Gly Lys Asp Gly Glu Ser Gly Arg Pro Gly Arg Pro Gly  
 225 230 235 240  
 Glu Arg Gly Leu Pro Gly Pro Pro Gly Ile Lys Gly Pro Ala Gly Ile  
 245 250 255  
 Pro Gly Phe Pro Gly Met Lys Gly His Arg Gly Phe Asp Gly Arg Asn  
 260 265 270  
 Gly Glu Lys Gly Glu Thr Gly Ala Pro Gly Leu Lys Gly Glu Asn Gly  
 275 280 285  
 Leu Pro Gly Glu Asn Gly Ala Pro Gly Pro Met Gly Pro Arg Gly Ala  
 290 295 300  
 Pro Gly Glu Arg Gly Arg Pro Gly Leu Pro Gly Ala Ala Gly Ala Arg  
 305 310 315 320  
 Gly Asn Asp Gly Ala Arg Gly Ser Asp Gly Gln Pro Gly Pro Pro Gly  
 325 330 335  
 Pro Pro Gly Thr Ala Gly Phe Pro Gly Ser Pro Gly Ala Lys Gly Glu  
 340 345 350  
 Val Gly Pro Ala Gly Ser Pro Gly Ser Asn Gly Ala Pro Gly Gln Arg  
 355 360 365  
 Gly Glu Pro Gly Pro Gln Gly His Ala Gly Ala Gln Gly Pro Pro Gly  
 370 375 380  
 Pro Pro Gly Ile Asn Gly Ser Pro Gly Gly Lys Gly Glu Met Gly Pro  
 385 390 395 400  
 Ala Gly Ile Pro Gly Ala Pro Gly Leu Met Gly Ala Arg Gly Pro Pro  
 405 410 415  
 Gly Pro Ala Gly Ala Asn Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly  
 420 425 430

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Glu Pro Gly Lys Asn Gly Ala Lys Gly Glu Pro Gly Pro Arg Gly Glu  
435 440 445

Arg Gly Glu Ala Gly Ile Pro Gly Val Pro Gly Ala Lys Gly Glu Asp  
450 455 460

Gly Lys Asp Gly Ser Pro Gly Glu Pro Gly Ala Asn Gly Leu Pro Gly  
465 470 475 480

Ala Ala Gly Glu Arg Gly Ala Pro Gly Phe Arg Gly Pro Ala Gly Pro  
485 490 495

Asn Gly Ile Pro Gly Glu Lys Gly Pro Ala Gly Glu Arg Gly Ala Pro  
500 505 510

Gly Pro Ala Gly Pro Arg Gly Ala Ala Gly Glu Pro Gly Arg Asp Gly  
515 520 525

Val Pro Gly Gly Pro Gly Met Arg Gly Met Pro Gly Ser Pro Gly Gly  
530 535 540

Pro Gly Ser Asp Gly Lys Pro Gly Pro Pro Gly Ser Gln Gly Glu Ser  
545 550 555 560

Gly Arg Pro Gly Pro Pro Gly Pro Ser Gly Pro Arg Gly Gln Pro Gly  
565 570 575

Val Met Gly Phe Pro Gly Pro Lys Gly Asn Asp Gly Ala Pro Gly Lys  
580 585 590

Asn Gly Glu Arg Gly Gly Pro Gly Gly Pro Gly Pro Gln Gly Pro Pro  
595 600 605

Gly Lys Asn Gly Glu Thr Gly Pro Gln Gly Pro Pro Gly Pro Thr Gly  
610 615 620

Pro Gly Gly Asp Lys Gly Asp Thr Gly Pro Pro Gly Pro Gln Gly Leu  
625 630 635 640

Gln Gly Leu Pro Gly Thr Gly Gly Pro Pro Gly Glu Asn Gly Lys Pro  
645 650 655

Gly Glu Pro Gly Pro Lys Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly  
660 665 670

Gly Lys Gly Asp Ala Gly Ala Pro Gly Glu Arg Gly Pro Pro Gly Leu  
675 680 685

Ala Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly Pro Pro Gly Pro Glu  
690 695 700

# FAB-008PC-SequenceListing

Gly 705 Gly Lys Gly Ala Ala 710 Gly Pro Pro Gly Pro 715 Gly Ala Ala Gly 720  
 Thr Pro Gly Leu Gln 725 Gly Met Pro Gly Glu 730 Arg Gly Gly Leu Gly 735 Ser  
 Pro Gly Pro Lys 740 Gly Asp Lys Gly Glu 745 Pro Gly Gly Pro Gly 750 Ala Asp  
 Gly Val Pro 755 Gly Lys Asp Gly Pro 760 Arg Gly Pro Thr Gly 765 Pro Ile Gly  
 Pro Pro 770 Gly Pro Ala Gly Gln 775 Pro Gly Asp Lys Gly 780 Glu Gly Gly Ala  
 Pro 785 Gly Leu Pro Gly Ile 790 Ala Gly Pro Arg Gly 795 Ser Pro Gly Glu Arg 800  
 Gly Glu Thr Gly Pro 805 Pro Gly Pro Ala Gly 810 Phe Pro Gly Ala Pro Gly 815  
 Gln Asn Gly Glu 820 Pro Gly Gly Lys Gly 825 Glu Arg Gly Ala Pro Gly Glu 830  
 Lys Gly Glu 835 Gly Gly Pro Pro Gly Val 840 Ala Gly Pro Pro Gly Gly Ser 845  
 Gly Pro 850 Ala Gly Pro Pro Gly 855 Pro Gln Gly Val Lys 860 Gly Glu Arg Gly  
 Ser 865 Pro Gly Gly Pro Gly 870 Ala Ala Gly Phe Pro 875 Gly Ala Arg Gly Leu 880  
 Pro Gly Pro Pro Gly 885 Ser Asn Gly Asn Pro 890 Gly Pro Pro Gly Pro 895 Ser  
 Gly Ser Pro Gly 900 Lys Asp Gly Pro Pro 905 Gly Pro Ala Gly Asn Thr Gly 910  
 Ala Pro Gly 915 Ser Pro Gly Val Ser 920 Gly Pro Lys Gly Asp 925 Ala Gly Gln  
 Pro Gly 930 Glu Lys Gly Ser Pro 935 Gly Ala Gln Gly Pro 940 Pro Gly Ala Pro  
 Gly 945 Pro Leu Gly Ile Ala 950 Gly Ile Thr Gly Ala 955 Arg Gly Leu Ala Gly 960  
 Pro Pro Gly Met Pro 965 Gly Pro Arg Gly Ser 970 Pro Gly Pro Gln Gly 975 Val



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Lys Gly Glu Ser Gly Lys Pro Gly Ala Asn Gly Leu Ser Gly Glu Arg  
                   980                                  985                                  990

Gly Pro Pro Gly Pro Gln Gly Leu Pro Gly Leu Ala Gly Thr Ala Gly  
                   995                                  1000                                  1005

Glu Pro Gly Arg Asp Gly Asn Pro Gly Ser Asp Gly Leu Pro Gly  
           1010                                  1015                                  1020

Arg Asp Gly Ser Pro Gly Gly Lys Gly Asp Arg Gly Glu Asn Gly  
           1025                                  1030                                  1035

Ser Pro Gly Ala Pro Gly Ala Pro Gly His Pro Gly Pro Pro Gly  
           1040                                  1045                                  1050

Pro Val Gly Pro Ala Gly Lys Ser Gly Asp Arg Gly Glu Ser Gly  
           1055                                  1060                                  1065

Pro Ala Gly Pro Ala Gly Ala Pro Gly Pro Ala Gly Ser Arg Gly  
           1070                                  1075                                  1080

Ala Pro Gly Pro Gln Gly Pro Arg Gly Asp Lys Gly Glu Thr Gly  
           1085                                  1090                                  1095

Glu Arg Gly Ala Ala Gly Ile Lys Gly His Arg Gly Phe Pro Gly  
           1100                                  1105                                  1110

Asn Pro Gly Ala Pro Gly Ser Pro Gly Pro Ala Gly Gln Gln Gly  
           1115                                  1120                                  1125

Ala Ile Gly Ser Pro Gly Pro Ala Gly Pro Arg Gly Pro Val Gly  
           1130                                  1135                                  1140

Pro Ser Gly Pro Pro Gly Lys Asp Gly Thr Ser Gly His Pro Gly  
           1145                                  1150                                  1155

Pro Ile Gly Pro Pro Gly Pro Arg Gly Asn Arg Gly Glu Arg Gly  
           1160                                  1165                                  1170

Ser Glu Gly Ser Pro Gly His Pro Gly Gln Pro Gly Pro Pro Gly  
           1175                                  1180                                  1185

Pro Pro Gly Ala Pro Gly Pro Cys Cys Gly Gly Val Gly Ala Ala  
           1190                                  1195                                  1200

Ala Ile Ala Gly Ile Gly Gly Glu Lys Ala Gly Gly Phe Ala Pro  
           1205                                  1210                                  1215

Tyr Tyr Gly Asp Glu Pro Met Asp Phe Lys Ile Asn Thr Asp Glu  
           1220                                  1225                                  1230

FAB-008PC-SequenceListing

Ile	Met	Thr	Ser	Leu	Lys	Ser	Val	Asn	Gly	Gln	Ile	Glu	Ser	Leu
	1235					1240					1245			
Ile	Ser	Pro	Asp	Gly	Ser	Arg	Lys	Asn	Pro	Ala	Arg	Asn	Cys	Arg
	1250					1255					1260			
Asp	Leu	Lys	Phe	Cys	His	Pro	Glu	Leu	Lys	Ser	Gly	Glu	Tyr	Trp
	1265					1270					1275			
Val	Asp	Pro	Asn	Gln	Gly	Cys	Lys	Leu	Asp	Ala	Ile	Lys	Val	Phe
	1280					1285					1290			
Cys	Asn	Met	Glu	Thr	Gly	Glu	Thr	Cys	Ile	Ser	Ala	Asn	Pro	Leu
	1295					1300					1305			
Asn	Val	Pro	Arg	Lys	His	Trp	Trp	Thr	Asp	Ser	Ser	Ala	Glu	Lys
	1310					1315					1320			
Lys	His	Val	Trp	Phe	Gly	Glu	Ser	Met	Asp	Gly	Gly	Phe	Gln	Phe
	1325					1330					1335			
Ser	Tyr	Gly	Asn	Pro	Glu	Leu	Pro	Glu	Asp	Val	Leu	Asp	Val	Gln
	1340					1345					1350			
Leu	Ala	Phe	Leu	Arg	Leu	Leu	Ser	Ser	Arg	Ala	Ser	Gln	Asn	Ile
	1355					1360					1365			
Thr	Tyr	His	Cys	Lys	Asn	Ser	Ile	Ala	Tyr	Met	Asp	Gln	Ala	Ser
	1370					1375					1380			
Gly	Asn	Val	Lys	Lys	Ala	Leu	Lys	Leu	Met	Gly	Ser	Asn	Glu	Gly
	1385					1390					1395			
Glu	Phe	Lys	Ala	Glu	Gly	Asn	Ser	Lys	Phe	Thr	Tyr	Thr	Val	Leu
	1400					1405					1410			
Glu	Asp	Gly	Cys	Thr	Lys	His	Thr	Gly	Glu	Trp	Ser	Lys	Thr	Val
	1415					1420					1425			
Phe	Glu	Tyr	Arg	Thr	Arg	Lys	Ala	Val	Arg	Leu	Pro	Ile	Val	Asp
	1430					1435					1440			
Ile	Ala	Pro	Tyr	Asp	Ile	Gly	Gly	Pro	Asp	Gln	Glu	Phe	Gly	Val
	1445					1450					1455			
Asp	Val	Gly	Pro	Val	Cys	Phe	Leu							
	1460					1465								

<210> 66  
 <211> 1669  
 <212> PRT

## FAB-008PC-SequenceListing

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

Met Gly Pro Arg Leu Ser Val Trp Leu Leu Leu Leu Pro Ala Ala Leu  
 1 5 10 15  
 Leu Leu His Glu Glu His Ser Arg Ala Ala Ala Lys Gly Gly Cys Ala  
 20 25 30  
 Gly Ser Gly Cys Gly Lys Cys Asp Cys His Gly Val Lys Gly Gln Lys  
 35 40 45  
 Gly Glu Arg Gly Leu Pro Gly Leu Gln Gly Val Ile Gly Phe Pro Gly  
 50 55 60  
 Met Gln Gly Pro Glu Gly Pro Gln Gly Pro Pro Gly Gln Lys Gly Asp  
 65 70 75 80  
 Thr Gly Glu Pro Gly Leu Pro Gly Thr Lys Gly Thr Arg Gly Pro Pro  
 85 90 95  
 Gly Ala Ser Gly Tyr Pro Gly Asn Pro Gly Leu Pro Gly Ile Pro Gly  
 100 105 110  
 Gln Asp Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly Cys Asn Gly Thr  
 115 120 125  
 Lys Gly Glu Arg Gly Pro Leu Gly Pro Pro Gly Leu Pro Gly Phe Ala  
 130 135 140  
 Gly Asn Pro Gly Pro Pro Gly Leu Pro Gly Met Lys Gly Asp Pro Gly  
 145 150 155 160  
 Glu Ile Leu Gly His Val Pro Gly Met Leu Leu Lys Gly Glu Arg Gly  
 165 170 175  
 Phe Pro Gly Ile Pro Gly Thr Pro Gly Pro Pro Gly Leu Pro Gly Leu  
 180 185 190  
 Gln Gly Pro Val Gly Pro Pro Gly Phe Thr Gly Pro Pro Gly Pro Pro  
 195 200 205  
 Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Gln Met Gly Leu Ser Phe  
 210 215 220  
 Gln Gly Pro Lys Gly Asp Lys Gly Asp Gln Gly Val Ser Gly Pro Pro  
 225 230 235 240  
 Gly Val Pro Gly Gln Ala Gln Val Gln Glu Lys Gly Asp Phe Ala Thr  
 245 250 255

## FAB-008PC-SequenceListing

Lys Gly Glu Lys Gly Gln Lys Gly Glu Pro Gly Phe Gln Gly Met Pro  
 260 265 270  
 Gly Val Gly Glu Lys Gly Glu Pro Gly Lys Pro Gly Pro Arg Gly Lys  
 275 280 285  
 Pro Gly Lys Asp Gly Asp Lys Gly Glu Lys Gly Ser Pro Gly Phe Pro  
 290 295 300  
 Gly Glu Pro Gly Tyr Pro Gly Leu Ile Gly Arg Gln Gly Pro Gln Gly  
 305 310 315 320  
 Glu Lys Gly Glu Ala Gly Pro Pro Gly Pro Gly Ile Val Ile Gly  
 325 330 335  
 Thr Gly Pro Leu Gly Glu Lys Gly Glu Arg Gly Tyr Pro Gly Thr Pro  
 340 345 350  
 Gly Pro Arg Gly Glu Pro Gly Pro Lys Gly Phe Pro Gly Leu Pro Gly  
 355 360 365  
 Gln Pro Gly Pro Pro Gly Leu Pro Val Pro Gly Gln Ala Gly Ala Pro  
 370 375 380  
 Gly Phe Pro Gly Glu Arg Gly Glu Lys Gly Asp Arg Gly Phe Pro Gly  
 385 390 395 400  
 Thr Ser Leu Pro Gly Pro Ser Gly Arg Asp Gly Leu Pro Gly Pro Pro  
 405 410 415  
 Gly Ser Pro Gly Pro Pro Gly Gln Pro Gly Tyr Thr Asn Gly Ile Val  
 420 425 430  
 Glu Cys Gln Pro Gly Pro Pro Gly Asp Gln Gly Pro Pro Gly Ile Pro  
 435 440 445  
 Gly Gln Pro Gly Phe Ile Gly Glu Ile Gly Glu Lys Gly Gln Lys Gly  
 450 455 460  
 Glu Ser Cys Leu Ile Cys Asp Ile Asp Gly Tyr Arg Gly Pro Pro Gly  
 465 470 475 480  
 Pro Gln Gly Pro Pro Gly Glu Ile Gly Phe Pro Gly Gln Pro Gly Ala  
 485 490 495  
 Lys Gly Asp Arg Gly Leu Pro Gly Arg Asp Gly Val Ala Gly Val Pro  
 500 505 510  
 Gly Pro Gln Gly Thr Pro Gly Leu Ile Gly Gln Pro Gly Ala Lys Gly  
 515 520 525

## FAB-008PC-SequenceListing

Glu Pro Gly Glu Phe Tyr Phe Asp Leu Arg Leu Lys Gly Asp Lys Gly  
 530 535 540

Asp Pro Gly Phe Pro Gly Gln Pro Gly Met Thr Gly Arg Ala Gly Ser  
 545 550 555 560

Pro Gly Arg Asp Gly His Pro Gly Leu Pro Gly Pro Lys Gly Ser Pro  
 565 570 575

Gly Ser Val Gly Leu Lys Gly Glu Arg Gly Pro Pro Gly Gly Val Gly  
 580 585 590

Phe Pro Gly Ser Arg Gly Asp Thr Gly Pro Pro Gly Pro Pro Gly Tyr  
 595 600 605

Gly Pro Ala Gly Pro Ile Gly Asp Lys Gly Gln Ala Gly Phe Pro Gly  
 610 615 620

Gly Pro Gly Ser Pro Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Lys  
 625 630 635 640

Ile Val Pro Leu Pro Gly Pro Pro Gly Ala Glu Gly Leu Pro Gly Ser  
 645 650 655

Pro Gly Phe Pro Gly Pro Gln Gly Asp Arg Gly Phe Pro Gly Thr Pro  
 660 665 670

Gly Arg Pro Gly Leu Pro Gly Glu Lys Gly Ala Val Gly Gln Pro Gly  
 675 680 685

Ile Gly Phe Pro Gly Pro Pro Gly Pro Lys Gly Val Asp Gly Leu Pro  
 690 695 700

Gly Asp Met Gly Pro Pro Gly Thr Pro Gly Arg Pro Gly Phe Asn Gly  
 705 710 715 720

Leu Pro Gly Asn Pro Gly Val Gln Gly Gln Lys Gly Glu Pro Gly Val  
 725 730 735

Gly Leu Pro Gly Leu Lys Gly Leu Pro Gly Leu Pro Gly Ile Pro Gly  
 740 745 750

Thr Pro Gly Glu Lys Gly Ser Ile Gly Val Pro Gly Val Pro Gly Glu  
 755 760 765

His Gly Ala Ile Gly Pro Pro Gly Leu Gln Gly Ile Arg Gly Glu Pro  
 770 775 780

Gly Pro Pro Gly Leu Pro Gly Ser Val Gly Ser Pro Gly Val Pro Gly  
 785 790 795 800

FAB-008PC-SequenceListing

Ile Gly Pro Pro Gly Ala Arg Gly Pro Gly Gly Gln Gly Pro Pro  
805 810 815

Gly Leu Ser Gly Pro Pro Gly Ile Lys Gly Glu Lys Gly Phe Pro Gly  
820 825 830

Phe Pro Gly Leu Asp Met Pro Gly Pro Lys Gly Asp Lys Gly Ala Gln  
835 840 845

Gly Leu Pro Gly Ile Thr Gly Gln Ser Gly Leu Pro Gly Leu Pro Gly  
850 855 860

Gln Gln Gly Ala Pro Gly Ile Pro Gly Phe Pro Gly Ser Lys Gly Glu  
865 870 875 880

Met Gly Val Met Gly Thr Pro Gly Gln Pro Gly Ser Pro Gly Pro Val  
885 890 895

Gly Ala Pro Gly Leu Pro Gly Glu Lys Gly Asp His Gly Phe Pro Gly  
900 905 910

Ser Ser Gly Pro Arg Gly Asp Pro Gly Leu Lys Gly Asp Lys Gly Asp  
915 920 925

Val Gly Leu Pro Gly Lys Pro Gly Ser Met Asp Lys Val Asp Met Gly  
930 935 940

Ser Met Lys Gly Gln Lys Gly Asp Gln Gly Glu Lys Gly Gln Ile Gly  
945 950 955 960

Pro Ile Gly Glu Lys Gly Ser Arg Gly Asp Pro Gly Thr Pro Gly Val  
965 970 975

Pro Gly Lys Asp Gly Gln Ala Gly Gln Pro Gly Gln Pro Gly Pro Lys  
980 985 990

Gly Asp Pro Gly Ile Ser Gly Thr Pro Gly Ala Pro Gly Leu Pro Gly  
995 1000 1005

Pro Lys Gly Ser Val Gly Gly Met Gly Leu Pro Gly Thr Pro Gly  
1010 1015 1020

Glu Lys Gly Val Pro Gly Ile Pro Gly Pro Gln Gly Ser Pro Gly  
1025 1030 1035

Leu Pro Gly Asp Lys Gly Ala Lys Gly Glu Lys Gly Gln Ala Gly  
1040 1045 1050

Pro Pro Gly Ile Gly Ile Pro Gly Leu Arg Gly Glu Lys Gly Asp  
1055 1060 1065

## FAB-008PC-SequenceListing

Gln Gly Ile Ala Gly Phe Pro Gly Ser Pro Gly Glu Lys Gly Glu  
 1070 1075 1080  
 Lys Gly Ser Ile Gly Ile Pro Gly Met Pro Gly Ser Pro Gly Leu  
 1085 1090 1095  
 Lys Gly Ser Pro Gly Ser Val Gly Tyr Pro Gly Ser Pro Gly Leu  
 1100 1105 1110  
 Pro Gly Glu Lys Gly Asp Lys Gly Leu Pro Gly Leu Asp Gly Ile  
 1115 1120 1125  
 Pro Gly Val Lys Gly Glu Ala Gly Leu Pro Gly Thr Pro Gly Pro  
 1130 1135 1140  
 Thr Gly Pro Ala Gly Gln Lys Gly Glu Pro Gly Ser Asp Gly Ile  
 1145 1150 1155  
 Pro Gly Ser Ala Gly Glu Lys Gly Glu Pro Gly Leu Pro Gly Arg  
 1160 1165 1170  
 Gly Phe Pro Gly Phe Pro Gly Ala Lys Gly Asp Lys Gly Ser Lys  
 1175 1180 1185  
 Gly Glu Val Gly Phe Pro Gly Leu Ala Gly Ser Pro Gly Ile Pro  
 1190 1195 1200  
 Gly Ser Lys Gly Glu Gln Gly Phe Met Gly Pro Pro Gly Pro Gln  
 1205 1210 1215  
 Gly Gln Pro Gly Leu Pro Gly Ser Pro Gly His Ala Thr Glu Gly  
 1220 1225 1230  
 Pro Lys Gly Asp Arg Gly Pro Gln Gly Gln Pro Gly Leu Pro Gly  
 1235 1240 1245  
 Leu Pro Gly Pro Met Gly Pro Pro Gly Leu Pro Gly Ile Asp Gly  
 1250 1255 1260  
 Val Lys Gly Asp Lys Gly Asn Pro Gly Trp Pro Gly Ala Pro Gly  
 1265 1270 1275  
 Val Pro Gly Pro Lys Gly Asp Pro Gly Phe Gln Gly Met Pro Gly  
 1280 1285 1290  
 Ile Gly Gly Ser Pro Gly Ile Thr Gly Ser Lys Gly Asp Met Gly  
 1295 1300 1305  
 Pro Pro Gly Val Pro Gly Phe Gln Gly Pro Lys Gly Leu Pro Gly  
 1310 1315 1320

## FAB-008PC-SequenceListing

Leu Gln Gly Ile Lys Gly Asp Gln Gly Asp Gln Gly Val Pro Gly  
 1325 1330 1335  
 Ala Lys Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Pro Tyr Asp  
 1340 1345 1350  
 Ile Ile Lys Gly Glu Pro Gly Leu Pro Gly Pro Glu Gly Pro Pro  
 1355 1360 1365  
 Gly Leu Lys Gly Leu Gln Gly Leu Pro Gly Pro Lys Gly Gln Gln  
 1370 1375 1380  
 Gly Val Thr Gly Leu Val Gly Ile Pro Gly Pro Pro Gly Ile Pro  
 1385 1390 1395  
 Gly Phe Asp Gly Ala Pro Gly Gln Lys Gly Glu Met Gly Pro Ala  
 1400 1405 1410  
 Gly Pro Thr Gly Pro Arg Gly Phe Pro Gly Pro Pro Gly Pro Asp  
 1415 1420 1425  
 Gly Leu Pro Gly Ser Met Gly Pro Pro Gly Thr Pro Ser Val Asp  
 1430 1435 1440  
 His Gly Phe Leu Val Thr Arg His Ser Gln Thr Ile Asp Asp Pro  
 1445 1450 1455  
 Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser Leu  
 1460 1465 1470  
 Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly  
 1475 1480 1485  
 Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu  
 1490 1495 1500  
 Phe Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp  
 1505 1510 1515  
 Tyr Ser Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met  
 1520 1525 1530  
 Ala Pro Ile Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys  
 1535 1540 1545  
 Ala Val Cys Glu Ala Pro Ala Met Val Met Ala Val His Ser Gln  
 1550 1555 1560  
 Thr Ile Gln Ile Pro Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp  
 1565 1570 1575



# FAB-008PC-SequenceListing

Ile Gly Tyr Ser Phe Val Met His Thr Ser Ala Gly Ala Glu Gly  
1580 1585 1590

Ser Gly Gln Ala Leu Ala Ser Pro Gly Ser Cys Leu Glu Glu Phe  
1595 1600 1605

Arg Ser Ala Pro Phe Ile Glu Cys His Gly Arg Gly Thr Cys Asn  
1610 1615 1620

Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp Leu Ala Thr Ile Glu Arg  
1625 1630 1635

Ser Glu Met Phe Lys Lys Pro Thr Pro Ser Thr Leu Lys Ala Gly  
1640 1645 1650

Glu Leu Arg Thr His Val Ser Arg Cys Gln Val Cys Met Arg Arg  
1655 1660 1665

Thr

<210> 67  
<211> 1712  
<212> PRT  
<213> Homo sapiens

<400> 67

Met Gly Arg Asp Gln Arg Ala Val Ala Gly Pro Ala Leu Arg Arg Trp  
1 5 10 15

Leu Leu Leu Gly Thr Val Thr Val Gly Phe Leu Ala Gln Ser Val Leu  
20 25 30

Ala Gly Val Lys Lys Phe Asp Val Pro Cys Gly Gly Arg Asp Cys Ser  
35 40 45

Gly Gly Cys Gln Cys Tyr Pro Glu Lys Gly Gly Arg Gly Gln Pro Gly  
50 55 60

Pro Val Gly Pro Gln Gly Tyr Asn Gly Pro Pro Gly Leu Gln Gly Phe  
65 70 75 80

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

Gly Val Thr Gly Pro Lys Gly Asp Val Gly Ala Arg Gly Val Ser Gly  
100 105 110

Phe Pro Gly Ala Asp Gly Ile Pro Gly His Pro Gly Gln Gly Gly Pro  
115 120 125

Arg Gly Arg Pro Gly Tyr Asp Gly Cys Asn Gly Thr Gln Gly Asp Ser

## FAB-008PC-SequenceListing

130

135

140

Gly Pro Gln Gly Pro Pro Gly Ser Glu Gly Phe Thr Gly Pro Pro Gly  
 145 150 155 160

Pro Gln Gly Pro Lys Gly Gln Lys Gly Glu Pro Tyr Ala Leu Pro Lys  
 165 170 175

Glu Glu Arg Asp Arg Tyr Arg Gly Glu Pro Gly Glu Pro Gly Leu Val  
 180 185 190

Gly Phe Gln Gly Pro Pro Gly Arg Pro Gly His Val Gly Gln Met Gly  
 195 200 205

Pro Val Gly Ala Pro Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Pro  
 210 215 220

Lys Gly Gln Gln Gly Asn Arg Gly Leu Gly Phe Tyr Gly Val Lys Gly  
 225 230 235 240

Glu Lys Gly Asp Val Gly Gln Pro Gly Pro Asn Gly Ile Pro Ser Asp  
 245 250 255

Thr Leu His Pro Ile Ile Ala Pro Thr Gly Val Thr Phe His Pro Asp  
 260 265 270

Gln Tyr Lys Gly Glu Lys Gly Ser Glu Gly Glu Pro Gly Ile Arg Gly  
 275 280 285

Ile Ser Leu Lys Gly Glu Glu Gly Ile Met Gly Phe Pro Gly Leu Arg  
 290 295 300

Gly Tyr Pro Gly Leu Ser Gly Glu Lys Gly Ser Pro Gly Gln Lys Gly  
 305 310 315 320

Ser Arg Gly Leu Asp Gly Tyr Gln Gly Pro Asp Gly Pro Arg Gly Pro  
 325 330 335

Lys Gly Glu Ala Gly Asp Pro Gly Pro Gly Leu Pro Ala Tyr Ser  
 340 345 350

Pro His Pro Ser Leu Ala Lys Gly Ala Arg Gly Asp Pro Gly Phe Pro  
 355 360 365

Gly Ala Gln Gly Glu Pro Gly Ser Gln Gly Glu Pro Gly Asp Pro Gly  
 370 375 380

Leu Pro Gly Pro Pro Gly Leu Ser Ile Gly Asp Gly Asp Gln Arg Arg  
 385 390 395 400

Gly Leu Pro Gly Glu Met Gly Pro Lys Gly Phe Ile Gly Asp Pro Gly  
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405

410

415

Ile Pro Ala Leu Tyr Gly Gly Pro Pro Gly Pro Asp Gly Lys Arg Gly  
420 425 430

Pro Pro Gly Pro Pro Gly Leu Pro Gly Pro Pro Gly Pro Asp Gly Phe  
435 440 445

Leu Phe Gly Leu Lys Gly Ala Lys Gly Arg Ala Gly Phe Pro Gly Leu  
450 455 460

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

Gly Glu Cys Arg Cys Thr Glu Gly Asp Glu Ala Ile Lys Gly Leu Pro  
485 490 495

Gly Leu Pro Gly Pro Lys Gly Phe Ala Gly Ile Asn Gly Glu Pro Gly  
500 505 510

Arg Lys Gly Asp Arg Gly Asp Pro Gly Gln His Gly Leu Pro Gly Phe  
515 520 525

Pro Gly Leu Lys Gly Val Pro Gly Asn Ile Gly Ala Pro Gly Pro Lys  
530 535 540

Gly Ala Lys Gly Asp Ser Arg Thr Ile Thr Thr Lys Gly Glu Arg Gly  
545 550 555 560

Gln Pro Gly Val Pro Gly Val Pro Gly Met Lys Gly Asp Asp Gly Ser  
565 570 575

Pro Gly Arg Asp Gly Leu Asp Gly Phe Pro Gly Leu Pro Gly Pro Pro  
580 585 590

Gly Asp Gly Ile Lys Gly Pro Pro Gly Asp Pro Gly Tyr Pro Gly Ile  
595 600 605

Pro Gly Thr Lys Gly Thr Pro Gly Glu Met Gly Pro Pro Gly Leu Gly  
610 615 620

Leu Pro Gly Leu Lys Gly Gln Arg Gly Phe Pro Gly Asp Ala Gly Leu  
625 630 635 640

Pro Gly Pro Pro Gly Phe Leu Gly Pro Pro Gly Pro Ala Gly Thr Pro  
645 650 655

Gly Gln Ile Asp Cys Asp Thr Asp Val Lys Arg Ala Val Gly Gly Asp  
660 665 670

Arg Gln Glu Ala Ile Gln Pro Gly Cys Ile Gly Gly Pro Lys Gly Leu

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675

680

685

Pro Gly Leu Pro Gly Pro Pro Gly Pro Thr Gly Ala Lys Gly Leu Arg  
690 695 700

Gly Ile Pro Gly Phe Ala Gly Ala Asp Gly Gly Pro Gly Pro Arg Gly  
705 710 715 720

Leu Pro Gly Asp Ala Gly Arg Glu Gly Phe Pro Gly Pro Pro Gly Phe  
725 730 735

Ile Gly Pro Arg Gly Ser Lys Gly Ala Val Gly Leu Pro Gly Pro Asp  
740 745 750

Gly Ser Pro Gly Pro Ile Gly Leu Pro Gly Pro Asp Gly Pro Pro Gly  
755 760 765

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

Gly Asp Ala Gly Val Pro Gly Gln Pro Gly Leu Lys Gly Leu Pro Gly  
785 790 795 800

Asp Arg Gly Pro Pro Gly Phe Arg Gly Ser Gln Gly Met Pro Gly Met  
805 810 815

Pro Gly Leu Lys Gly Gln Pro Gly Leu Pro Gly Pro Ser Gly Gln Pro  
820 825 830

Gly Leu Tyr Gly Pro Pro Gly Leu His Gly Phe Pro Gly Ala Pro Gly  
835 840 845

Gln Glu Gly Pro Leu Gly Leu Pro Gly Ile Pro Gly Arg Glu Gly Leu  
850 855 860

Pro Gly Asp Arg Gly Asp Pro Gly Asp Thr Gly Ala Pro Gly Pro Val  
865 870 875 880

Gly Met Lys Gly Leu Ser Gly Asp Arg Gly Asp Ala Gly Phe Thr Gly  
885 890 895

Glu Gln Gly His Pro Gly Ser Pro Gly Phe Lys Gly Ile Asp Gly Met  
900 905 910

Pro Gly Thr Pro Gly Leu Lys Gly Asp Arg Gly Ser Pro Gly Met Asp  
915 920 925

Gly Phe Gln Gly Met Pro Gly Leu Lys Gly Arg Pro Gly Phe Pro Gly  
930 935 940

Ser Lys Gly Glu Ala Gly Phe Phe Gly Ile Pro Gly Leu Lys Gly Leu

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FAB-008PC-SequenceListing															
945				950				955				960			
Ala	Gly	Glu	Pro	Gly 965	Phe	Lys	Gly	Ser	Arg 970	Gly	Asp	Pro	Gly	Pro 975	Pro
Gly	Pro	Pro	Pro	Val 980	Ile	Leu	Pro	Gly 985	Met	Lys	Asp	Ile	Lys 990	Gly	Glu
Lys	Gly	Asp 995	Glu	Gly	Pro	Met	Gly 1000	Leu	Lys	Gly	Tyr	Leu 1005	Gly	Ala	Lys
Gly	Ile 1010	Gln	Gly	Met	Pro	Gly 1015	Ile	Pro	Gly	Leu	Ser 1020	Gly	Ile	Pro	
Gly	Leu 1025	Pro	Gly	Arg	Pro	Gly 1030	His	Ile	Lys	Gly	Val 1035	Lys	Gly	Asp	
Ile	Gly 1040	Val	Pro	Gly	Ile	Pro 1045	Gly	Leu	Pro	Gly	Phe 1050	Pro	Gly	Val	
Ala	Gly 1055	Pro	Pro	Gly	Ile	Thr 1060	Gly	Phe	Pro	Gly	Phe 1065	Ile	Gly	Ser	
Arg	Gly 1070	Asp	Lys	Gly	Ala	Pro 1075	Gly	Arg	Ala	Gly	Leu 1080	Tyr	Gly	Glu	
Ile	Gly 1085	Ala	Thr	Gly	Asp	Phe 1090	Gly	Asp	Ile	Gly	Asp 1095	Thr	Ile	Asn	
Leu	Pro 1100	Gly	Arg	Pro	Gly	Leu 1105	Lys	Gly	Glu	Arg	Gly 1110	Thr	Thr	Gly	
Ile	Pro 1115	Gly	Leu	Lys	Gly	Phe 1120	Phe	Gly	Glu	Lys	Gly 1125	Thr	Glu	Gly	
Asp	Ile 1130	Gly	Phe	Pro	Gly	Ile 1135	Thr	Gly	Val	Thr	Gly 1140	Val	Gln	Gly	
Pro	Pro 1145	Gly	Leu	Lys	Gly	Gln 1150	Thr	Gly	Phe	Pro	Gly 1155	Leu	Thr	Gly	
Pro	Pro 1160	Gly	Ser	Gln	Gly	Glu 1165	Leu	Gly	Arg	Ile	Gly 1170	Leu	Pro	Gly	
Gly	Lys 1175	Gly	Asp	Asp	Gly	Trp 1180	Pro	Gly	Ala	Pro	Gly 1185	Leu	Pro	Gly	
Phe	Pro 1190	Gly	Leu	Arg	Gly	Ile 1195	Arg	Gly	Leu	His	Gly 1200	Leu	Pro	Gly	
Thr	Lys	Gly	Phe	Pro	Gly	Ser	Pro	Gly	Ser	Asp	Ile	His	Gly	Asp	

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1205						1210						1215			
Pro	Gly	Phe	Pro	Gly	Pro	Pro	Gly	Glu	Arg	Gly	Asp	Pro	Gly	Glu	
	1220					1225					1230				
Ala	Asn	Thr	Leu	Pro	Gly	Pro	Val	Gly	Val	Pro	Gly	Gln	Lys	Gly	
	1235					1240					1245				
Asp	Gln	Gly	Ala	Pro	Gly	Glu	Arg	Gly	Pro	Pro	Gly	Ser	Pro	Gly	
	1250					1255					1260				
Leu	Gln	Gly	Phe	Pro	Gly	Ile	Thr	Pro	Pro	Ser	Asn	Ile	Ser	Gly	
	1265					1270					1275				
Ala	Pro	Gly	Asp	Lys	Gly	Ala	Pro	Gly	Ile	Phe	Gly	Leu	Lys	Gly	
	1280					1285					1290				
Tyr	Arg	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ser	Ala	Ala	Leu	Pro	Gly	
	1295					1300					1305				
Ser	Lys	Gly	Asp	Thr	Gly	Asn	Pro	Gly	Ala	Pro	Gly	Thr	Pro	Gly	
	1310					1315					1320				
Thr	Lys	Gly	Trp	Ala	Gly	Asp	Ser	Gly	Pro	Gln	Gly	Arg	Pro	Gly	
	1325					1330					1335				
Val	Phe	Gly	Leu	Pro	Gly	Glu	Lys	Gly	Pro	Arg	Gly	Glu	Gln	Gly	
	1340					1345					1350				
Phe	Met	Gly	Asn	Thr	Gly	Pro	Thr	Gly	Ala	Val	Gly	Asp	Arg	Gly	
	1355					1360					1365				
Pro	Lys	Gly	Pro	Lys	Gly	Asp	Pro	Gly	Phe	Pro	Gly	Ala	Pro	Gly	
	1370					1375					1380				
Thr	Val	Gly	Ala	Pro	Gly	Ile	Ala	Gly	Ile	Pro	Gln	Lys	Ile	Ala	
	1385					1390					1395				
Val	Gln	Pro	Gly	Thr	Val	Gly	Pro	Gln	Gly	Arg	Arg	Gly	Pro	Pro	
	1400					1405					1410				
Gly	Ala	Pro	Gly	Glu	Met	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Glu	Pro	
	1415					1420					1425				
Gly	Phe	Arg	Gly	Ala	Pro	Gly	Lys	Ala	Gly	Pro	Gln	Gly	Arg	Gly	
	1430					1435					1440				
Gly	Val	Ser	Ala	Val	Pro	Gly	Phe	Arg	Gly	Asp	Glu	Gly	Pro	Ile	
	1445					1450					1455				
Gly	His	Gln	Gly	Pro	Ile	Gly	Gln	Glu	Gly	Ala	Pro	Gly	Arg	Pro	

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1460														
Gly	Ser	Pro	Gly	Leu	Pro	Gly	Met	Pro	Gly	Arg	Ser	Val	Ser	Ile
1475						1480					1485			
Gly	Tyr	Leu	Leu	Val	Lys	His	Ser	Gln	Thr	Asp	Gln	Glu	Pro	Met
1490						1495					1500			
Cys	Pro	Val	Gly	Met	Asn	Lys	Leu	Trp	Ser	Gly	Tyr	Ser	Leu	Leu
1505						1510					1515			
Tyr	Phe	Glu	Gly	Gln	Glu	Lys	Ala	His	Asn	Gln	Asp	Leu	Gly	Leu
1520						1525					1530			
Ala	Gly	Ser	Cys	Leu	Ala	Arg	Phe	Ser	Thr	Met	Pro	Phe	Leu	Tyr
1535						1540					1545			
Cys	Asn	Pro	Gly	Asp	Val	Cys	Tyr	Tyr	Ala	Ser	Arg	Asn	Asp	Lys
1550						1555					1560			
Ser	Tyr	Trp	Leu	Ser	Thr	Thr	Ala	Pro	Leu	Pro	Met	Met	Pro	Val
1565						1570					1575			
Ala	Glu	Asp	Glu	Ile	Lys	Pro	Tyr	Ile	Ser	Arg	Cys	Ser	Val	Cys
1580						1585					1590			
Glu	Ala	Pro	Ala	Ile	Ala	Ile	Ala	Val	His	Ser	Gln	Asp	Val	Ser
1595						1600					1605			
Ile	Pro	His	Cys	Pro	Ala	Gly	Trp	Arg	Ser	Leu	Trp	Ile	Gly	Tyr
1610						1615					1620			
Ser	Phe	Leu	Met	His	Thr	Ala	Ala	Gly	Asp	Glu	Gly	Gly	Gly	Gln
1625						1630					1635			
Ser	Leu	Val	Ser	Pro	Gly	Ser	Cys	Leu	Glu	Asp	Phe	Arg	Ala	Thr
1640						1645					1650			
Pro	Phe	Ile	Glu	Cys	Asn	Gly	Gly	Arg	Gly	Thr	Cys	His	Tyr	Tyr
1655						1660					1665			
Ala	Asn	Lys	Tyr	Ser	Phe	Trp	Leu	Thr	Thr	Ile	Pro	Glu	Gln	Ser
1670						1675					1680			
Phe	Gln	Gly	Ser	Pro	Ser	Ala	Asp	Thr	Leu	Lys	Ala	Gly	Leu	Ile
1685						1690					1695			
Arg	Thr	His	Ile	Ser	Arg	Cys	Gln	Val	Cys	Met	Lys	Asn	Leu	
1700						1705					1710			

&lt;210&gt; 68

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<211> 1670  
 <212> PRT  
 <213> Homo sapiens

<400> 68

Met Ser Ala Arg Thr Ala Pro Arg Pro Gln Val Leu Leu Leu Pro Leu  
 1 5 10 15

Leu Leu Val Leu Leu Ala Ala Ala Pro Ala Ala Ser Lys Gly Cys Val  
 20 25 30

Cys Lys Asp Lys Gly Gln Cys Phe Cys Asp Gly Ala Lys Gly Glu Lys  
 35 40 45

Gly Glu Lys Gly Phe Pro Gly Pro Pro Gly Ser Pro Gly Gln Lys Gly  
 50 55 60

Phe Thr Gly Pro Glu Gly Leu Pro Gly Pro Gln Gly Pro Lys Gly Phe  
 65 70 75 80

Pro Gly Leu Pro Gly Leu Thr Gly Ser Lys Gly Val Arg Gly Ile Ser  
 85 90 95

Gly Leu Pro Gly Phe Ser Gly Ser Pro Gly Leu Pro Gly Thr Pro Gly  
 100 105 110

Asn Thr Gly Pro Tyr Gly Leu Val Gly Val Pro Gly Cys Ser Gly Ser  
 115 120 125

Lys Gly Glu Gln Gly Phe Pro Gly Leu Pro Gly Thr Leu Gly Tyr Pro  
 130 135 140

Gly Ile Pro Gly Ala Ala Gly Leu Lys Gly Gln Lys Gly Ala Pro Ala  
 145 150 155 160

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

Gly Ala Pro Gly Pro Gln Gly Leu Pro Gly Pro Pro Gly Phe Pro Gly  
 180 185 190

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

Met Gly Pro Arg Gly Pro Lys Gly His Met Gly Glu Arg Val Ile Gly  
 210 215 220

His Lys Gly Glu Arg Gly Val Lys Gly Leu Thr Gly Pro Pro Gly Pro  
 225 230 235 240

Pro Gly Thr Val Ile Val Thr Leu Thr Gly Pro Asp Asn Arg Thr Asp  
 245 250 255



# FAB-008PC-SequenceListing

Leu Lys Gly Glu Lys Gly Asp Lys Gly Ala Met Gly Glu Pro Gly Pro  
 260 265 270  
 Pro Gly Pro Ser Gly Leu Pro Gly Glu Ser Tyr Gly Ser Glu Lys Gly  
 275 280 285  
 Ala Pro Gly Asp Pro Gly Leu Gln Gly Lys Pro Gly Lys Asp Gly Val  
 290 295 300  
 Pro Gly Phe Pro Gly Ser Glu Gly Val Lys Gly Asn Arg Gly Phe Pro  
 305 310 315 320  
 Gly Leu Met Gly Glu Asp Gly Ile Lys Gly Gln Lys Gly Asp Ile Gly  
 325 330 335  
 Pro Pro Gly Phe Arg Gly Pro Thr Glu Tyr Tyr Asp Thr Tyr Gln Glu  
 340 345 350  
 Lys Gly Asp Glu Gly Thr Pro Gly Pro Pro Gly Pro Arg Gly Ala Arg  
 355 360 365  
 Gly Pro Gln Gly Pro Ser Gly Pro Pro Gly Val Pro Gly Ser Pro Gly  
 370 375 380  
 Ser Ser Arg Pro Gly Leu Arg Gly Ala Pro Gly Trp Pro Gly Leu Lys  
 385 390 395 400  
 Gly Ser Lys Gly Glu Arg Gly Arg Pro Gly Lys Asp Ala Met Gly Thr  
 405 410 415  
 Pro Gly Ser Pro Gly Cys Ala Gly Ser Pro Gly Leu Pro Gly Ser Pro  
 420 425 430  
 Gly Pro Pro Gly Pro Pro Gly Asp Ile Val Phe Arg Lys Gly Pro Pro  
 435 440 445  
 Gly Asp His Gly Leu Pro Gly Tyr Leu Gly Ser Pro Gly Ile Pro Gly  
 450 455 460  
 Val Asp Gly Pro Lys Gly Glu Pro Gly Leu Leu Cys Thr Gln Cys Pro  
 465 470 475 480  
 Tyr Ile Pro Gly Pro Pro Gly Leu Pro Gly Leu Pro Gly Leu His Gly  
 485 490 495  
 Val Lys Gly Ile Pro Gly Arg Gln Gly Ala Ala Gly Leu Lys Gly Ser  
 500 505 510  
 Pro Gly Ser Pro Gly Asn Thr Gly Leu Pro Gly Phe Pro Gly Phe Pro  
 515 520 525

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Gly Ala Gln Gly Asp Pro Gly Leu Lys Gly Glu Lys Gly Glu Thr Leu  
 530 535 540  
 Gln Pro Glu Gly Gln Val Gly Val Pro Gly Asp Pro Gly Leu Arg Gly  
 545 550 555 560  
 Gln Pro Gly Arg Lys Gly Leu Asp Gly Ile Pro Gly Thr Pro Gly Val  
 565 570 575  
 Lys Gly Leu Pro Gly Pro Lys Gly Glu Leu Ala Leu Ser Gly Glu Lys  
 580 585 590  
 Gly Asp Gln Gly Pro Pro Gly Asp Pro Gly Ser Pro Gly Ser Pro Gly  
 595 600 605  
 Pro Ala Gly Pro Ala Gly Pro Pro Gly Tyr Gly Pro Gln Gly Glu Pro  
 610 615 620  
 Gly Leu Gln Gly Thr Gln Gly Val Pro Gly Ala Pro Gly Pro Pro Gly  
 625 630 635 640  
 Glu Ala Gly Pro Arg Gly Glu Leu Ser Val Ser Thr Pro Val Pro Gly  
 645 650 655  
 Pro Pro Gly Pro Pro Gly Pro Pro Gly His Pro Gly Pro Gln Gly Pro  
 660 665 670  
 Pro Gly Ile Pro Gly Ser Leu Gly Lys Cys Gly Asp Pro Gly Leu Pro  
 675 680 685  
 Gly Pro Asp Gly Glu Pro Gly Ile Pro Gly Ile Gly Phe Pro Gly Pro  
 690 695 700  
 Pro Gly Pro Lys Gly Asp Gln Gly Phe Pro Gly Thr Lys Gly Ser Leu  
 705 710 715 720  
 Gly Cys Pro Gly Lys Met Gly Glu Pro Gly Leu Pro Gly Lys Pro Gly  
 725 730 735  
 Leu Pro Gly Ala Lys Gly Glu Pro Ala Val Ala Met Pro Gly Gly Pro  
 740 745 750  
 Gly Thr Pro Gly Phe Pro Gly Glu Arg Gly Asn Ser Gly Glu His Gly  
 755 760 765  
 Glu Ile Gly Leu Pro Gly Leu Pro Gly Leu Pro Gly Thr Pro Gly Asn  
 770 775 780  
 Glu Gly Leu Asp Gly Pro Arg Gly Asp Pro Gly Gln Pro Gly Pro Pro  
 785 790 795 800

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Gly Glu Gln Gly Pro Pro Gly Arg Cys Ile Glu Gly Pro Arg Gly Ala  
 805 810 815  
 Gln Gly Leu Pro Gly Leu Asn Gly Leu Lys Gly Gln Gln Gly Arg Arg  
 820 825 830  
 Gly Lys Thr Gly Pro Lys Gly Asp Pro Gly Ile Pro Gly Leu Asp Arg  
 835 840 845  
 Ser Gly Phe Pro Gly Glu Thr Gly Ser Pro Gly Ile Pro Gly His Gln  
 850 855 860  
 Gly Glu Met Gly Pro Leu Gly Gln Arg Gly Tyr Pro Gly Asn Pro Gly  
 865 870 875 880  
 Ile Leu Gly Pro Pro Gly Glu Asp Gly Val Ile Gly Met Met Gly Phe  
 885 890 895  
 Pro Gly Ala Ile Gly Pro Pro Gly Pro Pro Gly Asn Pro Gly Thr Pro  
 900 905 910  
 Gly Gln Arg Gly Ser Pro Gly Ile Pro Gly Val Lys Gly Gln Arg Gly  
 915 920 925  
 Thr Pro Gly Ala Lys Gly Glu Gln Gly Asp Lys Gly Asn Pro Gly Pro  
 930 935 940  
 Ser Glu Ile Ser His Val Ile Gly Asp Lys Gly Glu Pro Gly Leu Lys  
 945 950 955 960  
 Gly Phe Ala Gly Asn Pro Gly Glu Lys Gly Asn Arg Gly Val Pro Gly  
 965 970 975  
 Met Pro Gly Leu Lys Gly Leu Lys Gly Leu Pro Gly Pro Ala Gly Pro  
 980 985 990  
 Pro Gly Pro Arg Gly Asp Leu Gly Ser Thr Gly Asn Pro Gly Glu Pro  
 995 1000 1005  
 Gly Leu Arg Gly Ile Pro Gly Ser Met Gly Asn Met Gly Met Pro  
 1010 1015 1020  
 Gly Ser Lys Gly Lys Arg Gly Thr Leu Gly Phe Pro Gly Arg Ala  
 1025 1030 1035  
 Gly Arg Pro Gly Leu Pro Gly Ile His Gly Leu Gln Gly Asp Lys  
 1040 1045 1050  
 Gly Glu Pro Gly Tyr Ser Glu Gly Thr Arg Pro Gly Pro Pro Gly  
 1055 1060 1065

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Pro	Thr	Gly	Asp	Pro	Gly	Leu	Pro	Gly	Asp	Met	Gly	Lys	Lys	Gly
	1070					1075					1080			
Glu	Met	Gly	Gln	Pro	Gly	Pro	Pro	Gly	His	Leu	Gly	Pro	Ala	Gly
	1085					1090					1095			
Pro	Glu	Gly	Ala	Pro	Gly	Ser	Pro	Gly	Ser	Pro	Gly	Leu	Pro	Gly
	1100					1105					1110			
Lys	Pro	Gly	Pro	His	Gly	Asp	Leu	Gly	Phe	Lys	Gly	Ile	Lys	Gly
	1115					1120					1125			
Leu	Leu	Gly	Pro	Pro	Gly	Ile	Arg	Gly	Pro	Pro	Gly	Leu	Pro	Gly
	1130					1135					1140			
Phe	Pro	Gly	Ser	Pro	Gly	Pro	Met	Gly	Ile	Arg	Gly	Asp	Gln	Gly
	1145					1150					1155			
Arg	Asp	Gly	Ile	Pro	Gly	Pro	Ala	Gly	Glu	Lys	Gly	Glu	Thr	Gly
	1160					1165					1170			
Leu	Leu	Arg	Ala	Pro	Pro	Gly	Pro	Arg	Gly	Asn	Pro	Gly	Ala	Gln
	1175					1180					1185			
Gly	Ala	Lys	Gly	Asp	Arg	Gly	Ala	Pro	Gly	Phe	Pro	Gly	Leu	Pro
	1190					1195					1200			
Gly	Arg	Lys	Gly	Ala	Met	Gly	Asp	Ala	Gly	Pro	Arg	Gly	Pro	Thr
	1205					1210					1215			
Gly	Ile	Glu	Gly	Phe	Pro	Gly	Pro	Pro	Gly	Leu	Pro	Gly	Ala	Ile
	1220					1225					1230			
Ile	Pro	Gly	Gln	Thr	Gly	Asn	Arg	Gly	Pro	Pro	Gly	Ser	Arg	Gly
	1235					1240					1245			
Ser	Pro	Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ser	His	Val
	1250					1255					1260			
Ile	Gly	Ile	Lys	Gly	Asp	Lys	Gly	Ser	Met	Gly	His	Pro	Gly	Pro
	1265					1270					1275			
Lys	Gly	Pro	Pro	Gly	Thr	Ala	Gly	Asp	Met	Gly	Pro	Pro	Gly	Arg
	1280					1285					1290			
Leu	Gly	Ala	Pro	Gly	Thr	Pro	Gly	Leu	Pro	Gly	Pro	Arg	Gly	Asp
	1295					1300					1305			
Pro	Gly	Phe	Gln	Gly	Phe	Pro	Gly	Val	Lys	Gly	Glu	Lys	Gly	Asn
	1310					1315					1320			

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Pro	Gly	Phe	Leu	Gly	Ser	Ile	Gly	Pro	Pro	Gly	Pro	Ile	Gly	Pro
	1325					1330					1335			
Lys	Gly	Pro	Pro	Gly	Val	Arg	Gly	Asp	Pro	Gly	Thr	Leu	Lys	Ile
	1340					1345					1350			
Ile	Ser	Leu	Pro	Gly	Ser	Pro	Gly	Pro	Pro	Gly	Thr	Pro	Gly	Glu
	1355					1360					1365			
Pro	Gly	Met	Gln	Gly	Glu	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Asn
	1370					1375					1380			
Leu	Gly	Pro	Cys	Gly	Pro	Arg	Gly	Lys	Pro	Gly	Lys	Asp	Gly	Lys
	1385					1390					1395			
Pro	Gly	Thr	Pro	Gly	Pro	Ala	Gly	Glu	Lys	Gly	Asn	Lys	Gly	Ser
	1400					1405					1410			
Lys	Gly	Glu	Pro	Gly	Pro	Ala	Gly	Ser	Asp	Gly	Leu	Pro	Gly	Leu
	1415					1420					1425			
Lys	Gly	Lys	Arg	Gly	Asp	Ser	Gly	Ser	Pro	Ala	Thr	Trp	Thr	Thr
	1430					1435					1440			
Arg	Gly	Phe	Val	Phe	Thr	Arg	His	Ser	Gln	Thr	Thr	Ala	Ile	Pro
	1445					1450					1455			
Ser	Cys	Pro	Glu	Gly	Thr	Val	Pro	Leu	Tyr	Ser	Gly	Phe	Ser	Phe
	1460					1465					1470			
Leu	Phe	Val	Gln	Gly	Asn	Gln	Arg	Ala	His	Gly	Gln	Asp	Leu	Gly
	1475					1480					1485			
Thr	Leu	Gly	Ser	Cys	Leu	Gln	Arg	Phe	Thr	Thr	Met	Pro	Phe	Leu
	1490					1495					1500			
Phe	Cys	Asn	Val	Asn	Asp	Val	Cys	Asn	Phe	Ala	Ser	Arg	Asn	Asp
	1505					1510					1515			
Tyr	Ser	Tyr	Trp	Leu	Ser	Thr	Pro	Ala	Leu	Met	Pro	Met	Asn	Met
	1520					1525					1530			
Ala	Pro	Ile	Thr	Gly	Arg	Ala	Leu	Glu	Pro	Tyr	Ile	Ser	Arg	Cys
	1535					1540					1545			
Thr	Val	Cys	Glu	Gly	Pro	Ala	Ile	Ala	Ile	Ala	Val	His	Ser	Gln
	1550					1555					1560			
Thr	Thr	Asp	Ile	Pro	Pro	Cys	Pro	His	Gly	Trp	Ile	Ser	Leu	Trp
	1565					1570					1575			

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Lys Gly Phe Ser Phe Ile Met Phe Thr Ser Ala Gly Ser Glu Gly  
1580 1585 1590

Thr Gly Gln Ala Leu Ala Ser Pro Gly Ser Cys Leu Glu Glu Phe  
1595 1600 1605

Arg Ala Ser Pro Phe Leu Glu Cys His Gly Arg Gly Thr Cys Asn  
1610 1615 1620

Tyr Tyr Ser Asn Ser Tyr Ser Phe Trp Leu Ala Ser Leu Asn Pro  
1625 1630 1635

Glu Arg Met Phe Arg Lys Pro Ile Pro Ser Thr Val Lys Ala Gly  
1640 1645 1650

Glu Leu Glu Lys Ile Ile Ser Arg Cys Gln Val Cys Met Lys Lys  
1655 1660 1665

Arg His  
1670

<210> 69  
<211> 1690  
<212> PRT  
<213> Homo sapiens

<400> 69

Met Trp Ser Leu His Ile Val Leu Met Arg Cys Ser Phe Arg Leu Thr  
1 5 10 15

Lys Ser Leu Ala Thr Gly Pro Trp Ser Leu Ile Leu Ile Leu Phe Ser  
20 25 30

Val Gln Tyr Val Tyr Gly Ser Gly Lys Lys Tyr Ile Gly Pro Cys Gly  
35 40 45

Gly Arg Asp Cys Ser Val Cys His Cys Val Pro Glu Lys Gly Ser Arg  
50 55 60

Gly Pro Pro Gly Pro Pro Gly Pro Gln Gly Pro Ile Gly Pro Leu Gly  
65 70 75 80

Ala Pro Gly Pro Ile Gly Leu Ser Gly Glu Lys Gly Met Arg Gly Asp  
85 90 95

Arg Gly Pro Pro Gly Ala Ala Gly Asp Lys Gly Asp Lys Gly Pro Thr  
100 105 110

Gly Val Pro Gly Phe Pro Gly Leu Asp Gly Ile Pro Gly His Pro Gly  
115 120 125

# FAB-008PC-SequenceListing

Pro Pro Gly Pro Arg Gly Lys Pro Gly Met Ser Gly His Asn Gly Ser  
 130 135 140  
 Arg Gly Asp Pro Gly Phe Pro Gly Gly Arg Gly Ala Leu Gly Pro Gly  
 145 150 155 160  
 Gly Pro Leu Gly His Pro Gly Glu Lys Gly Glu Lys Gly Asn Ser Val  
 165 170 175  
 Phe Ile Leu Gly Ala Val Lys Gly Ile Gln Gly Asp Arg Gly Asp Pro  
 180 185 190  
 Gly Leu Pro Gly Leu Pro Gly Ser Trp Gly Ala Gly Gly Pro Ala Gly  
 195 200 205  
 Pro Thr Gly Tyr Pro Gly Glu Pro Gly Leu Val Gly Pro Pro Gly Gln  
 210 215 220  
 Pro Gly Arg Pro Gly Leu Lys Gly Asn Pro Gly Val Gly Val Lys Gly  
 225 230 235 240  
 Gln Met Gly Asp Pro Gly Glu Val Gly Gln Gln Gly Ser Pro Gly Pro  
 245 250 255  
 Thr Leu Leu Val Glu Pro Pro Asp Phe Cys Leu Tyr Lys Gly Glu Lys  
 260 265 270  
 Gly Ile Lys Gly Ile Pro Gly Met Val Gly Leu Pro Gly Pro Pro Gly  
 275 280 285  
 Arg Lys Gly Glu Ser Gly Ile Gly Ala Lys Gly Glu Lys Gly Ile Pro  
 290 295 300  
 Gly Phe Pro Gly Pro Arg Gly Asp Pro Gly Ser Tyr Gly Ser Pro Gly  
 305 310 315 320  
 Phe Pro Gly Leu Lys Gly Glu Leu Gly Leu Val Gly Asp Pro Gly Leu  
 325 330 335  
 Phe Gly Leu Ile Gly Pro Lys Gly Asp Pro Gly Asn Arg Gly His Pro  
 340 345 350  
 Gly Pro Pro Gly Val Leu Val Thr Pro Pro Leu Pro Leu Lys Gly Pro  
 355 360 365  
 Pro Gly Asp Pro Gly Phe Pro Gly Arg Tyr Gly Glu Thr Gly Asp Val  
 370 375 380  
 Gly Pro Pro Gly Pro Pro Gly Leu Leu Gly Arg Pro Gly Glu Ala Cys  
 385 390 395 400

FAB-008PC-SequenceListing

Ala Gly Met Ile Gly Pro Pro Gly Pro Gln Gly Phe Pro Gly Leu Pro  
405 410 415

Gly Leu Pro Gly Glu Ala Gly Ile Pro Gly Arg Pro Asp Ser Ala Pro  
420 425 430

Gly Lys Pro Gly Lys Pro Gly Ser Pro Gly Leu Pro Gly Ala Pro Gly  
435 440 445

Leu Gln Gly Leu Pro Gly Ser Ser Val Ile Tyr Cys Ser Val Gly Asn  
450 455 460

Pro Gly Pro Gln Gly Ile Lys Gly Lys Val Gly Pro Pro Gly Gly Arg  
465 470 475 480

Gly Pro Lys Gly Glu Lys Gly Asn Glu Gly Leu Cys Ala Cys Glu Pro  
485 490 495

Gly Pro Met Gly Pro Pro Gly Pro Pro Gly Leu Pro Gly Arg Gln Gly  
500 505 510

Ser Lys Gly Asp Leu Gly Leu Pro Gly Trp Leu Gly Thr Lys Gly Asp  
515 520 525

Pro Gly Pro Pro Gly Ala Glu Gly Pro Pro Gly Leu Pro Gly Lys His  
530 535 540

Gly Ala Ser Gly Pro Pro Gly Asn Lys Gly Ala Lys Gly Asp Met Val  
545 550 555 560

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

Pro Gly Phe Pro Gly Gln Pro Gly Ser His Gly Arg Asp Gly His Ala  
580 585 590

Gly Glu Lys Gly Asp Pro Gly Pro Pro Gly Asp His Glu Asp Ala Thr  
595 600 605

Pro Gly Gly Lys Gly Phe Pro Gly Pro Leu Gly Pro Pro Gly Lys Ala  
610 615 620

Gly Pro Val Gly Pro Pro Gly Leu Gly Phe Pro Gly Pro Pro Gly Glu  
625 630 635 640

Arg Gly His Pro Gly Val Pro Gly His Pro Gly Val Arg Gly Pro Asp  
645 650 655

Gly Leu Lys Gly Gln Lys Gly Asp Thr Ile Ser Cys Asn Val Thr Tyr  
660 665 670



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Pro Gly Arg His Gly Pro Pro Gly Phe Asp Gly Pro Pro Gly Pro Lys  
675 680 685

Gly Phe Pro Gly Pro Gln Gly Ala Pro Gly Leu Ser Gly Ser Asp Gly  
690 695 700

His Lys Gly Arg Pro Gly Thr Pro Gly Thr Ala Glu Ile Pro Gly Pro  
705 710 715 720

Pro Gly Phe Arg Gly Asp Met Gly Asp Pro Gly Phe Gly Gly Glu Lys  
725 730 735

Gly Ser Ser Pro Val Gly Pro Pro Gly Pro Pro Gly Ser Pro Gly Val  
740 745 750

Asn Gly Gln Lys Gly Ile Pro Gly Asp Pro Ala Phe Gly His Leu Gly  
755 760 765

Pro Pro Gly Lys Arg Gly Leu Ser Gly Val Pro Gly Ile Lys Gly Pro  
770 775 780

Arg Gly Asp Pro Gly Cys Pro Gly Ala Glu Gly Pro Ala Gly Ile Pro  
785 790 795 800

Gly Phe Leu Gly Leu Lys Gly Pro Lys Gly Arg Glu Gly His Ala Gly  
805 810 815

Phe Pro Gly Val Pro Gly Pro Pro Gly His Ser Cys Glu Arg Gly Ala  
820 825 830

Pro Gly Ile Pro Gly Gln Pro Gly Leu Pro Gly Tyr Pro Gly Ser Pro  
835 840 845

Gly Ala Pro Gly Gly Lys Gly Gln Pro Gly Asp Val Gly Pro Pro Gly  
850 855 860

Pro Ala Gly Met Lys Gly Leu Pro Gly Leu Pro Gly Arg Pro Gly Ala  
865 870 875 880

His Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Phe Gly Asp Asp  
885 890 895

Gly Leu Pro Gly Pro Pro Gly Pro Lys Gly Pro Arg Gly Leu Pro Gly  
900 905 910

Phe Pro Gly Phe Pro Gly Glu Arg Gly Lys Pro Gly Ala Glu Gly Cys  
915 920 925

Pro Gly Ala Lys Gly Glu Pro Gly Glu Lys Gly Met Ser Gly Leu Pro  
930 935 940

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Gly Asp Arg Gly Leu Arg Gly Ala Lys Gly Ala Ile Gly Pro Pro Gly  
 945 950 955 960  
 Asp Glu Gly Glu Met Ala Ile Ile Ser Gln Lys Gly Thr Pro Gly Glu  
 965 970 975  
 Pro Gly Pro Pro Gly Asp Asp Gly Phe Pro Gly Glu Arg Gly Asp Lys  
 980 985 990  
 Gly Thr Pro Gly Met Gln Gly Arg Arg Gly Glu Pro Gly Arg Tyr Gly  
 995 1000 1005  
 Pro Pro Gly Phe His Arg Gly Glu Pro Gly Glu Lys Gly Gln Pro  
 1010 1015 1020  
 Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ser Thr Gly Leu Arg  
 1025 1030 1035  
 Gly Phe Ile Gly Phe Pro Gly Leu Pro Gly Asp Gln Gly Glu Pro  
 1040 1045 1050  
 Gly Ser Pro Gly Pro Pro Gly Phe Ser Gly Ile Asp Gly Ala Arg  
 1055 1060 1065  
 Gly Pro Lys Gly Asn Lys Gly Asp Pro Ala Ser His Phe Gly Pro  
 1070 1075 1080  
 Pro Gly Pro Lys Gly Glu Pro Gly Ser Pro Gly Cys Pro Gly His  
 1085 1090 1095  
 Phe Gly Ala Ser Gly Glu Gln Gly Leu Pro Gly Ile Gln Gly Pro  
 1100 1105 1110  
 Arg Gly Ser Pro Gly Arg Pro Gly Pro Pro Gly Ser Ser Gly Pro  
 1115 1120 1125  
 Pro Gly Cys Pro Gly Asp His Gly Met Pro Gly Leu Arg Gly Gln  
 1130 1135 1140  
 Pro Gly Glu Met Gly Asp Pro Gly Pro Arg Gly Leu Gln Gly Asp  
 1145 1150 1155  
 Pro Gly Ile Pro Gly Pro Pro Gly Ile Lys Gly Pro Ser Gly Ser  
 1160 1165 1170  
 Pro Gly Leu Asn Gly Leu His Gly Leu Lys Gly Gln Lys Gly Thr  
 1175 1180 1185  
 Lys Gly Ala Ser Gly Leu His Asp Val Gly Pro Pro Gly Pro Val  
 1190 1195 1200

FAB-008PC-SequenceListing

Gly	Ile	Pro	Gly	Leu	Lys	Gly	Glu	Arg	Gly	Asp	Pro	Gly	Ser	Pro
	1205					1210					1215			
Gly	Ile	Ser	Pro	Pro	Gly	Pro	Arg	Gly	Lys	Lys	Gly	Pro	Pro	Gly
	1220					1225					1230			
Pro	Pro	Gly	Ser	Ser	Gly	Pro	Pro	Gly	Pro	Ala	Gly	Ala	Thr	Gly
	1235					1240					1245			
Arg	Ala	Pro	Lys	Asp	Ile	Pro	Asp	Pro	Gly	Pro	Pro	Gly	Asp	Gln
	1250					1255					1260			
Gly	Pro	Pro	Gly	Pro	Asp	Gly	Pro	Arg	Gly	Ala	Pro	Gly	Pro	Pro
	1265					1270					1275			
Gly	Leu	Pro	Gly	Ser	Val	Asp	Leu	Leu	Arg	Gly	Glu	Pro	Gly	Asp
	1280					1285					1290			
Cys	Gly	Leu	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro
	1295					1300					1305			
Pro	Gly	Tyr	Lys	Gly	Phe	Pro	Gly	Cys	Asp	Gly	Lys	Asp	Gly	Gln
	1310					1315					1320			
Lys	Gly	Pro	Val	Gly	Phe	Pro	Gly	Pro	Gln	Gly	Pro	His	Gly	Phe
	1325					1330					1335			
Pro	Gly	Pro	Pro	Gly	Glu	Lys	Gly	Leu	Pro	Gly	Pro	Pro	Gly	Arg
	1340					1345					1350			
Lys	Gly	Pro	Thr	Gly	Leu	Pro	Gly	Pro	Arg	Gly	Glu	Pro	Gly	Pro
	1355					1360					1365			
Pro	Ala	Asp	Val	Asp	Asp	Cys	Pro	Arg	Ile	Pro	Gly	Leu	Pro	Gly
	1370					1375					1380			
Ala	Pro	Gly	Met	Arg	Gly	Pro	Glu	Gly	Ala	Met	Gly	Leu	Pro	Gly
	1385					1390					1395			
Met	Arg	Gly	Pro	Ser	Gly	Pro	Gly	Cys	Lys	Gly	Glu	Pro	Gly	Leu
	1400					1405					1410			
Asp	Gly	Arg	Arg	Gly	Val	Asp	Gly	Val	Pro	Gly	Ser	Pro	Gly	Pro
	1415					1420					1425			
Pro	Gly	Arg	Lys	Gly	Asp	Thr	Gly	Glu	Asp	Gly	Tyr	Pro	Gly	Gly
	1430					1435					1440			
Pro	Gly	Pro	Pro	Gly	Pro	Ile	Gly	Asp	Pro	Gly	Pro	Lys	Gly	Phe
	1445					1450					1455			

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Gly	Pro	Gly	Tyr	Leu	Gly	Gly	Phe	Leu	Leu	Val	Leu	His	Ser	Gln
	1460					1465					1470			
Thr	Asp	Gln	Glu	Pro	Thr	Cys	Pro	Leu	Gly	Met	Pro	Arg	Leu	Trp
	1475					1480					1485			
Thr	Gly	Tyr	Ser	Leu	Leu	Tyr	Leu	Glu	Gly	Gln	Glu	Lys	Ala	His
	1490					1495					1500			
Asn	Gln	Asp	Leu	Gly	Leu	Ala	Gly	Ser	Cys	Leu	Pro	Val	Phe	Ser
	1505					1510					1515			
Thr	Leu	Pro	Phe	Ala	Tyr	Cys	Asn	Ile	His	Gln	Val	Cys	His	Tyr
	1520					1525					1530			
Ala	Gln	Arg	Asn	Asp	Arg	Ser	Tyr	Trp	Leu	Ala	Ser	Ala	Ala	Pro
	1535					1540					1545			
Leu	Pro	Met	Met	Pro	Leu	Ser	Glu	Glu	Ala	Ile	Arg	Pro	Tyr	Val
	1550					1555					1560			
Ser	Arg	Cys	Ala	Val	Cys	Glu	Ala	Pro	Ala	Gln	Ala	Val	Ala	Val
	1565					1570					1575			
His	Ser	Gln	Asp	Gln	Ser	Ile	Pro	Pro	Cys	Pro	Gln	Thr	Trp	Arg
	1580					1585					1590			
Ser	Leu	Trp	Ile	Gly	Tyr	Ser	Phe	Leu	Met	His	Thr	Gly	Ala	Gly
	1595					1600					1605			
Asp	Gln	Gly	Gly	Gly	Gln	Ala	Leu	Met	Ser	Pro	Gly	Ser	Cys	Leu
	1610					1615					1620			
Glu	Asp	Phe	Arg	Ala	Ala	Pro	Phe	Leu	Glu	Cys	Gln	Gly	Arg	Gln
	1625					1630					1635			
Gly	Thr	Cys	His	Phe	Phe	Ala	Asn	Lys	Tyr	Ser	Phe	Trp	Leu	Thr
	1640					1645					1650			
Thr	Val	Lys	Ala	Asp	Leu	Gln	Phe	Ser	Ser	Ala	Pro	Ala	Pro	Asp
	1655					1660					1665			
Thr	Leu	Lys	Glu	Ser	Gln	Ala	Gln	Arg	Gln	Lys	Ile	Ser	Arg	Cys
	1670					1675					1680			
Gln	Val	Cys	Val	Lys	Tyr	Ser								
	1685					1690								

<210> 70  
 <211> 1685  
 <212> PRT

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<213> Homo sapiens

<400> 70

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

Leu Ser Leu Trp Gly Gln Pro Ala Glu Ala Ala Ala Cys Tyr Gly Cys
20     25     30

Ser Pro Gly Ser Lys Cys Asp Cys Ser Gly Ile Lys Gly Glu Lys Gly
35     40     45

Glu Arg Gly Phe Pro Gly Leu Glu Gly His Pro Gly Leu Pro Gly Phe
50     55     60

Pro Gly Pro Glu Gly Pro Pro Gly Pro Arg Gly Gln Lys Gly Asp Asp
65     70     75     80

Gly Ile Pro Gly Pro Pro Gly Pro Lys Gly Ile Arg Gly Pro Pro Gly
85     90     95

Leu Pro Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Met Pro Gly His
100    105    110

Asp Gly Ala Pro Gly Pro Gln Gly Ile Pro Gly Cys Asn Gly Thr Lys
115    120    125

Gly Glu Arg Gly Phe Pro Gly Ser Pro Gly Phe Pro Gly Leu Gln Gly
130    135    140

Pro Pro Gly Pro Pro Gly Ile Pro Gly Met Lys Gly Glu Pro Gly Ser
145    150    155    160

Ile Ile Met Ser Ser Leu Pro Gly Pro Lys Gly Asn Pro Gly Tyr Pro
165    170    175

Gly Pro Pro Gly Ile Gln Gly Leu Pro Gly Pro Thr Gly Ile Pro Gly
180    185    190

Pro Ile Gly Pro Pro Gly Pro Pro Gly Leu Met Gly Pro Pro Gly Pro
195    200    205

Pro Gly Leu Pro Gly Pro Lys Gly Asn Met Gly Leu Asn Phe Gln Gly
210    215    220

Pro Lys Gly Glu Lys Gly Glu Gln Gly Leu Gln Gly Pro Pro Gly Pro
225    230    235    240

Pro Gly Gln Ile Ser Glu Gln Lys Arg Pro Ile Asp Val Glu Phe Gln
245    250    255

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## FAB-008PC-SequenceListing

Lys Gly Asp Gln Gly Leu Pro Gly Asp Arg Gly Pro Pro Gly Pro Pro  
 260 265 270  
 Gly Ile Arg Gly Pro Pro Gly Pro Pro Gly Gly Glu Lys Gly Glu Lys  
 275 280 285  
 Gly Glu Gln Gly Glu Pro Gly Lys Arg Gly Lys Pro Gly Lys Asp Gly  
 290 295 300  
 Glu Asn Gly Gln Pro Gly Ile Pro Gly Leu Pro Gly Asp Pro Gly Tyr  
 305 310 315 320  
 Pro Gly Glu Pro Gly Arg Asp Gly Glu Lys Gly Gln Lys Gly Asp Thr  
 325 330 335  
 Gly Pro Pro Gly Pro Pro Gly Leu Val Ile Pro Arg Pro Gly Thr Gly  
 340 345 350  
 Ile Thr Ile Gly Glu Lys Gly Asn Ile Gly Leu Pro Gly Leu Pro Gly  
 355 360 365  
 Glu Lys Gly Glu Arg Gly Phe Pro Gly Ile Gln Gly Pro Pro Gly Leu  
 370 375 380  
 Pro Gly Pro Pro Gly Ala Ala Val Met Gly Pro Pro Gly Pro Pro Gly  
 385 390 395 400  
 Phe Pro Gly Glu Arg Gly Gln Lys Gly Asp Glu Gly Pro Pro Gly Ile  
 405 410 415  
 Ser Ile Pro Gly Pro Pro Gly Leu Asp Gly Gln Pro Gly Ala Pro Gly  
 420 425 430  
 Leu Pro Gly Pro Pro Gly Pro Ala Gly Pro His Ile Pro Pro Ser Asp  
 435 440 445  
 Glu Ile Cys Glu Pro Gly Pro Pro Gly Pro Pro Gly Ser Pro Gly Asp  
 450 455 460  
 Lys Gly Leu Gln Gly Glu Gln Gly Val Lys Gly Asp Lys Gly Asp Thr  
 465 470 475 480  
 Cys Phe Asn Cys Ile Gly Thr Gly Ile Ser Gly Pro Pro Gly Gln Pro  
 485 490 495  
 Gly Leu Pro Gly Leu Pro Gly Pro Pro Gly Ser Leu Gly Phe Pro Gly  
 500 505 510  
 Gln Lys Gly Glu Lys Gly Gln Ala Gly Ala Thr Gly Pro Lys Gly Leu  
 515 520 525

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Pro Gly Ile Pro Gly Ala Pro Gly Ala Pro Gly Phe Pro Gly Ser Lys  
530 535 540

Gly Glu Pro Gly Asp Ile Leu Thr Phe Pro Gly Met Lys Gly Asp Lys  
545 550 555 560

Gly Glu Leu Gly Ser Pro Gly Ala Pro Gly Leu Pro Gly Leu Pro Gly  
565 570 575

Thr Pro Gly Gln Asp Gly Leu Pro Gly Leu Pro Gly Pro Lys Gly Glu  
580 585 590

Pro Gly Gly Ile Thr Phe Lys Gly Glu Arg Gly Pro Pro Gly Asn Pro  
595 600 605

Gly Leu Pro Gly Leu Pro Gly Asn Ile Gly Pro Met Gly Pro Pro Gly  
610 615 620

Phe Gly Pro Pro Gly Pro Val Gly Glu Lys Gly Ile Gln Gly Val Ala  
625 630 635 640

Gly Asn Pro Gly Gln Pro Gly Ile Pro Gly Pro Lys Gly Asp Pro Gly  
645 650 655

Gln Thr Ile Thr Gln Pro Gly Lys Pro Gly Leu Pro Gly Asn Pro Gly  
660 665 670

Arg Asp Gly Asp Val Gly Leu Pro Gly Asp Pro Gly Leu Pro Gly Gln  
675 680 685

Pro Gly Leu Pro Gly Ile Pro Gly Ser Lys Gly Glu Pro Gly Ile Pro  
690 695 700

Gly Ile Gly Leu Pro Gly Pro Pro Gly Pro Lys Gly Phe Pro Gly Ile  
705 710 715 720

Pro Gly Pro Pro Gly Ala Pro Gly Thr Pro Gly Arg Ile Gly Leu Glu  
725 730 735

Gly Pro Pro Gly Pro Pro Gly Phe Pro Gly Pro Lys Gly Glu Pro Gly  
740 745 750

Phe Ala Leu Pro Gly Pro Pro Gly Pro Pro Gly Leu Pro Gly Phe Lys  
755 760 765

Gly Ala Leu Gly Pro Lys Gly Asp Arg Gly Phe Pro Gly Pro Pro Gly  
770 775 780

Pro Pro Gly Arg Thr Gly Leu Asp Gly Leu Pro Gly Pro Lys Gly Asp  
785 790 795 800

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Val Gly Pro Asn Gly Gln Pro Gly Pro Met Gly Pro Pro Gly Leu Pro  
805 810 815

Gly Ile Gly Val Gln Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly Pro  
820 825 830

Ile Gly Gln Pro Gly Leu His Gly Ile Pro Gly Glu Lys Gly Asp Pro  
835 840 845

Gly Pro Pro Gly Leu Asp Val Pro Gly Pro Pro Gly Glu Arg Gly Ser  
850 855 860

Pro Gly Ile Pro Gly Ala Pro Gly Pro Ile Gly Pro Pro Gly Ser Pro  
865 870 875 880

Gly Leu Pro Gly Lys Ala Gly Ala Ser Gly Phe Pro Gly Thr Lys Gly  
885 890 895

Glu Met Gly Met Met Gly Pro Pro Gly Pro Pro Gly Pro Leu Gly Ile  
900 905 910

Pro Gly Arg Ser Gly Val Pro Gly Leu Lys Gly Asp Asp Gly Leu Gln  
915 920 925

Gly Gln Pro Gly Leu Pro Gly Pro Thr Gly Glu Lys Gly Ser Lys Gly  
930 935 940

Glu Pro Gly Leu Pro Gly Pro Pro Gly Pro Met Asp Pro Asn Leu Leu  
945 950 955 960

Gly Ser Lys Gly Glu Lys Gly Glu Pro Gly Leu Pro Gly Ile Pro Gly  
965 970 975

Val Ser Gly Pro Lys Gly Tyr Gln Gly Leu Pro Gly Asp Pro Gly Gln  
980 985 990

Pro Gly Leu Ser Gly Gln Pro Gly Leu Pro Gly Pro Pro Gly Pro Lys  
995 1000 1005

Gly Asn Pro Gly Leu Pro Gly Gln Pro Gly Leu Ile Gly Pro Pro  
1010 1015 1020

Gly Leu Lys Gly Thr Ile Gly Asp Met Gly Phe Pro Gly Pro Gln  
1025 1030 1035

Gly Val Glu Gly Pro Pro Gly Pro Ser Gly Val Pro Gly Gln Pro  
1040 1045 1050

Gly Ser Pro Gly Leu Pro Gly Gln Lys Gly Asp Lys Gly Asp Pro  
1055 1060 1065



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Gly Ile 1070	Ser Ser Ile Gly	Leu Pro Gly Leu Pro Gly	Pro Lys Gly
Glu Pro 1085	Gly Leu Pro Gly Tyr	Pro Gly Asn Pro Gly	Ile Lys Gly
Ser Val 1100	Gly Asp Pro Gly Leu	Pro Gly Leu Pro Gly	Thr Pro Gly
Ala Lys 1115	Gly Gln Pro Gly Leu	Pro Gly Phe Pro Gly	Thr Pro Gly
Pro Pro 1130	Gly Pro Lys Gly Ile	Ser Gly Pro Pro Gly	Asn Pro Gly
Leu Pro 1145	Gly Glu Pro Gly Pro	Val Gly Gly Gly Gly	His Pro Gly
Gln Pro 1160	Gly Pro Pro Gly Glu	Lys Gly Lys Pro Gly	Gln Asp Gly
Ile Pro 1175	Gly Pro Ala Gly Gln	Lys Gly Glu Pro Gly	Gln Pro Gly
Phe Gly 1190	Asn Pro Gly Pro Pro	Gly Leu Pro Gly Leu	Ser Gly Gln
Lys Gly 1205	Asp Gly Gly Leu Pro	Gly Ile Pro Gly Asn	Pro Gly Leu
Pro Gly 1220	Pro Lys Gly Glu Pro	Gly Phe His Gly Phe	Pro Gly Val
Gln Gly 1235	Pro Pro Gly Pro Pro	Gly Ser Pro Gly Pro	Ala Leu Glu
Gly Pro 1250	Lys Gly Asn Pro Gly	Pro Gln Gly Pro Pro	Gly Arg Pro
Gly Leu 1265	Pro Gly Pro Glu Gly	Pro Pro Gly Leu Pro	Gly Asn Gly
Gly Ile 1280	Lys Gly Glu Lys Gly	Asn Pro Gly Gln Pro	Gly Leu Pro
Gly Leu 1295	Pro Gly Leu Lys Gly	Asp Gln Gly Pro Pro	Gly Leu Gln
Gly Asn 1310	Pro Gly Arg Pro Gly	Leu Asn Gly Met Lys	Gly Asp Pro

## FAB-008PC-SequenceListing

Gly Leu Pro Gly Val Pro Gly Phe Pro Gly Met Lys Gly Pro Ser  
 1325 1330 1335  
 Gly Val Pro Gly Ser Ala Gly Pro Glu Gly Glu Pro Gly Leu Ile  
 1340 1345 1350  
 Gly Pro Pro Gly Pro Pro Gly Leu Pro Gly Pro Ser Gly Gln Ser  
 1355 1360 1365  
 Ile Ile Ile Lys Gly Asp Ala Gly Pro Pro Gly Ile Pro Gly Gln  
 1370 1375 1380  
 Pro Gly Leu Lys Gly Leu Pro Gly Pro Gln Gly Pro Gln Gly Leu  
 1385 1390 1395  
 Pro Gly Pro Thr Gly Pro Pro Gly Asp Pro Gly Arg Asn Gly Leu  
 1400 1405 1410  
 Pro Gly Phe Asp Gly Ala Gly Gly Arg Lys Gly Asp Pro Gly Leu  
 1415 1420 1425  
 Pro Gly Gln Pro Gly Thr Arg Gly Leu Asp Gly Pro Pro Gly Pro  
 1430 1435 1440  
 Asp Gly Leu Gln Gly Pro Pro Gly Pro Pro Gly Thr Ser Ser Val  
 1445 1450 1455  
 Ala His Gly Phe Leu Ile Thr Arg His Ser Gln Thr Thr Asp Ala  
 1460 1465 1470  
 Pro Gln Cys Pro Gln Gly Thr Leu Gln Val Tyr Glu Gly Phe Ser  
 1475 1480 1485  
 Leu Leu Tyr Val Gln Gly Asn Lys Arg Ala His Gly Gln Asp Leu  
 1490 1495 1500  
 Gly Thr Ala Gly Ser Cys Leu Arg Arg Phe Ser Thr Met Pro Phe  
 1505 1510 1515  
 Met Phe Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn  
 1520 1525 1530  
 Asp Tyr Ser Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser  
 1535 1540 1545  
 Met Gln Pro Leu Lys Gly Gln Ser Ile Gln Pro Phe Ile Ser Arg  
 1550 1555 1560  
 Cys Ala Val Cys Glu Ala Pro Ala Val Val Ile Ala Val His Ser  
 1565 1570 1575

# FAB-008PC-SequenceListing

Gln Thr Ile Gln Ile Pro His Cys Pro Gln Gly Trp Asp Ser Leu  
1580 1585 1590

Trp Ile Gly Tyr Ser Phe Met Met His Thr Ser Ala Gly Ala Glu  
1595 1600 1605

Gly Ser Gly Gln Ala Leu Ala Ser Pro Gly Ser Cys Leu Glu Glu  
1610 1615 1620

Phe Arg Ser Ala Pro Phe Ile Glu Cys His Gly Arg Gly Thr Cys  
1625 1630 1635

Asn Tyr Tyr Ala Asn Ser Tyr Ser Phe Trp Leu Ala Thr Val Asp  
1640 1645 1650

Val Ser Asp Met Phe Ser Lys Pro Gln Ser Glu Thr Leu Lys Ala  
1655 1660 1665

Gly Asp Leu Arg Thr Arg Ile Ser Arg Cys Gln Val Cys Met Lys  
1670 1675 1680

Arg Thr  
1685

<210> 71  
<211> 1691  
<212> PRT  
<213> Homo sapiens

<400> 71

Met Leu Ile Asn Lys Leu Trp Leu Leu Leu Val Thr Leu Cys Leu Thr  
1 5 10 15

Glu Glu Leu Ala Ala Ala Gly Glu Lys Ser Tyr Gly Lys Pro Cys Gly  
20 25 30

Gly Gln Asp Cys Ser Gly Ser Cys Gln Cys Phe Pro Glu Lys Gly Ala  
35 40 45

Arg Gly Arg Pro Gly Pro Ile Gly Ile Gln Gly Pro Thr Gly Pro Gln  
50 55 60

Gly Phe Thr Gly Ser Thr Gly Leu Ser Gly Leu Lys Gly Glu Arg Gly  
65 70 75 80

Phe Pro Gly Leu Leu Gly Pro Tyr Gly Pro Lys Gly Asp Lys Gly Pro  
85 90 95

Met Gly Val Pro Gly Phe Leu Gly Ile Asn Gly Ile Pro Gly His Pro  
100 105 110

Gly Gln Pro Gly Pro Arg Gly Pro Pro Gly Leu Asp Gly Cys Asn Gly  
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115

120

125

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

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

Val Leu Ala Pro Gly Ser Phe Lys Gly Met Lys Gly Asp Pro Gly Leu  
 165 170 175

Pro Gly Leu Asp Gly Ile Thr Gly Pro Gln Gly Ala Pro Gly Phe Pro  
 180 185 190

Gly Ala Val Gly Pro Ala Gly Pro Pro Gly Leu Gln Gly Pro Pro Gly  
 195 200 205

Pro Pro Gly Pro Leu Gly Pro Asp Gly Asn Met Gly Leu Gly Phe Gln  
 210 215 220

Gly Glu Lys Gly Val Lys Gly Asp Val Gly Leu Pro Gly Pro Ala Gly  
 225 230 235 240

Pro Pro Pro Ser Thr Gly Glu Leu Glu Phe Met Gly Phe Pro Lys Gly  
 245 250 255

Lys Lys Gly Ser Lys Gly Glu Pro Gly Pro Lys Gly Phe Pro Gly Ile  
 260 265 270

Ser Gly Pro Pro Gly Phe Pro Gly Leu Gly Thr Thr Gly Glu Lys Gly  
 275 280 285

Glu Lys Gly Glu Lys Gly Ile Pro Gly Leu Pro Gly Pro Arg Gly Pro  
 290 295 300

Met Gly Ser Glu Gly Val Gln Gly Pro Pro Gly Gln Gln Gly Lys Lys  
 305 310 315 320

Gly Thr Leu Gly Phe Pro Gly Leu Asn Gly Phe Gln Gly Ile Glu Gly  
 325 330 335

Gln Lys Gly Asp Ile Gly Leu Pro Gly Pro Asp Val Phe Ile Asp Ile  
 340 345 350

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

Leu Pro Gly Leu Lys Gly Asp Glu Gly Ile Gln Gly Leu Arg Gly Pro  
 370 375 380

Ser Gly Val Pro Gly Leu Pro Ala Leu Ser Gly Val Pro Gly Ala Leu  
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## FAB-008PC-SequenceListing

385                      390                      395                      400  
 Gly Pro Gln Gly Phe<sub>405</sub> Pro Gly Leu Lys Gly<sub>410</sub> Asp Gln Gly Asn Pro Gly<sub>415</sub>  
 Arg Thr Thr Ile<sub>420</sub> Gly Ala Ala Gly<sub>425</sub> Leu Pro Gly Arg Asp Gly<sub>430</sub> Leu Pro  
 Gly Pro Pro<sub>435</sub> Gly Pro Pro Gly<sub>440</sub> Pro Ser Pro Glu Phe<sub>445</sub> Glu Thr Glu  
 Thr Leu<sub>450</sub> His Asn Lys Glu Ser<sub>455</sub> Gly Phe Pro Gly Leu<sub>460</sub> Arg Gly Glu Gln  
 Gly<sub>465</sub> Pro Lys Gly Asn Leu<sub>470</sub> Gly Leu Lys Gly<sub>475</sub> Ile Lys Gly Asp Ser Gly<sub>480</sub>  
 Phe Cys Ala Cys Asp<sub>485</sub> Gly Gly Val Pro Asn<sub>490</sub> Thr Gly Pro Pro Gly<sub>495</sub> Glu  
 Pro Gly Pro Pro<sub>500</sub> Gly Pro Trp Gly Leu<sub>505</sub> Ile Gly Leu Pro Gly<sub>510</sub> Leu Lys  
 Gly Ala Arg<sub>515</sub> Gly Asp Arg Gly Ser<sub>520</sub> Gly Gly Ala Gln Gly<sub>525</sub> Pro Ala Gly  
 Ala Pro<sub>530</sub> Gly Leu Val Gly Pro<sub>535</sub> Leu Gly Pro Ser Gly<sub>540</sub> Pro Lys Gly Lys  
 Lys<sub>545</sub> Gly Glu Pro Ile Leu<sub>550</sub> Ser Thr Ile Gln Gly<sub>555</sub> Met Pro Gly Asp Arg<sub>560</sub>  
 Gly Asp Ser Gly Ser<sub>565</sub> Gln Gly Phe Arg Gly<sub>570</sub> Val Ile Gly Glu Pro Gly<sub>575</sub>  
 Lys Asp Gly Val<sub>580</sub> Pro Gly Leu Pro Gly<sub>585</sub> Leu Pro Gly Leu Pro Gly<sub>590</sub> Asp  
 Gly Gly Gln Gly Phe Pro Gly Glu<sub>600</sub> Lys Gly Leu Pro Gly<sub>605</sub> Leu Pro Gly  
 Glu Lys<sub>610</sub> Gly His Pro Gly Pro<sub>615</sub> Pro Gly Leu Pro Gly<sub>620</sub> Asn Gly Leu Pro  
 Gly<sub>625</sub> Leu Pro Gly Pro Arg<sub>630</sub> Gly Leu Pro Gly Asp<sub>635</sub> Lys Gly Lys Asp Gly<sub>640</sub>  
 Leu Pro Gly Gln Gln Gly Leu Pro Gly Ser<sub>650</sub> Lys Gly Ile Thr Leu<sub>655</sub> Pro  
 Cys Ile Ile Pro Gly Ser Tyr Gly Pro Ser Gly Phe Pro Gly Thr Pro

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660

665

670

Gly Phe Pro Gly Pro Lys Gly Ser Arg Gly Leu Pro Gly Thr Pro Gly  
675 680 685

Gln Pro Gly Ser Ser Gly Ser Lys Gly Glu Pro Gly Ser Pro Gly Leu  
690 695 700

Val His Leu Pro Glu Leu Pro Gly Phe Pro Gly Pro Arg Gly Glu Lys  
705 710 715 720

Gly Leu Pro Gly Phe Pro Gly Leu Pro Gly Lys Asp Gly Leu Pro Gly  
725 730 735

Met Ile Gly Ser Pro Gly Leu Pro Gly Ser Lys Gly Ala Thr Gly Asp  
740 745 750

Ile Phe Gly Ala Glu Asn Gly Ala Pro Gly Glu Gln Gly Leu Gln Gly  
755 760 765

Leu Thr Gly His Lys Gly Phe Leu Gly Asp Ser Gly Leu Pro Gly Leu  
770 775 780

Lys Gly Val His Gly Lys Pro Gly Leu Leu Gly Pro Lys Gly Glu Arg  
785 790 795 800

Gly Ser Pro Gly Thr Pro Gly Gln Val Gly Gln Pro Gly Thr Pro Gly  
805 810 815

Ser Ser Gly Pro Tyr Gly Ile Lys Gly Lys Ser Gly Leu Pro Gly Ala  
820 825 830

Pro Gly Phe Pro Gly Ile Ser Gly His Pro Gly Lys Lys Gly Thr Arg  
835 840 845

Gly Lys Lys Gly Pro Pro Gly Ser Ile Val Lys Lys Gly Leu Pro Gly  
850 855 860

Leu Lys Gly Leu Pro Gly Asn Pro Gly Leu Val Gly Leu Lys Gly Ser  
865 870 875 880

Pro Gly Ser Pro Gly Val Ala Gly Leu Pro Ala Leu Ser Gly Pro Lys  
885 890 895

Gly Glu Lys Gly Ser Val Gly Phe Val Gly Phe Pro Gly Ile Pro Gly  
900 905 910

Leu Pro Gly Ile Pro Gly Thr Arg Gly Leu Lys Gly Ile Pro Gly Ser  
915 920 925

Thr Gly Lys Met Gly Pro Ser Gly Arg Ala Gly Thr Pro Gly Glu Lys

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930

935

940

Gly Asp Arg Gly Asn Pro Gly Pro Val Gly Ile Pro Ser Pro Arg Arg  
945 950 955 960

Pro Met Ser Asn Leu Trp Leu Lys Gly Asp Lys Gly Ser Gln Gly Ser  
965 970 975

Ala Gly Ser Asn Gly Phe Pro Gly Pro Arg Gly Asp Lys Gly Glu Ala  
980 985 990

Gly Arg Pro Gly Pro Pro Gly Leu Pro Gly Ala Pro Gly Leu Pro Gly  
995 1000 1005

Ile Ile Lys Gly Val Ser Gly Lys Pro Gly Pro Pro Gly Phe Met  
1010 1015 1020

Gly Ile Arg Gly Leu Pro Gly Leu Lys Gly Ser Ser Gly Ile Thr  
1025 1030 1035

Gly Phe Pro Gly Met Pro Gly Glu Ser Gly Ser Gln Gly Ile Arg  
1040 1045 1050

Gly Ser Pro Gly Leu Pro Gly Ala Ser Gly Leu Pro Gly Leu Lys  
1055 1060 1065

Gly Asp Asn Gly Gln Thr Val Glu Ile Ser Gly Ser Pro Gly Pro  
1070 1075 1080

Lys Gly Gln Pro Gly Glu Ser Gly Phe Lys Gly Thr Lys Gly Arg  
1085 1090 1095

Asp Gly Leu Ile Gly Asn Ile Gly Phe Pro Gly Asn Lys Gly Glu  
1100 1105 1110

Asp Gly Lys Val Gly Val Ser Gly Asp Val Gly Leu Pro Gly Ala  
1115 1120 1125

Pro Gly Phe Pro Gly Val Ala Gly Met Arg Gly Glu Pro Gly Leu  
1130 1135 1140

Pro Gly Ser Ser Gly His Gln Gly Ala Ile Gly Pro Leu Gly Ser  
1145 1150 1155

Pro Gly Leu Ile Gly Pro Lys Gly Phe Pro Gly Phe Pro Gly Leu  
1160 1165 1170

His Gly Leu Asn Gly Leu Pro Gly Thr Lys Gly Thr His Gly Thr  
1175 1180 1185

Pro Gly Pro Ser Ile Thr Gly Val Pro Gly Pro Ala Gly Leu Pro

## 1190

1195

1200

Gly Pro Lys Gly Glu Lys Gly Tyr Pro Gly Ile Gly Ile Gly Ala  
1205 1210 1215

Pro Gly Lys Pro Gly Leu Arg Gly Gln Lys Gly Asp Arg Gly Phe  
1220 1225 1230

Pro Gly Leu Gln Gly Pro Ala Gly Leu Pro Gly Ala Pro Gly Ile  
1235 1240 1245

Ser Leu Pro Ser Leu Ile Ala Gly Gln Pro Gly Asp Pro Gly Arg  
1250 1255 1260

Pro Gly Leu Asp Gly Glu Arg Gly Arg Pro Gly Pro Ala Gly Pro  
1265 1270 1275

Pro Gly Pro Pro Gly Pro Ser Ser Asn Gln Gly Asp Thr Gly Asp  
1280 1285 1290

Pro Gly Phe Pro Gly Ile Pro Gly Pro Lys Gly Pro Lys Gly Asp  
1295 1300 1305

Gln Gly Ile Pro Gly Phe Ser Gly Leu Pro Gly Glu Leu Gly Leu  
1310 1315 1320

Lys Gly Met Arg Gly Glu Pro Gly Phe Met Gly Thr Pro Gly Lys  
1325 1330 1335

Val Gly Pro Pro Gly Asp Pro Gly Phe Pro Gly Met Lys Gly Lys  
1340 1345 1350

Ala Gly Pro Arg Gly Ser Ser Gly Leu Gln Gly Asp Pro Gly Gln  
1355 1360 1365

Thr Pro Thr Ala Glu Ala Val Gln Val Pro Pro Gly Pro Leu Gly  
1370 1375 1380

Leu Pro Gly Ile Asp Gly Ile Pro Gly Leu Thr Gly Asp Pro Gly  
1385 1390 1395

Ala Gln Gly Pro Val Gly Leu Gln Gly Ser Lys Gly Leu Pro Gly  
1400 1405 1410

Ile Pro Gly Lys Asp Gly Pro Ser Gly Leu Pro Gly Pro Pro Gly  
1415 1420 1425

Ala Leu Gly Asp Pro Gly Leu Pro Gly Leu Gln Gly Pro Pro Gly  
1430 1435 1440

Phe Glu Gly Ala Pro Gly Gln Gln Gly Pro Phe Gly Met Pro Gly



## FAB-008PC-SequenceListing

1445													
Met	Pro	Gly	Gln	Ser	Met	Arg	Val	Gly	Tyr	Thr	Leu	Val	Lys His
1460						1465					1470		
Ser	Gln	Ser	Glu	Gln	Val	Pro	Pro	Cys	Pro	Ile	Gly	Met	Ser Gln
1475						1480					1485		
Leu	Trp	Val	Gly	Tyr	Ser	Leu	Leu	Phe	Val	Glu	Gly	Gln	Glu Lys
1490						1495					1500		
Ala	His	Asn	Gln	Asp	Leu	Gly	Phe	Ala	Gly	Ser	Cys	Leu	Pro Arg
1505						1510					1515		
Phe	Ser	Thr	Met	Pro	Phe	Ile	Tyr	Cys	Asn	Ile	Asn	Glu	Val Cys
1520						1525					1530		
His	Tyr	Ala	Arg	Arg	Asn	Asp	Lys	Ser	Tyr	Trp	Leu	Ser	Thr Thr
1535						1540					1545		
Ala	Pro	Ile	Pro	Met	Met	Pro	Val	Ser	Gln	Thr	Gln	Ile	Pro Gln
1550						1555					1560		
Tyr	Ile	Ser	Arg	Cys	Ser	Val	Cys	Glu	Ala	Pro	Ser	Gln	Ala Ile
1565						1570					1575		
Ala	Val	His	Ser	Gln	Asp	Ile	Thr	Ile	Pro	Gln	Cys	Pro	Leu Gly
1580						1585					1590		
Trp	Arg	Ser	Leu	Trp	Ile	Gly	Tyr	Ser	Phe	Leu	Met	His	Thr Ala
1595						1600					1605		
Ala	Gly	Ala	Glu	Gly	Gly	Gly	Gln	Ser	Leu	Val	Ser	Pro	Gly Ser
1610						1615					1620		
Cys	Leu	Glu	Asp	Phe	Arg	Ala	Thr	Pro	Phe	Ile	Glu	Cys	Ser Gly
1625						1630					1635		
Ala	Arg	Gly	Thr	Cys	His	Tyr	Phe	Ala	Asn	Lys	Tyr	Ser	Phe Trp
1640						1645					1650		
Leu	Thr	Thr	Val	Glu	Glu	Arg	Gln	Gln	Phe	Gly	Glu	Leu	Pro Val
1655						1660					1665		
Ser	Glu	Thr	Leu	Lys	Ala	Gly	Gln	Leu	His	Thr	Arg	Val	Ser Arg
1670						1675					1680		
Cys	Gln	Val	Cys	Met	Lys	Ser	Leu						
1685						1690							

&lt;210&gt; 72

FAB-008PC-SequenceListing

<211> 1838  
 <212> PRT  
 <213> Homo sapiens

<400> 72

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Met Asp Val His Thr Arg Trp Lys Ala Arg Ser Ala Leu Arg Pro Gly
1          5          10          15

Ala Pro Leu Leu Pro Pro Leu Leu Leu Leu Leu Trp Ala Pro Pro
20          25          30

Pro Ser Arg Ala Ala Gln Pro Ala Asp Leu Leu Lys Val Leu Asp Phe
35          40          45

His Asn Leu Pro Asp Gly Ile Thr Lys Thr Thr Gly Phe Cys Ala Thr
50          55          60

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

Ala Gln Leu Ser Ala Pro Thr Lys Gln Leu Tyr Pro Ala Ser Ala Phe
85          90          95

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

Gln Ala Phe Leu Val Ser Ile Tyr Asn Glu Gln Gly Ile Gln Gln Ile
115        120        125

Gly Leu Glu Leu Gly Arg Ser Pro Val Phe Leu Tyr Glu Asp His Thr
130        135        140

Gly Lys Pro Gly Pro Glu Asp Tyr Pro Leu Phe Arg Gly Ile Asn Leu
145        150        155        160

Ser Asp Gly Lys Trp His Arg Ile Ala Leu Ser Val His Lys Lys Asn
165        170        175

Val Thr Leu Ile Leu Asp Cys Lys Lys Lys Thr Thr Lys Phe Leu Asp
180        185        190

Arg Ser Asp His Pro Met Ile Asp Ile Asn Gly Ile Ile Val Phe Gly
195        200        205

Thr Arg Ile Leu Asp Glu Glu Val Phe Glu Gly Asp Ile Gln Gln Leu
210        215        220

Leu Phe Val Ser Asp His Arg Ala Ala Tyr Asp Tyr Cys Glu His Tyr
225        230        235        240

Ser Pro Asp Cys Asp Thr Ala Val Pro Asp Thr Pro Gln Ser Gln Asp
245        250        255
    
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# FAB-008PC-SequenceListing

Pro Asn Pro Asp Glu Tyr Tyr Thr Glu Gly Asp Gly Glu Gly Glu Thr  
 260 265 270  
 Tyr Tyr Tyr Glu Tyr Pro Tyr Tyr Glu Asp Pro Glu Asp Leu Gly Lys  
 275 280 285  
 Glu Pro Thr Pro Ser Lys Lys Pro Val Glu Ala Ala Lys Glu Thr Thr  
 290 295 300  
 Glu Val Pro Glu Glu Leu Thr Pro Thr Pro Thr Glu Ala Ala Pro Met  
 305 310 315 320  
 Pro Glu Thr Ser Glu Gly Ala Gly Lys Glu Glu Asp Val Gly Ile Gly  
 325 330 335  
 Asp Tyr Asp Tyr Val Pro Ser Glu Asp Tyr Tyr Thr Pro Ser Pro Tyr  
 340 345 350  
 Asp Asp Leu Thr Tyr Gly Glu Gly Glu Glu Asn Pro Asp Gln Pro Thr  
 355 360 365  
 Asp Pro Gly Ala Gly Ala Glu Ile Pro Thr Ser Thr Ala Asp Thr Ser  
 370 375 380  
 Asn Ser Ser Asn Pro Ala Pro Pro Pro Gly Glu Gly Ala Asp Asp Leu  
 385 390 395 400  
 Glu Gly Glu Phe Thr Glu Glu Thr Ile Arg Asn Leu Asp Glu Asn Tyr  
 405 410 415  
 Tyr Asp Pro Tyr Tyr Asp Pro Thr Ser Ser Pro Ser Glu Ile Gly Pro  
 420 425 430  
 Gly Met Pro Ala Asn Gln Asp Thr Ile Tyr Glu Gly Ile Gly Gly Pro  
 435 440 445  
 Arg Gly Glu Lys Gly Gln Lys Gly Glu Pro Ala Ile Ile Glu Pro Gly  
 450 455 460  
 Met Leu Ile Glu Gly Pro Pro Gly Pro Glu Gly Pro Ala Gly Leu Pro  
 465 470 475 480  
 Gly Pro Pro Gly Thr Met Gly Pro Thr Gly Gln Val Gly Asp Pro Gly  
 485 490 495  
 Glu Arg Gly Pro Pro Gly Arg Pro Gly Leu Pro Gly Ala Asp Gly Leu  
 500 505 510  
 Pro Gly Pro Pro Gly Thr Met Leu Met Leu Pro Phe Arg Phe Gly Gly  
 515 520 525

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Gly Gly Asp Ala Gly Ser Lys Gly Pro Met Val Ser Ala Gln Glu Ser  
 530 535 540  
 Gln Ala Gln Ala Ile Leu Gln Gln Ala Arg Leu Ala Leu Arg Gly Pro  
 545 550 555 560  
 Ala Gly Pro Met Gly Leu Thr Gly Arg Pro Gly Pro Val Gly Pro Pro  
 565 570 575  
 Gly Ser Gly Gly Leu Lys Gly Glu Pro Gly Asp Val Gly Pro Gln Gly  
 580 585 590  
 Pro Arg Gly Val Gln Gly Pro Pro Gly Pro Ala Gly Lys Pro Gly Arg  
 595 600 605  
 Arg Gly Arg Ala Gly Ser Asp Gly Ala Arg Gly Met Pro Gly Gln Thr  
 610 615 620  
 Gly Pro Lys Gly Asp Arg Gly Phe Asp Gly Leu Ala Gly Leu Pro Gly  
 625 630 635 640  
 Glu Lys Gly His Arg Gly Asp Pro Gly Pro Ser Gly Pro Pro Gly Pro  
 645 650 655  
 Pro Gly Asp Asp Gly Glu Arg Gly Asp Asp Gly Glu Val Gly Pro Arg  
 660 665 670  
 Gly Leu Pro Gly Glu Pro Gly Pro Arg Gly Leu Leu Gly Pro Lys Gly  
 675 680 685  
 Pro Pro Gly Pro Pro Gly Pro Pro Gly Val Thr Gly Met Asp Gly Gln  
 690 695 700  
 Pro Gly Pro Lys Gly Asn Val Gly Pro Gln Gly Glu Pro Gly Pro Pro  
 705 710 715 720  
 Gly Gln Gln Gly Asn Pro Gly Ala Gln Gly Leu Pro Gly Pro Gln Gly  
 725 730 735  
 Ala Ile Gly Pro Pro Gly Glu Lys Gly Pro Leu Gly Lys Pro Gly Leu  
 740 745 750  
 Pro Gly Met Pro Gly Ala Asp Gly Pro Pro Gly His Pro Gly Lys Glu  
 755 760 765  
 Gly Pro Pro Gly Glu Lys Gly Gly Gln Gly Pro Pro Gly Pro Gln Gly  
 770 775 780  
 Pro Ile Gly Tyr Pro Gly Pro Arg Gly Val Lys Gly Ala Asp Gly Ile  
 785 790 795 800

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Arg Gly Leu Lys Gly Thr Lys Gly Glu Lys Gly Glu Asp Gly Phe Pro  
805 810 815

Gly Phe Lys Gly Asp Met Gly Ile Lys Gly Asp Arg Gly Glu Ile Gly  
820 825 830

Pro Pro Gly Pro Arg Gly Glu Asp Gly Pro Glu Gly Pro Lys Gly Arg  
835 840 845

Gly Gly Pro Asn Gly Asp Pro Gly Pro Leu Gly Pro Pro Gly Glu Lys  
850 855 860

Gly Lys Leu Gly Val Pro Gly Leu Pro Gly Tyr Pro Gly Arg Gln Gly  
865 870 875 880

Pro Lys Gly Ser Ile Gly Phe Pro Gly Phe Pro Gly Ala Asn Gly Glu  
885 890 895

Lys Gly Gly Arg Gly Thr Pro Gly Lys Pro Gly Pro Arg Gly Gln Arg  
900 905 910

Gly Pro Thr Gly Pro Arg Gly Glu Arg Gly Pro Arg Gly Ile Thr Gly  
915 920 925

Lys Pro Gly Pro Lys Gly Asn Ser Gly Gly Asp Gly Pro Ala Gly Pro  
930 935 940

Pro Gly Glu Arg Gly Pro Asn Gly Pro Gln Gly Pro Thr Gly Phe Pro  
945 950 955 960

Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly Lys Asp Gly Leu Pro Gly  
965 970 975

His Pro Gly Gln Arg Gly Glu Thr Gly Phe Gln Gly Lys Thr Gly Pro  
980 985 990

Pro Gly Pro Pro Gly Val Val Gly Pro Gln Gly Pro Thr Gly Glu Thr  
995 1000 1005

Gly Pro Met Gly Glu Arg Gly His Pro Gly Pro Pro Gly Pro Pro  
1010 1015 1020

Gly Glu Gln Gly Leu Pro Gly Leu Ala Gly Lys Glu Gly Thr Lys  
1025 1030 1035

Gly Asp Pro Gly Pro Ala Gly Leu Pro Gly Lys Asp Gly Pro Pro  
1040 1045 1050

Gly Leu Arg Gly Phe Pro Gly Asp Arg Gly Leu Pro Gly Pro Val  
1055 1060 1065

# FAB-008PC-SequenceListing

Gly	Ala	Leu	Gly	Leu	Lys	Gly	Asn	Glu	Gly	Pro	Pro	Gly	Pro	Pro
1070						1075					1080			
Gly	Pro	Ala	Gly	Ser	Pro	Gly	Glu	Arg	Gly	Pro	Ala	Gly	Ala	Ala
1085						1090					1095			
Gly	Pro	Ile	Gly	Ile	Pro	Gly	Arg	Pro	Gly	Pro	Gln	Gly	Pro	Pro
1100						1105					1110			
Gly	Pro	Ala	Gly	Glu	Lys	Gly	Ala	Pro	Gly	Glu	Lys	Gly	Pro	Gln
1115						1120					1125			
Gly	Pro	Ala	Gly	Arg	Asp	Gly	Leu	Gln	Gly	Pro	Val	Gly	Leu	Pro
1130						1135					1140			
Gly	Pro	Ala	Gly	Pro	Val	Gly	Pro	Pro	Gly	Glu	Asp	Gly	Asp	Lys
1145						1150					1155			
Gly	Glu	Ile	Gly	Glu	Pro	Gly	Gln	Lys	Gly	Ser	Lys	Gly	Asp	Lys
1160						1165					1170			
Gly	Glu	Gln	Gly	Pro	Pro	Gly	Pro	Thr	Gly	Pro	Gln	Gly	Pro	Ile
1175						1180					1185			
Gly	Gln	Pro	Gly	Pro	Ser	Gly	Ala	Asp	Gly	Glu	Pro	Gly	Pro	Arg
1190						1195					1200			
Gly	Gln	Gln	Gly	Leu	Phe	Gly	Gln	Lys	Gly	Asp	Glu	Gly	Pro	Arg
1205						1210					1215			
Gly	Phe	Pro	Gly	Pro	Pro	Gly	Pro	Val	Gly	Leu	Gln	Gly	Leu	Pro
1220						1225					1230			
Gly	Pro	Pro	Gly	Glu	Lys	Gly	Glu	Thr	Gly	Asp	Val	Gly	Gln	Met
1235						1240					1245			
Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Arg	Gly	Pro	Ser	Gly	Ala	Pro
1250						1255					1260			
Gly	Ala	Asp	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Gly	Ile	Gly	Asn	Pro
1265						1270					1275			
Gly	Ala	Val	Gly	Glu	Lys	Gly	Glu	Pro	Gly	Glu	Ala	Gly	Glu	Pro
1280						1285					1290			
Gly	Leu	Pro	Gly	Glu	Gly	Gly	Pro	Pro	Gly	Pro	Lys	Gly	Glu	Arg
1295						1300					1305			
Gly	Glu	Lys	Gly	Glu	Ser	Gly	Pro	Ser	Gly	Ala	Ala	Gly	Pro	Pro
1310						1315					1320			

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Gly	Pro	Lys	Gly	Pro	Pro	Gly	Asp	Asp	Gly	Pro	Lys	Gly	Ser	Pro
1325						1330					1335			
Gly	Pro	Val	Gly	Phe	Pro	Gly	Asp	Pro	Gly	Pro	Pro	Gly	Glu	Pro
1340						1345					1350			
Gly	Pro	Ala	Gly	Gln	Asp	Gly	Pro	Pro	Gly	Asp	Lys	Gly	Asp	Asp
1355						1360					1365			
Gly	Glu	Pro	Gly	Gln	Thr	Gly	Ser	Pro	Gly	Pro	Thr	Gly	Glu	Pro
1370						1375					1380			
Gly	Pro	Ser	Gly	Pro	Pro	Gly	Lys	Arg	Gly	Pro	Pro	Gly	Pro	Ala
1385						1390					1395			
Gly	Pro	Glu	Gly	Arg	Gln	Gly	Glu	Lys	Gly	Ala	Lys	Gly	Glu	Ala
1400						1405					1410			
Gly	Leu	Glu	Gly	Pro	Pro	Gly	Lys	Thr	Gly	Pro	Ile	Gly	Pro	Gln
1415						1420					1425			
Gly	Ala	Pro	Gly	Lys	Pro	Gly	Pro	Asp	Gly	Leu	Arg	Gly	Ile	Pro
1430						1435					1440			
Gly	Pro	Val	Gly	Glu	Gln	Gly	Leu	Pro	Gly	Ser	Pro	Gly	Pro	Asp
1445						1450					1455			
Gly	Pro	Pro	Gly	Pro	Met	Gly	Pro	Pro	Gly	Leu	Pro	Gly	Leu	Lys
1460						1465					1470			
Gly	Asp	Ser	Gly	Pro	Lys	Gly	Glu	Lys	Gly	His	Pro	Gly	Leu	Ile
1475						1480					1485			
Gly	Leu	Ile	Gly	Pro	Pro	Gly	Glu	Gln	Gly	Glu	Lys	Gly	Asp	Arg
1490						1495					1500			
Gly	Leu	Pro	Gly	Pro	Gln	Gly	Ser	Ser	Gly	Pro	Lys	Gly	Glu	Gln
1505						1510					1515			
Gly	Ile	Thr	Gly	Pro	Ser	Gly	Pro	Ile	Gly	Pro	Pro	Gly	Pro	Pro
1520						1525					1530			
Gly	Leu	Pro	Gly	Pro	Pro	Gly	Pro	Lys	Gly	Ala	Lys	Gly	Ser	Ser
1535						1540					1545			
Gly	Pro	Thr	Gly	Pro	Lys	Gly	Glu	Ala	Gly	His	Pro	Gly	Pro	Pro
1550						1555					1560			
Gly	Pro	Pro	Gly	Pro	Pro	Gly	Glu	Val	Ile	Gln	Pro	Leu	Pro	Ile
1565						1570					1575			

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Gln	Ala	Ser	Arg	Thr	Arg	Arg	Asn	Ile	Asp	Ala	Ser	Gln	Leu	Leu
	1580					1585					1590			
Asp	Asp	Gly	Asn	Gly	Glu	Asn	Tyr	Val	Asp	Tyr	Ala	Asp	Gly	Met
	1595					1600					1605			
Glu	Glu	Ile	Phe	Gly	Ser	Leu	Asn	Ser	Leu	Lys	Leu	Glu	Ile	Glu
	1610					1615					1620			
Gln	Met	Lys	Arg	Pro	Leu	Gly	Thr	Gln	Gln	Asn	Pro	Ala	Arg	Thr
	1625					1630					1635			
Cys	Lys	Asp	Leu	Gln	Leu	Cys	His	Pro	Asp	Phe	Pro	Asp	Gly	Glu
	1640					1645					1650			
Tyr	Trp	Val	Asp	Pro	Asn	Gln	Gly	Cys	Ser	Arg	Asp	Ser	Phe	Lys
	1655					1660					1665			
Val	Tyr	Cys	Asn	Phe	Thr	Ala	Gly	Gly	Ser	Thr	Cys	Val	Phe	Pro
	1670					1675					1680			
Asp	Lys	Lys	Ser	Glu	Gly	Ala	Arg	Ile	Thr	Ser	Trp	Pro	Lys	Glu
	1685					1690					1695			
Asn	Pro	Gly	Ser	Trp	Phe	Ser	Glu	Phe	Lys	Arg	Gly	Lys	Leu	Leu
	1700					1705					1710			
Ser	Tyr	Val	Asp	Ala	Glu	Gly	Asn	Pro	Val	Gly	Val	Val	Gln	Met
	1715					1720					1725			
Thr	Phe	Leu	Arg	Leu	Leu	Ser	Ala	Ser	Ala	His	Gln	Asn	Val	Thr
	1730					1735					1740			
Tyr	His	Cys	Tyr	Gln	Ser	Val	Ala	Trp	Gln	Asp	Ala	Ala	Thr	Gly
	1745					1750					1755			
Ser	Tyr	Asp	Lys	Ala	Leu	Arg	Phe	Leu	Gly	Ser	Asn	Asp	Glu	Glu
	1760					1765					1770			
Met	Ser	Tyr	Asp	Asn	Asn	Pro	Tyr	Ile	Arg	Ala	Leu	Val	Asp	Gly
	1775					1780					1785			
Cys	Ala	Thr	Lys	Lys	Gly	Tyr	Gln	Lys	Thr	Val	Leu	Glu	Ile	Asp
	1790					1795					1800			
Thr	Pro	Lys	Val	Glu	Gln	Val	Pro	Ile	Val	Asp	Ile	Met	Phe	Asn
	1805					1810					1815			
Asp	Phe	Gly	Glu	Ala	Ser	Gln	Lys	Phe	Gly	Phe	Glu	Val	Gly	Pro
	1820					1825					1830			



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Ala Cys Phe Met Gly  
1835

<210> 73  
<211> 1499  
<212> PRT  
<213> Homo sapiens

<400> 73

Met Met Ala Asn Trp Ala Glu Ala Arg Pro Leu Leu Ile Leu Ile Val  
1 5 10 15

Leu Leu Gly Gln Phe Val Ser Ile Lys Ala Gln Glu Glu Asp Glu Asp  
20 25 30

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

Leu Asn Arg Asp Ile Trp Lys Pro Ala Pro Cys Gln Ile Cys Val Cys  
50 55 60

Asp Asn Gly Ala Ile Leu Cys Asp Lys Ile Glu Cys Gln Asp Val Leu  
65 70 75 80

Asp Cys Ala Asp Pro Val Thr Pro Pro Gly Glu Cys Cys Pro Val Cys  
85 90 95

Ser Gln Thr Pro Gly Gly Gly Asn Thr Asn Phe Gly Arg Gly Arg Lys  
100 105 110

Gly Gln Lys Gly Glu Pro Gly Leu Val Pro Val Val Thr Gly Ile Arg  
115 120 125

Gly Arg Pro Gly Pro Ala Gly Pro Pro Gly Ser Gln Gly Pro Arg Gly  
130 135 140

Glu Arg Gly Pro Lys Gly Arg Pro Gly Pro Arg Gly Pro Gln Gly Ile  
145 150 155 160

Asp Gly Glu Pro Gly Val Pro Gly Gln Pro Gly Ala Pro Gly Pro Pro  
165 170 175

Gly His Pro Ser His Pro Gly Pro Asp Gly Leu Ser Arg Pro Phe Ser  
180 185 190

Ala Gln Met Ala Gly Leu Asp Glu Lys Ser Gly Leu Gly Ser Gln Val  
195 200 205

Gly Leu Met Pro Gly Ser Val Gly Pro Val Gly Pro Arg Gly Pro Gln  
210 215 220

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Gly Leu Gln Gly Gln Gln Gly Gly Ala Gly Pro Thr Gly Pro Pro Gly  
 225 230 235 240  
 Glu Pro Gly Asp Pro Gly Pro Met Gly Pro Ile Gly Ser Arg Gly Pro  
 245 250 255  
 Glu Gly Pro Pro Gly Lys Pro Gly Glu Asp Gly Glu Pro Gly Arg Asn  
 260 265 270  
 Gly Asn Pro Gly Glu Val Gly Phe Ala Gly Ser Pro Gly Ala Arg Gly  
 275 280 285  
 Phe Pro Gly Ala Pro Gly Leu Pro Gly Leu Lys Gly His Arg Gly His  
 290 295 300  
 Lys Gly Leu Glu Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Ser Lys  
 305 310 315 320  
 Gly Glu Ala Gly Pro Thr Gly Pro Met Gly Ala Met Gly Pro Leu Gly  
 325 330 335  
 Pro Arg Gly Met Pro Gly Glu Arg Gly Arg Leu Gly Pro Gln Gly Ala  
 340 345 350  
 Pro Gly Gln Arg Gly Ala His Gly Met Pro Gly Lys Pro Gly Pro Met  
 355 360 365  
 Gly Pro Leu Gly Ile Pro Gly Ser Ser Gly Phe Pro Gly Asn Pro Gly  
 370 375 380  
 Met Lys Gly Glu Ala Gly Pro Thr Gly Ala Arg Gly Pro Glu Gly Pro  
 385 390 395 400  
 Gln Gly Gln Arg Gly Glu Thr Gly Pro Pro Gly Pro Val Gly Ser Pro  
 405 410 415  
 Gly Leu Pro Gly Ala Ile Gly Thr Asp Gly Thr Pro Gly Ala Lys Gly  
 420 425 430  
 Pro Thr Gly Ser Pro Gly Thr Ser Gly Pro Pro Gly Ser Ala Gly Pro  
 435 440 445  
 Pro Gly Ser Pro Gly Pro Gln Gly Ser Thr Gly Pro Gln Gly Ile Arg  
 450 455 460  
 Gly Gln Pro Gly Asp Pro Gly Val Pro Gly Phe Lys Gly Glu Ala Gly  
 465 470 475 480  
 Pro Lys Gly Glu Pro Gly Pro His Gly Ile Gln Gly Pro Ile Gly Pro  
 485 490 495

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Pro Gly Glu Glu Gly Lys Arg Gly Pro Arg Gly Asp Pro Gly Thr Val  
500 505 510

Gly Pro Pro Gly Pro Val Gly Glu Arg Gly Ala Pro Gly Asn Arg Gly  
515 520 525

Phe Pro Gly Ser Asp Gly Leu Pro Gly Pro Lys Gly Ala Gln Gly Glu  
530 535 540

Arg Gly Pro Val Gly Ser Ser Gly Pro Lys Gly Ser Gln Gly Asp Pro  
545 550 555 560

Gly Arg Pro Gly Glu Pro Gly Leu Pro Gly Ala Arg Gly Leu Thr Gly  
565 570 575

Asn Pro Gly Val Gln Gly Pro Glu Gly Lys Leu Gly Pro Leu Gly Ala  
580 585 590

Pro Gly Glu Asp Gly Arg Pro Gly Pro Pro Gly Ser Ile Gly Ile Arg  
595 600 605

Gly Gln Pro Gly Ser Met Gly Leu Pro Gly Pro Lys Gly Ser Ser Gly  
610 615 620

Asp Pro Gly Lys Pro Gly Glu Ala Gly Asn Ala Gly Val Pro Gly Gln  
625 630 635 640

Arg Gly Ala Pro Gly Lys Asp Gly Glu Val Gly Pro Ser Gly Pro Val  
645 650 655

Gly Pro Pro Gly Leu Ala Gly Glu Arg Gly Glu Gln Gly Pro Pro Gly  
660 665 670

Pro Thr Gly Phe Gln Gly Leu Pro Gly Pro Pro Gly Pro Pro Gly Glu  
675 680 685

Gly Gly Lys Pro Gly Asp Gln Gly Val Pro Gly Asp Pro Gly Ala Val  
690 695 700

Gly Pro Leu Gly Pro Arg Gly Glu Arg Gly Asn Pro Gly Glu Arg Gly  
705 710 715 720

Glu Pro Gly Ile Thr Gly Leu Pro Gly Glu Lys Gly Met Ala Gly Gly  
725 730 735

His Gly Pro Asp Gly Pro Lys Gly Ser Pro Gly Pro Ser Gly Thr Pro  
740 745 750

Gly Asp Thr Gly Pro Pro Gly Leu Gln Gly Met Pro Gly Glu Arg Gly  
755 760 765

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Ile Ala Gly Thr Pro Gly Pro Lys Gly Asp Arg Gly Gly Ile Gly Glu  
770 775 780

Lys Gly Ala Glu Gly Thr Ala Gly Asn Asp Gly Ala Arg Gly Leu Pro  
785 790 795 800

Gly Pro Leu Gly Pro Pro Gly Pro Ala Gly Pro Thr Gly Glu Lys Gly  
805 810 815

Glu Pro Gly Pro Arg Gly Leu Val Gly Pro Pro Gly Ser Arg Gly Asn  
820 825 830

Pro Gly Ser Arg Gly Glu Asn Gly Pro Thr Gly Ala Val Gly Phe Ala  
835 840 845

Gly Pro Gln Gly Pro Asp Gly Gln Pro Gly Val Lys Gly Glu Pro Gly  
850 855 860

Glu Pro Gly Gln Lys Gly Asp Ala Gly Ser Pro Gly Pro Gln Gly Leu  
865 870 875 880

Ala Gly Ser Pro Gly Pro His Gly Pro Asn Gly Val Pro Gly Leu Lys  
885 890 895

Gly Gly Arg Gly Thr Gln Gly Pro Pro Gly Ala Thr Gly Phe Pro Gly  
900 905 910

Ser Ala Gly Arg Val Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Pro  
915 920 925

Ala Gly Pro Leu Gly Glu Pro Gly Lys Glu Gly Pro Pro Gly Leu Arg  
930 935 940

Gly Asp Pro Gly Ser His Gly Arg Val Gly Asp Arg Gly Pro Ala Gly  
945 950 955 960

Pro Pro Gly Gly Pro Gly Asp Lys Gly Asp Pro Gly Glu Asp Gly Gln  
965 970 975

Pro Gly Pro Asp Gly Pro Pro Gly Pro Ala Gly Thr Thr Gly Gln Arg  
980 985 990

Gly Ile Val Gly Met Pro Gly Gln Arg Gly Glu Arg Gly Met Pro Gly  
995 1000 1005

Leu Pro Gly Pro Ala Gly Thr Pro Gly Lys Val Gly Pro Thr Gly  
1010 1015 1020

Ala Thr Gly Asp Lys Gly Pro Pro Gly Pro Val Gly Pro Pro Gly  
1025 1030 1035

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Ser	Asn 1040	Gly	Pro	Val	Gly	Glu 1045	Pro	Gly	Pro	Glu	Gly 1050	Pro	Ala	Gly
Asn	Asp 1055	Gly	Thr	Pro	Gly	Arg 1060	Asp	Gly	Ala	Val	Gly 1065	Glu	Arg	Gly
Asp	Arg 1070	Gly	Asp	Pro	Gly	Pro 1075	Ala	Gly	Leu	Pro	Gly 1080	Ser	Gln	Gly
Ala	Pro 1085	Gly	Thr	Pro	Gly	Pro 1090	Val	Gly	Ala	Pro	Gly 1095	Asp	Ala	Gly
Gln	Arg 1100	Gly	Asp	Pro	Gly	Ser 1105	Arg	Gly	Pro	Ile	Gly 1110	Pro	Pro	Gly
Arg	Ala 1115	Gly	Lys	Arg	Gly	Leu 1120	Pro	Gly	Pro	Gln	Gly 1125	Pro	Arg	Gly
Asp	Lys 1130	Gly	Asp	His	Gly	Asp 1135	Arg	Gly	Asp	Arg	Gly 1140	Gln	Lys	Gly
His	Arg 1145	Gly	Phe	Thr	Gly	Leu 1150	Gln	Gly	Leu	Pro	Gly 1155	Pro	Pro	Gly
Pro	Asn 1160	Gly	Glu	Gln	Gly	Ser 1165	Ala	Gly	Ile	Pro	Gly 1170	Pro	Phe	Gly
Pro	Arg 1175	Gly	Pro	Pro	Gly	Pro 1180	Val	Gly	Pro	Ser	Gly 1185	Lys	Glu	Gly
Asn	Pro 1190	Gly	Pro	Leu	Gly	Pro 1195	Ile	Gly	Pro	Pro	Gly 1200	Val	Arg	Gly
Ser	Val 1205	Gly	Glu	Ala	Gly	Pro 1210	Glu	Gly	Pro	Pro	Gly 1215	Glu	Pro	Gly
Pro	Pro 1220	Gly	Pro	Pro	Gly	Pro 1225	Pro	Gly	His	Leu	Thr 1230	Ala	Ala	Leu
Gly	Asp 1235	Ile	Met	Gly	His	Tyr 1240	Asp	Glu	Ser	Met	Pro 1245	Asp	Pro	Leu
Pro	Glu 1250	Phe	Thr	Glu	Asp	Gln 1255	Ala	Ala	Pro	Asp	Asp 1260	Lys	Asn	Lys
Thr	Asp 1265	Pro	Gly	Val	His	Ala 1270	Thr	Leu	Lys	Ser	Leu 1275	Ser	Ser	Gln
Ile	Glu 1280	Thr	Met	Arg	Ser	Pro 1285	Asp	Gly	Ser	Lys	Lys 1290	His	Pro	Ala

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Arg Thr Cys Asp Asp Leu Lys Leu Cys His Ser Ala Lys Gln Ser  
1295 1300 1305

Gly Glu Tyr Trp Ile Asp Pro Asn Gln Gly Ser Val Glu Asp Ala  
1310 1315 1320

Ile Lys Val Tyr Cys Asn Met Glu Thr Gly Glu Thr Cys Ile Ser  
1325 1330 1335

Ala Asn Pro Ser Ser Val Pro Arg Lys Thr Trp Trp Ala Ser Lys  
1340 1345 1350

Ser Pro Asp Asn Lys Pro Val Trp Tyr Gly Leu Asp Met Asn Arg  
1355 1360 1365

Gly Ser Gln Phe Ala Tyr Gly Asp His Gln Ser Pro Asn Thr Ala  
1370 1375 1380

Ile Thr Gln Met Thr Phe Leu Arg Leu Leu Ser Lys Glu Ala Ser  
1385 1390 1395

Gln Asn Ile Thr Tyr Ile Cys Lys Asn Ser Val Gly Tyr Met Asp  
1400 1405 1410

Asp Gln Ala Lys Asn Leu Lys Lys Ala Val Val Leu Lys Gly Ala  
1415 1420 1425

Asn Asp Leu Asp Ile Lys Ala Glu Gly Asn Ile Arg Phe Arg Tyr  
1430 1435 1440

Ile Val Leu Gln Asp Thr Cys Ser Lys Arg Asn Gly Asn Val Gly  
1445 1450 1455

Lys Thr Val Phe Glu Tyr Arg Thr Gln Asn Val Ala Arg Leu Pro  
1460 1465 1470

Ile Ile Asp Leu Ala Pro Val Asp Val Gly Gly Thr Asp Gln Glu  
1475 1480 1485

Phe Gly Val Glu Ile Gly Pro Val Cys Phe Val  
1490 1495

<210> 74  
<211> 1745  
<212> PRT  
<213> Homo sapiens

<400> 74

Met Gly Asn Arg Arg Asp Leu Gly Gln Pro Arg Ala Gly Leu Cys Leu  
1 5 10 15

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Leu Leu Ala Ala Leu Gln Leu Leu Pro Gly Thr Gln Ala Asp Pro Val  
20 25 30

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

Glu Gly Pro Gly Phe Cys Pro Gln Arg Thr Pro Glu Gly Asp Arg Ala  
50 55 60

Phe Arg Ile Gly Gln Ala Ser Thr Leu Gly Ile Pro Thr Trp Glu Leu  
65 70 75 80

Phe Pro Glu Gly His Phe Pro Glu Asn Phe Ser Leu Leu Ile Thr Leu  
85 90 95

Arg Gly Gln Pro Ala Asn Gln Ser Val Leu Leu Ser Ile Tyr Asp Glu  
100 105 110

Arg Gly Ala Arg Gln Leu Gly Leu Ala Leu Gly Pro Ala Leu Gly Leu  
115 120 125

Leu Gly Asp Pro Phe Arg Pro Leu Pro Gln Gln Val Asn Leu Thr Asp  
130 135 140

Gly Arg Trp His Arg Val Ala Val Ser Ile Asp Gly Glu Met Val Thr  
145 150 155 160

Leu Val Ala Asp Cys Glu Ala Gln Pro Pro Val Leu Gly His Gly Pro  
165 170 175

Arg Phe Ile Ser Ile Ala Gly Leu Thr Val Leu Gly Thr Gln Asp Leu  
180 185 190

Gly Glu Lys Thr Phe Glu Gly Asp Ile Gln Glu Leu Leu Ile Ser Pro  
195 200 205

Asp Pro Gln Ala Ala Phe Gln Ala Cys Glu Arg Tyr Leu Pro Asp Cys  
210 215 220

Asp Asn Leu Ala Pro Ala Ala Thr Val Ala Pro Gln Gly Glu Pro Glu  
225 230 235 240

Thr Pro Arg Pro Arg Arg Lys Gly Lys Gly Lys Gly Arg Lys Lys Gly  
245 250 255

Arg Gly Arg Lys Gly Lys Gly Arg Lys Lys Asn Lys Glu Ile Trp Thr  
260 265 270

Ser Ser Pro Pro Pro Asp Ser Ala Glu Asn Gln Thr Ser Thr Asp Ile  
275 280 285

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Pro Lys Thr Glu Thr Pro Ala Pro Asn Leu Pro Pro Thr Pro Thr Pro  
 290 295 300  
 Leu Val Val Thr Ser Thr Val Thr Thr Gly Leu Asn Ala Thr Ile Leu  
 305 310 315 320  
 Glu Arg Ser Leu Asp Pro Asp Ser Gly Thr Glu Leu Gly Thr Leu Glu  
 325 330 335  
 Thr Lys Ala Ala Arg Glu Asp Glu Glu Gly Asp Asp Ser Thr Met Gly  
 340 345 350  
 Pro Asp Phe Arg Ala Ala Glu Tyr Pro Ser Arg Thr Gln Phe Gln Ile  
 355 360 365  
 Phe Pro Gly Ala Gly Glu Lys Gly Ala Lys Gly Glu Pro Ala Val Ile  
 370 375 380  
 Glu Lys Gly Gln Gln Phe Glu Gly Pro Pro Gly Ala Pro Gly Pro Gln  
 385 390 395 400  
 Gly Val Val Gly Pro Ser Gly Pro Pro Gly Pro Pro Gly Phe Pro Gly  
 405 410 415  
 Asp Pro Gly Pro Pro Gly Pro Ala Gly Leu Pro Gly Ile Pro Gly Ile  
 420 425 430  
 Asp Gly Ile Arg Gly Pro Pro Gly Thr Val Ile Met Met Pro Phe Gln  
 435 440 445  
 Phe Ala Gly Gly Ser Phe Lys Gly Pro Pro Val Ser Phe Gln Gln Ala  
 450 455 460  
 Gln Ala Gln Ala Val Leu Gln Gln Thr Gln Leu Ser Met Lys Gly Pro  
 465 470 475 480  
 Pro Gly Pro Val Gly Leu Thr Gly Arg Pro Gly Pro Val Gly Leu Pro  
 485 490 495  
 Gly His Pro Gly Leu Lys Gly Glu Glu Gly Ala Glu Gly Pro Gln Gly  
 500 505 510  
 Pro Arg Gly Leu Gln Gly Pro His Gly Pro Pro Gly Arg Val Gly Lys  
 515 520 525  
 Met Gly Arg Pro Gly Ala Asp Gly Ala Arg Gly Leu Pro Gly Asp Thr  
 530 535 540  
 Gly Pro Lys Gly Asp Arg Gly Phe Asp Gly Leu Pro Gly Leu Pro Gly  
 545 550 555 560



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Glu Lys Gly Gln Arg Gly Asp Phe Gly His Val Gly Gln Pro Gly Pro  
565 570 575

Pro Gly Glu Asp Gly Glu Arg Gly Ala Glu Gly Pro Pro Gly Pro Thr  
580 585 590

Gly Gln Ala Gly Glu Pro Gly Pro Arg Gly Leu Leu Gly Pro Arg Gly  
595 600 605

Ser Pro Gly Pro Thr Gly Arg Pro Gly Val Thr Gly Ile Asp Gly Ala  
610 615 620

Pro Gly Ala Lys Gly Asn Val Gly Pro Pro Gly Glu Pro Gly Pro Pro  
625 630 635 640

Gly Gln Gln Gly Asn His Gly Ser Gln Gly Leu Pro Gly Pro Gln Gly  
645 650 655

Leu Ile Gly Thr Pro Gly Glu Lys Gly Pro Pro Gly Asn Pro Gly Ile  
660 665 670

Pro Gly Leu Pro Gly Ser Asp Gly Pro Leu Gly His Pro Gly His Glu  
675 680 685

Gly Pro Thr Gly Glu Lys Gly Ala Gln Gly Pro Pro Gly Ser Ala Gly  
690 695 700

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

Arg Gly Leu Gln Gly Glu Lys Gly Glu Lys Gly Glu Asp Gly Phe Pro  
725 730 735

Gly Phe Lys Gly Asp Val Gly Leu Lys Gly Asp Gln Gly Lys Pro Gly  
740 745 750

Ala Pro Gly Pro Arg Gly Glu Asp Gly Pro Glu Gly Pro Lys Gly Gln  
755 760 765

Ala Gly Gln Ala Gly Glu Glu Gly Pro Pro Gly Ser Ala Gly Glu Lys  
770 775 780

Gly Lys Leu Gly Val Pro Gly Leu Pro Gly Tyr Pro Gly Arg Pro Gly  
785 790 795 800

Pro Lys Gly Ser Ile Gly Phe Pro Gly Pro Leu Gly Pro Ile Gly Glu  
805 810 815

Lys Gly Lys Ser Gly Lys Thr Gly Gln Pro Gly Leu Glu Gly Glu Arg  
820 825 830

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Gly Pro Pro Gly Ser Arg Gly Glu Arg Gly Gln Pro Gly Ala Thr Gly  
 835 840 845

Gln Pro Gly Pro Lys Gly Asp Val Gly Gln Asp Gly Ala Pro Gly Ile  
 850 855 860

Pro Gly Glu Lys Gly Leu Pro Gly Leu Gln Gly Pro Pro Gly Phe Pro  
 865 870 875 880

Gly Pro Lys Gly Pro Pro Gly His Gln Gly Lys Asp Gly Arg Pro Gly  
 885 890 895

His Pro Gly Gln Arg Gly Glu Leu Gly Phe Gln Gly Gln Thr Gly Pro  
 900 905 910

Pro Gly Pro Ala Gly Val Leu Gly Pro Gln Gly Lys Thr Gly Glu Val  
 915 920 925

Gly Pro Leu Gly Glu Arg Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly  
 930 935 940

Glu Gln Gly Leu Pro Gly Leu Glu Gly Arg Glu Gly Ala Lys Gly Glu  
 945 950 955 960

Leu Gly Pro Pro Gly Pro Leu Gly Lys Glu Gly Pro Ala Gly Leu Arg  
 965 970 975

Gly Phe Pro Gly Pro Lys Gly Gly Pro Gly Asp Pro Gly Pro Thr Gly  
 980 985 990

Leu Lys Gly Asp Lys Gly Pro Pro Gly Pro Val Gly Ala Asn Gly Ser  
 995 1000 1005

Pro Gly Glu Arg Gly Pro Leu Gly Pro Ala Gly Gly Ile Gly Leu  
 1010 1015 1020

Pro Gly Gln Ser Gly Ser Glu Gly Pro Val Gly Pro Ala Gly Lys  
 1025 1030 1035

Lys Gly Ser Arg Gly Glu Arg Gly Pro Pro Gly Pro Thr Gly Lys  
 1040 1045 1050

Asp Gly Ile Pro Gly Pro Leu Gly Pro Leu Gly Pro Pro Gly Ala  
 1055 1060 1065

Ala Gly Pro Ser Gly Glu Glu Gly Asp Lys Gly Asp Val Gly Ala  
 1070 1075 1080

Pro Gly His Lys Gly Ser Lys Gly Asp Lys Gly Asp Ala Gly Pro  
 1085 1090 1095

## FAB-008PC-SequenceListing

Pro	Gly	Gln	Pro	Gly	Ile	Arg	Gly	Pro	Ala	Gly	His	Pro	Gly	Pro
	1100					1105					1110			
Pro	Gly	Ala	Asp	Gly	Ala	Gln	Gly	Arg	Arg	Gly	Pro	Pro	Gly	Leu
	1115					1120					1125			
Phe	Gly	Gln	Lys	Gly	Asp	Asp	Gly	Val	Arg	Gly	Phe	Val	Gly	Val
	1130					1135					1140			
Ile	Gly	Pro	Pro	Gly	Leu	Gln	Gly	Leu	Pro	Gly	Pro	Pro	Gly	Glu
	1145					1150					1155			
Lys	Gly	Glu	Val	Gly	Asp	Val	Gly	Ser	Met	Gly	Pro	His	Gly	Ala
	1160					1165					1170			
Pro	Gly	Pro	Arg	Gly	Pro	Gln	Gly	Pro	Thr	Gly	Ser	Glu	Gly	Thr
	1175					1180					1185			
Pro	Gly	Leu	Pro	Gly	Gly	Val	Gly	Gln	Pro	Gly	Ala	Val	Gly	Glu
	1190					1195					1200			
Lys	Gly	Glu	Arg	Gly	Asp	Ala	Gly	Asp	Pro	Gly	Pro	Pro	Gly	Ala
	1205					1210					1215			
Pro	Gly	Ile	Pro	Gly	Pro	Lys	Gly	Asp	Ile	Gly	Glu	Lys	Gly	Asp
	1220					1225					1230			
Ser	Gly	Pro	Ser	Gly	Ala	Ala	Gly	Pro	Pro	Gly	Lys	Lys	Gly	Pro
	1235					1240					1245			
Pro	Gly	Glu	Asp	Gly	Ala	Lys	Gly	Ser	Val	Gly	Pro	Thr	Gly	Leu
	1250					1255					1260			
Pro	Gly	Asp	Leu	Gly	Pro	Pro	Gly	Asp	Pro	Gly	Val	Ser	Gly	Ile
	1265					1270					1275			
Asp	Gly	Ser	Pro	Gly	Glu	Lys	Gly	Asp	Pro	Gly	Asp	Val	Gly	Gly
	1280					1285					1290			
Pro	Gly	Pro	Pro	Gly	Ala	Ser	Gly	Glu	Pro	Gly	Ala	Pro	Gly	Pro
	1295					1300					1305			
Pro	Gly	Lys	Arg	Gly	Pro	Ser	Gly	His	Met	Gly	Arg	Glu	Gly	Arg
	1310					1315					1320			
Glu	Gly	Glu	Lys	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Pro	Asp	Gly	Pro
	1325					1330					1335			
Pro	Gly	Arg	Thr	Gly	Pro	Met	Gly	Ala	Arg	Gly	Pro	Pro	Gly	Arg
	1340					1345					1350			

## FAB-008PC-SequenceListing

Val	Gly	Pro	Glu	Gly	Leu	Arg	Gly	Ile	Pro	Gly	Pro	Val	Gly	Glu
	1355					1360					1365			
Pro	Gly	Leu	Leu	Gly	Ala	Pro	Gly	Gln	Met	Gly	Pro	Pro	Gly	Pro
	1370					1375					1380			
Leu	Gly	Pro	Ser	Gly	Leu	Pro	Gly	Leu	Lys	Gly	Asp	Thr	Gly	Pro
	1385					1390					1395			
Lys	Gly	Glu	Lys	Gly	His	Ile	Gly	Leu	Ile	Gly	Leu	Ile	Gly	Pro
	1400					1405					1410			
Pro	Gly	Glu	Ala	Gly	Glu	Lys	Gly	Asp	Gln	Gly	Leu	Pro	Gly	Val
	1415					1420					1425			
Gln	Gly	Pro	Pro	Gly	Pro	Lys	Gly	Asp	Pro	Gly	Pro	Pro	Gly	Pro
	1430					1435					1440			
Ile	Gly	Ser	Leu	Gly	His	Pro	Gly	Pro	Pro	Gly	Val	Ala	Gly	Pro
	1445					1450					1455			
Leu	Gly	Gln	Lys	Gly	Ser	Lys	Gly	Ser	Pro	Gly	Ser	Met	Gly	Pro
	1460					1465					1470			
Arg	Gly	Asp	Thr	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ala
	1475					1480					1485			
Pro	Ala	Glu	Leu	His	Gly	Leu	Arg	Arg	Arg	Arg	Arg	Phe	Val	Pro
	1490					1495					1500			
Val	Pro	Leu	Pro	Val	Val	Glu	Gly	Gly	Leu	Glu	Glu	Val	Leu	Ala
	1505					1510					1515			
Ser	Leu	Thr	Ser	Leu	Ser	Leu	Glu	Leu	Glu	Gln	Leu	Arg	Arg	Pro
	1520					1525					1530			
Pro	Gly	Thr	Ala	Glu	Arg	Pro	Gly	Leu	Val	Cys	His	Glu	Leu	His
	1535					1540					1545			
Arg	Asn	His	Pro	His	Leu	Pro	Asp	Gly	Glu	Tyr	Trp	Ile	Asp	Pro
	1550					1555					1560			
Asn	Gln	Gly	Cys	Ala	Arg	Asp	Ser	Phe	Arg	Val	Phe	Cys	Asn	Phe
	1565					1570					1575			
Thr	Ala	Gly	Gly	Glu	Thr	Cys	Leu	Tyr	Pro	Asp	Lys	Lys	Phe	Glu
	1580					1585					1590			
Ile	Val	Lys	Leu	Ala	Ser	Trp	Ser	Lys	Glu	Lys	Pro	Gly	Gly	Trp
	1595					1600					1605			

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Tyr Ser Thr Phe Arg Arg Gly Lys Lys Phe Ser Tyr Val Asp Ala  
1610 1615 1620

Asp Gly Ser Pro Val Asn Val Val Gln Leu Asn Phe Leu Lys Leu  
1625 1630 1635

Leu Ser Ala Thr Ala Arg Gln Asn Phe Thr Tyr Ser Cys Gln Asn  
1640 1645 1650

Ala Ala Ala Trp Leu Asp Glu Ala Thr Gly Asp Tyr Ser His Ser  
1655 1660 1665

Ala Arg Phe Leu Gly Thr Asn Gly Glu Glu Leu Ser Phe Asn Gln  
1670 1675 1680

Thr Thr Ala Ala Thr Val Ser Val Pro Gln Asp Gly Cys Arg Leu  
1685 1690 1695

Arg Lys Gly Gln Thr Lys Thr Leu Phe Glu Phe Ser Ser Ser Arg  
1700 1705 1710

Ala Gly Phe Leu Pro Leu Trp Asp Val Ala Ala Thr Asp Phe Gly  
1715 1720 1725

Gln Thr Asn Gln Lys Phe Gly Phe Glu Leu Gly Pro Val Cys Phe  
1730 1735 1740

Ser Ser  
1745

<210> 75  
<211> 1028  
<212> PRT  
<213> Homo sapiens

<400> 75

Met Arg Ala Ala Arg Ala Leu Leu Pro Leu Leu Leu Gln Ala Cys Trp  
1 5 10 15

Thr Ala Ala Gln Asp Glu Pro Glu Thr Pro Arg Ala Val Ala Phe Gln  
20 25 30

Asp Cys Pro Val Asp Leu Phe Phe Val Leu Asp Thr Ser Glu Ser Val  
35 40 45

Ala Leu Arg Leu Lys Pro Tyr Gly Ala Leu Val Asp Lys Val Lys Ser  
50 55 60

Phe Thr Lys Arg Phe Ile Asp Asn Leu Arg Asp Arg Tyr Tyr Arg Cys  
65 70 75 80

Asp Arg Asn Leu Val Trp Asn Ala Gly Ala Leu His Tyr Ser Asp Glu

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85

90

95

Val Glu Ile Ile Gln Gly Leu Thr Arg Met Pro Gly Gly Arg Asp Ala  
100 105 110

Leu Lys Ser Ser Val Asp Ala Val Lys Tyr Phe Gly Lys Gly Thr Tyr  
115 120 125

Thr Asp Cys Ala Ile Lys Lys Gly Leu Glu Gln Leu Leu Val Gly Gly  
130 135 140

Ser His Leu Lys Glu Asn Lys Tyr Leu Ile Val Val Thr Asp Gly His  
145 150 155 160

Pro Leu Glu Gly Tyr Lys Glu Pro Cys Gly Gly Leu Glu Asp Ala Val  
165 170 175

Asn Glu Ala Lys His Leu Gly Val Lys Val Phe Ser Val Ala Ile Thr  
180 185 190

Pro Asp His Leu Glu Pro Arg Leu Ser Ile Ile Ala Thr Asp His Thr  
195 200 205

Tyr Arg Arg Asn Phe Thr Ala Ala Asp Trp Gly Gln Ser Arg Asp Ala  
210 215 220

Glu Glu Ala Ile Ser Gln Thr Ile Asp Thr Ile Val Asp Met Ile Lys  
225 230 235 240

Asn Asn Val Glu Gln Val Cys Cys Ser Phe Glu Cys Gln Pro Ala Arg  
245 250 255

Gly Pro Pro Gly Leu Arg Gly Asp Pro Gly Phe Glu Gly Glu Arg Gly  
260 265 270

Lys Pro Gly Leu Pro Gly Glu Lys Gly Glu Ala Gly Asp Pro Gly Arg  
275 280 285

Pro Gly Asp Leu Gly Pro Val Gly Tyr Gln Gly Met Lys Gly Glu Lys  
290 295 300

Gly Ser Arg Gly Glu Lys Gly Ser Arg Gly Pro Lys Gly Tyr Lys Gly  
305 310 315 320

Glu Lys Gly Lys Arg Gly Ile Asp Gly Val Asp Gly Val Lys Gly Glu  
325 330 335

Met Gly Tyr Pro Gly Leu Pro Gly Cys Lys Gly Ser Pro Gly Phe Asp  
340 345 350

Gly Ile Gln Gly Pro Pro Gly Pro Lys Gly Asp Pro Gly Ala Phe Gly

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355

360

365

Leu Lys Gly Glu Lys Gly Glu Pro Gly Ala Asp Gly Glu Ala Gly Arg  
 370 375 380

Pro Gly Ser Ser Gly Pro Ser Gly Asp Glu Gly Gln Pro Gly Glu Pro  
 385 390 395 400

Gly Pro Pro Gly Glu Lys Gly Glu Ala Gly Asp Glu Gly Asn Pro Gly  
 405 410 415

Pro Asp Gly Ala Pro Gly Glu Arg Gly Gly Pro Gly Glu Arg Gly Pro  
 420 425 430

Arg Gly Thr Pro Gly Thr Arg Gly Pro Arg Gly Asp Pro Gly Glu Ala  
 435 440 445

Gly Pro Gln Gly Asp Gln Gly Arg Glu Gly Pro Val Gly Val Pro Gly  
 450 455 460

Asp Pro Gly Glu Ala Gly Pro Ile Gly Pro Lys Gly Tyr Arg Gly Asp  
 465 470 475 480

Glu Gly Pro Pro Gly Ser Glu Gly Ala Arg Gly Ala Pro Gly Pro Ala  
 485 490 495

Gly Pro Pro Gly Asp Pro Gly Leu Met Gly Glu Arg Gly Glu Asp Gly  
 500 505 510

Pro Ala Gly Asn Gly Thr Glu Gly Phe Pro Gly Phe Pro Gly Tyr Pro  
 515 520 525

Gly Asn Arg Gly Ala Pro Gly Ile Asn Gly Thr Lys Gly Tyr Pro Gly  
 530 535 540

Leu Lys Gly Asp Glu Gly Glu Ala Gly Asp Pro Gly Asp Asp Asn Asn  
 545 550 555 560

Asp Ile Ala Pro Arg Gly Val Lys Gly Ala Lys Gly Tyr Arg Gly Pro  
 565 570 575

Glu Gly Pro Gln Gly Pro Pro Gly His Gln Gly Pro Pro Gly Pro Asp  
 580 585 590

Glu Cys Glu Ile Leu Asp Ile Ile Met Lys Met Cys Ser Cys Cys Glu  
 595 600 605

Cys Lys Cys Gly Pro Ile Asp Leu Leu Phe Val Leu Asp Ser Ser Glu  
 610 615 620

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

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625					630					635					640
Val	Ile	Asp	Arg	Leu 645	Ser	Arg	Asp	Glu	Leu 650	Val	Lys	Phe	Glu	Pro 655	Gly
Gln	Ser	Tyr	Ala 660	Gly	Val	Val	Gln	Tyr 665	Ser	His	Ser	Gln	Met 670	Gln	Glu
His	Val	Ser 675	Leu	Arg	Ser	Pro	Ser 680	Ile	Arg	Asn	Val	Gln 685	Glu	Leu	Lys
Glu	Ala 690	Ile	Lys	Ser	Leu	Gln 695	Trp	Met	Ala	Gly	Gly 700	Thr	Phe	Thr	Gly
Glu 705	Ala	Leu	Gln	Tyr	Thr 710	Arg	Asp	Gln	Leu	Leu 715	Pro	Pro	Ser	Pro	Asn 720
Asn	Arg	Ile	Ala	Leu 725	Val	Ile	Thr	Asp	Gly 730	Arg	Ser	Asp	Thr	Gln 735	Arg
Asp	Thr	Thr	Pro 740	Leu	Asn	Val	Leu	Cys 745	Ser	Pro	Gly	Ile	Gln 750	Val	Val
Ser	Val	Gly 755	Ile	Lys	Asp	Val	Phe 760	Asp	Phe	Ile	Pro	Gly 765	Ser	Asp	Gln
Leu	Asn 770	Val	Ile	Ser	Cys	Gln 775	Gly	Leu	Ala	Pro	Ser 780	Gln	Gly	Arg	Pro
Gly 785	Leu	Ser	Leu	Val	Lys 790	Glu	Asn	Tyr	Ala	Glu 795	Leu	Leu	Glu	Asp	Ala 800
Phe	Leu	Lys	Asn	Val 805	Thr	Ala	Gln	Ile	Cys 810	Ile	Asp	Lys	Lys	Cys 815	Pro
Asp	Tyr	Thr	Cys 820	Pro	Ile	Thr	Phe	Ser 825	Ser	Pro	Ala	Asp	Ile 830	Thr	Ile
Leu	Leu	Asp 835	Gly	Ser	Ala	Ser	Val 840	Gly	Ser	His	Asn	Phe 845	Asp	Thr	Thr
Lys	Arg 850	Phe	Ala	Lys	Arg	Leu 855	Ala	Glu	Arg	Phe	Leu 860	Thr	Ala	Gly	Arg
Thr 865	Asp	Pro	Ala	His	Asp 870	Val	Arg	Val	Ala	Val 875	Val	Gln	Tyr	Ser	Gly 880
Thr	Gly	Gln	Gln	Arg 885	Pro	Glu	Arg	Ala	Ser 890	Leu	Gln	Phe	Leu	Gln 895	Asn
Tyr	Thr	Ala	Leu	Ala	Ser	Ala	Val	Asp	Ala	Met	Asp	Phe	Ile	Asn	Asp



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900

905

910

Ala Thr Asp Val Asn Asp Ala Leu Gly Tyr Val Thr Arg Phe Tyr Arg  
915 920 925

Glu Ala Ser Ser Gly Ala Ala Lys Lys Arg Leu Leu Leu Phe Ser Asp  
930 935 940

Gly Asn Ser Gln Gly Ala Thr Pro Ala Ala Ile Glu Lys Ala Val Gln  
945 950 955 960

Glu Ala Gln Arg Ala Gly Ile Glu Ile Phe Val Val Val Val Gly Arg  
965 970 975

Gln Val Asn Glu Pro His Ile Arg Val Leu Val Thr Gly Lys Thr Ala  
980 985 990

Glu Tyr Asp Val Ala Tyr Gly Glu Ser His Leu Phe Arg Val Pro Ser  
995 1000 1005

Tyr Gln Ala Leu Leu Arg Gly Val Phe His Gln Thr Val Ser Arg  
1010 1015 1020

Lys Val Ala Leu Gly  
1025

<210> 76  
<211> 1019  
<212> PRT  
<213> Homo sapiens

<400> 76

Met Leu Gln Gly Thr Cys Ser Val Leu Leu Leu Trp Gly Ile Leu Gly  
1 5 10 15

Ala Ile Gln Ala Gln Gln Gln Glu Val Ile Ser Pro Asp Thr Thr Glu  
20 25 30

Arg Asn Asn Asn Cys Pro Glu Lys Thr Asp Cys Pro Ile His Val Tyr  
35 40 45

Phe Val Leu Asp Thr Ser Glu Ser Val Thr Met Gln Ser Pro Thr Asp  
50 55 60

Ile Leu Leu Phe His Met Lys Gln Phe Val Pro Gln Phe Ile Ser Gln  
65 70 75 80

Leu Gln Asn Glu Phe Tyr Leu Asp Gln Val Ala Leu Ser Trp Arg Tyr  
85 90 95

Gly Gly Leu His Phe Ser Asp Gln Val Glu Val Phe Ser Pro Pro Gly  
100 105 110

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Ser Asp Arg Ala Ser Phe Ile Lys Asn Leu Gln Gly Ile Ser Ser Phe  
 115 120 125  
 Arg Arg Gly Thr Phe Thr Asp Cys Ala Leu Ala Asn Met Thr Glu Gln  
 130 135 140  
 Ile Arg Gln Asp Arg Ser Lys Gly Thr Val His Phe Ala Val Val Ile  
 145 150 155 160  
 Thr Asp Gly His Val Thr Gly Ser Pro Cys Gly Gly Ile Lys Leu Gln  
 165 170 175  
 Ala Glu Arg Ala Arg Glu Glu Gly Ile Arg Leu Phe Ala Val Ala Pro  
 180 185 190  
 Asn Gln Asn Leu Lys Glu Gln Gly Leu Arg Asp Ile Ala Ser Thr Pro  
 195 200 205  
 His Glu Leu Tyr Arg Asn Asp Tyr Ala Thr Met Leu Pro Asp Ser Thr  
 210 215 220  
 Glu Ile Asp Gln Asp Thr Ile Asn Arg Ile Ile Lys Val Met Lys His  
 225 230 235 240  
 Glu Ala Tyr Gly Glu Cys Tyr Lys Val Ser Cys Leu Glu Ile Pro Gly  
 245 250 255  
 Pro Ser Gly Pro Lys Gly Tyr Arg Gly Gln Lys Gly Ala Lys Gly Asn  
 260 265 270  
 Met Gly Glu Pro Gly Glu Pro Gly Gln Lys Gly Arg Gln Gly Asp Pro  
 275 280 285  
 Gly Ile Glu Gly Pro Ile Gly Phe Pro Gly Pro Lys Gly Val Pro Gly  
 290 295 300  
 Phe Lys Gly Glu Lys Gly Glu Phe Gly Ala Asp Gly Arg Lys Gly Ala  
 305 310 315 320  
 Pro Gly Leu Ala Gly Lys Asn Gly Thr Asp Gly Gln Lys Gly Lys Leu  
 325 330 335  
 Gly Arg Ile Gly Pro Pro Gly Cys Lys Gly Asp Pro Gly Asn Arg Gly  
 340 345 350  
 Pro Asp Gly Tyr Pro Gly Glu Ala Gly Ser Pro Gly Glu Arg Gly Asp  
 355 360 365  
 Gln Gly Gly Lys Gly Asp Pro Gly Arg Pro Gly Arg Arg Gly Pro Pro  
 370 375 380

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Gly Glu Ile Gly Ala Lys Gly Ser Lys Gly Tyr Gln Gly Asn Ser Gly  
 385 390 395 400  
 Ala Pro Gly Ser Pro Gly Val Lys Gly Ala Lys Gly Gly Pro Gly Pro  
 405 410 415  
 Arg Gly Pro Lys Gly Glu Pro Gly Arg Arg Gly Asp Pro Gly Thr Lys  
 420 425 430  
 Gly Ser Pro Gly Ser Asp Gly Pro Lys Gly Glu Lys Gly Asp Pro Gly  
 435 440 445  
 Pro Glu Gly Pro Arg Gly Leu Ala Gly Glu Val Gly Asn Lys Gly Ala  
 450 455 460  
 Lys Gly Asp Arg Gly Leu Pro Gly Pro Arg Gly Pro Gln Gly Ala Leu  
 465 470 475 480  
 Gly Glu Pro Gly Lys Gln Gly Ser Arg Gly Asp Pro Gly Asp Ala Gly  
 485 490 495  
 Pro Arg Gly Asp Ser Gly Gln Pro Gly Pro Lys Gly Asp Pro Gly Arg  
 500 505 510  
 Pro Gly Phe Ser Tyr Pro Gly Pro Arg Gly Ala Pro Gly Glu Lys Gly  
 515 520 525  
 Glu Pro Gly Pro Arg Gly Pro Glu Gly Gly Arg Gly Asp Phe Gly Leu  
 530 535 540  
 Lys Gly Glu Pro Gly Arg Lys Gly Glu Lys Gly Glu Pro Ala Asp Pro  
 545 550 555 560  
 Gly Pro Pro Gly Glu Pro Gly Pro Arg Gly Pro Arg Gly Val Pro Gly  
 565 570 575  
 Pro Glu Gly Glu Pro Gly Pro Pro Gly Asp Pro Gly Leu Thr Glu Cys  
 580 585 590  
 Asp Val Met Thr Tyr Val Arg Glu Thr Cys Gly Cys Cys Asp Cys Glu  
 595 600 605  
 Lys Arg Cys Gly Ala Leu Asp Val Val Phe Val Ile Asp Ser Ser Glu  
 610 615 620  
 Ser Ile Gly Tyr Thr Asn Phe Thr Leu Glu Lys Asn Phe Val Ile Asn  
 625 630 635 640  
 Val Val Asn Arg Leu Gly Ala Ile Ala Lys Asp Pro Lys Ser Glu Thr  
 645 650 655

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Gly Thr Arg Val Gly Val Val Gln Tyr Ser His Glu Gly Thr Phe Glu  
 660 665 670  
 Ala Ile Gln Leu Asp Asp Glu Arg Ile Asp Ser Leu Ser Ser Phe Lys  
 675 680 685  
 Glu Ala Val Lys Asn Leu Glu Trp Ile Ala Gly Gly Thr Trp Thr Pro  
 690 695 700  
 Ser Ala Leu Lys Phe Ala Tyr Asp Arg Leu Ile Lys Glu Ser Arg Arg  
 705 710 715 720  
 Gln Lys Thr Arg Val Phe Ala Val Val Ile Thr Asp Gly Arg His Asp  
 725 730 735  
 Pro Arg Asp Asp Asp Leu Asn Leu Arg Ala Leu Cys Asp Arg Asp Val  
 740 745 750  
 Thr Val Thr Ala Ile Gly Ile Gly Asp Met Phe His Glu Lys His Glu  
 755 760 765  
 Ser Glu Asn Leu Tyr Ser Ile Ala Cys Asp Lys Pro Gln Gln Val Arg  
 770 775 780  
 Asn Met Thr Leu Phe Ser Asp Leu Val Ala Glu Lys Phe Ile Asp Asp  
 785 790 795 800  
 Met Glu Asp Val Leu Cys Pro Asp Pro Gln Ile Val Cys Pro Asp Leu  
 805 810 815  
 Pro Cys Gln Thr Glu Leu Ser Val Ala Gln Cys Thr Gln Arg Pro Val  
 820 825 830  
 Asp Ile Val Phe Leu Leu Asp Gly Ser Glu Arg Leu Gly Glu Gln Asn  
 835 840 845  
 Phe His Lys Ala Arg Arg Phe Val Glu Gln Val Ala Arg Arg Leu Thr  
 850 855 860  
 Leu Ala Arg Arg Asp Asp Asp Pro Leu Asn Ala Arg Val Ala Leu Leu  
 865 870 875 880  
 Gln Phe Gly Gly Pro Gly Glu Gln Gln Val Ala Phe Pro Leu Ser His  
 885 890 895  
 Asn Leu Thr Ala Ile His Glu Ala Leu Glu Thr Thr Gln Tyr Leu Asn  
 900 905 910  
 Ser Phe Ser His Val Gly Ala Gly Val Val His Ala Ile Asn Ala Ile  
 915 920 925

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Val Arg Ser Pro Arg Gly Gly Ala Arg Arg His Ala Glu Leu Ser Phe  
930 935 940

Val Phe Leu Thr Asp Gly Val Thr Gly Asn Asp Ser Leu His Glu Ser  
945 950 955 960

Ala His Ser Met Arg Lys Gln Asn Val Val Pro Thr Val Leu Ala Leu  
965 970 975

Gly Ser Asp Val Asp Met Asp Val Leu Thr Thr Leu Ser Leu Gly Asp  
980 985 990

Arg Ala Ala Val Phe His Glu Lys Asp Tyr Asp Ser Leu Ala Gln Pro  
995 1000 1005

Gly Phe Phe Asp Arg Phe Ile Arg Trp Ile Cys  
1010 1015

<210> 77  
<211> 3177  
<212> PRT  
<213> Homo sapiens

<400> 77

Met Arg Lys His Arg His Leu Pro Leu Val Ala Val Phe Cys Leu Phe  
1 5 10 15

Leu Ser Gly Phe Pro Thr Thr His Ala Gln Gln Gln Gln Ala Asp Val  
20 25 30

Lys Asn Gly Ala Ala Ala Asp Ile Ile Phe Leu Val Asp Ser Ser Trp  
35 40 45

Thr Ile Gly Glu Glu His Phe Gln Leu Val Arg Glu Phe Leu Tyr Asp  
50 55 60

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

Val Gln Phe Asn Gly Asn Pro His Thr Glu Phe Leu Leu Asn Thr Tyr  
85 90 95

Arg Thr Lys Gln Glu Val Leu Ser His Ile Ser Asn Met Ser Tyr Ile  
100 105 110

Gly Gly Thr Asn Gln Thr Gly Lys Gly Leu Glu Tyr Ile Met Gln Ser  
115 120 125

His Leu Thr Lys Ala Ala Gly Ser Arg Ala Gly Asp Gly Val Pro Gln  
130 135 140

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Val Ile Val Val Leu Thr Asp Gly His Ser Lys Asp Gly Leu Ala Leu  
 145 150 155 160  
 Pro Ser Ala Glu Leu Lys Ser Ala Asp Val Asn Val Phe Ala Ile Gly  
 165 170 175  
 Val Glu Asp Ala Asp Glu Gly Ala Leu Lys Glu Ile Ala Ser Glu Pro  
 180 185 190  
 Leu Asn Met His Met Phe Asn Leu Glu Asn Phe Thr Ser Leu His Asp  
 195 200 205  
 Ile Val Gly Asn Leu Val Ser Cys Val His Ser Ser Val Ser Pro Glu  
 210 215 220  
 Arg Ala Gly Asp Thr Glu Thr Leu Lys Asp Ile Thr Ala Gln Asp Ser  
 225 230 235 240  
 Ala Asp Ile Ile Phe Leu Ile Asp Gly Ser Asn Asn Thr Gly Ser Val  
 245 250 255  
 Asn Phe Ala Val Ile Leu Asp Phe Leu Val Asn Leu Leu Glu Lys Leu  
 260 265 270  
 Pro Ile Gly Thr Gln Gln Ile Arg Val Gly Val Val Gln Phe Ser Asp  
 275 280 285  
 Glu Pro Arg Thr Met Phe Ser Leu Asp Thr Tyr Ser Thr Lys Ala Gln  
 290 295 300  
 Val Leu Gly Ala Val Lys Ala Leu Gly Phe Ala Gly Gly Glu Leu Ala  
 305 310 315 320  
 Asn Ile Gly Leu Ala Leu Asp Phe Val Val Glu Asn His Phe Thr Arg  
 325 330 335  
 Ala Gly Gly Ser Arg Val Glu Glu Gly Val Pro Gln Val Leu Val Leu  
 340 345 350  
 Ile Ser Ala Gly Pro Ser Ser Asp Glu Ile Arg Tyr Gly Val Val Ala  
 355 360 365  
 Leu Lys Gln Ala Ser Val Phe Ser Phe Gly Leu Gly Ala Gln Ala Ala  
 370 375 380  
 Ser Arg Ala Glu Leu Gln His Ile Ala Thr Asp Asp Asn Leu Val Phe  
 385 390 395 400  
 Thr Val Pro Glu Phe Arg Ser Phe Gly Asp Leu Gln Glu Lys Leu Leu  
 405 410 415

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Pro Tyr Ile Val Gly Val Ala Gln Arg His Ile Val Leu Lys Pro Pro  
420 425 430

Thr Ile Val Thr Gln Val Ile Glu Val Asn Lys Arg Asp Ile Val Phe  
435 440 445

Leu Val Asp Gly Ser Ser Ala Leu Gly Leu Ala Asn Phe Asn Ala Ile  
450 455 460

Arg Asp Phe Ile Ala Lys Val Ile Gln Arg Leu Glu Ile Gly Gln Asp  
465 470 475 480

Leu Ile Gln Val Ala Val Ala Gln Tyr Ala Asp Thr Val Arg Pro Glu  
485 490 495

Phe Tyr Phe Asn Thr His Pro Thr Lys Arg Glu Val Ile Thr Ala Val  
500 505 510

Arg Lys Met Lys Pro Leu Asp Gly Ser Ala Leu Tyr Thr Gly Ser Ala  
515 520 525

Leu Asp Phe Val Arg Asn Asn Leu Phe Thr Ser Ser Ala Gly Tyr Arg  
530 535 540

Ala Ala Glu Gly Ile Pro Lys Leu Leu Val Leu Ile Thr Gly Gly Lys  
545 550 555 560

Ser Leu Asp Glu Ile Ser Gln Pro Ala Gln Glu Leu Lys Arg Ser Ser  
565 570 575

Ile Met Ala Phe Ala Ile Gly Asn Lys Gly Ala Asp Gln Ala Glu Leu  
580 585 590

Glu Glu Ile Ala Phe Asp Ser Ser Leu Val Phe Ile Pro Ala Glu Phe  
595 600 605

Arg Ala Ala Pro Leu Gln Gly Met Leu Pro Gly Leu Leu Ala Pro Leu  
610 615 620

Arg Thr Leu Ser Gly Thr Pro Glu Val His Ser Asn Lys Arg Asp Ile  
625 630 635 640

Ile Phe Leu Leu Asp Gly Ser Ala Asn Val Gly Lys Thr Asn Phe Pro  
645 650 655

Tyr Val Arg Asp Phe Val Met Asn Leu Val Asn Ser Leu Asp Ile Gly  
660 665 670

Asn Asp Asn Ile Arg Val Gly Leu Val Gln Phe Ser Asp Thr Pro Val  
675 680 685

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Thr Glu Phe Ser Leu Asn Thr Tyr Gln Thr Lys Ser Asp Ile Leu Gly  
 690 695 700  
 His Leu Arg Gln Leu Gln Leu Gln Gly Gly Ser Gly Leu Asn Thr Gly  
 705 710 715 720  
 Ser Ala Leu Ser Tyr Val Tyr Ala Asn His Phe Thr Glu Ala Gly Gly  
 725 730 735  
 Ser Arg Ile Arg Glu His Val Pro Gln Leu Leu Leu Leu Leu Thr Ala  
 740 745 750  
 Gly Gln Ser Glu Asp Ser Tyr Leu Gln Ala Ala Asn Ala Leu Thr Arg  
 755 760 765  
 Ala Gly Ile Leu Thr Phe Cys Val Gly Ala Ser Gln Ala Asn Lys Ala  
 770 775 780  
 Glu Leu Glu Gln Ile Ala Phe Asn Pro Ser Leu Val Tyr Leu Met Asp  
 785 790 795 800  
 Asp Phe Ser Ser Leu Pro Ala Leu Pro Gln Gln Leu Ile Gln Pro Leu  
 805 810 815  
 Thr Thr Tyr Val Ser Gly Gly Val Glu Glu Val Pro Leu Ala Gln Pro  
 820 825 830  
 Glu Ser Lys Arg Asp Ile Leu Phe Leu Phe Asp Gly Ser Ala Asn Leu  
 835 840 845  
 Val Gly Gln Phe Pro Val Val Arg Asp Phe Leu Tyr Lys Ile Ile Asp  
 850 855 860  
 Glu Leu Asn Val Lys Pro Glu Gly Thr Arg Ile Ala Val Ala Gln Tyr  
 865 870 875 880  
 Ser Asp Asp Val Lys Val Glu Ser Arg Phe Asp Glu His Gln Ser Lys  
 885 890 895  
 Pro Glu Ile Leu Asn Leu Val Lys Arg Met Lys Ile Lys Thr Gly Lys  
 900 905 910  
 Ala Leu Asn Leu Gly Tyr Ala Leu Asp Tyr Ala Gln Arg Tyr Ile Phe  
 915 920 925  
 Val Lys Ser Ala Gly Ser Arg Ile Glu Asp Gly Val Leu Gln Phe Leu  
 930 935 940  
 Val Leu Leu Val Ala Gly Arg Ser Ser Asp Arg Val Asp Gly Pro Ala  
 945 950 955 960



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Ser Asn Leu Lys Gln Ser Gly Val Val Pro Phe Ile Phe Gln Ala Lys  
965 970 975

Asn Ala Asp Pro Ala Glu Leu Glu Gln Ile Val Leu Ser Pro Ala Phe  
980 985 990

Ile Leu Ala Ala Glu Ser Leu Pro Lys Ile Gly Asp Leu His Pro Gln  
995 1000 1005

Ile Val Asn Leu Leu Lys Ser Val His Asn Gly Ala Pro Ala Pro  
1010 1015 1020

Val Ser Gly Glu Lys Asp Val Val Phe Leu Leu Asp Gly Ser Glu  
1025 1030 1035

Gly Val Arg Ser Gly Phe Pro Leu Leu Lys Glu Phe Val Gln Arg  
1040 1045 1050

Val Val Glu Ser Leu Asp Val Gly Gln Asp Arg Val Arg Val Ala  
1055 1060 1065

Val Val Gln Tyr Ser Asp Arg Thr Arg Pro Glu Phe Tyr Leu Asn  
1070 1075 1080

Ser Tyr Met Asn Lys Gln Asp Val Val Asn Ala Val Arg Gln Leu  
1085 1090 1095

Thr Leu Leu Gly Gly Pro Thr Pro Asn Thr Gly Ala Ala Leu Glu  
1100 1105 1110

Phe Val Leu Arg Asn Ile Leu Val Ser Ser Ala Gly Ser Arg Ile  
1115 1120 1125

Thr Glu Gly Val Pro Gln Leu Leu Ile Val Leu Thr Ala Asp Arg  
1130 1135 1140

Ser Gly Asp Asp Val Arg Asn Pro Ser Val Val Val Lys Arg Gly  
1145 1150 1155

Gly Ala Val Pro Ile Gly Ile Gly Ile Gly Asn Ala Asp Ile Thr  
1160 1165 1170

Glu Met Gln Thr Ile Ser Phe Ile Pro Asp Phe Ala Val Ala Ile  
1175 1180 1185

Pro Thr Phe Arg Gln Leu Gly Thr Val Gln Gln Val Ile Ser Glu  
1190 1195 1200

Arg Val Thr Gln Leu Thr Arg Glu Glu Leu Ser Arg Leu Gln Pro  
1205 1210 1215

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Val	Leu	Gln	Pro	Leu	Pro	Ser	Pro	Gly	Val	Gly	Gly	Lys	Arg	Asp
	1220					1225					1230			
Val	Val	Phe	Leu	Ile	Asp	Gly	Ser	Gln	Ser	Ala	Gly	Pro	Glu	Phe
	1235					1240					1245			
Gln	Tyr	Val	Arg	Thr	Leu	Ile	Glu	Arg	Leu	Val	Asp	Tyr	Leu	Asp
	1250					1255					1260			
Val	Gly	Phe	Asp	Thr	Thr	Arg	Val	Ala	Val	Ile	Gln	Phe	Ser	Asp
	1265					1270					1275			
Asp	Pro	Lys	Val	Glu	Phe	Leu	Leu	Asn	Ala	His	Ser	Ser	Lys	Asp
	1280					1285					1290			
Glu	Val	Gln	Asn	Ala	Val	Gln	Arg	Leu	Arg	Pro	Lys	Gly	Gly	Arg
	1295					1300					1305			
Gln	Ile	Asn	Val	Gly	Asn	Ala	Leu	Glu	Tyr	Val	Ser	Arg	Asn	Ile
	1310					1315					1320			
Phe	Lys	Arg	Pro	Leu	Gly	Ser	Arg	Ile	Glu	Glu	Gly	Val	Pro	Gln
	1325					1330					1335			
Phe	Leu	Val	Leu	Ile	Ser	Ser	Gly	Lys	Ser	Asp	Asp	Glu	Val	Asp
	1340					1345					1350			
Asp	Pro	Ala	Val	Glu	Leu	Lys	Gln	Phe	Gly	Val	Ala	Pro	Phe	Thr
	1355					1360					1365			
Ile	Ala	Arg	Asn	Ala	Asp	Gln	Glu	Glu	Leu	Val	Lys	Ile	Ser	Leu
	1370					1375					1380			
Ser	Pro	Glu	Tyr	Val	Phe	Ser	Val	Ser	Thr	Phe	Arg	Glu	Leu	Pro
	1385					1390					1395			
Ser	Leu	Glu	Gln	Lys	Leu	Leu	Thr	Pro	Ile	Thr	Thr	Leu	Thr	Ser
	1400					1405					1410			
Glu	Gln	Ile	Gln	Lys	Leu	Leu	Ala	Ser	Thr	Arg	Tyr	Pro	Pro	Pro
	1415					1420					1425			
Ala	Val	Glu	Ser	Asp	Ala	Ala	Asp	Ile	Val	Phe	Leu	Ile	Asp	Ser
	1430					1435					1440			
Ser	Glu	Gly	Val	Arg	Pro	Asp	Gly	Phe	Ala	His	Ile	Arg	Asp	Phe
	1445					1450					1455			
Val	Ser	Arg	Ile	Val	Arg	Arg	Leu	Asn	Ile	Gly	Pro	Ser	Lys	Val
	1460					1465					1470			

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Arg	Val	Gly	Val	Val	Gln	Phe	Ser	Asn	Asp	Val	Phe	Pro	Glu	Phe
1475						1480					1485			
Tyr	Leu	Lys	Thr	Tyr	Arg	Ser	Gln	Ala	Pro	Val	Leu	Asp	Ala	Ile
1490						1495					1500			
Arg	Arg	Leu	Arg	Leu	Arg	Gly	Gly	Ser	Pro	Leu	Asn	Thr	Gly	Lys
1505						1510					1515			
Ala	Leu	Glu	Phe	Val	Ala	Arg	Asn	Leu	Phe	Val	Lys	Ser	Ala	Gly
1520						1525					1530			
Ser	Arg	Ile	Glu	Asp	Gly	Val	Pro	Gln	His	Leu	Val	Leu	Val	Leu
1535						1540					1545			
Gly	Gly	Lys	Ser	Gln	Asp	Asp	Val	Ser	Arg	Phe	Ala	Gln	Val	Ile
1550						1555					1560			
Arg	Ser	Ser	Gly	Ile	Val	Ser	Leu	Gly	Val	Gly	Asp	Arg	Asn	Ile
1565						1570					1575			
Asp	Arg	Thr	Glu	Leu	Gln	Thr	Ile	Thr	Asn	Asp	Pro	Arg	Leu	Val
1580						1585					1590			
Phe	Thr	Val	Arg	Glu	Phe	Arg	Glu	Leu	Pro	Asn	Ile	Glu	Glu	Arg
1595						1600					1605			
Ile	Met	Asn	Ser	Phe	Gly	Pro	Ser	Ala	Ala	Thr	Pro	Ala	Pro	Pro
1610						1615					1620			
Gly	Val	Asp	Thr	Pro	Pro	Pro	Ser	Arg	Pro	Glu	Lys	Lys	Lys	Ala
1625						1630					1635			
Asp	Ile	Val	Phe	Leu	Leu	Asp	Gly	Ser	Ile	Asn	Phe	Arg	Arg	Asp
1640						1645					1650			
Ser	Phe	Gln	Glu	Val	Leu	Arg	Phe	Val	Ser	Glu	Ile	Val	Asp	Thr
1655						1660					1665			
Val	Tyr	Glu	Asp	Gly	Asp	Ser	Ile	Gln	Val	Gly	Leu	Val	Gln	Tyr
1670						1675					1680			
Asn	Ser	Asp	Pro	Thr	Asp	Glu	Phe	Phe	Leu	Lys	Asp	Phe	Ser	Thr
1685						1690					1695			
Lys	Arg	Gln	Ile	Ile	Asp	Ala	Ile	Asn	Lys	Val	Val	Tyr	Lys	Gly
1700						1705					1710			
Gly	Arg	His	Ala	Asn	Thr	Lys	Val	Gly	Leu	Glu	His	Leu	Arg	Val
1715						1720					1725			

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Asn	His	Phe	Val	Pro	Glu	Ala	Gly	Ser	Arg	Leu	Asp	Gln	Arg	Val
1730						1735					1740			
Pro	Gln	Ile	Ala	Phe	Val	Ile	Thr	Gly	Gly	Lys	Ser	Val	Glu	Asp
1745						1750					1755			
Ala	Gln	Asp	Val	Ser	Leu	Ala	Leu	Thr	Gln	Arg	Gly	Val	Lys	Val
1760						1765					1770			
Phe	Ala	Val	Gly	Val	Arg	Asn	Ile	Asp	Ser	Glu	Glu	Val	Gly	Lys
1775						1780					1785			
Ile	Ala	Ser	Asn	Ser	Ala	Thr	Ala	Phe	Arg	Val	Gly	Asn	Val	Gln
1790						1795					1800			
Glu	Leu	Ser	Glu	Leu	Ser	Glu	Gln	Val	Leu	Glu	Thr	Leu	His	Asp
1805						1810					1815			
Ala	Met	His	Glu	Thr	Leu	Cys	Pro	Gly	Val	Thr	Asp	Ala	Ala	Lys
1820						1825					1830			
Ala	Cys	Asn	Leu	Asp	Val	Ile	Leu	Gly	Phe	Asp	Gly	Ser	Arg	Asp
1835						1840					1845			
Gln	Asn	Val	Phe	Val	Ala	Gln	Lys	Gly	Phe	Glu	Ser	Lys	Val	Asp
1850						1855					1860			
Ala	Ile	Leu	Asn	Arg	Ile	Ser	Gln	Met	His	Arg	Val	Ser	Cys	Ser
1865						1870					1875			
Gly	Gly	Arg	Ser	Pro	Thr	Val	Arg	Val	Ser	Val	Val	Ala	Asn	Thr
1880						1885					1890			
Pro	Ser	Gly	Pro	Val	Glu	Ala	Phe	Asp	Phe	Asp	Glu	Tyr	Gln	Pro
1895						1900					1905			
Glu	Met	Leu	Glu	Lys	Phe	Arg	Asn	Met	Arg	Ser	Gln	His	Pro	Tyr
1910						1915					1920			
Val	Leu	Thr	Glu	Asp	Thr	Leu	Lys	Val	Tyr	Leu	Asn	Lys	Phe	Arg
1925						1930					1935			
Gln	Ser	Ser	Pro	Asp	Ser	Val	Lys	Val	Val	Ile	His	Phe	Thr	Asp
1940						1945					1950			
Gly	Ala	Asp	Gly	Asp	Leu	Ala	Asp	Leu	His	Arg	Ala	Ser	Glu	Asn
1955						1960					1965			
Leu	Arg	Gln	Glu	Gly	Val	Arg	Ala	Leu	Ile	Leu	Val	Gly	Leu	Glu
1970						1975					1980			

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Arg	Val	Val	Asn	Leu	Glu	Arg	Leu	Met	His	Leu	Glu	Phe	Gly	Arg
1985						1990					1995			
Gly	Phe	Met	Tyr	Asp	Arg	Pro	Leu	Arg	Leu	Asn	Leu	Leu	Asp	Leu
2000						2005					2010			
Asp	Tyr	Glu	Leu	Ala	Glu	Gln	Leu	Asp	Asn	Ile	Ala	Glu	Lys	Ala
2015						2020					2025			
Cys	Cys	Gly	Val	Pro	Cys	Lys	Cys	Ser	Gly	Gln	Arg	Gly	Asp	Arg
2030						2035					2040			
Gly	Pro	Ile	Gly	Ser	Ile	Gly	Pro	Lys	Gly	Ile	Pro	Gly	Glu	Asp
2045						2050					2055			
Gly	Tyr	Arg	Gly	Tyr	Pro	Gly	Asp	Glu	Gly	Gly	Pro	Gly	Glu	Arg
2060						2065					2070			
Gly	Pro	Pro	Gly	Val	Asn	Gly	Thr	Gln	Gly	Phe	Gln	Gly	Cys	Pro
2075						2080					2085			
Gly	Gln	Arg	Gly	Val	Lys	Gly	Ser	Arg	Gly	Phe	Pro	Gly	Glu	Lys
2090						2095					2100			
Gly	Glu	Val	Gly	Glu	Ile	Gly	Leu	Asp	Gly	Leu	Asp	Gly	Glu	Asp
2105						2110					2115			
Gly	Asp	Lys	Gly	Leu	Pro	Gly	Ser	Ser	Gly	Glu	Lys	Gly	Asn	Pro
2120						2125					2130			
Gly	Arg	Arg	Gly	Asp	Lys	Gly	Pro	Arg	Gly	Glu	Lys	Gly	Glu	Arg
2135						2140					2145			
Gly	Asp	Val	Gly	Ile	Arg	Gly	Asp	Pro	Gly	Asn	Pro	Gly	Gln	Asp
2150						2155					2160			
Ser	Gln	Glu	Arg	Gly	Pro	Lys	Gly	Glu	Thr	Gly	Asp	Leu	Gly	Pro
2165						2170					2175			
Met	Gly	Val	Pro	Gly	Arg	Asp	Gly	Val	Pro	Gly	Gly	Pro	Gly	Glu
2180						2185					2190			
Thr	Gly	Lys	Asn	Gly	Gly	Phe	Gly	Arg	Arg	Gly	Pro	Pro	Gly	Ala
2195						2200					2205			
Lys	Gly	Asn	Lys	Gly	Gly	Pro	Gly	Gln	Pro	Gly	Phe	Glu	Gly	Glu
2210						2215					2220			
Gln	Gly	Thr	Arg	Gly	Ala	Gln	Gly	Pro	Ala	Gly	Pro	Ala	Gly	Pro
2225						2230					2235			

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Pro	Gly	Leu	Ile	Gly	Glu	Gln	Gly	Ile	Ser	Gly	Pro	Arg	Gly	Ser
	2240					2245					2250			
Gly	Gly	Ala	Ala	Gly	Ala	Pro	Gly	Glu	Arg	Gly	Arg	Thr	Gly	Pro
	2255					2260					2265			
Leu	Gly	Arg	Lys	Gly	Glu	Pro	Gly	Glu	Pro	Gly	Pro	Lys	Gly	Gly
	2270					2275					2280			
Ile	Gly	Asn	Arg	Gly	Pro	Arg	Gly	Glu	Thr	Gly	Asp	Asp	Gly	Arg
	2285					2290					2295			
Asp	Gly	Val	Gly	Ser	Glu	Gly	Arg	Arg	Gly	Lys	Lys	Gly	Glu	Arg
	2300					2305					2310			
Gly	Phe	Pro	Gly	Tyr	Pro	Gly	Pro	Lys	Gly	Asn	Pro	Gly	Glu	Pro
	2315					2320					2325			
Gly	Leu	Asn	Gly	Thr	Thr	Gly	Pro	Lys	Gly	Ile	Arg	Gly	Arg	Arg
	2330					2335					2340			
Gly	Asn	Ser	Gly	Pro	Pro	Gly	Ile	Val	Gly	Gln	Lys	Gly	Asp	Pro
	2345					2350					2355			
Gly	Tyr	Pro	Gly	Pro	Ala	Gly	Pro	Lys	Gly	Asn	Arg	Gly	Asp	Ser
	2360					2365					2370			
Ile	Asp	Gln	Cys	Ala	Leu	Ile	Gln	Ser	Ile	Lys	Asp	Lys	Cys	Pro
	2375					2380					2385			
Cys	Cys	Tyr	Gly	Pro	Leu	Glu	Cys	Pro	Val	Phe	Pro	Thr	Glu	Leu
	2390					2395					2400			
Ala	Phe	Ala	Leu	Asp	Thr	Ser	Glu	Gly	Val	Asn	Gln	Asp	Thr	Phe
	2405					2410					2415			
Gly	Arg	Met	Arg	Asp	Val	Val	Leu	Ser	Ile	Val	Asn	Asp	Leu	Thr
	2420					2425					2430			
Ile	Ala	Glu	Ser	Asn	Cys	Pro	Arg	Gly	Ala	Arg	Val	Ala	Val	Val
	2435					2440					2445			
Thr	Tyr	Asn	Asn	Glu	Val	Thr	Thr	Glu	Ile	Arg	Phe	Ala	Asp	Ser
	2450					2455					2460			
Lys	Arg	Lys	Ser	Val	Leu	Leu	Asp	Lys	Ile	Lys	Asn	Leu	Gln	Val
	2465					2470					2475			
Ala	Leu	Thr	Ser	Lys	Gln	Gln	Ser	Leu	Glu	Thr	Ala	Met	Ser	Phe
	2480					2485					2490			

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Val	Ala	Arg	Asn	Thr	Phe	Lys	Arg	Val	Arg	Asn	Gly	Phe	Leu	Met
	2495					2500					2505			
Arg	Lys	Val	Ala	Val	Phe	Phe	Ser	Asn	Thr	Pro	Thr	Arg	Ala	Ser
	2510					2515					2520			
Pro	Gln	Leu	Arg	Glu	Ala	Val	Leu	Lys	Leu	Ser	Asp	Ala	Gly	Ile
	2525					2530					2535			
Thr	Pro	Leu	Phe	Leu	Thr	Arg	Gln	Glu	Asp	Arg	Gln	Leu	Ile	Asn
	2540					2545					2550			
Ala	Leu	Gln	Ile	Asn	Asn	Thr	Ala	Val	Gly	His	Ala	Leu	Val	Leu
	2555					2560					2565			
Pro	Ala	Gly	Arg	Asp	Leu	Thr	Asp	Phe	Leu	Glu	Asn	Val	Leu	Thr
	2570					2575					2580			
Cys	His	Val	Cys	Leu	Asp	Ile	Cys	Asn	Ile	Asp	Pro	Ser	Cys	Gly
	2585					2590					2595			
Phe	Gly	Ser	Trp	Arg	Pro	Ser	Phe	Arg	Asp	Arg	Arg	Ala	Ala	Gly
	2600					2605					2610			
Ser	Asp	Val	Asp	Ile	Asp	Met	Ala	Phe	Ile	Leu	Asp	Ser	Ala	Glu
	2615					2620					2625			
Thr	Thr	Thr	Leu	Phe	Gln	Phe	Asn	Glu	Met	Lys	Lys	Tyr	Ile	Ala
	2630					2635					2640			
Tyr	Leu	Val	Arg	Gln	Leu	Asp	Met	Ser	Pro	Asp	Pro	Lys	Ala	Ser
	2645					2650					2655			
Gln	His	Phe	Ala	Arg	Val	Ala	Val	Val	Gln	His	Ala	Pro	Ser	Glu
	2660					2665					2670			
Ser	Val	Asp	Asn	Ala	Ser	Met	Pro	Pro	Val	Lys	Val	Glu	Phe	Ser
	2675					2680					2685			
Leu	Thr	Asp	Tyr	Gly	Ser	Lys	Glu	Lys	Leu	Val	Asp	Phe	Leu	Ser
	2690					2695					2700			
Arg	Gly	Met	Thr	Gln	Leu	Gln	Gly	Thr	Arg	Ala	Leu	Gly	Ser	Ala
	2705					2710					2715			
Ile	Glu	Tyr	Thr	Ile	Glu	Asn	Val	Phe	Glu	Ser	Ala	Pro	Asn	Pro
	2720					2725					2730			
Arg	Asp	Leu	Lys	Ile	Val	Val	Leu	Met	Leu	Thr	Gly	Glu	Val	Pro
	2735					2740					2745			

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Glu	Gln	Gln	Leu	Glu	Glu	Ala	Gln	Arg	Val	Ile	Leu	Gln	Ala	Lys
	2750					2755					2760			
Cys	Lys	Gly	Tyr	Phe	Phe	Val	Val	Leu	Gly	Ile	Gly	Arg	Lys	Val
	2765					2770					2775			
Asn	Ile	Lys	Glu	Val	Tyr	Thr	Phe	Ala	Ser	Glu	Pro	Asn	Asp	Val
	2780					2785					2790			
Phe	Phe	Lys	Leu	Val	Asp	Lys	Ser	Thr	Glu	Leu	Asn	Glu	Glu	Pro
	2795					2800					2805			
Leu	Met	Arg	Phe	Gly	Arg	Leu	Leu	Pro	Ser	Phe	Val	Ser	Ser	Glu
	2810					2815					2820			
Asn	Ala	Phe	Tyr	Leu	Ser	Pro	Asp	Ile	Arg	Lys	Gln	Cys	Asp	Trp
	2825					2830					2835			
Phe	Gln	Gly	Asp	Gln	Pro	Thr	Lys	Asn	Leu	Val	Lys	Phe	Gly	His
	2840					2845					2850			
Lys	Gln	Val	Asn	Val	Pro	Asn	Asn	Val	Thr	Ser	Ser	Pro	Thr	Ser
	2855					2860					2865			
Asn	Pro	Val	Thr	Thr	Thr	Lys	Pro	Val	Thr	Thr	Thr	Lys	Pro	Val
	2870					2875					2880			
Thr	Thr	Thr	Thr	Lys	Pro	Val	Thr	Thr	Thr	Thr	Lys	Pro	Val	Thr
	2885					2890					2895			
Ile	Ile	Asn	Gln	Pro	Ser	Val	Lys	Pro	Ala	Ala	Ala	Lys	Pro	Ala
	2900					2905					2910			
Pro	Ala	Lys	Pro	Val	Ala	Ala	Lys	Pro	Val	Ala	Thr	Lys	Met	Ala
	2915					2920					2925			
Thr	Val	Arg	Pro	Pro	Val	Ala	Val	Lys	Pro	Ala	Thr	Ala	Ala	Lys
	2930					2935					2940			
Pro	Val	Ala	Ala	Lys	Pro	Ala	Ala	Val	Arg	Pro	Pro	Ala	Ala	Ala
	2945					2950					2955			
Ala	Ala	Lys	Pro	Val	Ala	Thr	Lys	Pro	Glu	Val	Pro	Arg	Pro	Gln
	2960					2965					2970			
Ala	Ala	Lys	Pro	Ala	Ala	Thr	Lys	Pro	Ala	Thr	Thr	Lys	Pro	Met
	2975					2980					2985			
Val	Lys	Met	Ser	Arg	Glu	Val	Gln	Val	Phe	Glu	Ile	Thr	Glu	Asn
	2990					2995					3000			



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Ser Ala Lys Leu His Trp Glu Arg Ala Glu Pro Pro Gly Pro Tyr  
3005 3010 3015

Phe Tyr Asp Leu Thr Val Thr Ser Ala His Asp Gln Ser Leu Val  
3020 3025 3030

Leu Lys Gln Asn Leu Thr Val Thr Asp Arg Val Ile Gly Gly Leu  
3035 3040 3045

Leu Ala Gly Gln Thr Tyr His Val Ala Val Val Cys Tyr Leu Arg  
3050 3055 3060

Ser Gln Val Arg Ala Thr Tyr His Gly Ser Phe Ser Thr Lys Lys  
3065 3070 3075

Ser Gln Pro Pro Pro Pro Gln Pro Ala Arg Ser Ala Ser Ser Ser  
3080 3085 3090

Thr Ile Asn Leu Met Val Ser Thr Glu Pro Leu Ala Leu Thr Glu  
3095 3100 3105

Thr Asp Ile Cys Lys Leu Pro Lys Asp Glu Gly Thr Cys Arg Asp  
3110 3115 3120

Phe Ile Leu Lys Trp Tyr Tyr Asp Pro Asn Thr Lys Ser Cys Ala  
3125 3130 3135

Arg Phe Trp Tyr Gly Gly Cys Gly Gly Asn Glu Asn Lys Phe Gly  
3140 3145 3150

Ser Gln Lys Glu Cys Glu Lys Val Cys Ala Pro Val Leu Ala Lys  
3155 3160 3165

Pro Gly Val Ile Ser Val Met Gly Thr  
3170 3175

<210> 78  
<211> 2944  
<212> PRT  
<213> Homo sapiens

<400> 78

Met Thr Leu Arg Leu Leu Val Ala Ala Leu Cys Ala Gly Ile Leu Ala  
1 5 10 15

Glu Ala Pro Arg Val Arg Ala Gln His Arg Glu Arg Val Thr Cys Thr  
20 25 30

Arg Leu Tyr Ala Ala Asp Ile Val Phe Leu Leu Asp Gly Ser Ser Ser  
35 40 45

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Ile Gly Arg Ser Asn Phe Arg Glu Val Arg Ser Phe Leu Glu Gly Leu  
 50 55 60  
 Val Leu Pro Phe Ser Gly Ala Ala Ser Ala Gln Gly Val Arg Phe Ala  
 65 70 75 80  
 Thr Val Gln Tyr Ser Asp Asp Pro Arg Thr Glu Phe Gly Leu Asp Ala  
 85 90 95  
 Leu Gly Ser Gly Gly Asp Val Ile Arg Ala Ile Arg Glu Leu Ser Tyr  
 100 105 110  
 Lys Gly Gly Asn Thr Arg Thr Gly Ala Ala Ile Leu His Val Ala Asp  
 115 120 125  
 His Val Phe Leu Pro Gln Leu Ala Arg Pro Gly Val Pro Lys Val Cys  
 130 135 140  
 Ile Leu Ile Thr Asp Gly Lys Ser Gln Asp Leu Val Asp Thr Ala Ala  
 145 150 155 160  
 Gln Arg Leu Lys Gly Gln Gly Val Lys Leu Phe Ala Val Gly Ile Lys  
 165 170 175  
 Asn Ala Asp Pro Glu Glu Leu Lys Arg Val Ala Ser Gln Pro Thr Ser  
 180 185 190  
 Asp Phe Phe Phe Phe Val Asn Asp Phe Ser Ile Leu Arg Thr Leu Leu  
 195 200 205  
 Pro Leu Val Ser Arg Arg Val Cys Thr Thr Ala Gly Gly Val Pro Val  
 210 215 220  
 Thr Arg Pro Pro Asp Asp Ser Thr Ser Ala Pro Arg Asp Leu Val Leu  
 225 230 235 240  
 Ser Glu Pro Ser Ser Gln Ser Leu Arg Val Gln Trp Thr Ala Ala Ser  
 245 250 255  
 Gly Pro Val Thr Gly Tyr Lys Val Gln Tyr Thr Pro Leu Thr Gly Leu  
 260 265 270  
 Gly Gln Pro Leu Pro Ser Glu Arg Gln Glu Val Asn Val Pro Ala Gly  
 275 280 285  
 Glu Thr Ser Val Arg Leu Arg Gly Leu Arg Pro Leu Thr Glu Tyr Gln  
 290 295 300  
 Val Thr Val Ile Ala Leu Tyr Ala Asn Ser Ile Gly Glu Ala Val Ser  
 305 310 315 320

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Gly Thr Ala Arg Thr Thr Ala Leu Glu Gly Pro Glu Leu Thr Ile Gln  
325 330 335

Asn Thr Thr Ala His Ser Leu Leu Val Ala Trp Arg Ser Val Pro Gly  
340 345 350

Ala Thr Gly Tyr Arg Val Thr Trp Arg Val Leu Ser Gly Gly Pro Thr  
355 360 365

Gln Gln Gln Glu Leu Gly Pro Gly Gln Gly Ser Val Leu Leu Arg Asp  
370 375 380

Leu Glu Pro Gly Thr Asp Tyr Glu Val Thr Val Ser Thr Leu Phe Gly  
385 390 395 400

Arg Ser Val Gly Pro Ala Thr Ser Leu Met Ala Arg Thr Asp Ala Ser  
405 410 415

Val Glu Gln Thr Leu Arg Pro Val Ile Leu Gly Pro Thr Ser Ile Leu  
420 425 430

Leu Ser Trp Asn Leu Val Pro Glu Ala Arg Gly Tyr Arg Leu Glu Trp  
435 440 445

Arg Arg Glu Thr Gly Leu Glu Pro Pro Gln Lys Val Val Leu Pro Ser  
450 455 460

Asp Val Thr Arg Tyr Gln Leu Asp Gly Leu Gln Pro Gly Thr Glu Tyr  
465 470 475 480

Arg Leu Thr Leu Tyr Thr Leu Leu Glu Gly His Glu Val Ala Thr Pro  
485 490 495

Ala Thr Val Val Pro Thr Gly Pro Glu Leu Pro Val Ser Pro Val Thr  
500 505 510

Asp Leu Gln Ala Thr Glu Leu Pro Gly Gln Arg Val Arg Val Ser Trp  
515 520 525

Ser Pro Val Pro Gly Ala Thr Gln Tyr Arg Ile Ile Val Arg Ser Thr  
530 535 540

Gln Gly Val Glu Arg Thr Leu Val Leu Pro Gly Ser Gln Thr Ala Phe  
545 550 555 560

Asp Leu Asp Asp Val Gln Ala Gly Leu Ser Tyr Thr Val Arg Val Ser  
565 570 575

Ala Arg Val Gly Pro Arg Glu Gly Ser Ala Ser Val Leu Thr Val Arg  
580 585 590

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Arg Glu Pro Glu Thr Pro Leu Ala Val Pro Gly Leu Arg Val Val Val  
595 600 605

Ser Asp Ala Thr Arg Val Arg Val Ala Trp Gly Pro Val Pro Gly Ala  
610 615 620

Ser Gly Phe Arg Ile Ser Trp Ser Thr Gly Ser Gly Pro Glu Ser Ser  
625 630 635 640

Gln Thr Leu Pro Pro Asp Ser Thr Ala Thr Asp Ile Thr Gly Leu Gln  
645 650 655

Pro Gly Thr Thr Tyr Gln Val Ala Val Ser Val Leu Arg Gly Arg Glu  
660 665 670

Glu Gly Pro Ala Ala Val Ile Val Ala Arg Thr Asp Pro Leu Gly Pro  
675 680 685

Val Arg Thr Val His Val Thr Gln Ala Ser Ser Ser Ser Val Thr Ile  
690 695 700

Thr Trp Thr Arg Val Pro Gly Ala Thr Gly Tyr Arg Val Ser Trp His  
705 710 715 720

Ser Ala His Gly Pro Glu Lys Ser Gln Leu Val Ser Gly Glu Ala Thr  
725 730 735

Val Ala Glu Leu Asp Gly Leu Glu Pro Asp Thr Glu Tyr Thr Val His  
740 745 750

Val Arg Ala His Val Ala Gly Val Asp Gly Pro Pro Ala Ser Val Val  
755 760 765

Val Arg Thr Ala Pro Glu Pro Val Gly Arg Val Ser Arg Leu Gln Ile  
770 775 780

Leu Asn Ala Ser Ser Asp Val Leu Arg Ile Thr Trp Val Gly Val Thr  
785 790 795 800

Gly Ala Thr Ala Tyr Arg Leu Ala Trp Gly Arg Ser Glu Gly Gly Pro  
805 810 815

Met Arg His Gln Ile Leu Pro Gly Asn Thr Asp Ser Ala Glu Ile Arg  
820 825 830

Gly Leu Glu Gly Gly Val Ser Tyr Ser Val Arg Val Thr Ala Leu Val  
835 840 845

Gly Asp Arg Glu Gly Thr Pro Val Ser Ile Val Val Thr Thr Pro Pro  
850 855 860

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Glu Ala Pro Pro Ala Leu Gly Thr Leu His Val Val Gln Arg Gly Glu  
 865 870 875 880  
 His Ser Leu Arg Leu Arg Trp Glu Pro Val Pro Arg Ala Gln Gly Phe  
 885 890 895  
 Leu Leu His Trp Gln Pro Glu Gly Gly Gln Glu Gln Ser Arg Val Leu  
 900 905 910  
 Gly Pro Glu Leu Ser Ser Tyr His Leu Asp Gly Leu Glu Pro Ala Thr  
 915 920 925  
 Gln Tyr Arg Val Arg Leu Ser Val Leu Gly Pro Ala Gly Glu Gly Pro  
 930 935 940  
 Ser Ala Glu Val Thr Ala Arg Thr Glu Ser Pro Arg Val Pro Ser Ile  
 945 950 955 960  
 Glu Leu Arg Val Val Asp Thr Ser Ile Asp Ser Val Thr Leu Ala Trp  
 965 970 975  
 Thr Pro Val Ser Arg Ala Ser Ser Tyr Ile Leu Ser Trp Arg Pro Leu  
 980 985 990  
 Arg Gly Pro Gly Gln Glu Val Pro Gly Ser Pro Gln Thr Leu Pro Gly  
 995 1000 1005  
 Ile Ser Ser Ser Gln Arg Val Thr Gly Leu Glu Pro Gly Val Ser  
 1010 1015 1020  
 Tyr Ile Phe Ser Leu Thr Pro Val Leu Asp Gly Val Arg Gly Pro  
 1025 1030 1035  
 Glu Ala Ser Val Thr Gln Thr Pro Val Cys Pro Arg Gly Leu Ala  
 1040 1045 1050  
 Asp Val Val Phe Leu Pro His Ala Thr Gln Asp Asn Ala His Arg  
 1055 1060 1065  
 Ala Glu Ala Thr Arg Arg Val Leu Glu Arg Leu Val Leu Ala Leu  
 1070 1075 1080  
 Gly Pro Leu Gly Pro Gln Ala Val Gln Val Gly Leu Leu Ser Tyr  
 1085 1090 1095  
 Ser His Arg Pro Ser Pro Leu Phe Pro Leu Asn Gly Ser His Asp  
 1100 1105 1110  
 Leu Gly Ile Ile Leu Gln Arg Ile Arg Asp Met Pro Tyr Met Asp  
 1115 1120 1125

## FAB-008PC-SequenceListing

Pro	Ser	Gly	Asn	Asn	Leu	Gly	Thr	Ala	Val	Val	Thr	Ala	His	Arg
	1130					1135					1140			
Tyr	Met	Leu	Ala	Pro	Asp	Ala	Pro	Gly	Arg	Arg	Gln	His	Val	Pro
	1145					1150					1155			
Gly	Val	Met	Val	Leu	Leu	Val	Asp	Glu	Pro	Leu	Arg	Gly	Asp	Ile
	1160					1165					1170			
Phe	Ser	Pro	Ile	Arg	Glu	Ala	Gln	Ala	Ser	Gly	Leu	Asn	Val	Val
	1175					1180					1185			
Met	Leu	Gly	Met	Ala	Gly	Ala	Asp	Pro	Glu	Gln	Leu	Arg	Arg	Leu
	1190					1195					1200			
Ala	Pro	Gly	Met	Asp	Ser	Val	Gln	Thr	Phe	Phe	Ala	Val	Asp	Asp
	1205					1210					1215			
Gly	Pro	Ser	Leu	Asp	Gln	Ala	Val	Ser	Gly	Leu	Ala	Thr	Ala	Leu
	1220					1225					1230			
Cys	Gln	Ala	Ser	Phe	Thr	Thr	Gln	Pro	Arg	Pro	Glu	Pro	Cys	Pro
	1235					1240					1245			
Val	Tyr	Cys	Pro	Lys	Gly	Gln	Lys	Gly	Glu	Pro	Gly	Glu	Met	Gly
	1250					1255					1260			
Leu	Arg	Gly	Gln	Val	Gly	Pro	Pro	Gly	Asp	Pro	Gly	Leu	Pro	Gly
	1265					1270					1275			
Arg	Thr	Gly	Ala	Pro	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Ser	Ala	Thr
	1280					1285					1290			
Ala	Lys	Gly	Glu	Arg	Gly	Phe	Pro	Gly	Ala	Asp	Gly	Arg	Pro	Gly
	1295					1300					1305			
Ser	Pro	Gly	Arg	Ala	Gly	Asn	Pro	Gly	Thr	Pro	Gly	Ala	Pro	Gly
	1310					1315					1320			
Leu	Lys	Gly	Ser	Pro	Gly	Leu	Pro	Gly	Pro	Arg	Gly	Asp	Pro	Gly
	1325					1330					1335			
Glu	Arg	Gly	Pro	Arg	Gly	Pro	Lys	Gly	Glu	Pro	Gly	Ala	Pro	Gly
	1340					1345					1350			
Gln	Val	Ile	Gly	Gly	Glu	Gly	Pro	Gly	Leu	Pro	Gly	Arg	Lys	Gly
	1355					1360					1365			
Asp	Pro	Gly	Pro	Ser	Gly	Pro	Pro	Gly	Pro	Arg	Gly	Pro	Leu	Gly
	1370					1375					1380			

## FAB-008PC-SequenceListing

Asp	Pro	Gly	Pro	Arg	Gly	Pro	Pro	Gly	Leu	Pro	Gly	Thr	Ala	Met
1385						1390					1395			
Lys	Gly	Asp	Lys	Gly	Asp	Arg	Gly	Glu	Arg	Gly	Pro	Pro	Gly	Pro
1400						1405					1410			
Gly	Glu	Gly	Gly	Ile	Ala	Pro	Gly	Glu	Pro	Gly	Leu	Pro	Gly	Leu
1415						1420					1425			
Pro	Gly	Ser	Pro	Gly	Pro	Gln	Gly	Pro	Val	Gly	Pro	Pro	Gly	Lys
1430						1435					1440			
Lys	Gly	Glu	Lys	Gly	Asp	Ser	Glu	Asp	Gly	Ala	Pro	Gly	Leu	Pro
1445						1450					1455			
Gly	Gln	Pro	Gly	Ser	Pro	Gly	Glu	Gln	Gly	Pro	Arg	Gly	Pro	Pro
1460						1465					1470			
Gly	Ala	Ile	Gly	Pro	Lys	Gly	Asp	Arg	Gly	Phe	Pro	Gly	Pro	Leu
1475						1480					1485			
Gly	Glu	Ala	Gly	Glu	Lys	Gly	Glu	Arg	Gly	Pro	Pro	Gly	Pro	Ala
1490						1495					1500			
Gly	Ser	Arg	Gly	Leu	Pro	Gly	Val	Ala	Gly	Arg	Pro	Gly	Ala	Lys
1505						1510					1515			
Gly	Pro	Glu	Gly	Pro	Pro	Gly	Pro	Thr	Gly	Arg	Gln	Gly	Glu	Lys
1520						1525					1530			
Gly	Glu	Pro	Gly	Arg	Pro	Gly	Asp	Pro	Ala	Val	Val	Gly	Pro	Ala
1535						1540					1545			
Val	Ala	Gly	Pro	Lys	Gly	Glu	Lys	Gly	Asp	Val	Gly	Pro	Ala	Gly
1550						1555					1560			
Pro	Arg	Gly	Ala	Thr	Gly	Val	Gln	Gly	Glu	Arg	Gly	Pro	Pro	Gly
1565						1570					1575			
Leu	Val	Leu	Pro	Gly	Asp	Pro	Gly	Pro	Lys	Gly	Asp	Pro	Gly	Asp
1580						1585					1590			
Arg	Gly	Pro	Ile	Gly	Leu	Thr	Gly	Arg	Ala	Gly	Pro	Pro	Gly	Asp
1595						1600					1605			
Ser	Gly	Pro	Pro	Gly	Glu	Lys	Gly	Asp	Pro	Gly	Arg	Pro	Gly	Pro
1610						1615					1620			
Pro	Gly	Pro	Val	Gly	Pro	Arg	Gly	Arg	Asp	Gly	Glu	Val	Gly	Glu
1625						1630					1635			

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Lys	Gly	Asp	Glu	Gly	Pro	Pro	Gly	Asp	Pro	Gly	Leu	Pro	Gly	Lys
	1640					1645					1650			
Ala	Gly	Glu	Arg	Gly	Leu	Arg	Gly	Ala	Pro	Gly	Val	Arg	Gly	Pro
	1655					1660					1665			
Val	Gly	Glu	Lys	Gly	Asp	Gln	Gly	Asp	Pro	Gly	Glu	Asp	Gly	Arg
	1670					1675					1680			
Asn	Gly	Ser	Pro	Gly	Ser	Ser	Gly	Pro	Lys	Gly	Asp	Arg	Gly	Glu
	1685					1690					1695			
Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Arg	Leu	Val	Asp	Thr	Gly	Pro
	1700					1705					1710			
Gly	Ala	Arg	Glu	Lys	Gly	Glu	Pro	Gly	Asp	Arg	Gly	Gln	Glu	Gly
	1715					1720					1725			
Pro	Arg	Gly	Pro	Lys	Gly	Asp	Pro	Gly	Leu	Pro	Gly	Ala	Pro	Gly
	1730					1735					1740			
Glu	Arg	Gly	Ile	Glu	Gly	Phe	Arg	Gly	Pro	Pro	Gly	Pro	Gln	Gly
	1745					1750					1755			
Asp	Pro	Gly	Val	Arg	Gly	Pro	Ala	Gly	Glu	Lys	Gly	Asp	Arg	Gly
	1760					1765					1770			
Pro	Pro	Gly	Leu	Asp	Gly	Arg	Ser	Gly	Leu	Asp	Gly	Lys	Pro	Gly
	1775					1780					1785			
Ala	Ala	Gly	Pro	Ser	Gly	Pro	Asn	Gly	Ala	Ala	Gly	Lys	Ala	Gly
	1790					1795					1800			
Asp	Pro	Gly	Arg	Asp	Gly	Leu	Pro	Gly	Leu	Arg	Gly	Glu	Gln	Gly
	1805					1810					1815			
Leu	Pro	Gly	Pro	Ser	Gly	Pro	Pro	Gly	Leu	Pro	Gly	Lys	Pro	Gly
	1820					1825					1830			
Glu	Asp	Gly	Lys	Pro	Gly	Leu	Asn	Gly	Lys	Asn	Gly	Glu	Pro	Gly
	1835					1840					1845			
Asp	Pro	Gly	Glu	Asp	Gly	Arg	Lys	Gly	Glu	Lys	Gly	Asp	Ser	Gly
	1850					1855					1860			
Ala	Ser	Gly	Arg	Glu	Gly	Arg	Asp	Gly	Pro	Lys	Gly	Glu	Arg	Gly
	1865					1870					1875			
Ala	Pro	Gly	Ile	Leu	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Leu	Pro	Gly
	1880					1885					1890			



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Pro	Val	Gly	Pro	Pro	Gly	Gln	Gly	Phe	Pro	Gly	Val	Pro	Gly	Gly
	1895					1900					1905			
Thr	Gly	Pro	Lys	Gly	Asp	Arg	Gly	Glu	Thr	Gly	Ser	Lys	Gly	Glu
	1910					1915					1920			
Gln	Gly	Leu	Pro	Gly	Glu	Arg	Gly	Leu	Arg	Gly	Glu	Pro	Gly	Ser
	1925					1930					1935			
Val	Pro	Asn	Val	Asp	Arg	Leu	Leu	Glu	Thr	Ala	Gly	Ile	Lys	Ala
	1940					1945					1950			
Ser	Ala	Leu	Arg	Glu	Ile	Val	Glu	Thr	Trp	Asp	Glu	Ser	Ser	Gly
	1955					1960					1965			
Ser	Phe	Leu	Pro	Val	Pro	Glu	Arg	Arg	Arg	Gly	Pro	Lys	Gly	Asp
	1970					1975					1980			
Ser	Gly	Glu	Gln	Gly	Pro	Pro	Gly	Lys	Glu	Gly	Pro	Ile	Gly	Phe
	1985					1990					1995			
Pro	Gly	Glu	Arg	Gly	Leu	Lys	Gly	Asp	Arg	Gly	Asp	Pro	Gly	Pro
	2000					2005					2010			
Gln	Gly	Pro	Pro	Gly	Leu	Ala	Leu	Gly	Glu	Arg	Gly	Pro	Pro	Gly
	2015					2020					2025			
Pro	Ser	Gly	Leu	Ala	Gly	Glu	Pro	Gly	Lys	Pro	Gly	Ile	Pro	Gly
	2030					2035					2040			
Leu	Pro	Gly	Arg	Ala	Gly	Gly	Val	Gly	Glu	Ala	Gly	Arg	Pro	Gly
	2045					2050					2055			
Glu	Arg	Gly	Glu	Arg	Gly	Glu	Lys	Gly	Glu	Arg	Gly	Glu	Gln	Gly
	2060					2065					2070			
Arg	Asp	Gly	Pro	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	Pro	Pro	Gly
	2075					2080					2085			
Pro	Pro	Gly	Pro	Lys	Val	Ser	Val	Asp	Glu	Pro	Gly	Pro	Gly	Leu
	2090					2095					2100			
Ser	Gly	Glu	Gln	Gly	Pro	Pro	Gly	Leu	Lys	Gly	Ala	Lys	Gly	Glu
	2105					2110					2115			
Pro	Gly	Ser	Asn	Gly	Asp	Gln	Gly	Pro	Lys	Gly	Asp	Arg	Gly	Val
	2120					2125					2130			
Pro	Gly	Ile	Lys	Gly	Asp	Arg	Gly	Glu	Pro	Gly	Pro	Arg	Gly	Gln
	2135					2140					2145			

## FAB-008PC-SequenceListing

Asp Gly 2150 Asn Pro Gly Leu Pro 2155 Gly Glu Arg Gly Met 2160 Ala Gly Pro  
 Glu Gly 2165 Lys Pro Gly Leu Gln 2170 Gly Pro Arg Gly Pro 2175 Pro Gly Pro  
 Val Gly 2180 Gly His Gly Asp Pro 2185 Gly Pro Pro Gly Ala 2190 Pro Gly Leu  
 Ala Gly 2195 Pro Ala Gly Pro Gln 2200 Gly Pro Ser Gly Leu 2205 Lys Gly Glu  
 Pro Gly 2210 Glu Thr Gly Pro Pro 2215 Gly Arg Gly Leu Thr 2220 Gly Pro Thr  
 Gly Ala 2225 Val Gly Leu Pro Gly 2230 Pro Pro Gly Pro Ser 2235 Gly Leu Val  
 Gly Pro 2240 Gln Gly Ser Pro Gly 2245 Leu Pro Gly Gln Val 2250 Gly Glu Thr  
 Gly Lys 2255 Pro Gly Ala Pro Gly 2260 Arg Asp Gly Ala Ser 2265 Gly Lys Asp  
 Gly Asp 2270 Arg Gly Ser Pro Gly 2275 Val Pro Gly Ser Pro 2280 Gly Leu Pro  
 Gly Pro 2285 Val Gly Pro Lys Gly 2290 Glu Pro Gly Pro Thr 2295 Gly Ala Pro  
 Gly Gln 2300 Ala Val Val Gly Leu 2305 Pro Gly Ala Lys Gly 2310 Glu Lys Gly  
 Ala Pro 2315 Gly Gly Leu Ala Gly 2320 Asp Leu Val Gly Glu 2325 Pro Gly Ala  
 Lys Gly 2330 Asp Arg Gly Leu Pro 2335 Gly Pro Arg Gly Glu 2340 Lys Gly Glu  
 Ala Gly 2345 Arg Ala Gly Glu Pro 2350 Gly Asp Pro Gly Glu 2355 Asp Gly Gln  
 Lys Gly 2360 Ala Pro Gly Pro Lys 2365 Gly Phe Lys Gly Asp 2370 Pro Gly Val  
 Gly Val 2375 Pro Gly Ser Pro Gly 2380 Pro Pro Gly Pro Pro 2385 Gly Val Lys  
 Gly Asp 2390 Leu Gly Leu Pro Gly 2395 Leu Pro Gly Ala Pro 2400 Gly Val Val

## FAB-008PC-SequenceListing

Gly Phe Pro Gly Gln Thr Gly Pro Arg Gly Glu Met Gly Gln Pro  
 2405 2410 2415  
 Gly Pro Ser Gly Glu Arg Gly Leu Ala Gly Pro Pro Gly Arg Glu  
 2420 2425 2430  
 Gly Ile Pro Gly Pro Leu Gly Pro Pro Gly Pro Pro Gly Ser Val  
 2435 2440 2445  
 Gly Pro Pro Gly Ala Ser Gly Leu Lys Gly Asp Lys Gly Asp Pro  
 2450 2455 2460  
 Gly Val Gly Leu Pro Gly Pro Arg Gly Glu Arg Gly Glu Pro Gly  
 2465 2470 2475  
 Ile Arg Gly Glu Asp Gly Arg Pro Gly Gln Glu Gly Pro Arg Gly  
 2480 2485 2490  
 Leu Thr Gly Pro Pro Gly Ser Arg Gly Glu Arg Gly Glu Lys Gly  
 2495 2500 2505  
 Asp Val Gly Ser Ala Gly Leu Lys Gly Asp Lys Gly Asp Ser Ala  
 2510 2515 2520  
 Val Ile Leu Gly Pro Pro Gly Pro Arg Gly Ala Lys Gly Asp Met  
 2525 2530 2535  
 Gly Glu Arg Gly Pro Arg Gly Leu Asp Gly Asp Lys Gly Pro Arg  
 2540 2545 2550  
 Gly Asp Asn Gly Asp Pro Gly Asp Lys Gly Ser Lys Gly Glu Pro  
 2555 2560 2565  
 Gly Asp Lys Gly Ser Ala Gly Leu Pro Gly Leu Arg Gly Leu Leu  
 2570 2575 2580  
 Gly Pro Gln Gly Gln Pro Gly Ala Ala Gly Ile Pro Gly Asp Pro  
 2585 2590 2595  
 Gly Ser Pro Gly Lys Asp Gly Val Pro Gly Ile Arg Gly Glu Lys  
 2600 2605 2610  
 Gly Asp Val Gly Phe Met Gly Pro Arg Gly Leu Lys Gly Glu Arg  
 2615 2620 2625  
 Gly Val Lys Gly Ala Cys Gly Leu Asp Gly Glu Lys Gly Asp Lys  
 2630 2635 2640  
 Gly Glu Ala Gly Pro Pro Gly Arg Pro Gly Leu Ala Gly His Lys  
 2645 2650 2655

## FAB-008PC-SequenceListing

Gly Glu Met Gly Glu Pro Gly Val Pro Gly Gln Ser Gly Ala Pro  
 2660 2665 2670  
 Gly Lys Glu Gly Leu Ile Gly Pro Lys Gly Asp Arg Gly Phe Asp  
 2675 2680 2685  
 Gly Gln Pro Gly Pro Lys Gly Asp Gln Gly Glu Lys Gly Glu Arg  
 2690 2695 2700  
 Gly Thr Pro Gly Ile Gly Gly Phe Pro Gly Pro Ser Gly Asn Asp  
 2705 2710 2715  
 Gly Ser Ala Gly Pro Pro Gly Pro Pro Gly Ser Val Gly Pro Arg  
 2720 2725 2730  
 Gly Pro Glu Gly Leu Gln Gly Gln Lys Gly Glu Arg Gly Pro Pro  
 2735 2740 2745  
 Gly Glu Arg Val Val Gly Ala Pro Gly Val Pro Gly Ala Pro Gly  
 2750 2755 2760  
 Glu Arg Gly Glu Gln Gly Arg Pro Gly Pro Ala Gly Pro Arg Gly  
 2765 2770 2775  
 Glu Lys Gly Glu Ala Ala Leu Thr Glu Asp Asp Ile Arg Gly Phe  
 2780 2785 2790  
 Val Arg Gln Glu Met Ser Gln His Cys Ala Cys Gln Gly Gln Phe  
 2795 2800 2805  
 Ile Ala Ser Gly Ser Arg Pro Leu Pro Ser Tyr Ala Ala Asp Thr  
 2810 2815 2820  
 Ala Gly Ser Gln Leu His Ala Val Pro Val Leu Arg Val Ser His  
 2825 2830 2835  
 Ala Glu Glu Glu Glu Arg Val Pro Pro Glu Asp Asp Glu Tyr Ser  
 2840 2845 2850  
 Glu Tyr Ser Glu Tyr Ser Val Glu Glu Tyr Gln Asp Pro Glu Ala  
 2855 2860 2865  
 Pro Trp Asp Ser Asp Asp Pro Cys Ser Leu Pro Leu Asp Glu Gly  
 2870 2875 2880  
 Ser Cys Thr Ala Tyr Thr Leu Arg Trp Tyr His Arg Ala Val Thr  
 2885 2890 2895  
 Gly Ser Thr Glu Ala Cys His Pro Phe Val Tyr Gly Gly Cys Gly  
 2900 2905 2910

# FAB-008PC-SequenceListing

Gly Asn Ala Asn Arg Phe Gly Thr Arg Glu Ala Cys Glu Arg Arg  
2915 2920 2925

Cys Pro Pro Arg Val Val Gln Ser Gln Gly Thr Gly Thr Ala Gln  
2930 2935 2940

Asp

<210> 79  
<211> 724  
<212> PRT  
<213> Homo sapiens

<400> 79

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

## FAB-008PC-SequenceListing

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 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  
 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 Lys  
 435 440 445

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

Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala  
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FAB-008PC-SequenceListing

465 470 475 480

Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly  
485 490 495

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

Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala  
515 520 525

Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala  
530 535 540

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

Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly  
565 570 575

Val Pro Gly Phe Gly Ala Val Pro Gly Ala Leu Ala Ala Ala Lys Ala  
580 585 590

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

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

Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly  
625 630 635 640

Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly  
645 650 655

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

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

Ala Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly  
690 695 700

Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly  
705 710 715 720

Arg Lys Arg Lys

<210> 80

FAB-008PC-SequenceListing

<211> 677  
<212> PRT  
<213> Homo sapiens

<400> 80

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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 Ala Leu Gly Pro
 35          40          45

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

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

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

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly
100          105          110

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

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val
130          135          140

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

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

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

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly
195          200          205

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

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

Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe
245          250          255

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# FAB-008PC-SequenceListing

Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val  
 260 265 270  
 Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val  
 275 280 285  
 Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala  
 290 295 300  
 Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly  
 305 310 315 320  
 Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val  
 325 330 335  
 Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala  
 340 345 350  
 Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala  
 355 360 365  
 Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile  
 370 375 380  
 Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly  
 385 390 395 400  
 Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val  
 405 410 415  
 Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln  
 420 425 430  
 Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Leu Val Pro Gly Val  
 435 440 445  
 Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro  
 450 455 460  
 Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val  
 465 470 475 480  
 Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala  
 485 490 495  
 Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg  
 500 505 510  
 Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val  
 515 520 525

FAB-008PC-SequenceListing

Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val  
 530 535 540  
 Gly Ala Gly Val Pro Gly Phe Gly Ala Val Pro Gly Ala Leu Ala Ala  
 545 550 555 560  
 Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly  
 565 570 575  
 Leu Gly Ala Leu Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala  
 580 585 590  
 Gly Pro Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala  
 595 600 605  
 Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly  
 610 615 620  
 Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala  
 625 630 635 640  
 Ala Ala Ala Lys Ala Ala Lys Tyr Gly Val Ala Ala Arg Pro Gly Phe  
 645 650 655  
 Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys  
 660 665 670  
 Gly Arg Lys Arg Lys  
 675  
 <210> 81  
 <211> 692  
 <212> PRT  
 <213> Homo sapiens  
 <400> 81  
 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

FAB-008PC-SequenceListing

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

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

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

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

Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val Leu  
145 150 155 160

Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro Thr  
165 170 175

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

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

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

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

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

Pro Gln Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe Gly  
260 265 270

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

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

Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys  
305 310 315 320

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

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

FAB-008PC-SequenceListing

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

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

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

Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val  
405 410 415

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

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

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

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

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

Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala  
500 505 510

Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg Ala  
515 520 525

Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val Gly  
530 535 540

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

Ala Gly Val Pro Gly Phe Gly Ala Val Pro Gly Ala Leu Ala Ala Ala  
565 570 575

Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu  
580 585 590

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

Pro Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln  
610 615 620

FAB-008PC-SequenceListing

Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly  
625 630 635 640

Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala  
645 650 655

Ala Ala Lys Ala Ala Lys Tyr Gly Val Ala Ala Arg Pro Gly Phe Gly  
660 665 670

Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly  
675 680 685

Arg Lys Arg Lys  
690

<210> 82  
<211> 711  
<212> PRT  
<213> Homo sapiens

<400> 82

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 Ala Pro Ser  
115 120 125

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

Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val Leu  
145 150 155 160

## FAB-008PC-SequenceListing

Pro Gly Ala Arg Phe Pro Gly Val Gly Val Leu Pro Gly Val Pro Thr  
 165 170 175  
 Gly Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Gly Ala Phe Ala  
 180 185 190  
 Gly Ile Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val Pro  
 195 200 205  
 Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly Leu  
 210 215 220  
 Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly Val  
 225 230 235 240  
 Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val Gly  
 245 250 255  
 Pro Gln Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe Gly  
 260 265 270  
 Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val Pro  
 275 280 285  
 Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val Gly  
 290 295 300  
 Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys  
 305 310 315 320  
 Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro  
 325 330 335  
 Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val Pro  
 340 345 350  
 Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala Ala  
 355 360 365  
 Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys  
 370 375 380  
 Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro  
 385 390 395 400  
 Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val  
 405 410 415  
 Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val Pro  
 420 425 430

FAB-008PC-SequenceListing

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

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

Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro  
465 470 475 480

Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val  
485 490 495

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

Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly  
515 520 525

Val Ala Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln  
530 535 540

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

Gly Val Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu  
565 570 575

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

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

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

Gly Ala Gly Pro Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys  
625 630 635 640

Ala Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly  
645 650 655

Val Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile Pro  
660 665 670

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

Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys  
690 695 700

FAB-008PC-SequenceListing

Ala Cys Gly Arg Lys Arg Lys  
705 710

<210> 83  
<211> 705  
<212> PRT  
<213> Homo sapiens

<400> 83

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  
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## FAB-008PC-SequenceListing

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 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  
                                  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 Lys  
                                  435                      440                      445  
 Ala Ala Lys Tyr Gly Leu Val Pro Gly Val Gly Val Ala Pro Gly Val  
                                  450                      455                      460  
 Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Leu Ala Pro  
 465                      470                      475                      480  
 Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val  
                                  485                      490                      495  
 Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala Lys Ser Ala

FAB-008PC-SequenceListing

500

505

510

Ala Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala Gly Leu Gly  
515 520 525

Ala Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro Gly Leu Gly  
530 535 540

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

Phe Gly Ala Val Pro Gly Ala Leu Ala Ala Lys Ala Ala Lys Tyr  
565 570 575

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

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

Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Gly  
610 615 620

Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly Val Pro Gly  
625 630 635 640

Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys Ala Ala  
645 650 655

Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala Gly Gln  
660 665 670

Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro  
675 680 685

Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg  
690 695 700

Lys  
705

<210> 84  
<211> 706  
<212> PRT  
<213> Homo sapiens

<400> 84

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

# FAB-008PC-SequenceListing

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 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

# FAB-008PC-SequenceListing

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  
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 Val Gly Thr Pro Ala Ala Ala Ala Ala Lys Ala  
450 455 460

Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Pro Gly Val Gly Val Ala  
465 470 475 480

Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly  
485 490 495

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

Val Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Ala Ala Ala  
515 520 525

Lys Ser Ala Ala Lys Val Ala Ala Lys Ala Gln Leu Arg Ala Ala Ala  
530 535 540

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

Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly  
565 570 575

# FAB-008PC-SequenceListing

Val Pro Gly Phe Gly Ala Val Pro Gly Ala Leu Ala Ala Ala Lys Ala  
580 585 590

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

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

Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly  
625 630 635 640

Leu Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly  
645 650 655

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

Lys Ala Ala Lys Tyr Gly Val Ala Ala Arg Pro Gly Phe Gly Leu Ser  
675 680 685

Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys  
690 695 700

Arg Lys  
705

<210> 85  
<211> 643  
<212> PRT  
<213> Homo sapiens

<400> 85

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

Pro Gly Gly Val Ala Asp Ala Ala Ala Ala Tyr Lys Ala Ala Lys Ala  
85 90 95

FAB-008PC-SequenceListing

Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly Val Ser  
100 105 110

Ala Gly Ala Val Val Pro Gln Pro Gly Ala Gly Val Lys Pro Gly Lys  
115 120 125

Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val Leu Pro  
130 135 140

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

Ala Gly Val Lys Pro Lys Ala Pro Gly Val Gly Pro Phe Gly Gly Pro  
165 170 175

Gln Pro Gly Val Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro  
180 185 190

Gly Tyr Gly Pro Gly Gly Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr  
195 200 205

Pro Thr Gly Thr Gly Val Gly Pro Gln Ala Ala Ala Ala Ala Ala Ala  
210 215 220

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

Val Gly Gly Ala Gly Val Pro Gly Val Pro Gly Ala Ile Pro Gly Ile  
245 250 255

Gly Gly Ile Ala Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala  
260 265 270

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

Gly Gly Pro Gly Phe Gly Pro Gly Val Val Gly Val Pro Gly Ala Gly  
290 295 300

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

Ala Gly Ile Pro Gly Ala Ala Val Pro Gly Val Val Ser Pro Glu Ala  
325 330 335

Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly  
340 345 350

Val Gly Val Gly Gly Ile Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe  
355 360 365

# FAB-008PC-SequenceListing

Pro Gly Phe Gly Val Gly Val Gly Ala Glu Ala Gln Ala Ala Ala Ala  
 370 375 380  
 Ala Lys Ala Ala Lys Tyr 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 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 Val Pro Gly Ala Leu Ala Ala Ala Lys Ala Ala  
 500 505 510  
 Lys Tyr Gly Ala Ala Val Pro Gly Val Leu Gly Gly Leu Gly Ala Leu  
 515 520 525  
 Gly Gly Val Gly Ile Pro Gly Gly Val Val Gly Ala Gly Pro Ala Ala  
 530 535 540  
 Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu  
 545 550 555 560  
 Val Gly Ala Ala Gly Leu Gly Gly Leu Gly Val Gly Gly Leu Gly Val  
 565 570 575  
 Pro Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys  
 580 585 590  
 Ala Ala Lys Tyr Gly Ala Ala Gly Leu Gly Gly Val Leu Gly Gly Ala  
 595 600 605  
 Gly Gln Phe Pro Leu Gly Gly Val Ala Ala Arg Pro Gly Phe Gly Leu  
 610 615 620  
 Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg  
 625 630 635 640

# FAB-008PC-SequenceListing

Lys Arg Lys

<210> 86  
<211> 700  
<212> PRT  
<213> Homo sapiens

<400> 86

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 Ala Leu Gly Pro  
35 40 45

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

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

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

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly  
100 105 110

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

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

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

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

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

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

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



# FAB-008PC-SequenceListing

Tyr Gly Pro Gly Gly Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro  
 225 230 235 240  
 Thr Gly Thr Gly Val Gly Pro Gln Ala Ala Ala Ala Ala Ala Lys  
 245 250 255  
 Ala Ala Ala Lys Phe Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val  
 260 265 270  
 Gly Gly Ala Gly Val Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly  
 275 280 285  
 Gly Ile Ala Gly Val Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala  
 290 295 300  
 Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly  
 305 310 315 320  
 Gly Pro Gly Phe Gly Pro Gly Val Val Gly Val Pro Gly Ala Gly Val  
 325 330 335  
 Pro Gly Val Gly Val Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala  
 340 345 350  
 Gly Ile Pro Gly Ala Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala  
 355 360 365  
 Ala Lys Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val  
 370 375 380  
 Gly Val Gly Gly Ile Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro  
 385 390 395 400  
 Gly Phe Gly Val Gly Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro  
 405 410 415  
 Gly Val Gly Gly Val Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile  
 420 425 430  
 Ser Pro Glu Ala Gln Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly  
 435 440 445  
 Leu Val Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly  
 450 455 460  
 Val Gly Val Ala Pro Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala  
 465 470 475 480  
 Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly  
 485 490 495

# FAB-008PC-SequenceListing

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

Lys Ala Gln Leu Arg Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly  
515 520 525

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

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

Gly Ala Leu Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro  
565 570 575

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

Gly Val Val Gly Ala Gly Pro Ala Ala Ala Ala Ala Ala Ala Lys Ala  
595 600 605

Ala Ala Lys Ala Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly  
610 615 620

Gly Leu Gly Val Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly  
625 630 635 640

Gly Ile Pro Pro Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala  
645 650 655

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

Val Ala Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly  
675 680 685

Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys  
690 695 700

<210> 87  
<211> 730  
<212> PRT  
<213> Homo sapiens

<400> 87

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  
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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 Lys Ala Ala Lys Tyr Gly Ala Ala Ala

FAB-008PC-SequenceListing

305                  310                  315                  320

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580

585

590

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

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

Val Gly Ala Gly Pro Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala  
625 630 635 640

Lys Ala Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu  
645 650 655

Gly Val Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile  
660 665 670

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

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

Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys  
705 710 715 720

Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys  
725 730

<210> 88  
<211> 658  
<212> PRT  
<213> Homo sapiens

<400> 88

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

# FAB-008PC-SequenceListing

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 Tyr Gly Pro Gly Gly Val Ala Gly Ala  
210 215 220

Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val Gly Pro Gln Ala  
225 230 235 240

Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe Gly Ala Gly Ala  
245 250 255

Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val Pro Gly Val Pro  
260 265 270

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

Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala  
290 295 300

Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly Pro Gly Val Val  
305 310 315 320

Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val Pro Gly Ala Gly  
325 330 335

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

Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Lys  
355 360 365

FAB-008PC-SequenceListing

Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr Tyr Gly  
 370 375 380  
 Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly Gly Ile  
 385 390 395 400  
 Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val Pro Gly Val Gly  
 405 410 415  
 Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln Ala Ala Ala Ala  
 420 425 430  
 Ala Lys Ala Ala Lys Tyr Gly Leu Val Pro Gly Val Gly Val Ala Pro  
 435 440 445  
 Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Leu  
 450 455 460  
 Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val  
 465 470 475 480  
 Gly Val Ala Pro Gly Ile Gly Pro Gly Gly Val Ala Gly Ala Ala Ala  
 485 490 495  
 Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly Val Gly Val Gly Val Pro  
 500 505 510  
 Gly Leu Gly Val Gly Ala Gly Val Pro Gly Leu Gly Val Gly Ala Gly  
 515 520 525  
 Val Pro Gly Phe Gly Ala 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  
 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 Val Ala Ala Arg Pro Gly Phe Gly Leu Ser  
 625 630 635 640

FAB-008PC-SequenceListing

Pro Ile Phe Pro Gly Gly Ala Cys Leu Gly Lys Ala Cys Gly Arg Lys  
645 650 655

Arg Lys

<210> 89  
<211> 714  
<212> PRT  
<213> Homo sapiens  
<400> 89

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 Ala Leu Gly Pro  
35 40 45

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

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

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

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly  
100 105 110

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

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val  
130 135 140

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

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

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

Pro Leu Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly  
195 200 205



FAB-008PC-SequenceListing

Leu Pro Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly  
 210 215 220  
 Val Ala Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val  
 225 230 235 240  
 Gly Pro Gln Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe  
 245 250 255  
 Gly Ala Gly Ala Ala Gly Val Leu Pro Gly Val Gly Gly Ala Gly Val  
 260 265 270  
 Pro Gly Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val  
 275 280 285  
 Gly Thr Pro Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala  
 290 295 300  
 Lys Tyr Gly Ala Ala Ala Gly Leu Val Pro Gly Gly Pro Gly Phe Gly  
 305 310 315 320  
 Pro Gly Val Val Gly Val Pro Gly Ala Gly Val Pro Gly Val Gly Val  
 325 330 335  
 Pro Gly Ala Gly Ile Pro Val Val Pro Gly Ala Gly Ile Pro Gly Ala  
 340 345 350  
 Ala Val Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala  
 355 360 365  
 Lys Ala Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile  
 370 375 380  
 Pro Thr Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly  
 385 390 395 400  
 Val Gly Gly Ile Pro Gly Val Ala Gly Val Pro Gly Val Gly Gly Val  
 405 410 415  
 Pro Gly Val Gly Gly Val Pro Gly Val Gly Ile Ser Pro Glu Ala Gln  
 420 425 430  
 Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Val Gly Thr Pro Ala  
 435 440 445  
 Ala Ala Ala Ala Lys Ala Ala Ala Lys Ala Ala Gln Phe Gly Leu Val  
 450 455 460  
 Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val Gly  
 465 470 475 480

FAB-008PC-SequenceListing

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

Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Ile Gly Pro Gly  
500 505 510

Gly Val Ala Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys Ala  
515 520 525

Gln Leu Arg Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu Gly  
530 535 540

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

Leu Gly Val Gly Ala Gly Val Pro Gly Phe Gly Ala Val Pro Gly Ala  
565 570 575

Leu Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly Val  
580 585 590

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

Val Gly Ala Gly Pro Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala  
610 615 620

Lys Ala Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly Leu  
625 630 635 640

Gly Val Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly Ile  
645 650 655

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

Gly Gly Val Leu Gly Gly Ala Gly Gln Phe Pro Leu Gly Gly Val Ala  
675 680 685

Ala Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys  
690 695 700

Leu Gly Lys Ala Cys Gly Arg Lys Arg Lys  
705 710

<210> 90  
<211> 617  
<212> PRT  
<213> Homo sapiens

<400> 90

# FAB-008PC-SequenceListing

Met Ala Gly Leu Thr Ala Ala Ala Pro Arg Pro Gly Val 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 Ala Leu Gly Pro  
35 40 45

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

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

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

Lys Ala Gly Ala Gly Leu Gly Gly Val Pro Gly Val Gly Gly Leu Gly  
100 105 110

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

Gly Lys Val Pro Gly Val Gly Leu Pro Gly Val Tyr Pro Gly Gly Val  
130 135 140

Leu Pro Gly Val Gly Pro Phe Gly Gly Pro Gln Pro Gly Val Pro Leu  
145 150 155 160

Gly Tyr Pro Ile Lys Ala Pro Lys Leu Pro Gly Gly Tyr Gly Leu Pro  
165 170 175

Tyr Thr Thr Gly Lys Leu Pro Tyr Gly Tyr Gly Pro Gly Gly Val Ala  
180 185 190

Gly Ala Ala Gly Lys Ala Gly Tyr Pro Thr Gly Thr Gly Val Gly Pro  
195 200 205

Gln Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Ala Lys Phe Gly Ala  
210 215 220

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

Val Pro Gly Ala Ile Pro Gly Ile Gly Gly Ile Ala Gly Val Gly Thr  
245 250 255

Pro Ala Ala Ala Ala Ala Ala Ala Ala Ala Lys Ala Ala Lys Tyr  
260 265 270

FAB-008PC-SequenceListing

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

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

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

Pro Gly Val Val Ser Pro Glu Ala Ala Ala Lys Ala Ala Ala Lys Ala  
325 330 335

Ala Lys Tyr Gly Ala Arg Pro Gly Val Gly Val Gly Gly Ile Pro Thr  
340 345 350

Tyr Gly Val Gly Ala Gly Gly Phe Pro Gly Phe Gly Val Gly Val Gly  
355 360 365

Ala Glu Ala Gln Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Leu  
370 375 380

Val Pro Gly Val Gly Val Ala Pro Gly Val Gly Val Ala Pro Gly Val  
385 390 395 400

Gly Val Ala Pro Gly Val Gly Leu Ala Pro Gly Val Gly Val Ala Pro  
405 410 415

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

Gly Gly Val Ala Ala Ala Ala Lys Ser Ala Ala Lys Val Ala Ala Lys  
435 440 445

Ala Gln Leu Arg Ala Ala Ala Gly Leu Gly Ala Gly Ile Pro Gly Leu  
450 455 460

Gly Val Gly Val Gly Val Pro Gly Leu Gly Val Gly Ala Gly Val Pro  
465 470 475 480

Gly Leu Gly Val Gly Ala Gly Val Pro Gly Phe Gly Ala Val Pro Gly  
485 490 495

Ala Leu Ala Ala Ala Lys Ala Ala Lys Tyr Gly Ala Ala Val Pro Gly  
500 505 510

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

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

# FAB-008PC-SequenceListing

Ala Lys Ala Ala Gln Phe Gly Leu Val Gly Ala Ala Gly Leu Gly Gly  
545 550 555 560

Leu Gly Val Gly Gly Leu Gly Val Pro Gly Val Gly Gly Leu Gly Gly  
565 570 575

Ile Pro Pro Ala Ala Ala Ala Lys Ala Ala Lys Tyr Gly Val Ala Ala  
580 585 590

Arg Pro Gly Phe Gly Leu Ser Pro Ile Phe Pro Gly Gly Ala Cys Leu  
595 600 605

Gly Lys Ala Cys Gly Arg Lys Arg Lys  
610 615

<210> 91  
<211> 786  
<212> PRT  
<213> Homo sapiens

<400> 91

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  
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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  
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

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435

440

445

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

Pro Gly Ala Pro Gly 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 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  
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705 710 715 720

Gly Val Gly Gly Leu Gly Gly Ile Pro Pro Ala Ala Ala Ala Lys Ala  
725 730 735

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> 92  
<211> 417  
<212> PRT  
<213> Homo sapiens

<400> 92

Met Arg Phe Ala Trp Thr Val Leu Leu Leu Gly Pro Leu Gln Leu Cys  
1 5 10 15

Ala Leu Val His Cys Ala Pro Pro Ala Ala Gly Gln Gln Gln Pro Pro  
20 25 30

Arg Glu Pro Pro Ala Ala Pro Gly Ala Trp Arg Gln Gln Ile Gln Trp  
35 40 45

Glu Asn Asn Gly Gln Val Phe Ser Leu Leu Ser Leu Gly Ser Gln Tyr  
50 55 60

Gln Pro Gln Arg Arg Arg Asp Pro Gly Ala Ala Val Pro Gly Ala Ala  
65 70 75 80

Asn Ala Ser Ala Gln Gln Pro Arg Thr Pro Ile Leu Leu Ile Arg Asp  
85 90 95

Asn Arg Thr Ala Ala Ala Arg Thr Arg Thr Ala Gly Ser Ser Gly Val  
100 105 110

Thr Ala Gly Arg Pro Arg Pro Thr Ala Arg His Trp Phe Gln Ala Gly  
115 120 125

Tyr Ser Thr Ser Arg Ala Arg Glu Ala Gly Ala Ser Arg Ala Glu Asn  
130 135 140

Gln Thr Ala Pro Gly Glu Val Pro Ala Leu Ser Asn Leu Arg Pro Pro  
145 150 155 160



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Ser Arg Val Asp Gly Met Val Gly Asp Asp Pro Tyr Asn Pro Tyr Lys  
165 170 175

Tyr Ser Asp Asp Asn Pro Tyr Tyr Asn Tyr Tyr Asp Thr Tyr Glu Arg  
180 185 190

Pro Arg Pro Gly Gly Arg Tyr Arg Pro Gly Tyr Gly Thr Gly Tyr Phe  
195 200 205

Gln Tyr Gly Leu Pro Asp Leu Val Ala Asp Pro Tyr Tyr Ile Gln Ala  
210 215 220

Ser Thr Tyr Val Gln Lys Met Ser Met Tyr Asn Leu Arg Cys Ala Ala  
225 230 235 240

Glu Glu Asn Cys Leu Ala Ser Thr Ala Tyr Arg Ala Asp Val Arg Asp  
245 250 255

Tyr Asp His Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln  
260 265 270

Gly Thr Ser Asp Phe Leu Pro Ser Arg Pro Arg Tyr Ser Trp Glu Trp  
275 280 285

His Ser Cys His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr  
290 295 300

Asp Leu Leu Asp Ala Asn Thr Gln Arg Arg Val Ala Glu Gly His Lys  
305 310 315 320

Ala Ser Phe Cys Leu Glu Asp Thr Ser Cys Asp Tyr Gly Tyr His Arg  
325 330 335

Arg Phe Ala Cys Thr Ala His Thr Gln Gly Leu Ser Pro Gly Cys Tyr  
340 345 350

Asp Thr Tyr Gly Ala Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp  
355 360 365

Val Lys Pro Gly Asn Tyr Ile Leu Lys Val Ser Val Asn Pro Ser Tyr  
370 375 380

Leu Val Pro Glu Ser Asp Tyr Thr Asn Asn Val Val Arg Cys Asp Ile  
385 390 395 400

Arg Tyr Thr Gly His His Ala Tyr Ala Ser Gly Cys Thr Ile Ser Pro  
405 410 415

Tyr

FAB-008PC-SequenceListing

<210> 93  
 <211> 187  
 <212> PRT  
 <213> Homo sapiens

<400> 93

Met Ser Met Tyr Asn Leu Arg Cys Ala Ala Glu Glu Asn Cys Leu Ala  
 1 5 10 15

Ser Thr Ala Tyr Arg Ala Asp Val Arg Asp Tyr Asp His Arg Val Leu  
 20 25 30

Leu Arg Phe Pro Gln Arg Val Lys Asn Gln Gly Thr Ser Asp Phe Leu  
 35 40 45

Pro Ser Arg Pro Arg Tyr Ser Trp Glu Trp His Ser Cys His Gln His  
 50 55 60

Tyr His Ser Met Asp Glu Phe Ser His Tyr Asp Leu Leu Asp Ala Asn  
 65 70 75 80

Thr Gln Arg Arg Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu  
 85 90 95

Asp Thr Ser Cys Asp Tyr Gly Tyr His Arg Arg Phe Ala Cys Thr Ala  
 100 105 110

His Thr Gln Gly Leu Ser Pro Gly Cys Tyr Asp Thr Tyr Gly Ala Asp  
 115 120 125

Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn Tyr  
 130 135 140

Ile Leu Lys Val Ser Val Asn Pro Ser Tyr Leu Val Pro Glu Ser Asp  
 145 150 155 160

Tyr Thr Asn Asn Val Val Arg Cys Asp Ile Arg Tyr Thr Gly His His  
 165 170 175

Ala Tyr Ala Ser Gly Cys Thr Ile Ser Pro Tyr  
 180 185

<210> 94  
 <211> 1132  
 <212> PRT  
 <213> Homo sapiens

<400> 94

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15

## FAB-008PC-SequenceListing

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80  
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95  
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110  
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 115 120 125  
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130 135 140  
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
 145 150 155 160  
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
 165 170 175  
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 180 185 190  
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
 195 200 205  
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
 210 215 220  
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225 230 235 240  
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245 250 255  
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
 260 265 270  
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285

## FAB-008PC-SequenceListing

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
 500 505 510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560

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Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg  
675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile  
705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln  
725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His  
740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp  
755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser  
770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu  
785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His  
805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro  
820 825 830

## FAB-008PC-SequenceListing

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp  
 835 840 845  
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu  
 850 855 860  
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala  
 865 870 875 880  
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys  
 885 890 895  
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu  
 900 905 910  
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe  
 915 920 925  
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser  
 930 935 940  
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe  
 945 950 955 960  
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly  
 965 970 975  
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn  
 980 985 990  
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln  
 995 1000 1005  
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln  
 1010 1015 1020  
 Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp  
 1025 1030 1035  
 Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly  
 1040 1045 1050  
 Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu  
 1055 1060 1065  
 Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr  
 1070 1075 1080  
 Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr  
 1085 1090 1095

## FAB-008PC-SequenceListing

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr  
 1100 1105 1110

Ala Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys  
 1115 1120 1125

Thr Ile Leu Asp  
 1130

<210> 95  
 <211> 1069  
 <212> PRT  
 <213> Homo sapiens

<400> 95

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
 145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
 165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
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## FAB-008PC-SequenceListing

195

200

205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
 210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
 260 265 270

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

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300

Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335

Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350

Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365

Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380

Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400

Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415

Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445

Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460

Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
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## FAB-008PC-SequenceListing

465                      470                      475                      480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
                                  485                                   490                                   495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
                                  500                                   505                                   510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
                                  515                                   520                                   525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
                                  530                                   535                                   540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
                                  545                                   550                                   555                                   560  
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
                                  565                                   570                                   575  
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
                                  580                                   585                                   590  
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
                                  595                                   600                                   605  
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
                                  610                                   615                                   620  
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
                                  625                                   630                                   635                                   640  
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
                                  645                                   650                                   655  
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
                                  660                                   665                                   670  
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg  
                                  675                                   680                                   685  
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
                                  690                                   695                                   700  
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile  
                                  705                                   710                                   715                                   720  
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln  
                                  725                                   730                                   735  
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His

## FAB-008PC-SequenceListing

740

745

750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp  
 755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser  
 770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu  
 785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His  
 805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro  
 820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp  
 835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu  
 850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala  
 865 870 875 880

Lys Thr Phe Leu Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr  
 885 890 895

Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe  
 900 905 910

Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val  
 915 920 925

Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu  
 930 935 940

Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln  
 945 950 955 960

Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr  
 965 970 975

Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser  
 980 985 990

Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln  
 995 1000 1005

Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg

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1010

1015

1020

Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr  
1025 1030 1035

Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu  
1040 1045 1050

Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu  
1055 1060 1065

Asp

<210> 96  
<211> 2477  
<212> PRT  
<213> Homo sapiens

<400> 96

Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys  
1 5 10 15

Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln  
20 25 30

Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser  
35 40 45

Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln  
50 55 60

Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly  
65 70 75 80

Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr  
85 90 95

Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr  
100 105 110

Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala  
115 120 125

Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly  
130 135 140

Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr  
145 150 155 160

Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu  
165 170 175

# FAB-008PC-SequenceListing

Trp Thr Cys Lys 180 Pro Ile Ala Glu Lys 185 Cys Phe Asp His Ala 190 Ala Gly  
 Thr Ser Tyr 195 Val Val Gly Glu Thr 200 Trp Glu Lys Pro Tyr 205 Gln Gly Trp  
 Met Met 210 Val Asp Cys Thr Cys 215 Leu Gly Glu Gly Ser 220 Gly Arg Ile Thr  
 Cys 225 Thr Ser Arg Asn Arg 230 Cys Asn Asp Gln Asp 235 Thr Arg Thr Ser Tyr 240  
 Arg Ile Gly Asp Thr 245 Trp Ser Lys Lys Asp 250 Asn Arg Gly Asn Leu 255 Leu  
 Gln Cys Ile Cys 260 Thr Gly Asn Gly Arg 265 Gly Glu Trp Lys Cys 270 Glu Arg  
 His Thr Ser 275 Val Gln Thr Thr Ser 280 Ser Gly Ser Gly Pro 285 Phe Thr Asp  
 Val Arg 290 Ala Ala Val Tyr Gln 295 Pro Gln Pro His Pro 300 Gln Pro Pro Pro  
 Tyr Gly His Cys Val Thr 310 Asp Ser Gly Val Val 315 Tyr Ser Val Gly Met 320  
 Gln Trp Leu Lys Thr 325 Gln Gly Asn Lys Gln 330 Met Leu Cys Thr Cys 335 Leu  
 Gly Asn Gly Val 340 Ser Cys Gln Glu Thr 345 Ala Val Thr Gln Thr 350 Tyr Gly  
 Gly Asn Ser 355 Asn Gly Glu Pro Cys 360 Val Leu Pro Phe Thr 365 Tyr Asn Gly  
 Arg Thr 370 Phe Tyr Ser Cys Thr 375 Thr Glu Gly Arg Gln 380 Asp Gly His Leu  
 Trp Cys Ser Thr Thr Ser 390 Asn Tyr Glu Gln Asp 395 Gln Lys Tyr Ser Phe 400  
 Cys Thr Asp His Thr 405 Val Leu Val Gln Thr 410 Arg Gly Gly Asn Ser 415 Asn  
 Gly Ala Leu Cys 420 His Phe Pro Phe Leu 425 Tyr Asn Asn His Asn 430 Tyr Thr  
 Asp Cys Thr 435 Ser Glu Gly Arg Arg 440 Asp Asn Met Lys Trp 445 Cys Gly Thr

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Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met Ala  
 450 455 460  
 Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg Ile  
 465 470 475 480  
 Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg Cys  
 485 490 495  
 Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr Ser  
 500 505 510  
 Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val Asn  
 515 520 525  
 Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys Thr  
 530 535 540  
 Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp Gln  
 545 550 555 560  
 Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser Trp  
 565 570 575  
 Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly Arg  
 580 585 590  
 Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser Ser  
 595 600 605  
 Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro Asn  
 610 615 620  
 Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser Lys  
 625 630 635 640  
 Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg Trp Lys Glu  
 645 650 655  
 Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu Lys  
 660 665 670  
 Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr Gly  
 675 680 685  
 His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser Thr  
 690 695 700  
 Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr Pro Phe Ser Pro  
 705 710 715 720

# FAB-008PC-SequenceListing

Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr Ala Ser Ser Phe  
 725 730 735  
 Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg Val  
 740 745 750  
 Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp Leu  
 755 760 765  
 Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly Arg  
 770 775 780  
 Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp Gly Glu Gln Ser  
 785 790 795 800  
 Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp Ala Pro Pro Asp  
 805 810 815  
 Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val Val Arg Trp Ser  
 820 825 830  
 Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val Tyr Ser Pro Ser  
 835 840 845  
 Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu Thr Ala Asn Ser  
 850 855 860  
 Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr Asn Ile Thr Ile  
 865 870 875 880  
 Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val Val Ile Gln Gln  
 885 890 895  
 Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro Ser Pro Arg Asp  
 900 905 910  
 Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr Ile Met Trp Thr  
 915 920 925  
 Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp Val Ile Pro Val  
 930 935 940  
 Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile Ser Arg Asn Thr  
 945 950 955 960  
 Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr Tyr Tyr Phe Lys  
 965 970 975  
 Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro Leu Thr Ala Gln  
 980 985 990

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Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu Gln Phe Val Asn Glu  
 995 1000 1005  
 Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro Pro Arg Ala Gln  
 1010 1015 1020  
 Ile Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg Arg Gly Gln  
 1025 1030 1035  
 Pro Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr Pro Leu  
 1040 1045 1050  
 Arg Asn Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu Val Ala  
 1055 1060 1065  
 Ile Lys Gly Asn Gln Glu Ser Pro Lys Ala Thr Gly Val Phe Thr  
 1070 1075 1080  
 Thr Leu Gln Pro Gly Ser Ser Ile Pro Pro Tyr Asn Thr Glu Val  
 1085 1090 1095  
 Thr Glu Thr Thr Ile Val Ile Thr Trp Thr Pro Ala Pro Arg Ile  
 1100 1105 1110  
 Gly Phe Lys Leu Gly Val Arg Pro Ser Gln Gly Gly Glu Ala Pro  
 1115 1120 1125  
 Arg Glu Val Thr Ser Asp Ser Gly Ser Ile Val Val Ser Gly Leu  
 1130 1135 1140  
 Thr Pro Gly Val Glu Tyr Val Tyr Thr Ile Gln Val Leu Arg Asp  
 1145 1150 1155  
 Gly Gln Glu Arg Asp Ala Pro Ile Val Asn Lys Val Val Thr Pro  
 1160 1165 1170  
 Leu Ser Pro Pro Thr Asn Leu His Leu Glu Ala Asn Pro Asp Thr  
 1175 1180 1185  
 Gly Val Leu Thr Val Ser Trp Glu Arg Ser Thr Thr Pro Asp Ile  
 1190 1195 1200  
 Thr Gly Tyr Arg Ile Thr Thr Thr Pro Thr Asn Gly Gln Gln Gly  
 1205 1210 1215  
 Asn Ser Leu Glu Glu Val Val His Ala Asp Gln Ser Ser Cys Thr  
 1220 1225 1230  
 Phe Asp Asn Leu Ser Pro Gly Leu Glu Tyr Asn Val Ser Val Tyr  
 1235 1240 1245

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Thr	Val	Lys	Asp	Asp	Lys	Glu	Ser	Val	Pro	Ile	Ser	Asp	Thr	Ile
	1250					1255					1260			
Ile	Pro	Glu	Val	Pro	Gln	Leu	Thr	Asp	Leu	Ser	Phe	Val	Asp	Ile
	1265					1270					1275			
Thr	Asp	Ser	Ser	Ile	Gly	Leu	Arg	Trp	Thr	Pro	Leu	Asn	Ser	Ser
	1280					1285					1290			
Thr	Ile	Ile	Gly	Tyr	Arg	Ile	Thr	Val	Val	Ala	Ala	Gly	Glu	Gly
	1295					1300					1305			
Ile	Pro	Ile	Phe	Glu	Asp	Phe	Val	Asp	Ser	Ser	Val	Gly	Tyr	Tyr
	1310					1315					1320			
Thr	Val	Thr	Gly	Leu	Glu	Pro	Gly	Ile	Asp	Tyr	Asp	Ile	Ser	Val
	1325					1330					1335			
Ile	Thr	Leu	Ile	Asn	Gly	Gly	Glu	Ser	Ala	Pro	Thr	Thr	Leu	Thr
	1340					1345					1350			
Gln	Gln	Thr	Ala	Val	Pro	Pro	Pro	Thr	Asp	Leu	Arg	Phe	Thr	Asn
	1355					1360					1365			
Ile	Gly	Pro	Asp	Thr	Met	Arg	Val	Thr	Trp	Ala	Pro	Pro	Pro	Ser
	1370					1375					1380			
Ile	Asp	Leu	Thr	Asn	Phe	Leu	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn
	1385					1390					1395			
Glu	Glu	Asp	Val	Ala	Glu	Leu	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala
	1400					1405					1410			
Val	Val	Leu	Thr	Asn	Leu	Leu	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser
	1415					1420					1425			
Val	Ser	Ser	Val	Tyr	Glu	Gln	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly
	1430					1435					1440			
Arg	Gln	Lys	Thr	Gly	Leu	Asp	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser
	1445					1450					1455			
Asp	Ile	Thr	Ala	Asn	Ser	Phe	Thr	Val	His	Trp	Ile	Ala	Pro	Arg
	1460					1465					1470			
Ala	Thr	Ile	Thr	Gly	Tyr	Arg	Ile	Arg	His	His	Pro	Glu	His	Phe
	1475					1480					1485			
Ser	Gly	Arg	Pro	Arg	Glu	Asp	Arg	Val	Pro	His	Ser	Arg	Asn	Ser
	1490					1495					1500			



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Ile	Thr	Leu	Thr	Asn	Leu	Thr	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser
1505						1510					1515			
Ile	Val	Ala	Leu	Asn	Gly	Arg	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly
1520						1525					1530			
Gln	Gln	Ser	Thr	Val	Ser	Asp	Val	Pro	Arg	Asp	Leu	Glu	Val	Val
1535						1540					1545			
Ala	Ala	Thr	Pro	Thr	Ser	Leu	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala
1550						1555					1560			
Val	Thr	Val	Arg	Tyr	Tyr	Arg	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly
1565						1570					1575			
Asn	Ser	Pro	Val	Gln	Glu	Phe	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr
1580						1585					1590			
Ala	Thr	Ile	Ser	Gly	Leu	Lys	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr
1595						1600					1605			
Val	Tyr	Ala	Val	Thr	Gly	Arg	Gly	Asp	Ser	Pro	Ala	Ser	Ser	Lys
1610						1615					1620			
Pro	Ile	Ser	Ile	Asn	Tyr	Arg	Thr	Glu	Ile	Asp	Lys	Pro	Ser	Gln
1625						1630					1635			
Met	Gln	Val	Thr	Asp	Val	Gln	Asp	Asn	Ser	Ile	Ser	Val	Lys	Trp
1640						1645					1650			
Leu	Pro	Ser	Ser	Ser	Pro	Val	Thr	Gly	Tyr	Arg	Val	Thr	Thr	Thr
1655						1660					1665			
Pro	Lys	Asn	Gly	Pro	Gly	Pro	Thr	Lys	Thr	Lys	Thr	Ala	Gly	Pro
1670						1675					1680			
Asp	Gln	Thr	Glu	Met	Thr	Ile	Glu	Gly	Leu	Gln	Pro	Thr	Val	Glu
1685						1690					1695			
Tyr	Val	Val	Ser	Val	Tyr	Ala	Gln	Asn	Pro	Ser	Gly	Glu	Ser	Gln
1700						1705					1710			
Pro	Leu	Val	Gln	Thr	Ala	Val	Thr	Asn	Ile	Asp	Arg	Pro	Lys	Gly
1715						1720					1725			
Leu	Ala	Phe	Thr	Asp	Val	Asp	Val	Asp	Ser	Ile	Lys	Ile	Ala	Trp
1730						1735					1740			
Glu	Ser	Pro	Gln	Gly	Gln	Val	Ser	Arg	Tyr	Arg	Val	Thr	Tyr	Ser
1745						1750					1755			

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Ser	Pro	Glu	Asp	Gly	Ile	His	Glu	Leu	Phe	Pro	Ala	Pro	Asp	Gly
	1760					1765					1770			
Glu	Glu	Asp	Thr	Ala	Glu	Leu	Gln	Gly	Leu	Arg	Pro	Gly	Ser	Glu
	1775					1780					1785			
Tyr	Thr	Val	Ser	Val	Val	Ala	Leu	His	Asp	Asp	Met	Glu	Ser	Gln
	1790					1795					1800			
Pro	Leu	Ile	Gly	Thr	Gln	Ser	Thr	Ala	Ile	Pro	Ala	Pro	Thr	Asp
	1805					1810					1815			
Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	Gln	Trp
	1820					1825					1830			
Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr
	1835					1840					1845			
Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro
	1850					1855					1860			
Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys
	1865					1870					1875			
Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg
	1880					1885					1890			
Pro	Ala	Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro
	1895					1900					1905			
Arg	Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile
	1910					1915					1920			
Ser	Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp
	1925					1930					1935			
Ala	Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys
	1940					1945					1950			
Pro	Asp	Val	Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr
	1955					1960					1965			
Asp	Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser
	1970					1975					1980			
Ser	Pro	Val	Val	Ile	Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser
	1985					1990					1995			
Asn	Leu	Arg	Phe	Leu	Ala	Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser
	2000					2005					2010			

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Trp	Gln	Pro	Pro	Arg	Ala	Arg	Ile	Thr	Gly	Tyr	Ile	Ile	Lys	Tyr
	2015					2020					2025			
Glu	Lys	Pro	Gly	Ser	Pro	Pro	Arg	Glu	Val	Val	Pro	Arg	Pro	Arg
	2030					2035					2040			
Pro	Gly	Val	Thr	Glu	Ala	Thr	Ile	Thr	Gly	Leu	Glu	Pro	Gly	Thr
	2045					2050					2055			
Glu	Tyr	Thr	Ile	Tyr	Val	Ile	Ala	Leu	Lys	Asn	Asn	Gln	Lys	Ser
	2060					2065					2070			
Glu	Pro	Leu	Ile	Gly	Arg	Lys	Lys	Thr	Asp	Glu	Leu	Pro	Gln	Leu
	2075					2080					2085			
Val	Thr	Leu	Pro	His	Pro	Asn	Leu	His	Gly	Pro	Glu	Ile	Leu	Asp
	2090					2095					2100			
Val	Pro	Ser	Thr	Val	Gln	Lys	Thr	Pro	Phe	Val	Thr	His	Pro	Gly
	2105					2110					2115			
Tyr	Asp	Thr	Gly	Asn	Gly	Ile	Gln	Leu	Pro	Gly	Thr	Ser	Gly	Gln
	2120					2125					2130			
Gln	Pro	Ser	Val	Gly	Gln	Gln	Met	Ile	Phe	Glu	Glu	His	Gly	Phe
	2135					2140					2145			
Arg	Arg	Thr	Thr	Pro	Pro	Thr	Thr	Ala	Thr	Pro	Ile	Arg	His	Arg
	2150					2155					2160			
Pro	Arg	Pro	Tyr	Pro	Pro	Asn	Val	Gly	Glu	Glu	Ile	Gln	Ile	Gly
	2165					2170					2175			
His	Ile	Pro	Arg	Glu	Asp	Val	Asp	Tyr	His	Leu	Tyr	Pro	His	Gly
	2180					2185					2190			
Pro	Gly	Leu	Asn	Pro	Asn	Ala	Ser	Thr	Gly	Gln	Glu	Ala	Leu	Ser
	2195					2200					2205			
Gln	Thr	Thr	Ile	Ser	Trp	Ala	Pro	Phe	Gln	Asp	Thr	Ser	Glu	Tyr
	2210					2215					2220			
Ile	Ile	Ser	Cys	His	Pro	Val	Gly	Thr	Asp	Glu	Glu	Pro	Leu	Gln
	2225					2230					2235			
Phe	Arg	Val	Pro	Gly	Thr	Ser	Thr	Ser	Ala	Thr	Leu	Thr	Gly	Leu
	2240					2245					2250			
Thr	Arg	Gly	Ala	Thr	Tyr	Asn	Ile	Ile	Val	Glu	Ala	Leu	Lys	Asp
	2255					2260					2265			

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Gln Gln Arg His Lys Val Arg Glu Glu Val Val Thr Val Gly Asn  
2270 2275 2280

Ser Val Asn Glu Gly Leu Asn Gln Pro Thr Asp Asp Ser Cys Phe  
2285 2290 2295

Asp Pro Tyr Thr Val Ser His Tyr Ala Val Gly Asp Glu Trp Glu  
2300 2305 2310

Arg Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu Gly  
2315 2320 2325

Phe Gly Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys His  
2330 2335 2340

Asp Asn Gly Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln  
2345 2350 2355

Gly Glu Asn Gly Gln Met Met Ser Cys Thr Cys Leu Gly Asn Gly  
2360 2365 2370

Lys Gly Glu Phe Lys Cys Asp Pro His Glu Ala Thr Cys Tyr Asp  
2375 2380 2385

Asp Gly Lys Thr Tyr His Val Gly Glu Gln Trp Gln Lys Glu Tyr  
2390 2395 2400

Leu Gly Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly  
2405 2410 2415

Trp Arg Cys Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro  
2420 2425 2430

Glu Gly Thr Thr Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr  
2435 2440 2445

His Gln Arg Thr Asn Thr Asn Val Asn Cys Pro Ile Glu Cys Phe  
2450 2455 2460

Met Pro Leu Asp Val Gln Ala Asp Arg Glu Asp Ser Arg Glu  
2465 2470 2475

<210> 97  
<211> 2355  
<212> PRT  
<213> Homo sapiens  
<400> 97

Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Ala Val Gln Cys  
1 5 10 15

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Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln  
 20 25 30  
 Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser  
 35 40 45  
 Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln  
 50 55 60  
 Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly  
 65 70 75 80  
 Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr  
 85 90 95  
 Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr  
 100 105 110  
 Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala  
 115 120 125  
 Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly  
 130 135 140  
 Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr  
 145 150 155 160  
 Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu  
 165 170 175  
 Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly  
 180 185 190  
 Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp  
 195 200 205  
 Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr  
 210 215 220  
 Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr  
 225 230 235 240  
 Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu  
 245 250 255  
 Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg  
 260 265 270  
 His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp  
 275 280 285

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Val	Arg	Ala	Ala	Val	Tyr	Gln	Pro	Gln	Pro	His	Pro	Gln	Pro	Pro	Pro
	290					295					300				
Tyr	Gly	His	Cys	Val	Thr	Asp	Ser	Gly	Val	Val	Tyr	Ser	Val	Gly	Met
305					310					315					320
Gln	Trp	Leu	Lys	Thr	Gln	Gly	Asn	Lys	Gln	Met	Leu	Cys	Thr	Cys	Leu
				325					330					335	
Gly	Asn	Gly	Val	Ser	Cys	Gln	Glu	Thr	Ala	Val	Thr	Gln	Thr	Tyr	Gly
			340					345					350		
Gly	Asn	Ser	Asn	Gly	Glu	Pro	Cys	Val	Leu	Pro	Phe	Thr	Tyr	Asn	Gly
		355					360					365			
Arg	Thr	Phe	Tyr	Ser	Cys	Thr	Thr	Glu	Gly	Arg	Gln	Asp	Gly	His	Leu
	370					375					380				
Trp	Cys	Ser	Thr	Thr	Ser	Asn	Tyr	Glu	Gln	Asp	Gln	Lys	Tyr	Ser	Phe
385					390					395					400
Cys	Thr	Asp	His	Thr	Val	Leu	Val	Gln	Thr	Arg	Gly	Gly	Asn	Ser	Asn
				405					410					415	
Gly	Ala	Leu	Cys	His	Phe	Pro	Phe	Leu	Tyr	Asn	Asn	His	Asn	Tyr	Thr
			420					425					430		
Asp	Cys	Thr	Ser	Glu	Gly	Arg	Arg	Asp	Asn	Met	Lys	Trp	Cys	Gly	Thr
		435					440					445			
Thr	Gln	Asn	Tyr	Asp	Ala	Asp	Gln	Lys	Phe	Gly	Phe	Cys	Pro	Met	Ala
	450					455					460				
Ala	His	Glu	Glu	Ile	Cys	Thr	Thr	Asn	Glu	Gly	Val	Met	Tyr	Arg	Ile
465					470					475					480
Gly	Asp	Gln	Trp	Asp	Lys	Gln	His	Asp	Met	Gly	His	Met	Met	Arg	Cys
				485					490					495	
Thr	Cys	Val	Gly	Asn	Gly	Arg	Gly	Glu	Trp	Thr	Cys	Ile	Ala	Tyr	Ser
			500					505					510		
Gln	Leu	Arg	Asp	Gln	Cys	Ile	Val	Asp	Asp	Ile	Thr	Tyr	Asn	Val	Asn
		515					520					525			
Asp	Thr	Phe	His	Lys	Arg	His	Glu	Glu	Gly	His	Met	Leu	Asn	Cys	Thr
	530					535					540				
Cys	Phe	Gly	Gln	Gly	Arg	Gly	Arg	Trp	Lys	Cys	Asp	Pro	Val	Asp	Gln
545					550					555					560

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Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser Trp  
 565 570 575  
 Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly Arg  
 580 585 590  
 Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser Ser  
 595 600 605  
 Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro Asn  
 610 615 620  
 Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser Lys  
 625 630 635 640  
 Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg Trp Lys Glu  
 645 650 655  
 Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu Lys  
 660 665 670  
 Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr Gly  
 675 680 685  
 His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser Thr  
 690 695 700  
 Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr Pro Phe Ser Pro  
 705 710 715 720  
 Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr Ala Ser Ser Phe  
 725 730 735  
 Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg Val  
 740 745 750  
 Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp Leu  
 755 760 765  
 Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly Arg  
 770 775 780  
 Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp Gly Glu Gln Ser  
 785 790 795 800  
 Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp Ala Pro Pro Asp  
 805 810 815  
 Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val Val Arg Trp Ser  
 820 825 830

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Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val Tyr Ser Pro Ser  
835 840 845

Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu Thr Ala Asn Ser  
850 855 860

Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr Asn Ile Thr Ile  
865 870 875 880

Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val Val Ile Gln Gln  
885 890 895

Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro Ser Pro Arg Asp  
900 905 910

Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr Ile Met Trp Thr  
915 920 925

Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp Val Ile Pro Val  
930 935 940

Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile Ser Arg Asn Thr  
945 950 955 960

Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr Tyr Tyr Phe Lys  
965 970 975

Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro Leu Thr Ala Gln  
980 985 990

Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu Gln Phe Val Asn Glu  
995 1000 1005

Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro Pro Arg Ala Gln  
1010 1015 1020

Ile Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg Arg Gly Gln  
1025 1030 1035

Pro Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr Pro Leu  
1040 1045 1050

Arg Asn Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu Val Ala  
1055 1060 1065

Ile Lys Gly Asn Gln Glu Ser Pro Lys Ala Thr Gly Val Phe Thr  
1070 1075 1080

Thr Leu Gln Pro Gly Ser Ser Ile Pro Pro Tyr Asn Thr Glu Val  
1085 1090 1095



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Thr	Glu	Thr	Thr	Ile	Val	Ile	Thr	Trp	Thr	Pro	Ala	Pro	Arg	Ile
	1100					1105					1110			
Gly	Phe	Lys	Leu	Gly	Val	Arg	Pro	Ser	Gln	Gly	Gly	Glu	Ala	Pro
	1115					1120					1125			
Arg	Glu	Val	Thr	Ser	Asp	Ser	Gly	Ser	Ile	Val	Val	Ser	Gly	Leu
	1130					1135					1140			
Thr	Pro	Gly	Val	Glu	Tyr	Val	Tyr	Thr	Ile	Gln	Val	Leu	Arg	Asp
	1145					1150					1155			
Gly	Gln	Glu	Arg	Asp	Ala	Pro	Ile	Val	Asn	Lys	Val	Val	Thr	Pro
	1160					1165					1170			
Leu	Ser	Pro	Pro	Thr	Asn	Leu	His	Leu	Glu	Ala	Asn	Pro	Asp	Thr
	1175					1180					1185			
Gly	Val	Leu	Thr	Val	Ser	Trp	Glu	Arg	Ser	Thr	Thr	Pro	Asp	Ile
	1190					1195					1200			
Thr	Gly	Tyr	Arg	Ile	Thr	Thr	Thr	Pro	Thr	Asn	Gly	Gln	Gln	Gly
	1205					1210					1215			
Asn	Ser	Leu	Glu	Glu	Val	Val	His	Ala	Asp	Gln	Ser	Ser	Cys	Thr
	1220					1225					1230			
Phe	Asp	Asn	Leu	Ser	Pro	Gly	Leu	Glu	Tyr	Asn	Val	Ser	Val	Tyr
	1235					1240					1245			
Thr	Val	Lys	Asp	Asp	Lys	Glu	Ser	Val	Pro	Ile	Ser	Asp	Thr	Ile
	1250					1255					1260			
Ile	Pro	Ala	Val	Pro	Pro	Pro	Thr	Asp	Leu	Arg	Phe	Thr	Asn	Ile
	1265					1270					1275			
Gly	Pro	Asp	Thr	Met	Arg	Val	Thr	Trp	Ala	Pro	Pro	Pro	Ser	Ile
	1280					1285					1290			
Asp	Leu	Thr	Asn	Phe	Leu	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn	Glu
	1295					1300					1305			
Glu	Asp	Val	Ala	Glu	Leu	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val
	1310					1315					1320			
Val	Leu	Thr	Asn	Leu	Leu	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val
	1325					1330					1335			
Ser	Ser	Val	Tyr	Glu	Gln	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg
	1340					1345					1350			

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Gln	Lys	Thr	Gly	Leu	Asp	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp
	1355					1360					1365			
Ile	Thr	Ala	Asn	Ser	Phe	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala
	1370					1375					1380			
Thr	Ile	Thr	Gly	Tyr	Arg	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser
	1385					1390					1395			
Gly	Arg	Pro	Arg	Glu	Asp	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile
	1400					1405					1410			
Thr	Leu	Thr	Asn	Leu	Thr	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile
	1415					1420					1425			
Val	Ala	Leu	Asn	Gly	Arg	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln
	1430					1435					1440			
Gln	Ser	Thr	Val	Ser	Asp	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala
	1445					1450					1455			
Ala	Thr	Pro	Thr	Ser	Leu	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val
	1460					1465					1470			
Thr	Val	Arg	Tyr	Tyr	Arg	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn
	1475					1480					1485			
Ser	Pro	Val	Gln	Glu	Phe	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala
	1490					1495					1500			
Thr	Ile	Ser	Gly	Leu	Lys	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val
	1505					1510					1515			
Tyr	Ala	Val	Thr	Gly	Arg	Gly	Asp	Ser	Pro	Ala	Ser	Ser	Lys	Pro
	1520					1525					1530			
Ile	Ser	Ile	Asn	Tyr	Arg	Thr	Glu	Ile	Asp	Lys	Pro	Ser	Gln	Met
	1535					1540					1545			
Gln	Val	Thr	Asp	Val	Gln	Asp	Asn	Ser	Ile	Ser	Val	Lys	Trp	Leu
	1550					1555					1560			
Pro	Ser	Ser	Ser	Pro	Val	Thr	Gly	Tyr	Arg	Val	Thr	Thr	Thr	Pro
	1565					1570					1575			
Lys	Asn	Gly	Pro	Gly	Pro	Thr	Lys	Thr	Lys	Thr	Ala	Gly	Pro	Asp
	1580					1585					1590			
Gln	Thr	Glu	Met	Thr	Ile	Glu	Gly	Leu	Gln	Pro	Thr	Val	Glu	Tyr
	1595					1600					1605			

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Val	Val	Ser	Val	Tyr	Ala	Gln	Asn	Pro	Ser	Gly	Glu	Ser	Gln	Pro
	1610					1615					1620			
Leu	Val	Gln	Thr	Ala	Val	Thr	Asn	Ile	Asp	Arg	Pro	Lys	Gly	Leu
	1625					1630					1635			
Ala	Phe	Thr	Asp	Val	Asp	Val	Asp	Ser	Ile	Lys	Ile	Ala	Trp	Glu
	1640					1645					1650			
Ser	Pro	Gln	Gly	Gln	Val	Ser	Arg	Tyr	Arg	Val	Thr	Tyr	Ser	Ser
	1655					1660					1665			
Pro	Glu	Asp	Gly	Ile	His	Glu	Leu	Phe	Pro	Ala	Pro	Asp	Gly	Glu
	1670					1675					1680			
Glu	Asp	Thr	Ala	Glu	Leu	Gln	Gly	Leu	Arg	Pro	Gly	Ser	Glu	Tyr
	1685					1690					1695			
Thr	Val	Ser	Val	Val	Ala	Leu	His	Asp	Asp	Met	Glu	Ser	Gln	Pro
	1700					1705					1710			
Leu	Ile	Gly	Thr	Gln	Ser	Thr	Ala	Ile	Pro	Ala	Pro	Thr	Asp	Leu
	1715					1720					1725			
Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	Gln	Trp	Thr
	1730					1735					1740			
Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr	Pro
	1745					1750					1755			
Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro	Asp
	1760					1765					1770			
Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys	Tyr
	1775					1780					1785			
Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg	Pro
	1790					1795					1800			
Ala	Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	Arg
	1805					1810					1815			
Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser
	1820					1825					1830			
Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala
	1835					1840					1845			
Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro
	1850					1855					1860			

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Asp	Val 1865	Arg	Ser	Tyr	Thr	Ile 1870	Thr	Gly	Leu	Gln	Pro 1875	Gly	Thr	Asp
Tyr	Lys 1880	Ile	Tyr	Leu	Tyr	Thr 1885	Leu	Asn	Asp	Asn	Ala 1890	Arg	Ser	Ser
Pro	Val 1895	Val	Ile	Asp	Ala	Ser 1900	Thr	Ala	Ile	Asp	Ala 1905	Pro	Ser	Asn
Leu	Arg 1910	Phe	Leu	Ala	Thr	Thr 1915	Pro	Asn	Ser	Leu	Leu 1920	Val	Ser	Trp
Gln	Pro 1925	Pro	Arg	Ala	Arg	Ile 1930	Thr	Gly	Tyr	Ile	Ile 1935	Lys	Tyr	Glu
Lys	Pro 1940	Gly	Ser	Pro	Pro	Arg 1945	Glu	Val	Val	Pro	Arg 1950	Pro	Arg	Pro
Gly	Val 1955	Thr	Glu	Ala	Thr	Ile 1960	Thr	Gly	Leu	Glu	Pro 1965	Gly	Thr	Glu
Tyr	Thr 1970	Ile	Tyr	Val	Ile	Ala 1975	Leu	Lys	Asn	Asn	Gln 1980	Lys	Ser	Glu
Pro	Leu 1985	Ile	Gly	Arg	Lys	Lys 1990	Thr	Asp	Glu	Leu	Pro 1995	Gln	Leu	Val
Thr	Leu 2000	Pro	His	Pro	Asn	Leu 2005	His	Gly	Pro	Glu	Ile 2010	Leu	Asp	Val
Pro	Ser 2015	Thr	Val	Gln	Lys	Thr 2020	Pro	Phe	Val	Thr	His 2025	Pro	Gly	Tyr
Asp	Thr 2030	Gly	Asn	Gly	Ile	Gln 2035	Leu	Pro	Gly	Thr	Ser 2040	Gly	Gln	Gln
Pro	Ser 2045	Val	Gly	Gln	Gln	Met 2050	Ile	Phe	Glu	Glu	His 2055	Gly	Phe	Arg
Arg	Thr 2060	Thr	Pro	Pro	Thr	Thr 2065	Ala	Thr	Pro	Ile	Arg 2070	His	Arg	Pro
Arg	Pro 2075	Tyr	Pro	Pro	Asn	Val 2080	Gly	Gln	Glu	Ala	Leu 2085	Ser	Gln	Thr
Thr	Ile 2090	Ser	Trp	Ala	Pro	Phe 2095	Gln	Asp	Thr	Ser	Glu 2100	Tyr	Ile	Ile
Ser	Cys 2105	His	Pro	Val	Gly	Thr 2110	Asp	Glu	Glu	Pro	Leu 2115	Gln	Phe	Arg

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Val	Pro	Gly	Thr	Ser	Thr	Ser	Ala	Thr	Leu	Thr	Gly	Leu	Thr	Arg
	2120					2125					2130			
Gly	Ala	Thr	Tyr	Asn	Ile	Ile	Val	Glu	Ala	Leu	Lys	Asp	Gln	Gln
	2135					2140					2145			
Arg	His	Lys	Val	Arg	Glu	Glu	Val	Val	Thr	Val	Gly	Asn	Ser	Val
	2150					2155					2160			
Asn	Glu	Gly	Leu	Asn	Gln	Pro	Thr	Asp	Asp	Ser	Cys	Phe	Asp	Pro
	2165					2170					2175			
Tyr	Thr	Val	Ser	His	Tyr	Ala	Val	Gly	Asp	Glu	Trp	Glu	Arg	Met
	2180					2185					2190			
Ser	Glu	Ser	Gly	Phe	Lys	Leu	Leu	Cys	Gln	Cys	Leu	Gly	Phe	Gly
	2195					2200					2205			
Ser	Gly	His	Phe	Arg	Cys	Asp	Ser	Ser	Arg	Trp	Cys	His	Asp	Asn
	2210					2215					2220			
Gly	Val	Asn	Tyr	Lys	Ile	Gly	Glu	Lys	Trp	Asp	Arg	Gln	Gly	Glu
	2225					2230					2235			
Asn	Gly	Gln	Met	Met	Ser	Cys	Thr	Cys	Leu	Gly	Asn	Gly	Lys	Gly
	2240					2245					2250			
Glu	Phe	Lys	Cys	Asp	Pro	His	Glu	Ala	Thr	Cys	Tyr	Asp	Asp	Gly
	2255					2260					2265			
Lys	Thr	Tyr	His	Val	Gly	Glu	Gln	Trp	Gln	Lys	Glu	Tyr	Leu	Gly
	2270					2275					2280			
Ala	Ile	Cys	Ser	Cys	Thr	Cys	Phe	Gly	Gly	Gln	Arg	Gly	Trp	Arg
	2285					2290					2295			
Cys	Asp	Asn	Cys	Arg	Arg	Pro	Gly	Gly	Glu	Pro	Ser	Pro	Glu	Gly
	2300					2305					2310			
Thr	Thr	Gly	Gln	Ser	Tyr	Asn	Gln	Tyr	Ser	Gln	Arg	Tyr	His	Gln
	2315					2320					2325			
Arg	Thr	Asn	Thr	Asn	Val	Asn	Cys	Pro	Ile	Glu	Cys	Phe	Met	Pro
	2330					2335					2340			
Leu	Asp	Val	Gln	Ala	Asp	Arg	Glu	Asp	Ser	Arg	Glu			
	2345					2350					2355			

<210> 98  
 <211> 2330  
 <212> PRT

## FAB-008PC-SequenceListing

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys  
 1 5 10 15  
 Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln  
 20 25 30  
 Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser  
 35 40 45  
 Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln  
 50 55 60  
 Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly  
 65 70 75 80  
 Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr  
 85 90 95  
 Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr  
 100 105 110  
 Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala  
 115 120 125  
 Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly  
 130 135 140  
 Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr  
 145 150 155 160  
 Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu  
 165 170 175  
 Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly  
 180 185 190  
 Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp  
 195 200 205  
 Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr  
 210 215 220  
 Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr  
 225 230 235 240  
 Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu  
 245 250 255

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Gln Cys Ile Cys<sub>260</sub> Thr Gly Asn Gly Arg<sub>265</sub> Gly Glu Trp Lys Cys<sub>270</sub> Glu Arg

His Thr Ser<sub>275</sub> Val Gln Thr Thr Ser<sub>280</sub> Ser Gly Ser Gly Pro<sub>285</sub> Phe Thr Asp

Val Arg<sub>290</sub> Ala Ala Val Tyr Gln<sub>295</sub> Pro Gln Pro His Pro<sub>300</sub> Gln Pro Pro Pro

Tyr<sub>305</sub> Gly His Cys Val Thr<sub>310</sub> Asp Ser Gly Val Val<sub>315</sub> Tyr Ser Val Gly Met<sub>320</sub>

Gln Trp Leu Lys Thr<sub>325</sub> Gln Gly Asn Lys Gln<sub>330</sub> Met Leu Cys Thr Cys<sub>335</sub> Leu

Gly Asn Gly Val<sub>340</sub> Ser Cys Gln Glu Thr<sub>345</sub> Ala Val Thr Gln Thr<sub>350</sub> Tyr Gly

Gly Asn Ser<sub>355</sub> Asn Gly Glu Pro Cys<sub>360</sub> Val Leu Pro Phe Thr<sub>365</sub> Tyr Asn Gly

Arg Thr<sub>370</sub> Phe Tyr Ser Cys Thr<sub>375</sub> Thr Glu Gly Arg Gln<sub>380</sub> Asp Gly His Leu

Trp<sub>385</sub> Cys Ser Thr Thr Ser<sub>390</sub> Asn Tyr Glu Gln Asp<sub>395</sub> Gln Lys Tyr Ser Phe<sub>400</sub>

Cys Thr Asp His Thr<sub>405</sub> Val Leu Val Gln Thr<sub>410</sub> Arg Gly Gly Asn Ser<sub>415</sub> Asn

Gly Ala Leu Cys<sub>420</sub> His Phe Pro Phe Leu<sub>425</sub> Tyr Asn Asn His Asn<sub>430</sub> Tyr Thr

Asp Cys Thr<sub>435</sub> Ser Glu Gly Arg Arg<sub>440</sub> Asp Asn Met Lys Trp<sub>445</sub> Cys Gly Thr

Thr Gln<sub>450</sub> Asn Tyr Asp Ala Asp<sub>455</sub> Gln Lys Phe Gly Phe<sub>460</sub> Cys Pro Met Ala

Ala<sub>465</sub> His Glu Glu Ile Cys<sub>470</sub> Thr Thr Asn Glu Gly<sub>475</sub> Val Met Tyr Arg Ile<sub>480</sub>

Gly Asp Gln Trp Asp<sub>485</sub> Lys Gln His Asp Met<sub>490</sub> Gly His Met Met Arg<sub>495</sub> Cys

Thr Cys Val Gly<sub>500</sub> Asn Gly Arg Gly Glu<sub>505</sub> Trp Thr Cys Ile Ala<sub>510</sub> Tyr Ser

Gln Leu Arg<sub>515</sub> Asp Gln Cys Ile Val<sub>520</sub> Asp Asp Ile Thr Tyr<sub>525</sub> Asn Val Asn

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Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys Thr  
530 535 540

Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp Gln  
545 550 555 560

Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser Trp  
565 570 575

Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly Arg  
580 585 590

Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser Ser  
595 600 605

Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro Asn  
610 615 620

Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser Lys  
625 630 635 640

Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg Trp Lys Glu  
645 650 655

Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu Lys  
660 665 670

Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr Gly  
675 680 685

His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser Thr  
690 695 700

Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr Pro Phe Ser Pro  
705 710 715 720

Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr Ala Ser Ser Phe  
725 730 735

Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg Val  
740 745 750

Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp Leu  
755 760 765

Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly Arg  
770 775 780

Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp Gly Glu Gln Ser  
785 790 795 800



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Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp Ala Pro Pro Asp  
805 810 815

Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val Val Arg Trp Ser  
820 825 830

Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val Tyr Ser Pro Ser  
835 840 845

Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu Thr Ala Asn Ser  
850 855 860

Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr Asn Ile Thr Ile  
865 870 875 880

Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val Val Ile Gln Gln  
885 890 895

Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro Ser Pro Arg Asp  
900 905 910

Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr Ile Met Trp Thr  
915 920 925

Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp Val Ile Pro Val  
930 935 940

Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile Ser Arg Asn Thr  
945 950 955 960

Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr Tyr Tyr Phe Lys  
965 970 975

Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro Leu Thr Ala Gln  
980 985 990

Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu Gln Phe Val Asn Glu  
995 1000 1005

Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro Pro Arg Ala Gln  
1010 1015 1020

Ile Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg Arg Gly Gln  
1025 1030 1035

Pro Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr Pro Leu  
1040 1045 1050

Arg Asn Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu Val Ala  
1055 1060 1065

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Ile	Lys	Gly	Asn	Gln	Glu	Ser	Pro	Lys	Ala	Thr	Gly	Val	Phe	Thr
	1070					1075					1080			
Thr	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Pro	Pro	Tyr	Asn	Thr	Glu	Val
	1085					1090					1095			
Thr	Glu	Thr	Thr	Ile	Val	Ile	Thr	Trp	Thr	Pro	Ala	Pro	Arg	Ile
	1100					1105					1110			
Gly	Phe	Lys	Leu	Gly	Val	Arg	Pro	Ser	Gln	Gly	Gly	Glu	Ala	Pro
	1115					1120					1125			
Arg	Glu	Val	Thr	Ser	Asp	Ser	Gly	Ser	Ile	Val	Val	Ser	Gly	Leu
	1130					1135					1140			
Thr	Pro	Gly	Val	Glu	Tyr	Val	Tyr	Thr	Ile	Gln	Val	Leu	Arg	Asp
	1145					1150					1155			
Gly	Gln	Glu	Arg	Asp	Ala	Pro	Ile	Val	Asn	Lys	Val	Val	Thr	Pro
	1160					1165					1170			
Leu	Ser	Pro	Pro	Thr	Asn	Leu	His	Leu	Glu	Ala	Asn	Pro	Asp	Thr
	1175					1180					1185			
Gly	Val	Leu	Thr	Val	Ser	Trp	Glu	Arg	Ser	Thr	Thr	Pro	Asp	Ile
	1190					1195					1200			
Thr	Gly	Tyr	Arg	Ile	Thr	Thr	Thr	Pro	Thr	Asn	Gly	Gln	Gln	Gly
	1205					1210					1215			
Asn	Ser	Leu	Glu	Glu	Val	Val	His	Ala	Asp	Gln	Ser	Ser	Cys	Thr
	1220					1225					1230			
Phe	Asp	Asn	Leu	Ser	Pro	Gly	Leu	Glu	Tyr	Asn	Val	Ser	Val	Tyr
	1235					1240					1245			
Thr	Val	Lys	Asp	Asp	Lys	Glu	Ser	Val	Pro	Ile	Ser	Asp	Thr	Ile
	1250					1255					1260			
Ile	Pro	Ala	Val	Pro	Pro	Pro	Thr	Asp	Leu	Arg	Phe	Thr	Asn	Ile
	1265					1270					1275			
Gly	Pro	Asp	Thr	Met	Arg	Val	Thr	Trp	Ala	Pro	Pro	Pro	Ser	Ile
	1280					1285					1290			
Asp	Leu	Thr	Asn	Phe	Leu	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn	Glu
	1295					1300					1305			
Glu	Asp	Val	Ala	Glu	Leu	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val
	1310					1315					1320			

## FAB-008PC-SequenceListing

Val	Leu	Thr	Asn	Leu	Leu	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val
	1325					1330					1335			
Ser	Ser	Val	Tyr	Glu	Gln	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg
	1340					1345					1350			
Gln	Lys	Thr	Gly	Leu	Asp	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp
	1355					1360					1365			
Ile	Thr	Ala	Asn	Ser	Phe	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala
	1370					1375					1380			
Thr	Ile	Thr	Gly	Tyr	Arg	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser
	1385					1390					1395			
Gly	Arg	Pro	Arg	Glu	Asp	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile
	1400					1405					1410			
Thr	Leu	Thr	Asn	Leu	Thr	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile
	1415					1420					1425			
Val	Ala	Leu	Asn	Gly	Arg	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln
	1430					1435					1440			
Gln	Ser	Thr	Val	Ser	Asp	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala
	1445					1450					1455			
Ala	Thr	Pro	Thr	Ser	Leu	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val
	1460					1465					1470			
Thr	Val	Arg	Tyr	Tyr	Arg	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn
	1475					1480					1485			
Ser	Pro	Val	Gln	Glu	Phe	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala
	1490					1495					1500			
Thr	Ile	Ser	Gly	Leu	Lys	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val
	1505					1510					1515			
Tyr	Ala	Val	Thr	Gly	Arg	Gly	Asp	Ser	Pro	Ala	Ser	Ser	Lys	Pro
	1520					1525					1530			
Ile	Ser	Ile	Asn	Tyr	Arg	Thr	Glu	Ile	Asp	Lys	Pro	Ser	Gln	Met
	1535					1540					1545			
Gln	Val	Thr	Asp	Val	Gln	Asp	Asn	Ser	Ile	Ser	Val	Lys	Trp	Leu
	1550					1555					1560			
Pro	Ser	Ser	Ser	Pro	Val	Thr	Gly	Tyr	Arg	Val	Thr	Thr	Thr	Pro
	1565					1570					1575			

## FAB-008PC-SequenceListing

Lys Asn Gly Pro Gly Pro Thr Lys Thr Lys Thr Ala Gly Pro Asp  
 1580 1585 1590  
 Gln Thr Glu Met Thr Ile Glu Gly Leu Gln Pro Thr Val Glu Tyr  
 1595 1600 1605  
 Val Val Ser Val Tyr Ala Gln Asn Pro Ser Gly Glu Ser Gln Pro  
 1610 1615 1620  
 Leu Val Gln Thr Ala Val Thr Asn Ile Asp Arg Pro Lys Gly Leu  
 1625 1630 1635  
 Ala Phe Thr Asp Val Asp Val Asp Ser Ile Lys Ile Ala Trp Glu  
 1640 1645 1650  
 Ser Pro Gln Gly Gln Val Ser Arg Tyr Arg Val Thr Tyr Ser Ser  
 1655 1660 1665  
 Pro Glu Asp Gly Ile His Glu Leu Phe Pro Ala Pro Asp Gly Glu  
 1670 1675 1680  
 Glu Asp Thr Ala Glu Leu Gln Gly Leu Arg Pro Gly Ser Glu Tyr  
 1685 1690 1695  
 Thr Val Ser Val Val Ala Leu His Asp Asp Met Glu Ser Gln Pro  
 1700 1705 1710  
 Leu Ile Gly Thr Gln Ser Thr Ala Ile Pro Ala Pro Thr Asp Leu  
 1715 1720 1725  
 Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr  
 1730 1735 1740  
 Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro  
 1745 1750 1755  
 Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp  
 1760 1765 1770  
 Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr  
 1775 1780 1785  
 Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro  
 1790 1795 1800  
 Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg  
 1805 1810 1815  
 Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser  
 1820 1825 1830

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Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala
	1835					1840					1845			
Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro
	1850					1855					1860			
Asp	Val	Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp
	1865					1870					1875			
Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser
	1880					1885					1890			
Pro	Val	Val	Ile	Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser	Asn
	1895					1900					1905			
Leu	Arg	Phe	Leu	Ala	Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser	Trp
	1910					1915					1920			
Gln	Pro	Pro	Arg	Ala	Arg	Ile	Thr	Gly	Tyr	Ile	Ile	Lys	Tyr	Glu
	1925					1930					1935			
Lys	Pro	Gly	Ser	Pro	Pro	Arg	Glu	Val	Val	Pro	Arg	Pro	Arg	Pro
	1940					1945					1950			
Gly	Val	Thr	Glu	Ala	Thr	Ile	Thr	Gly	Leu	Glu	Pro	Gly	Thr	Glu
	1955					1960					1965			
Tyr	Thr	Ile	Tyr	Val	Ile	Ala	Leu	Lys	Asn	Asn	Gln	Lys	Ser	Glu
	1970					1975					1980			
Pro	Leu	Ile	Gly	Arg	Lys	Lys	Thr	Val	Gln	Lys	Thr	Pro	Phe	Val
	1985					1990					1995			
Thr	His	Pro	Gly	Tyr	Asp	Thr	Gly	Asn	Gly	Ile	Gln	Leu	Pro	Gly
	2000					2005					2010			
Thr	Ser	Gly	Gln	Gln	Pro	Ser	Val	Gly	Gln	Gln	Met	Ile	Phe	Glu
	2015					2020					2025			
Glu	His	Gly	Phe	Arg	Arg	Thr	Thr	Pro	Pro	Thr	Thr	Ala	Thr	Pro
	2030					2035					2040			
Ile	Arg	His	Arg	Pro	Arg	Pro	Tyr	Pro	Pro	Asn	Val	Gly	Gln	Glu
	2045					2050					2055			
Ala	Leu	Ser	Gln	Thr	Thr	Ile	Ser	Trp	Ala	Pro	Phe	Gln	Asp	Thr
	2060					2065					2070			
Ser	Glu	Tyr	Ile	Ile	Ser	Cys	His	Pro	Val	Gly	Thr	Asp	Glu	Glu
	2075					2080					2085			

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Pro	Leu	Gln	Phe	Arg	Val	Pro	Gly	Thr	Ser	Thr	Ser	Ala	Thr	Leu
	2090					2095					2100			
Thr	Gly	Leu	Thr	Arg	Gly	Ala	Thr	Tyr	Asn	Ile	Ile	Val	Glu	Ala
	2105					2110					2115			
Leu	Lys	Asp	Gln	Gln	Arg	His	Lys	Val	Arg	Glu	Glu	Val	Val	Thr
	2120					2125					2130			
Val	Gly	Asn	Ser	Val	Asn	Glu	Gly	Leu	Asn	Gln	Pro	Thr	Asp	Asp
	2135					2140					2145			
Ser	Cys	Phe	Asp	Pro	Tyr	Thr	Val	Ser	His	Tyr	Ala	Val	Gly	Asp
	2150					2155					2160			
Glu	Trp	Glu	Arg	Met	Ser	Glu	Ser	Gly	Phe	Lys	Leu	Leu	Cys	Gln
	2165					2170					2175			
Cys	Leu	Gly	Phe	Gly	Ser	Gly	His	Phe	Arg	Cys	Asp	Ser	Ser	Arg
	2180					2185					2190			
Trp	Cys	His	Asp	Asn	Gly	Val	Asn	Tyr	Lys	Ile	Gly	Glu	Lys	Trp
	2195					2200					2205			
Asp	Arg	Gln	Gly	Glu	Asn	Gly	Gln	Met	Met	Ser	Cys	Thr	Cys	Leu
	2210					2215					2220			
Gly	Asn	Gly	Lys	Gly	Glu	Phe	Lys	Cys	Asp	Pro	His	Glu	Ala	Thr
	2225					2230					2235			
Cys	Tyr	Asp	Asp	Gly	Lys	Thr	Tyr	His	Val	Gly	Glu	Gln	Trp	Gln
	2240					2245					2250			
Lys	Glu	Tyr	Leu	Gly	Ala	Ile	Cys	Ser	Cys	Thr	Cys	Phe	Gly	Gly
	2255					2260					2265			
Gln	Arg	Gly	Trp	Arg	Cys	Asp	Asn	Cys	Arg	Arg	Pro	Gly	Gly	Glu
	2270					2275					2280			
Pro	Ser	Pro	Glu	Gly	Thr	Thr	Gly	Gln	Ser	Tyr	Asn	Gln	Tyr	Ser
	2285					2290					2295			
Gln	Arg	Tyr	His	Gln	Arg	Thr	Asn	Thr	Asn	Val	Asn	Cys	Pro	Ile
	2300					2305					2310			
Glu	Cys	Phe	Met	Pro	Leu	Asp	Val	Gln	Ala	Asp	Arg	Glu	Asp	Ser
	2315					2320					2325			
Arg	Glu													
	2330													

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<210> 99  
 <211> 2296  
 <212> PRT  
 <213> Homo sapiens

<400> 99

Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys  
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Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln  
 20 25 30

Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser  
 35 40 45

Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln  
 50 55 60

Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly  
 65 70 75 80

Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr  
 85 90 95

Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr  
 100 105 110

Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala  
 115 120 125

Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly  
 130 135 140

Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr  
 145 150 155 160

Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu  
 165 170 175

Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly  
 180 185 190

Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp  
 195 200 205

Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr  
 210 215 220

Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr  
 225 230 235 240

Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu  
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245

250

255

Gln Cys Ile Cys<sub>260</sub> Thr Gly Asn Gly Arg<sub>265</sub> Gly Glu Trp Lys Cys<sub>270</sub> Glu Arg

His Thr Ser<sub>275</sub> Val Gln Thr Thr Ser<sub>280</sub> Ser Gly Ser Gly Pro<sub>285</sub> Phe Thr Asp

Val Arg<sub>290</sub> Ala Ala Val Tyr Gln<sub>295</sub> Pro Gln Pro His Pro<sub>300</sub> Gln Pro Pro Pro

Tyr Gly His Cys Val Thr<sub>310</sub> Asp Ser Gly Val Val<sub>315</sub> Tyr Ser Val Gly Met<sub>320</sub>

Gln Trp Leu Lys Thr<sub>325</sub> Gln Gly Asn Lys Gln<sub>330</sub> Met Leu Cys Thr Cys<sub>335</sub> Leu

Gly Asn Gly Val<sub>340</sub> Ser Cys Gln Glu Thr<sub>345</sub> Ala Val Thr Gln Thr<sub>350</sub> Tyr Gly

Gly Asn Ser<sub>355</sub> Asn Gly Glu Pro Cys<sub>360</sub> Val Leu Pro Phe Thr<sub>365</sub> Tyr Asn Gly

Arg Thr<sub>370</sub> Phe Tyr Ser Cys Thr<sub>375</sub> Thr Glu Gly Arg Gln<sub>380</sub> Asp Gly His Leu

Trp Cys Ser Thr Thr Ser<sub>390</sub> Asn Tyr Glu Gln Asp<sub>395</sub> Gln Lys Tyr Ser Phe<sub>400</sub>

Cys Thr Asp His Thr<sub>405</sub> Val Leu Val Gln Thr<sub>410</sub> Arg Gly Gly Asn Ser<sub>415</sub> Asn

Gly Ala Leu Cys<sub>420</sub> His Phe Pro Phe Leu<sub>425</sub> Tyr Asn Asn His Asn<sub>430</sub> Tyr Thr

Asp Cys Thr<sub>435</sub> Ser Glu Gly Arg Arg<sub>440</sub> Asp Asn Met Lys Trp<sub>445</sub> Cys Gly Thr

Thr Gln<sub>450</sub> Asn Tyr Asp Ala Asp<sub>455</sub> Gln Lys Phe Gly Phe<sub>460</sub> Cys Pro Met Ala

Ala His Glu Glu Ile Cys<sub>470</sub> Thr Thr Asn Glu Gly<sub>475</sub> Val Met Tyr Arg Ile<sub>480</sub>

Gly Asp Gln Trp Asp<sub>485</sub> Lys Gln His Asp Met<sub>490</sub> Gly His Met Met Arg<sub>495</sub> Cys

Thr Cys Val Gly<sub>500</sub> Asn Gly Arg Gly Glu<sub>505</sub> Trp Thr Cys Ile Ala<sub>510</sub> Tyr Ser

Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val Asn



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515

520

525

Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys Thr  
530 535 540

Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp Gln  
545 550 555 560

Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser Trp  
565 570 575

Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly Arg  
580 585 590

Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser Ser  
595 600 605

Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro Asn  
610 615 620

Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser Lys  
625 630 635 640

Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg Trp Lys Glu  
645 650 655

Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu Lys  
660 665 670

Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr Gly  
675 680 685

His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser Thr  
690 695 700

Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr Pro Phe Ser Pro  
705 710 715 720

Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr Ala Ser Ser Phe  
725 730 735

Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg Val  
740 745 750

Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp Leu  
755 760 765

Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly Arg  
770 775 780

Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp Gly Glu Gln Ser

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785					790					795					800
Leu	Ile	Leu	Ser	Thr 805	Ser	Gln	Thr	Thr	Ala 810	Pro	Asp	Ala	Pro	Pro 815	Asp
Pro	Thr	Val	Asp 820	Gln	Val	Asp	Asp	Thr 825	Ser	Ile	Val	Val	Arg 830	Trp	Ser
Arg	Pro	Gln 835	Ala	Pro	Ile	Thr	Gly 840	Tyr	Arg	Ile	Val	Tyr 845	Ser	Pro	Ser
Val	Glu 850	Gly	Ser	Ser	Thr	Glu 855	Leu	Asn	Leu	Pro	Glu 860	Thr	Ala	Asn	Ser
Val 865	Thr	Leu	Ser	Asp	Leu 870	Gln	Pro	Gly	Val	Gln 875	Tyr	Asn	Ile	Thr	Ile 880
Tyr	Ala	Val	Glu	Glu 885	Asn	Gln	Glu	Ser	Thr 890	Pro	Val	Val	Ile	Gln 895	Gln
Glu	Thr	Thr	Gly 900	Thr	Pro	Arg	Ser	Asp 905	Thr	Val	Pro	Ser	Pro 910	Arg	Asp
Leu	Gln	Phe 915	Val	Glu	Val	Thr	Asp 920	Val	Lys	Val	Thr	Ile 925	Met	Trp	Thr
Pro	Pro 930	Glu	Ser	Ala	Val	Thr 935	Gly	Tyr	Arg	Val	Asp 940	Val	Ile	Pro	Val
Asn 945	Leu	Pro	Gly	Glu	His 950	Gly	Gln	Arg	Leu	Pro 955	Ile	Ser	Arg	Asn	Thr 960
Phe	Ala	Glu	Val	Thr 965	Gly	Leu	Ser	Pro	Gly 970	Val	Thr	Tyr	Tyr	Phe 975	Lys
Val	Phe	Ala	Val 980	Ser	His	Gly	Arg	Glu 985	Ser	Lys	Pro	Leu	Thr 990	Ala	Gln
Gln	Thr	Thr 995	Lys	Leu	Asp	Ala	Pro 1000	Thr	Asn	Leu	Gln	Phe 1005	Val	Asn	Glu
Thr	Asp 1010	Ser	Thr	Val	Leu	Val 1015	Arg	Trp	Thr	Pro	Pro 1020	Arg	Ala	Gln	
Ile	Thr 1025	Gly	Tyr	Arg	Leu	Thr 1030	Val	Gly	Leu	Thr	Arg 1035	Arg	Gly	Gln	
Pro	Arg 1040	Gln	Tyr	Asn	Val	Gly 1045	Pro	Ser	Val	Ser	Lys 1050	Tyr	Pro	Leu	
Arg	Asn	Leu	Gln	Pro	Ala	Ser	Glu	Tyr	Thr	Val	Ser	Leu	Val	Ala	

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1055														
Ile	Lys	Gly	Asn	Gln	Glu	Ser	Pro	Lys	Ala	Thr	Gly	Val	Phe	Thr
	1070					1075					1080			
Thr	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Pro	Pro	Tyr	Asn	Thr	Glu	Val
	1085					1090					1095			
Thr	Glu	Thr	Thr	Ile	Val	Ile	Thr	Trp	Thr	Pro	Ala	Pro	Arg	Ile
	1100					1105					1110			
Gly	Phe	Lys	Leu	Gly	Val	Arg	Pro	Ser	Gln	Gly	Gly	Glu	Ala	Pro
	1115					1120					1125			
Arg	Glu	Val	Thr	Ser	Asp	Ser	Gly	Ser	Ile	Val	Val	Ser	Gly	Leu
	1130					1135					1140			
Thr	Pro	Gly	Val	Glu	Tyr	Val	Tyr	Thr	Ile	Gln	Val	Leu	Arg	Asp
	1145					1150					1155			
Gly	Gln	Glu	Arg	Asp	Ala	Pro	Ile	Val	Asn	Lys	Val	Val	Thr	Pro
	1160					1165					1170			
Leu	Ser	Pro	Pro	Thr	Asn	Leu	His	Leu	Glu	Ala	Asn	Pro	Asp	Thr
	1175					1180					1185			
Gly	Val	Leu	Thr	Val	Ser	Trp	Glu	Arg	Ser	Thr	Thr	Pro	Asp	Ile
	1190					1195					1200			
Thr	Gly	Tyr	Arg	Ile	Thr	Thr	Thr	Pro	Thr	Asn	Gly	Gln	Gln	Gly
	1205					1210					1215			
Asn	Ser	Leu	Glu	Glu	Val	Val	His	Ala	Asp	Gln	Ser	Ser	Cys	Thr
	1220					1225					1230			
Phe	Asp	Asn	Leu	Ser	Pro	Gly	Leu	Glu	Tyr	Asn	Val	Ser	Val	Tyr
	1235					1240					1245			
Thr	Val	Lys	Asp	Asp	Lys	Glu	Ser	Val	Pro	Ile	Ser	Asp	Thr	Ile
	1250					1255					1260			
Ile	Pro	Ala	Val	Pro	Pro	Pro	Thr	Asp	Leu	Arg	Phe	Thr	Asn	Ile
	1265					1270					1275			
Gly	Pro	Asp	Thr	Met	Arg	Val	Thr	Trp	Ala	Pro	Pro	Pro	Ser	Ile
	1280					1285					1290			
Asp	Leu	Thr	Asn	Phe	Leu	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn	Glu
	1295					1300					1305			
Glu	Asp	Val	Ala	Glu	Leu	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val

## 1320

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1565													
Lys	Asn	Gly	Pro	Gly	Pro	Thr	Lys	Thr	Lys	Thr	Ala	Gly	Pro Asp
	1580					1585					1590		
Gln	Thr	Glu	Met	Thr	Ile	Glu	Gly	Leu	Gln	Pro	Thr	Val	Glu Tyr
	1595					1600					1605		
Val	Val	Ser	Val	Tyr	Ala	Gln	Asn	Pro	Ser	Gly	Glu	Ser	Gln Pro
	1610					1615					1620		
Leu	Val	Gln	Thr	Ala	Val	Thr	Thr	Ile	Pro	Ala	Pro	Thr	Asp Leu
	1625					1630					1635		
Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	Gln	Trp Thr
	1640					1645					1650		
Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr Pro
	1655					1660					1665		
Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro Asp
	1670					1675					1680		
Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys Tyr
	1685					1690					1695		
Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg Pro
	1700					1705					1710		
Ala	Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro Arg
	1715					1720					1725		
Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile Ser
	1730					1735					1740		
Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp Ala
	1745					1750					1755		
Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys Pro
	1760					1765					1770		
Asp	Val	Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr Asp
	1775					1780					1785		
Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser Ser
	1790					1795					1800		
Pro	Val	Val	Ile	Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser Asn
	1805					1810					1815		
Leu	Arg	Phe	Leu	Ala	Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser Trp

## FAB-008PC-SequenceListing

1820														
Gln	Pro	Pro	Arg	Ala	Arg	Ile	Thr	Gly	Tyr	Ile	Ile	Lys	Tyr	Glu
1835						1840					1845			
Lys	Pro	Gly	Ser	Pro	Pro	Arg	Glu	Val	Val	Pro	Arg	Pro	Arg	Pro
1850						1855					1860			
Gly	Val	Thr	Glu	Ala	Thr	Ile	Thr	Gly	Leu	Glu	Pro	Gly	Thr	Glu
1865						1870					1875			
Tyr	Thr	Ile	Tyr	Val	Ile	Ala	Leu	Lys	Asn	Asn	Gln	Lys	Ser	Glu
1880						1885					1890			
Pro	Leu	Ile	Gly	Arg	Lys	Lys	Thr	Asp	Glu	Leu	Pro	Gln	Leu	Val
1895						1900					1905			
Thr	Leu	Pro	His	Pro	Asn	Leu	His	Gly	Pro	Glu	Ile	Leu	Asp	Val
1910						1915					1920			
Pro	Ser	Thr	Val	Gln	Lys	Thr	Pro	Phe	Val	Thr	His	Pro	Gly	Tyr
1925						1930					1935			
Asp	Thr	Gly	Asn	Gly	Ile	Gln	Leu	Pro	Gly	Thr	Ser	Gly	Gln	Gln
1940						1945					1950			
Pro	Ser	Val	Gly	Gln	Gln	Met	Ile	Phe	Glu	Glu	His	Gly	Phe	Arg
1955						1960					1965			
Arg	Thr	Thr	Pro	Pro	Thr	Thr	Ala	Thr	Pro	Ile	Arg	His	Arg	Pro
1970						1975					1980			
Arg	Pro	Tyr	Pro	Pro	Asn	Val	Gly	Glu	Glu	Ile	Gln	Ile	Gly	His
1985						1990					1995			
Ile	Pro	Arg	Glu	Asp	Val	Asp	Tyr	His	Leu	Tyr	Pro	His	Gly	Pro
2000						2005					2010			
Gly	Leu	Asn	Pro	Asn	Ala	Ser	Thr	Gly	Gln	Glu	Ala	Leu	Ser	Gln
2015						2020					2025			
Thr	Thr	Ile	Ser	Trp	Ala	Pro	Phe	Gln	Asp	Thr	Ser	Glu	Tyr	Ile
2030						2035					2040			
Ile	Ser	Cys	His	Pro	Val	Gly	Thr	Asp	Glu	Glu	Pro	Leu	Gln	Phe
2045						2050					2055			
Arg	Val	Pro	Gly	Thr	Ser	Thr	Ser	Ala	Thr	Leu	Thr	Gly	Leu	Thr
2060						2065					2070			
Arg	Gly	Ala	Thr	Tyr	Asn	Ile	Ile	Val	Glu	Ala	Leu	Lys	Asp	Gln

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2075

2080

2085

Gln Arg His Lys Val Arg Glu Glu Val Val Thr Val Gly Asn Ser  
2090 2095 2100

Val Asn Glu Gly Leu Asn Gln Pro Thr Asp Asp Ser Cys Phe Asp  
2105 2110 2115

Pro Tyr Thr Val Ser His Tyr Ala Val Gly Asp Glu Trp Glu Arg  
2120 2125 2130

Met Ser Glu Ser Gly Phe Lys Leu Leu Cys Gln Cys Leu Gly Phe  
2135 2140 2145

Gly Ser Gly His Phe Arg Cys Asp Ser Ser Arg Trp Cys His Asp  
2150 2155 2160

Asn Gly Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp Arg Gln Gly  
2165 2170 2175

Glu Asn Gly Gln Met Met Ser Cys Thr Cys Leu Gly Asn Gly Lys  
2180 2185 2190

Gly Glu Phe Lys Cys Asp Pro His Glu Ala Thr Cys Tyr Asp Asp  
2195 2200 2205

Gly Lys Thr Tyr His Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu  
2210 2215 2220

Gly Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly Trp  
2225 2230 2235

Arg Cys Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro Glu  
2240 2245 2250

Gly Thr Thr Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr His  
2255 2260 2265

Gln Arg Thr Asn Thr Asn Val Asn Cys Pro Ile Glu Cys Phe Met  
2270 2275 2280

Pro Leu Asp Val Gln Ala Asp Arg Glu Asp Ser Arg Glu  
2285 2290 2295

<210> 100  
<211> 2176  
<212> PRT  
<213> Homo sapiens

<400> 100

Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys  
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Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln  
 20 25 30  
 Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser  
 35 40 45  
 Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln  
 50 55 60  
 Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly  
 65 70 75 80  
 Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr  
 85 90 95  
 Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr  
 100 105 110  
 Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala  
 115 120 125  
 Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly  
 130 135 140  
 Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr  
 145 150 155 160  
 Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu  
 165 170 175  
 Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly  
 180 185 190  
 Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp  
 195 200 205  
 Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile Thr  
 210 215 220  
 Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser Tyr  
 225 230 235 240  
 Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu Leu  
 245 250 255  
 Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu Arg  
 260 265 270  
 His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr Asp  
 275 280 285



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Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro  
 290 295 300  
 Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met  
 305 310 315 320  
 Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu  
 325 330 335  
 Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly  
 340 345 350  
 Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly  
 355 360 365  
 Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln Asp Gly His Leu  
 370 375 380  
 Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser Phe  
 385 390 395 400  
 Cys Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser Asn  
 405 410 415  
 Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr Thr  
 420 425 430  
 Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly Thr  
 435 440 445  
 Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met Ala  
 450 455 460  
 Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg Ile  
 465 470 475 480  
 Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg Cys  
 485 490 495  
 Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr Ser  
 500 505 510  
 Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val Asn  
 515 520 525  
 Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys Thr  
 530 535 540  
 Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp Gln  
 545 550 555 560

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Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser Trp  
 565 570 575  
 Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly Arg  
 580 585 590  
 Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser Ser  
 595 600 605  
 Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro Asn  
 610 615 620  
 Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser Lys  
 625 630 635 640  
 Tyr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg Trp Lys Glu  
 645 650 655  
 Ala Thr Ile Pro Gly His Leu Asn Ser Tyr Thr Ile Lys Gly Leu Lys  
 660 665 670  
 Pro Gly Val Val Tyr Glu Gly Gln Leu Ile Ser Ile Gln Gln Tyr Gly  
 675 680 685  
 His Gln Glu Val Thr Arg Phe Asp Phe Thr Thr Thr Ser Thr Ser Thr  
 690 695 700  
 Pro Val Thr Ser Asn Thr Val Thr Gly Glu Thr Thr Pro Phe Ser Pro  
 705 710 715 720  
 Leu Val Ala Thr Ser Glu Ser Val Thr Glu Ile Thr Ala Ser Ser Phe  
 725 730 735  
 Val Val Ser Trp Val Ser Ala Ser Asp Thr Val Ser Gly Phe Arg Val  
 740 745 750  
 Glu Tyr Glu Leu Ser Glu Glu Gly Asp Glu Pro Gln Tyr Leu Asp Leu  
 755 760 765  
 Pro Ser Thr Ala Thr Ser Val Asn Ile Pro Asp Leu Leu Pro Gly Arg  
 770 775 780  
 Lys Tyr Ile Val Asn Val Tyr Gln Ile Ser Glu Asp Gly Glu Gln Ser  
 785 790 795 800  
 Leu Ile Leu Ser Thr Ser Gln Thr Thr Ala Pro Asp Ala Pro Pro Asp  
 805 810 815  
 Pro Thr Val Asp Gln Val Asp Asp Thr Ser Ile Val Val Arg Trp Ser  
 820 825 830

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Arg Pro Gln Ala Pro Ile Thr Gly Tyr Arg Ile Val Tyr Ser Pro Ser  
 835 840 845  
 Val Glu Gly Ser Ser Thr Glu Leu Asn Leu Pro Glu Thr Ala Asn Ser  
 850 855 860  
 Val Thr Leu Ser Asp Leu Gln Pro Gly Val Gln Tyr Asn Ile Thr Ile  
 865 870 875 880  
 Tyr Ala Val Glu Glu Asn Gln Glu Ser Thr Pro Val Val Ile Gln Gln  
 885 890 895  
 Glu Thr Thr Gly Thr Pro Arg Ser Asp Thr Val Pro Ser Pro Arg Asp  
 900 905 910  
 Leu Gln Phe Val Glu Val Thr Asp Val Lys Val Thr Ile Met Trp Thr  
 915 920 925  
 Pro Pro Glu Ser Ala Val Thr Gly Tyr Arg Val Asp Val Ile Pro Val  
 930 935 940  
 Asn Leu Pro Gly Glu His Gly Gln Arg Leu Pro Ile Ser Arg Asn Thr  
 945 950 955 960  
 Phe Ala Glu Val Thr Gly Leu Ser Pro Gly Val Thr Tyr Tyr Phe Lys  
 965 970 975  
 Val Phe Ala Val Ser His Gly Arg Glu Ser Lys Pro Leu Thr Ala Gln  
 980 985 990  
 Gln Thr Thr Lys Leu Asp Ala Pro Thr Asn Leu Gln Phe Val Asn Glu  
 995 1000 1005  
 Thr Asp Ser Thr Val Leu Val Arg Trp Thr Pro Pro Arg Ala Gln  
 1010 1015 1020  
 Ile Thr Gly Tyr Arg Leu Thr Val Gly Leu Thr Arg Arg Gly Gln  
 1025 1030 1035  
 Pro Arg Gln Tyr Asn Val Gly Pro Ser Val Ser Lys Tyr Pro Leu  
 1040 1045 1050  
 Arg Asn Leu Gln Pro Ala Ser Glu Tyr Thr Val Ser Leu Val Ala  
 1055 1060 1065  
 Ile Lys Gly Asn Gln Glu Ser Pro Lys Ala Thr Gly Val Phe Thr  
 1070 1075 1080  
 Thr Leu Gln Pro Gly Ser Ser Ile Pro Pro Tyr Asn Thr Glu Val  
 1085 1090 1095

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Thr	Glu	Thr	Thr	Ile	Val	Ile	Thr	Trp	Thr	Pro	Ala	Pro	Arg	Ile
	1100					1105					1110			
Gly	Phe	Lys	Leu	Gly	Val	Arg	Pro	Ser	Gln	Gly	Gly	Glu	Ala	Pro
	1115					1120					1125			
Arg	Glu	Val	Thr	Ser	Asp	Ser	Gly	Ser	Ile	Val	Val	Ser	Gly	Leu
	1130					1135					1140			
Thr	Pro	Gly	Val	Glu	Tyr	Val	Tyr	Thr	Ile	Gln	Val	Leu	Arg	Asp
	1145					1150					1155			
Gly	Gln	Glu	Arg	Asp	Ala	Pro	Ile	Val	Asn	Lys	Val	Val	Thr	Pro
	1160					1165					1170			
Leu	Ser	Pro	Pro	Thr	Asn	Leu	His	Leu	Glu	Ala	Asn	Pro	Asp	Thr
	1175					1180					1185			
Gly	Val	Leu	Thr	Val	Ser	Trp	Glu	Arg	Ser	Thr	Thr	Pro	Asp	Ile
	1190					1195					1200			
Thr	Gly	Tyr	Arg	Ile	Thr	Thr	Thr	Pro	Thr	Asn	Gly	Gln	Gln	Gly
	1205					1210					1215			
Asn	Ser	Leu	Glu	Glu	Val	Val	His	Ala	Asp	Gln	Ser	Ser	Cys	Thr
	1220					1225					1230			
Phe	Asp	Asn	Leu	Ser	Pro	Gly	Leu	Glu	Tyr	Asn	Val	Ser	Val	Tyr
	1235					1240					1245			
Thr	Val	Lys	Asp	Asp	Lys	Glu	Ser	Val	Pro	Ile	Ser	Asp	Thr	Ile
	1250					1255					1260			
Ile	Pro	Ala	Val	Pro	Pro	Pro	Thr	Asp	Leu	Arg	Phe	Thr	Asn	Ile
	1265					1270					1275			
Gly	Pro	Asp	Thr	Met	Arg	Val	Thr	Trp	Ala	Pro	Pro	Pro	Ser	Ile
	1280					1285					1290			
Asp	Leu	Thr	Asn	Phe	Leu	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn	Glu
	1295					1300					1305			
Glu	Asp	Val	Ala	Glu	Leu	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val
	1310					1315					1320			
Val	Leu	Thr	Asn	Leu	Leu	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val
	1325					1330					1335			
Ser	Ser	Val	Tyr	Glu	Gln	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg
	1340					1345					1350			

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Gln	Lys	Thr	Gly	Leu	Asp	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp
	1355					1360					1365			
Ile	Thr	Ala	Asn	Ser	Phe	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala
	1370					1375					1380			
Thr	Ile	Thr	Gly	Tyr	Arg	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser
	1385					1390					1395			
Gly	Arg	Pro	Arg	Glu	Asp	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile
	1400					1405					1410			
Thr	Leu	Thr	Asn	Leu	Thr	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile
	1415					1420					1425			
Val	Ala	Leu	Asn	Gly	Arg	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln
	1430					1435					1440			
Gln	Ser	Thr	Val	Ser	Asp	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala
	1445					1450					1455			
Ala	Thr	Pro	Thr	Ser	Leu	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val
	1460					1465					1470			
Thr	Val	Arg	Tyr	Tyr	Arg	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn
	1475					1480					1485			
Ser	Pro	Val	Gln	Glu	Phe	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala
	1490					1495					1500			
Thr	Ile	Ser	Gly	Leu	Lys	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val
	1505					1510					1515			
Tyr	Ala	Val	Thr	Gly	Arg	Gly	Asp	Ser	Pro	Ala	Ser	Ser	Lys	Pro
	1520					1525					1530			
Ile	Ser	Ile	Asn	Tyr	Arg	Thr	Glu	Ile	Asp	Lys	Pro	Ser	Gln	Met
	1535					1540					1545			
Gln	Val	Thr	Asp	Val	Gln	Asp	Asn	Ser	Ile	Ser	Val	Lys	Trp	Leu
	1550					1555					1560			
Pro	Ser	Ser	Ser	Pro	Val	Thr	Gly	Tyr	Arg	Val	Thr	Thr	Thr	Pro
	1565					1570					1575			
Lys	Asn	Gly	Pro	Gly	Pro	Thr	Lys	Thr	Lys	Thr	Ala	Gly	Pro	Asp
	1580					1585					1590			
Gln	Thr	Glu	Met	Thr	Ile	Glu	Gly	Leu	Gln	Pro	Thr	Val	Glu	Tyr
	1595					1600					1605			

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Val	Val	Ser	Val	Tyr	Ala	Gln	Asn	Pro	Ser	Gly	Glu	Ser	Gln	Pro
	1610					1615					1620			
Leu	Val	Gln	Thr	Ala	Val	Thr	Thr	Ile	Pro	Ala	Pro	Thr	Asp	Leu
	1625					1630					1635			
Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	Gln	Trp	Thr
	1640					1645					1650			
Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr	Pro
	1655					1660					1665			
Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro	Asp
	1670					1675					1680			
Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys	Tyr
	1685					1690					1695			
Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg	Pro
	1700					1705					1710			
Ala	Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	Arg
	1715					1720					1725			
Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser
	1730					1735					1740			
Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala
	1745					1750					1755			
Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro
	1760					1765					1770			
Asp	Val	Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp
	1775					1780					1785			
Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser
	1790					1795					1800			
Pro	Val	Val	Ile	Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser	Asn
	1805					1810					1815			
Leu	Arg	Phe	Leu	Ala	Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser	Trp
	1820					1825					1830			
Gln	Pro	Pro	Arg	Ala	Arg	Ile	Thr	Gly	Tyr	Ile	Ile	Lys	Tyr	Glu
	1835					1840					1845			
Lys	Pro	Gly	Ser	Pro	Pro	Arg	Glu	Val	Val	Pro	Arg	Pro	Arg	Pro
	1850					1855					1860			

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Gly	Val	Thr	Glu	Ala	Thr	Ile	Thr	Gly	Leu	Glu	Pro	Gly	Thr	Glu
1865						1870					1875			
Tyr	Thr	Ile	Tyr	Val	Ile	Ala	Leu	Lys	Asn	Asn	Gln	Lys	Ser	Glu
1880						1885					1890			
Pro	Leu	Ile	Gly	Arg	Lys	Lys	Thr	Gly	Gln	Glu	Ala	Leu	Ser	Gln
1895						1900					1905			
Thr	Thr	Ile	Ser	Trp	Ala	Pro	Phe	Gln	Asp	Thr	Ser	Glu	Tyr	Ile
1910						1915					1920			
Ile	Ser	Cys	His	Pro	Val	Gly	Thr	Asp	Glu	Glu	Pro	Leu	Gln	Phe
1925						1930					1935			
Arg	Val	Pro	Gly	Thr	Ser	Thr	Ser	Ala	Thr	Leu	Thr	Gly	Leu	Thr
1940						1945					1950			
Arg	Gly	Ala	Thr	Tyr	Asn	Ile	Ile	Val	Glu	Ala	Leu	Lys	Asp	Gln
1955						1960					1965			
Gln	Arg	His	Lys	Val	Arg	Glu	Glu	Val	Val	Thr	Val	Gly	Asn	Ser
1970						1975					1980			
Val	Asn	Glu	Gly	Leu	Asn	Gln	Pro	Thr	Asp	Asp	Ser	Cys	Phe	Asp
1985						1990					1995			
Pro	Tyr	Thr	Val	Ser	His	Tyr	Ala	Val	Gly	Asp	Glu	Trp	Glu	Arg
2000						2005					2010			
Met	Ser	Glu	Ser	Gly	Phe	Lys	Leu	Leu	Cys	Gln	Cys	Leu	Gly	Phe
2015						2020					2025			
Gly	Ser	Gly	His	Phe	Arg	Cys	Asp	Ser	Ser	Arg	Trp	Cys	His	Asp
2030						2035					2040			
Asn	Gly	Val	Asn	Tyr	Lys	Ile	Gly	Glu	Lys	Trp	Asp	Arg	Gln	Gly
2045						2050					2055			
Glu	Asn	Gly	Gln	Met	Met	Ser	Cys	Thr	Cys	Leu	Gly	Asn	Gly	Lys
2060						2065					2070			
Gly	Glu	Phe	Lys	Cys	Asp	Pro	His	Glu	Ala	Thr	Cys	Tyr	Asp	Asp
2075						2080					2085			
Gly	Lys	Thr	Tyr	His	Val	Gly	Glu	Gln	Trp	Gln	Lys	Glu	Tyr	Leu
2090						2095					2100			
Gly	Ala	Ile	Cys	Ser	Cys	Thr	Cys	Phe	Gly	Gly	Gln	Arg	Gly	Trp
2105						2110					2115			

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Arg Cys Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro Glu  
2120 2125 2130

Gly Thr Thr Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr His  
2135 2140 2145

Gln Arg Thr Asn Thr Asn Val Asn Cys Pro Ile Glu Cys Phe Met  
2150 2155 2160

Pro Leu Asp Val Gln Ala Asp Arg Glu Asp Ser Arg Glu  
2165 2170 2175

<210> 101  
<211> 657  
<212> PRT  
<213> Homo sapiens

<400> 101

Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Ala Val Gln Cys  
1 5 10 15

Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg Gln  
20 25 30

Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln Ser  
35 40 45

Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln Gln  
50 55 60

Trp Glu Arg Thr Tyr Leu Gly Asn Ala Leu Val Cys Thr Cys Tyr Gly  
65 70 75 80

Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu Thr  
85 90 95

Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr  
100 105 110

Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala  
115 120 125

Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly  
130 135 140

Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr  
145 150 155 160

Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu  
165 170 175



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Trp Thr Cys Lys<sub>180</sub> Pro Ile Ala Glu Lys<sub>185</sub> Cys Phe Asp His Ala<sub>190</sub> Ala Gly  
 Thr Ser Tyr<sub>195</sub> Val Val Gly Glu Thr<sub>200</sub> Trp Glu Lys Pro Tyr<sub>205</sub> Gln Gly Trp  
 Met Met<sub>210</sub> Val Asp Cys Thr Cys<sub>215</sub> Leu Gly Glu Gly Ser<sub>220</sub> Gly Arg Ile Thr  
 Cys<sub>225</sub> Thr Ser Arg Asn Arg<sub>230</sub> Cys Asn Asp Gln Asp<sub>235</sub> Thr Arg Thr Ser Tyr<sub>240</sub>  
 Arg Ile Gly Asp Thr<sub>245</sub> Trp Ser Lys Lys Asp<sub>250</sub> Asn Arg Gly Asn Leu<sub>255</sub> Leu  
 Gln Cys Ile Cys<sub>260</sub> Thr Gly Asn Gly Arg<sub>265</sub> Gly Glu Trp Lys Cys<sub>270</sub> Glu Arg  
 His Thr Ser<sub>275</sub> Val Gln Thr Thr Ser<sub>280</sub> Ser Gly Ser Gly Pro<sub>285</sub> Phe Thr Asp  
 Val Arg<sub>290</sub> Ala Ala Val Tyr Gln<sub>295</sub> Pro Gln Pro His Pro<sub>300</sub> Gln Pro Pro Pro  
 Tyr Gly His Cys Val Thr<sub>310</sub> Asp Ser Gly Val Val<sub>315</sub> Tyr Ser Val Gly Met<sub>320</sub>  
 Gln Trp Leu Lys Thr<sub>325</sub> Gln Gly Asn Lys Gln<sub>330</sub> Met Leu Cys Thr Cys<sub>335</sub> Leu  
 Gly Asn Gly Val<sub>340</sub> Ser Cys Gln Glu Thr<sub>345</sub> Ala Val Thr Gln<sub>350</sub> Thr Tyr Gly  
 Gly Asn Ser<sub>355</sub> Asn Gly Glu Pro Cys<sub>360</sub> Val Leu Pro Phe Thr<sub>365</sub> Tyr Asn Gly  
 Arg Thr<sub>370</sub> Phe Tyr Ser Cys Thr<sub>375</sub> Thr Glu Gly Arg Gln<sub>380</sub> Asp Gly His Leu  
 Trp Cys Ser Thr Thr Ser<sub>390</sub> Asn Tyr Glu Gln Asp<sub>395</sub> Gln Lys Tyr Ser Phe<sub>400</sub>  
 Cys Thr Asp His Thr<sub>405</sub> Val Leu Val Gln Thr<sub>410</sub> Arg Gly Gly Asn Ser<sub>415</sub> Asn  
 Gly Ala Leu Cys<sub>420</sub> His Phe Pro Phe Leu<sub>425</sub> Tyr Asn Asn His Asn<sub>430</sub> Tyr Thr  
 Asp Cys Thr<sub>435</sub> Ser Glu Gly Arg Arg<sub>440</sub> Asp Asn Met Lys Trp<sub>445</sub> Cys Gly Thr

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Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met Ala  
450 455 460

Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg Ile  
465 470 475 480

Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg Cys  
485 490 495

Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr Ser  
500 505 510

Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val Asn  
515 520 525

Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys Thr  
530 535 540

Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp Gln  
545 550 555 560

Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser Trp  
565 570 575

Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly Arg  
580 585 590

Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser Ser  
595 600 605

Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro Asn  
610 615 620

Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile Ser Lys  
625 630 635 640

Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn Leu Gly  
645 650 655

Tyr

<210> 102  
<211> 478  
<212> PRT  
<213> Homo sapiens

<400> 102

Met Ala Pro Leu Arg Pro Leu Leu Ile Leu Ala Leu Leu Ala Trp Val  
1 5 10 15

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Ala Leu Ala Asp Gln Glu Ser Cys Lys Gly Arg Cys Thr Glu Gly Phe  
20 25 30

Asn Val Asp Lys Lys Cys Gln Cys Asp Glu Leu Cys Ser Tyr Tyr Gln  
35 40 45

Ser Cys Cys Thr Asp Tyr Thr Ala Glu Cys Lys Pro Gln Val Thr Arg  
50 55 60

Gly Asp Val Phe Thr Met Pro Glu Asp Glu Tyr Thr Val Tyr Asp Asp  
65 70 75 80

Gly Glu Glu Lys Asn Asn Ala Thr Val His Glu Gln Val Gly Gly Pro  
85 90 95

Ser Leu Thr Ser Asp Leu Gln Ala Gln Ser Lys Gly Asn Pro Glu Gln  
100 105 110

Thr Pro Val Leu Lys Pro Glu Glu Glu Ala Pro Ala Pro Glu Val Gly  
115 120 125

Ala Ser Lys Pro Glu Gly Ile Asp Ser Arg Pro Glu Thr Leu His Pro  
130 135 140

Gly Arg Pro Gln Pro Pro Ala Glu Glu Glu Leu Cys Ser Gly Lys Pro  
145 150 155 160

Phe Asp Ala Phe Thr Asp Leu Lys Asn Gly Ser Leu Phe Ala Phe Arg  
165 170 175

Gly Gln Tyr Cys Tyr Glu Leu Asp Glu Lys Ala Val Arg Pro Gly Tyr  
180 185 190

Pro Lys Leu Ile Arg Asp Val Trp Gly Ile Glu Gly Pro Ile Asp Ala  
195 200 205

Ala Phe Thr Arg Ile Asn Cys Gln Gly Lys Thr Tyr Leu Phe Lys Gly  
210 215 220

Ser Gln Tyr Trp Arg Phe Glu Asp Gly Val Leu Asp Pro Asp Tyr Pro  
225 230 235 240

Arg Asn Ile Ser Asp Gly Phe Asp Gly Ile Pro Asp Asn Val Asp Ala  
245 250 255

Ala Leu Ala Leu Pro Ala His Ser Tyr Ser Gly Arg Glu Arg Val Tyr  
260 265 270

Phe Phe Lys Gly Lys Gln Tyr Trp Glu Tyr Gln Phe Gln His Gln Pro  
275 280 285

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Ser Gln Glu Glu Cys Glu Gly Ser Ser Leu Ser Ala Val Phe Glu His  
290 295 300

Phe Ala Met Met Gln Arg Asp Ser Trp Glu Asp Ile Phe Glu Leu Leu  
305 310 315 320

Phe Trp Gly Arg Thr Ser Ala Gly Thr Arg Gln Pro Gln Phe Ile Ser  
325 330 335

Arg Asp Trp His Gly Val Pro Gly Gln Val Asp Ala Ala Met Ala Gly  
340 345 350

Arg Ile Tyr Ile Ser Gly Met Ala Pro Arg Pro Ser Leu Ala Lys Lys  
355 360 365

Gln Arg Phe Arg His Arg Asn Arg Lys Gly Tyr Arg Ser Gln Arg Gly  
370 375 380

His Ser Arg Gly Arg Asn Gln Asn Ser Arg Arg Pro Ser Arg Ala Thr  
385 390 395 400

Trp Leu Ser Leu Phe Ser Ser Glu Glu Ser Asn Leu Gly Ala Asn Asn  
405 410 415

Tyr Asp Asp Tyr Arg Met Asp Trp Leu Val Pro Ala Thr Cys Glu Pro  
420 425 430

Ile Gln Ser Val Phe Phe Phe Ser Gly Asp Lys Tyr Tyr Arg Val Asn  
435 440 445

Leu Arg Thr Arg Arg Val Asp Thr Val Asp Pro Pro Tyr Pro Arg Ser  
450 455 460

Ile Ala Gln Tyr Trp Leu Gly Cys Pro Ala Pro Gly His Leu  
465 470 475

<210> 103  
<211> 1247  
<212> PRT  
<213> Homo sapiens

<400> 103

Met Leu Ala Ser Ser Ser Arg Ile Arg Ala Ala Trp Thr Arg Ala Leu  
1 5 10 15

Leu Leu Pro Leu Leu Leu Ala Gly Pro Val Gly Cys Leu Ser Arg Gln  
20 25 30

Glu Leu Phe Pro Phe Gly Pro Gly Gln Gly Asp Leu Glu Leu Glu Asp  
35 40 45

Gly Asp Asp Phe Val Ser Pro Ala Leu Glu Leu Ser Gly Ala Leu Arg  
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50

55

60

Phe Tyr Asp Arg Ser Asp Ile Asp Ala Val Tyr Val Thr Thr Asn Gly  
65 70 75 80

Ile Ile Ala Thr Ser Glu Pro Pro Ala Lys Glu Ser His Pro Gly Leu  
85 90 95

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

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

Ser Ile Thr Gln Arg Ala Ala Glu Cys Val His Arg Gly Phe Pro Glu  
130 135 140

Ile Ser Phe Gln Pro Ser Ser Ala Val Val Val Thr Trp Glu Ser Val  
145 150 155 160

Ala Pro Tyr Gln Gly Pro Ser Arg Asp Pro Asp Gln Lys Gly Lys Arg  
165 170 175

Asn Thr Phe Gln Ala Val Leu Ala Ser Ser Asp Ser Ser Ser Tyr Ala  
180 185 190

Ile Phe Leu Tyr Pro Glu Asp Gly Leu Gln Phe His Thr Thr Phe Ser  
195 200 205

Lys Lys Glu Asn Asn Gln Val Pro Ala Val Val Ala Phe Ser Gln Gly  
210 215 220

Ser Val Gly Phe Leu Trp Lys Ser Asn Gly Ala Tyr Asn Ile Phe Ala  
225 230 235 240

Asn Asp Arg Glu Ser Val Glu Asn Leu Ala Lys Ser Ser Asn Ser Gly  
245 250 255

Gln Gln Gly Val Trp Val Phe Glu Ile Gly Ser Pro Ala Thr Thr Asn  
260 265 270

Gly Val Val Pro Ala Asp Val Ile Leu Gly Thr Glu Asp Gly Ala Glu  
275 280 285

Tyr Asp Asp Glu Asp Glu Asp Tyr Asp Leu Ala Thr Thr Arg Leu Gly  
290 295 300

Leu Glu Asp Val Gly Thr Thr Pro Phe Ser Tyr Lys Ala Leu Arg Arg  
305 310 315 320

Gly Gly Ala Asp Thr Tyr Ser Val Pro Ser Val Leu Ser Pro Arg Arg  
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325

330

335

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

Phe Gln Leu Ala Val Glu Thr Phe His Gln Gln His Pro Gln Val Ile  
355 360 365

Asp Val Asp Glu Val Glu Glu Thr Gly Val Val Phe Ser Tyr Asn Thr  
370 375 380

Asp Ser Arg Gln Thr Cys Ala Asn Asn Arg His Gln Cys Ser Val His  
385 390 395 400

Ala Glu Cys Arg Asp Tyr Ala Thr Gly Phe Cys Cys Ser Cys Val Ala  
405 410 415

Gly Tyr Thr Gly Asn Gly Arg Gln Cys Val Ala Glu Gly Ser Pro Gln  
420 425 430

Arg Val Asn Gly Lys Val Lys Gly Arg Ile Phe Val Gly Ser Ser Gln  
435 440 445

Val Pro Ile Val Phe Glu Asn Thr Asp Leu His Ser Tyr Val Val Met  
450 455 460

Asn His Gly Arg Ser Tyr Thr Ala Ile Ser Thr Ile Pro Glu Thr Val  
465 470 475 480

Gly Tyr Ser Leu Leu Pro Leu Ala Pro Val Gly Gly Ile Ile Gly Trp  
485 490 495

Met Phe Ala Val Glu Gln Asp Gly Phe Lys Asn Gly Phe Ser Ile Thr  
500 505 510

Gly Gly Glu Phe Thr Arg Gln Ala Glu Val Thr Phe Val Gly His Pro  
515 520 525

Gly Asn Leu Val Ile Lys Gln Arg Phe Ser Gly Ile Asp Glu His Gly  
530 535 540

His Leu Thr Ile Asp Thr Glu Leu Glu Gly Arg Val Pro Gln Ile Pro  
545 550 555 560

Phe Gly Ser Ser Val His Ile Glu Pro Tyr Thr Glu Leu Tyr His Tyr  
565 570 575

Ser Thr Ser Val Ile Thr Ser Ser Ser Thr Arg Glu Tyr Thr Val Thr  
580 585 590

Glu Pro Glu Arg Asp Gly Ala Ser Pro Ser Arg Ile Tyr Thr Tyr Gln

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595

600

605

Trp Arg Gln Thr Ile Thr Phe Gln Glu Cys Val His Asp Asp Ser Arg  
610 615 620

Pro Ala Leu Pro Ser Thr Gln Gln Leu Ser Val Asp Ser Val Phe Val  
625 630 635 640

Leu Tyr Asn Gln Glu Glu Lys Ile Leu Arg Tyr Ala Leu Ser Asn Ser  
645 650 655

Ile Gly Pro Val Arg Glu Gly Ser Pro Asp Ala Leu Gln Asn Pro Cys  
660 665 670

Tyr Ile Gly Thr His Gly Cys Asp Thr Asn Ala Ala Cys Arg Pro Gly  
675 680 685

Pro Arg Thr Gln Phe Thr Cys Glu Cys Ser Ile Gly Phe Arg Gly Asp  
690 695 700

Gly Arg Thr Cys Tyr Asp Ile Asp Glu Cys Ser Glu Gln Pro Ser Val  
705 710 715 720

Cys Gly Ser His Thr Ile Cys Asn Asn His Pro Gly Thr Phe Arg Cys  
725 730 735

Glu Cys Val Glu Gly Tyr Gln Phe Ser Asp Glu Gly Thr Cys Val Ala  
740 745 750

Val Val Asp Gln Arg Pro Ile Asn Tyr Cys Glu Thr Gly Leu His Asn  
755 760 765

Cys Asp Ile Pro Gln Arg Ala Gln Cys Ile Tyr Thr Gly Gly Ser Ser  
770 775 780

Tyr Thr Cys Ser Cys Leu Pro Gly Phe Ser Gly Asp Gly Gln Ala Cys  
785 790 795 800

Gln Asp Val Asp Glu Cys Gln Pro Ser Arg Cys His Pro Asp Ala Phe  
805 810 815

Cys Tyr Asn Thr Pro Gly Ser Phe Thr Cys Gln Cys Lys Pro Gly Tyr  
820 825 830

Gln Gly Asp Gly Phe Arg Cys Val Pro Gly Glu Val Glu Lys Thr Arg  
835 840 845

Cys Gln His Glu Arg Glu His Ile Leu Gly Ala Ala Gly Ala Thr Asp  
850 855 860

Pro Gln Arg Pro Ile Pro Pro Gly Leu Phe Val Pro Glu Cys Asp Ala

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865											870											875											880
His	Gly	His	Tyr	Ala	Pro	Thr	Gln	Cys	His	Gly	Ser	Thr	Gly	Tyr	Cys																		
				885					890					895																			
Trp	Cys	Val	Asp	Arg	Asp	Gly	Arg	Glu	Val	Glu	Gly	Thr	Arg	Thr	Arg																		
			900				905				910																						
Pro	Gly	Met	Thr	Pro	Pro	Cys	Leu	Ser	Thr	Val	Ala	Pro	Pro	Ile	His																		
		915					920					925																					
Gln	Gly	Pro	Ala	Val	Pro	Thr	Ala	Val	Ile	Pro	Leu	Pro	Pro	Gly	Thr																		
		930				935				940																							
His	Leu	Leu	Phe	Ala	Gln	Thr	Gly	Lys	Ile	Glu	Arg	Leu	Pro	Leu	Glu																		
		945				950				955																							
Gly	Asn	Thr	Met	Arg	Lys	Thr	Glu	Ala	Lys	Ala	Phe	Leu	His	Val	Pro																		
			965				970																										
Ala	Lys	Val	Ile	Ile	Gly	Leu	Ala	Phe	Asp	Cys	Val	Asp	Lys	Met	Val																		
			980				985				990																						
Tyr	Trp	Thr	Asp	Ile	Thr	Glu	Pro	Ser	Ile	Gly	Arg	Ala	Ser	Leu	His																		
		995				1000																											
Gly	Gly	Glu	Pro	Thr	Thr	Ile	Ile	Arg	Gln	Asp	Leu	Gly	Ser	Pro																			
		1010				1015				1020																							
Glu	Gly	Ile	Ala	Val	Asp	His	Leu	Gly	Arg	Asn	Ile	Phe	Trp	Thr																			
		1025				1030				1035																							
Asp	Ser	Asn	Leu	Asp	Arg	Ile	Glu	Val	Ala	Lys	Leu	Asp	Gly	Thr																			
		1040				1045				1050																							
Gln	Arg	Arg	Val	Leu	Phe	Glu	Thr	Asp	Leu	Val	Asn	Pro	Arg	Gly																			
		1055				1060				1065																							
Ile	Val	Thr	Asp	Ser	Val	Arg	Gly	Asn	Leu	Tyr	Trp	Thr	Asp	Trp																			
		1070				1075				1080																							
Asn	Arg	Asp	Asn	Pro	Lys	Ile	Glu	Thr	Ser	Tyr	Met	Asp	Gly	Thr																			
		1085				1090				1095																							
Asn	Arg	Arg	Ile	Leu	Val	Gln	Asp	Asp	Leu	Gly	Leu	Pro	Asn	Gly																			
		1100				1105				1110																							
Leu	Thr	Phe	Asp	Ala	Phe	Ser	Ser	Gln	Leu	Cys	Trp	Val	Asp	Ala																			
		1115				1120				1125																							
Gly	Thr	Asn	Arg	Ala	Glu	Cys	Leu	Asn	Pro	Ser	Gln	Pro	Ser	Arg																			



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1130

1135

1140

Arg Lys Ala Leu Glu Gly Leu Gln Tyr Pro Phe Ala Val Thr Ser  
1145 1150 1155

Tyr Gly Lys Asn Leu Tyr Phe Thr Asp Trp Lys Met Asn Ser Val  
1160 1165 1170

Val Ala Leu Asp Leu Ala Ile Ser Lys Glu Thr Asp Ala Phe Gln  
1175 1180 1185

Pro His Lys Gln Thr Arg Leu Tyr Gly Ile Thr Thr Ala Leu Ser  
1190 1195 1200

Gln Cys Pro Gln Gly His Asn Tyr Cys Ser Val Asn Asn Gly Gly  
1205 1210 1215

Cys Thr His Leu Cys Leu Ala Thr Pro Gly Ser Arg Thr Cys Arg  
1220 1225 1230

Cys Pro Asp Asn Thr Leu Gly Val Asp Cys Ile Glu Gln Lys  
1235 1240 1245

<210> 104  
<211> 3075  
<212> PRT  
<213> Homo sapiens  
<400> 104

Met Arg Gly Gly Val Leu Leu Val Leu Leu Leu Cys Val Ala Ala Gln  
1 5 10 15

Cys Arg Gln Arg Gly Leu Phe Pro Ala Ile Leu Asn Leu Ala Ser Asn  
20 25 30

Ala His Ile Ser Thr Asn Ala Thr Cys Gly Glu Lys Gly Pro Glu Met  
35 40 45

Phe Cys Lys Leu Val Glu His Val Pro Gly Arg Pro Val Arg Asn Pro  
50 55 60

Gln Cys Arg Ile Cys Asp Gly Asn Ser Ala Asn Pro Arg Glu Arg His  
65 70 75 80

Pro Ile Ser His Ala Ile Asp Gly Thr Asn Asn Trp Trp Gln Ser Pro  
85 90 95

Ser Ile Gln Asn Gly Arg Glu Tyr His Trp Val Thr Ile Thr Leu Asp  
100 105 110

Leu Arg Gln Val Phe Gln Val Ala Tyr Val Ile Ile Lys Ala Ala Asn  
115 120 125

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Ala Pro Arg Pro Gly Asn Trp Ile Leu Glu Arg Ser Leu Asp Gly Thr  
 130 135 140  
 Thr Phe Ser Pro Trp Gln Tyr Tyr Ala Val Ser Asp Ser Glu Cys Leu  
 145 150 155 160  
 Ser Arg Tyr Asn Ile Thr Pro Arg Arg Gly Pro Pro Thr Tyr Arg Ala  
 165 170 175  
 Asp Asp Glu Val Ile Cys Thr Ser Tyr Tyr Ser Arg Leu Val Pro Leu  
 180 185 190  
 Glu His Gly Glu Ile His Thr Ser Leu Ile Asn Gly Arg Pro Ser Ala  
 195 200 205  
 Asp Asp Leu Ser Pro Lys Leu Leu Glu Phe Thr Ser Ala Arg Tyr Ile  
 210 215 220  
 Arg Leu Arg Leu Gln Arg Ile Arg Thr Leu Asn Ala Asp Leu Met Thr  
 225 230 235 240  
 Leu Ser His Arg Glu Pro Lys Glu Leu Asp Pro Ile Val Thr Arg Arg  
 245 250 255  
 Tyr Tyr Tyr Ser Ile Lys Asp Ile Ser Val Gly Gly Met Cys Ile Cys  
 260 265 270  
 Tyr Gly His Ala Ser Ser Cys Pro Trp Asp Glu Thr Thr Lys Lys Leu  
 275 280 285  
 Gln Cys Gln Cys Glu His Asn Thr Cys Gly Glu Ser Cys Asn Arg Cys  
 290 295 300  
 Cys Pro Gly Tyr His Gln Gln Pro Trp Arg Pro Gly Thr Val Ser Ser  
 305 310 315 320  
 Gly Asn Thr Cys Glu Ala Cys Asn Cys His Asn Lys Ala Lys Asp Cys  
 325 330 335  
 Tyr Tyr Asp Glu Ser Val Ala Lys Gln Lys Lys Ser Leu Asn Thr Ala  
 340 345 350  
 Gly Gln Phe Arg Gly Gly Gly Val Cys Ile Asn Cys Leu Gln Asn Thr  
 355 360 365  
 Met Gly Ile Asn Cys Glu Thr Cys Ile Asp Gly Tyr Tyr Arg Pro His  
 370 375 380  
 Lys Val Ser Pro Tyr Glu Asp Glu Pro Cys Arg Pro Cys Asn Cys Asp  
 385 390 395 400

# FAB-008PC-SequenceListing

Pro Val Gly Ser Leu Ser Ser Val Cys Ile Lys Asp Asp Leu His Ser  
 405 410 415  
 Asp Leu His Asn Gly Lys Gln Pro Gly Gln Cys Pro Cys Lys Glu Gly  
 420 425 430  
 Tyr Thr Gly Glu Lys Cys Asp Arg Cys Gln Leu Gly Tyr Lys Asp Tyr  
 435 440 445  
 Pro Thr Cys Val Ser Cys Gly Cys Asn Pro Val Gly Ser Ala Ser Asp  
 450 455 460  
 Glu Pro Cys Thr Gly Pro Cys Val Cys Lys Glu Asn Val Glu Gly Lys  
 465 470 475 480  
 Ala Cys Asp Arg Cys Lys Pro Gly Phe Tyr Asn Leu Lys Glu Lys Asn  
 485 490 495  
 Pro Arg Gly Cys Ser Glu Cys Phe Cys Phe Gly Val Ser Asp Val Cys  
 500 505 510  
 Ser Ser Leu Ser Trp Pro Val Gly Gln Val Asn Ser Met Ser Gly Trp  
 515 520 525  
 Leu Val Thr Asp Leu Ile Ser Pro Arg Lys Ile Pro Ser Gln Gln Asp  
 530 535 540  
 Ala Leu Gly Gly Arg His Gln Val Ser Ile Asn Asn Thr Ala Val Met  
 545 550 555 560  
 Gln Arg Leu Ala Pro Lys Tyr Tyr Trp Ala Ala Pro Glu Ala Tyr Leu  
 565 570 575  
 Gly Asn Lys Leu Thr Ala Phe Gly Gly Phe Leu Lys Tyr Thr Val Ser  
 580 585 590  
 Tyr Asp Ile Pro Val Glu Thr Val Asp Ser Asn Leu Met Ser His Ala  
 595 600 605  
 Asp Val Ile Ile Lys Gly Asn Gly Leu Thr Leu Ser Thr Gln Ala Glu  
 610 615 620  
 Gly Leu Ser Leu Gln Pro Tyr Glu Glu Tyr Leu Asn Val Val Arg Leu  
 625 630 635 640  
 Val Pro Glu Asn Phe Gln Asp Phe His Ser Lys Arg Gln Ile Asp Arg  
 645 650 655  
 Asp Gln Leu Met Thr Val Leu Ala Asn Val Thr His Leu Leu Ile Arg  
 660 665 670

# FAB-008PC-SequenceListing

Ala Asn Tyr Asn Ser Ala Lys Met Ala Leu Tyr Arg Leu Glu Ser Val  
 675 680 685  
 Ser Leu Asp Ile Ala Ser Ser Asn Ala Ile Asp Leu Val Val Ala Ala  
 690 695 700  
 Asp Val Glu His Cys Glu Cys Pro Gln Gly Tyr Thr Gly Thr Ser Cys  
 705 710 715 720  
 Glu Ser Cys Leu Ser Gly Tyr Tyr Arg Val Asp Gly Ile Leu Phe Gly  
 725 730 735  
 Gly Ile Cys Gln Pro Cys Glu Cys His Gly His Ala Ala Glu Cys Asn  
 740 745 750  
 Val His Gly Val Cys Ile Ala Cys Ala His Asn Thr Thr Gly Val His  
 755 760 765  
 Cys Glu Gln Cys Leu Pro Gly Phe Tyr Gly Glu Pro Ser Arg Gly Thr  
 770 775 780  
 Pro Gly Asp Cys Gln Pro Cys Ala Cys Pro Leu Thr Ile Ala Ser Asn  
 785 790 795 800  
 Asn Phe Ser Pro Thr Cys His Leu Asn Asp Gly Asp Glu Val Val Cys  
 805 810 815  
 Asp Trp Cys Ala Pro Gly Tyr Ser Gly Ala Trp Cys Glu Arg Cys Ala  
 820 825 830  
 Asp Gly Tyr Tyr Gly Asn Pro Thr Val Pro Gly Glu Ser Cys Val Pro  
 835 840 845  
 Cys Asp Cys Ser Gly Asn Val Asp Pro Ser Glu Ala Gly His Cys Asp  
 850 855 860  
 Ser Val Thr Gly Glu Cys Leu Lys Cys Leu Gly Asn Thr Asp Gly Ala  
 865 870 875 880  
 His Cys Glu Arg Cys Ala Asp Gly Phe Tyr Gly Asp Ala Val Thr Ala  
 885 890 895  
 Lys Asn Cys Arg Ala Cys Glu Cys His Val Lys Gly Ser His Ser Ala  
 900 905 910  
 Val Cys His Leu Glu Thr Gly Leu Cys Asp Cys Lys Pro Asn Val Thr  
 915 920 925  
 Gly Gln Gln Cys Asp Gln Cys Leu His Gly Tyr Tyr Gly Leu Asp Ser  
 930 935 940

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Gly His Gly Cys Arg Pro Cys Asn Cys Ser Val Ala Gly Ser Val Ser  
 945 950 955 960  
 Asp Gly Cys Thr Asp Glu Gly Gln Cys His Cys Val Pro Gly Val Ala  
 965 970 975  
 Gly Lys Arg Cys Asp Arg Cys Ala His Gly Phe Tyr Ala Tyr Gln Asp  
 980 985 990  
 Gly Ser Cys Thr Pro Cys Asp Cys Pro His Thr Gln Asn Thr Cys Asp  
 995 1000 1005  
 Pro Glu Thr Gly Glu Cys Val Cys Pro Pro His Thr Gln Gly Val  
 1010 1015 1020  
 Lys Cys Glu Glu Cys Glu Asp Gly His Trp Gly Tyr Asp Ala Glu  
 1025 1030 1035  
 Val Gly Cys Gln Ala Cys Asn Cys Ser Leu Val Gly Ser Thr His  
 1040 1045 1050  
 His Arg Cys Asp Val Val Thr Gly His Cys Gln Cys Lys Ser Lys  
 1055 1060 1065  
 Phe Gly Gly Arg Ala Cys Asp Gln Cys Ser Leu Gly Tyr Arg Asp  
 1070 1075 1080  
 Phe Pro Asp Cys Val Pro Cys Asp Cys Asp Leu Arg Gly Thr Ser  
 1085 1090 1095  
 Gly Asp Ala Cys Asn Leu Glu Gln Gly Leu Cys Gly Cys Val Glu  
 1100 1105 1110  
 Glu Thr Gly Ala Cys Pro Cys Lys Glu Asn Val Phe Gly Pro Gln  
 1115 1120 1125  
 Cys Asn Glu Cys Arg Glu Gly Thr Phe Ala Leu Arg Ala Asp Asn  
 1130 1135 1140  
 Pro Leu Gly Cys Ser Pro Cys Phe Cys Ser Gly Leu Ser His Leu  
 1145 1150 1155  
 Cys Ser Glu Leu Glu Asp Tyr Val Arg Thr Pro Val Thr Leu Gly  
 1160 1165 1170  
 Ser Asp Gln Pro Leu Leu Arg Val Val Ser Gln Ser Asn Leu Arg  
 1175 1180 1185  
 Gly Thr Thr Glu Gly Val Tyr Tyr Gln Ala Pro Asp Phe Leu Leu  
 1190 1195 1200

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Asp	Ala	Ala	Thr	Val	Arg	Gln	His	Ile	Arg	Ala	Glu	Pro	Phe	Tyr
	1205					1210					1215			
Trp	Arg	Leu	Pro	Gln	Gln	Phe	Gln	Gly	Asp	Gln	Leu	Met	Ala	Tyr
	1220					1225					1230			
Gly	Gly	Lys	Leu	Lys	Tyr	Ser	Val	Ala	Phe	Tyr	Ser	Leu	Asp	Gly
	1235					1240					1245			
Val	Gly	Thr	Ser	Asn	Phe	Glu	Pro	Gln	Val	Leu	Ile	Lys	Gly	Gly
	1250					1255					1260			
Arg	Ile	Arg	Lys	Gln	Val	Ile	Tyr	Met	Asp	Ala	Pro	Ala	Pro	Glu
	1265					1270					1275			
Asn	Gly	Val	Arg	Gln	Glu	Gln	Glu	Val	Ala	Met	Arg	Glu	Asn	Phe
	1280					1285					1290			
Trp	Lys	Tyr	Phe	Asn	Ser	Val	Ser	Glu	Lys	Pro	Val	Thr	Arg	Glu
	1295					1300					1305			
Asp	Phe	Met	Ser	Val	Leu	Ser	Asp	Ile	Glu	Tyr	Ile	Leu	Ile	Lys
	1310					1315					1320			
Ala	Ser	Tyr	Gly	Gln	Gly	Leu	Gln	Gln	Ser	Arg	Ile	Ser	Asp	Ile
	1325					1330					1335			
Ser	Met	Glu	Val	Gly	Arg	Lys	Ala	Glu	Lys	Leu	His	Pro	Glu	Glu
	1340					1345					1350			
Glu	Val	Ala	Ser	Leu	Leu	Glu	Asn	Cys	Val	Cys	Pro	Pro	Gly	Thr
	1355					1360					1365			
Val	Gly	Phe	Ser	Cys	Gln	Asp	Cys	Ala	Pro	Gly	Tyr	His	Arg	Gly
	1370					1375					1380			
Lys	Leu	Pro	Ala	Gly	Ser	Asp	Arg	Gly	Pro	Arg	Pro	Leu	Val	Ala
	1385					1390					1395			
Pro	Cys	Val	Pro	Cys	Ser	Cys	Asn	Asn	His	Ser	Asp	Thr	Cys	Asp
	1400					1405					1410			
Pro	Asn	Thr	Gly	Lys	Cys	Leu	Asn	Cys	Gly	Asp	Asn	Thr	Ala	Gly
	1415					1420					1425			
Asp	His	Cys	Asp	Val	Cys	Thr	Ser	Gly	Tyr	Tyr	Gly	Lys	Val	Thr
	1430					1435					1440			
Gly	Ser	Ala	Ser	Asp	Cys	Ala	Leu	Cys	Ala	Cys	Pro	His	Ser	Pro
	1445					1450					1455			

# FAB-008PC-SequenceListing

Pro	Ala	Ser	Phe	Ser	Pro	Thr	Cys	Val	Leu	Glu	Gly	Asp	His	Asp
	1460					1465					1470			
Phe	Arg	Cys	Asp	Ala	Cys	Leu	Leu	Gly	Tyr	Glu	Gly	Lys	His	Cys
	1475					1480					1485			
Glu	Arg	Cys	Ser	Ser	Ser	Tyr	Tyr	Gly	Asn	Pro	Gln	Thr	Pro	Gly
	1490					1495					1500			
Gly	Ser	Cys	Gln	Lys	Cys	Asp	Cys	Asn	Pro	His	Gly	Ser	Val	His
	1505					1510					1515			
Gly	Asp	Cys	Asp	Arg	Thr	Ser	Gly	Gln	Cys	Val	Cys	Arg	Leu	Gly
	1520					1525					1530			
Ala	Ser	Gly	Leu	Arg	Cys	Asp	Glu	Cys	Glu	Pro	Arg	His	Ile	Leu
	1535					1540					1545			
Met	Glu	Thr	Asp	Cys	Val	Ser	Cys	Asp	Asp	Glu	Cys	Val	Gly	Val
	1550					1555					1560			
Leu	Leu	Asn	Asp	Leu	Asp	Glu	Ile	Gly	Asp	Ala	Val	Leu	Ser	Leu
	1565					1570					1575			
Asn	Leu	Thr	Gly	Ile	Ile	Pro	Val	Pro	Tyr	Gly	Ile	Leu	Ser	Asn
	1580					1585					1590			
Leu	Glu	Asn	Thr	Thr	Lys	Tyr	Leu	Gln	Glu	Ser	Leu	Leu	Lys	Glu
	1595					1600					1605			
Asn	Met	Gln	Lys	Asp	Leu	Gly	Lys	Ile	Lys	Leu	Glu	Gly	Val	Ala
	1610					1615					1620			
Glu	Glu	Thr	Asp	Asn	Leu	Gln	Lys	Lys	Leu	Thr	Arg	Met	Leu	Ala
	1625					1630					1635			
Ser	Thr	Gln	Lys	Val	Asn	Arg	Ala	Thr	Glu	Arg	Ile	Phe	Lys	Glu
	1640					1645					1650			
Ser	Gln	Asp	Leu	Ala	Ile	Ala	Ile	Glu	Arg	Leu	Gln	Met	Ser	Ile
	1655					1660					1665			
Thr	Glu	Ile	Met	Glu	Lys	Thr	Thr	Leu	Asn	Gln	Thr	Leu	Asp	Glu
	1670					1675					1680			
Asp	Phe	Leu	Leu	Pro	Asn	Ser	Thr	Leu	Gln	Asn	Met	Gln	Gln	Asn
	1685					1690					1695			
Gly	Thr	Ser	Leu	Leu	Glu	Ile	Met	Gln	Ile	Arg	Asp	Phe	Thr	Gln
	1700					1705					1710			

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Leu	His	Gln	Asn	Ala	Thr	Leu	Glu	Leu	Lys	Ala	Ala	Glu	Asp	Leu
	1715					1720					1725			
Leu	Ser	Gln	Ile	Gln	Glu	Asn	Tyr	Gln	Lys	Pro	Leu	Glu	Glu	Leu
	1730					1735					1740			
Glu	Val	Leu	Lys	Glu	Ala	Ala	Ser	His	Val	Leu	Ser	Lys	His	Asn
	1745					1750					1755			
Asn	Glu	Leu	Lys	Ala	Ala	Glu	Ala	Leu	Val	Arg	Glu	Ala	Glu	Ala
	1760					1765					1770			
Lys	Met	Gln	Glu	Ser	Asn	His	Leu	Leu	Leu	Met	Val	Asn	Ala	Asn
	1775					1780					1785			
Leu	Arg	Glu	Phe	Ser	Asp	Lys	Lys	Leu	His	Val	Gln	Glu	Glu	Gln
	1790					1795					1800			
Asn	Leu	Thr	Ser	Glu	Leu	Ile	Val	Gln	Gly	Arg	Gly	Leu	Ile	Asp
	1805					1810					1815			
Ala	Ala	Ala	Ala	Gln	Thr	Asp	Ala	Val	Gln	Asp	Ala	Leu	Glu	His
	1820					1825					1830			
Leu	Glu	Asp	His	Gln	Asp	Lys	Leu	Leu	Leu	Trp	Ser	Ala	Lys	Ile
	1835					1840					1845			
Arg	His	His	Ile	Asp	Asp	Leu	Val	Met	His	Met	Ser	Gln	Arg	Asn
	1850					1855					1860			
Ala	Val	Asp	Leu	Val	Tyr	Arg	Ala	Glu	Asp	His	Ala	Ala	Glu	Phe
	1865					1870					1875			
Gln	Arg	Leu	Ala	Asp	Val	Leu	Tyr	Ser	Gly	Leu	Glu	Asn	Ile	Arg
	1880					1885					1890			
Asn	Val	Ser	Leu	Asn	Ala	Thr	Ser	Ala	Ala	Tyr	Val	His	Tyr	Asn
	1895					1900					1905			
Ile	Gln	Ser	Leu	Ile	Glu	Glu	Ser	Glu	Glu	Leu	Ala	Arg	Asp	Ala
	1910					1915					1920			
His	Arg	Thr	Val	Thr	Glu	Thr	Ser	Leu	Leu	Ser	Glu	Ser	Leu	Val
	1925					1930					1935			
Ser	Asn	Gly	Lys	Ala	Ala	Val	Gln	Arg	Ser	Ser	Arg	Phe	Leu	Lys
	1940					1945					1950			
Glu	Gly	Asn	Asn	Leu	Ser	Arg	Lys	Leu	Pro	Gly	Ile	Ala	Leu	Glu
	1955					1960					1965			



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Leu	Ser	Glu	Leu	Arg	Asn	Lys	Thr	Asn	Arg	Phe	Gln	Glu	Asn	Ala
	1970					1975					1980			
Val	Glu	Ile	Thr	Arg	Gln	Thr	Asn	Glu	Ser	Leu	Leu	Ile	Leu	Arg
	1985					1990					1995			
Ala	Ile	Pro	Lys	Gly	Ile	Arg	Asp	Lys	Gly	Ala	Lys	Thr	Lys	Glu
	2000					2005					2010			
Leu	Ala	Thr	Ser	Ala	Ser	Gln	Ser	Ala	Val	Ser	Thr	Leu	Arg	Asp
	2015					2020					2025			
Val	Ala	Gly	Leu	Ser	Gln	Glu	Leu	Leu	Asn	Thr	Ser	Ala	Ser	Leu
	2030					2035					2040			
Ser	Arg	Val	Asn	Thr	Thr	Leu	Arg	Glu	Thr	His	Gln	Leu	Leu	Gln
	2045					2050					2055			
Asp	Ser	Thr	Met	Ala	Thr	Leu	Leu	Ala	Gly	Arg	Lys	Val	Lys	Asp
	2060					2065					2070			
Val	Glu	Ile	Gln	Ala	Asn	Leu	Leu	Phe	Asp	Arg	Leu	Lys	Pro	Leu
	2075					2080					2085			
Lys	Met	Leu	Glu	Glu	Asn	Leu	Ser	Arg	Asn	Leu	Ser	Glu	Ile	Lys
	2090					2095					2100			
Leu	Leu	Ile	Ser	Gln	Ala	Arg	Lys	Gln	Ala	Ala	Ser	Ile	Lys	Val
	2105					2110					2115			
Ala	Val	Ser	Ala	Asp	Arg	Asp	Cys	Ile	Arg	Ala	Tyr	Gln	Pro	Gln
	2120					2125					2130			
Ile	Ser	Ser	Thr	Asn	Tyr	Asn	Thr	Leu	Thr	Leu	Asn	Val	Lys	Thr
	2135					2140					2145			
Gln	Glu	Pro	Asp	Asn	Leu	Leu	Phe	Tyr	Leu	Gly	Ser	Ser	Thr	Ala
	2150					2155					2160			
Ser	Asp	Phe	Leu	Ala	Val	Glu	Met	Arg	Arg	Gly	Arg	Val	Ala	Phe
	2165					2170					2175			
Leu	Trp	Asp	Leu	Gly	Ser	Gly	Ser	Thr	Arg	Leu	Glu	Phe	Pro	Asp
	2180					2185					2190			
Phe	Pro	Ile	Asp	Asp	Asn	Arg	Trp	His	Ser	Ile	His	Val	Ala	Arg
	2195					2200					2205			
Phe	Gly	Asn	Ile	Gly	Ser	Leu	Ser	Val	Lys	Glu	Met	Ser	Ser	Asn
	2210					2215					2220			

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Gln	Lys	Ser	Pro	Thr	Lys	Thr	Ser	Lys	Ser	Pro	Gly	Thr	Ala	Asn
	2225					2230					2235			
Val	Leu	Asp	Val	Asn	Asn	Ser	Thr	Leu	Met	Phe	Val	Gly	Gly	Leu
	2240					2245					2250			
Gly	Gly	Gln	Ile	Lys	Lys	Ser	Pro	Ala	Val	Lys	Val	Thr	His	Phe
	2255					2260					2265			
Lys	Gly	Cys	Leu	Gly	Glu	Ala	Phe	Leu	Asn	Gly	Lys	Ser	Ile	Gly
	2270					2275					2280			
Leu	Trp	Asn	Tyr	Ile	Glu	Arg	Glu	Gly	Lys	Cys	Arg	Gly	Cys	Phe
	2285					2290					2295			
Gly	Ser	Ser	Gln	Asn	Glu	Asp	Pro	Ser	Phe	His	Phe	Asp	Gly	Ser
	2300					2305					2310			
Gly	Tyr	Ser	Val	Val	Glu	Lys	Ser	Leu	Pro	Ala	Thr	Val	Thr	Gln
	2315					2320					2325			
Ile	Ile	Met	Leu	Phe	Asn	Thr	Phe	Ser	Pro	Asn	Gly	Leu	Leu	Leu
	2330					2335					2340			
Tyr	Leu	Gly	Ser	Tyr	Gly	Thr	Lys	Asp	Phe	Leu	Ser	Ile	Glu	Leu
	2345					2350					2355			
Phe	Arg	Gly	Arg	Val	Lys	Val	Met	Thr	Asp	Leu	Gly	Ser	Gly	Pro
	2360					2365					2370			
Ile	Thr	Leu	Leu	Thr	Asp	Arg	Arg	Tyr	Asn	Asn	Gly	Thr	Trp	Tyr
	2375					2380					2385			
Lys	Ile	Ala	Phe	Gln	Arg	Asn	Arg	Lys	Gln	Gly	Val	Leu	Ala	Val
	2390					2395					2400			
Ile	Asp	Ala	Tyr	Asn	Thr	Ser	Asn	Lys	Glu	Thr	Lys	Gln	Gly	Glu
	2405					2410					2415			
Thr	Pro	Gly	Ala	Ser	Ser	Asp	Leu	Asn	Arg	Leu	Asp	Lys	Asp	Pro
	2420					2425					2430			
Ile	Tyr	Val	Gly	Gly	Leu	Pro	Arg	Ser	Arg	Val	Val	Arg	Arg	Gly
	2435					2440					2445			
Val	Thr	Thr	Lys	Ser	Phe	Val	Gly	Cys	Ile	Lys	Asn	Leu	Glu	Ile
	2450					2455					2460			
Ser	Arg	Ser	Thr	Phe	Asp	Leu	Leu	Arg	Asn	Ser	Tyr	Gly	Val	Arg
	2465					2470					2475			

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Lys	Gly	Cys	Leu	Leu	Glu	Pro	Ile	Arg	Ser	Val	Ser	Phe	Leu	Lys
	2480					2485					2490			
Gly	Gly	Tyr	Ile	Glu	Leu	Pro	Pro	Lys	Ser	Leu	Ser	Pro	Glu	Ser
	2495					2500					2505			
Glu	Trp	Leu	Val	Thr	Phe	Ala	Thr	Thr	Asn	Ser	Ser	Gly	Ile	Ile
	2510					2515					2520			
Leu	Ala	Ala	Leu	Gly	Gly	Asp	Val	Glu	Lys	Arg	Gly	Asp	Arg	Glu
	2525					2530					2535			
Glu	Ala	His	Val	Pro	Phe	Phe	Ser	Val	Met	Leu	Ile	Gly	Gly	Asn
	2540					2545					2550			
Ile	Glu	Val	His	Val	Asn	Pro	Gly	Asp	Gly	Thr	Gly	Leu	Arg	Lys
	2555					2560					2565			
Ala	Leu	Leu	His	Ala	Pro	Thr	Gly	Thr	Cys	Ser	Asp	Gly	Gln	Ala
	2570					2575					2580			
His	Ser	Ile	Ser	Leu	Val	Arg	Asn	Arg	Arg	Ile	Ile	Thr	Val	Gln
	2585					2590					2595			
Leu	Asp	Glu	Asn	Asn	Pro	Val	Glu	Met	Lys	Leu	Gly	Thr	Leu	Val
	2600					2605					2610			
Glu	Ser	Arg	Thr	Ile	Asn	Val	Ser	Asn	Leu	Tyr	Val	Gly	Gly	Ile
	2615					2620					2625			
Pro	Glu	Gly	Glu	Gly	Thr	Ser	Leu	Leu	Thr	Met	Arg	Arg	Ser	Phe
	2630					2635					2640			
His	Gly	Cys	Ile	Lys	Asn	Leu	Ile	Phe	Asn	Leu	Glu	Leu	Leu	Asp
	2645					2650					2655			
Phe	Asn	Ser	Ala	Val	Gly	His	Glu	Gln	Val	Asp	Leu	Asp	Thr	Cys
	2660					2665					2670			
Trp	Leu	Ser	Glu	Arg	Pro	Lys	Leu	Ala	Pro	Asp	Ala	Glu	Asp	Ser
	2675					2680					2685			
Lys	Leu	Leu	Pro	Glu	Pro	Arg	Ala	Phe	Pro	Glu	Gln	Cys	Val	Val
	2690					2695					2700			
Asp	Ala	Ala	Leu	Glu	Tyr	Val	Pro	Gly	Ala	His	Gln	Phe	Gly	Leu
	2705					2710					2715			
Thr	Gln	Asn	Ser	His	Phe	Ile	Leu	Pro	Phe	Asn	Gln	Ser	Ala	Val
	2720					2725					2730			

# FAB-008PC-SequenceListing

Arg	Lys	Lys	Leu	Ser	Val	Glu	Leu	Ser	Ile	Arg	Thr	Phe	Ala	Ser
	2735					2740					2745			
Ser	Gly	Leu	Ile	Tyr	Tyr	Met	Ala	His	Gln	Asn	Gln	Ala	Asp	Tyr
	2750					2755					2760			
Ala	Val	Leu	Gln	Leu	His	Gly	Gly	Arg	Leu	His	Phe	Met	Phe	Asp
	2765					2770					2775			
Leu	Gly	Lys	Gly	Arg	Thr	Lys	Val	Ser	His	Pro	Ala	Leu	Leu	Ser
	2780					2785					2790			
Asp	Gly	Lys	Trp	His	Thr	Val	Lys	Thr	Asp	Tyr	Val	Lys	Arg	Lys
	2795					2800					2805			
Gly	Phe	Ile	Thr	Val	Asp	Gly	Arg	Glu	Ser	Pro	Met	Val	Thr	Val
	2810					2815					2820			
Val	Gly	Asp	Gly	Thr	Met	Leu	Asp	Val	Glu	Gly	Leu	Phe	Tyr	Leu
	2825					2830					2835			
Gly	Gly	Leu	Pro	Ser	Gln	Tyr	Gln	Ala	Arg	Lys	Ile	Gly	Asn	Ile
	2840					2845					2850			
Thr	His	Ser	Ile	Pro	Ala	Cys	Ile	Gly	Asp	Val	Thr	Val	Asn	Ser
	2855					2860					2865			
Lys	Gln	Leu	Asp	Lys	Asp	Ser	Pro	Val	Ser	Ala	Phe	Thr	Val	Asn
	2870					2875					2880			
Arg	Cys	Tyr	Ala	Val	Ala	Gln	Glu	Gly	Thr	Tyr	Phe	Asp	Gly	Ser
	2885					2890					2895			
Gly	Tyr	Ala	Ala	Leu	Val	Lys	Glu	Gly	Tyr	Lys	Val	Gln	Ser	Asp
	2900					2905					2910			
Val	Asn	Ile	Thr	Leu	Glu	Phe	Arg	Thr	Ser	Ser	Gln	Asn	Gly	Val
	2915					2920					2925			
Leu	Leu	Gly	Ile	Ser	Thr	Ala	Lys	Val	Asp	Ala	Ile	Gly	Leu	Glu
	2930					2935					2940			
Leu	Val	Asp	Gly	Lys	Val	Leu	Phe	His	Val	Asn	Asn	Gly	Ala	Gly
	2945					2950					2955			
Arg	Ile	Thr	Ala	Ala	Tyr	Glu	Pro	Lys	Thr	Ala	Thr	Val	Leu	Cys
	2960					2965					2970			
Asp	Gly	Lys	Trp	His	Thr	Leu	Gln	Ala	Asn	Lys	Ser	Lys	His	Arg
	2975					2980					2985			

FAB-008PC-SequenceListing

Ile Thr Leu Ile Val Asp Gly Asn Ala Val Gly Ala Glu Ser Pro  
2990 2995 3000

His Thr Gln Ser Thr Ser Val Asp Thr Asn Asn Pro Ile Tyr Val  
3005 3010 3015

Gly Gly Tyr Pro Ala Gly Val Lys Gln Lys Cys Leu Arg Ser Gln  
3020 3025 3030

Thr Ser Phe Arg Gly Cys Leu Arg Lys Leu Ala Leu Ile Lys Ser  
3035 3040 3045

Pro Gln Val Gln Ser Phe Asp Phe Ser Arg Ala Phe Glu Leu His  
3050 3055 3060

Gly Val Phe Leu His Ser Cys Pro Gly Thr Glu Ser  
3065 3070 3075

<210> 105  
<211> 158  
<212> PRT  
<213> Homo sapiens

<400> 105

Met Gly Lys Ile Ser Ser Leu Pro Thr Gln Leu Phe Lys Cys Cys Phe  
1 5 10 15

Cys Asp Phe Leu Lys Val Lys Met His Thr Met Ser Ser Ser His Leu  
20 25 30

Phe Tyr Leu Ala Leu Cys Leu Leu Thr Phe Thr Ser Ser Ala Thr Ala  
35 40 45

Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe  
50 55 60

Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly  
65 70 75 80

Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys  
85 90 95

Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Leu  
100 105 110

Lys Pro Ala Lys Ser Ala Arg Ser Val Arg Ala Gln Arg His Thr Asp  
115 120 125

Met Pro Lys Thr Gln Lys Tyr Gln Pro Pro Ser Thr Asn Lys Asn Thr  
130 135 140

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Lys Ser Gln Arg Arg Lys Gly Ser Thr Phe Glu Glu Arg Lys  
145 150 155

<210> 106  
<211> 155  
<212> PRT  
<213> Homo sapiens

<400> 106

Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe  
1 5 10 15

Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser  
20 25 30

Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly  
35 40 45

Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu  
50 55 60

Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu  
65 70 75 80

Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu  
85 90 95

Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr  
100 105 110

Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys  
115 120 125

Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala  
130 135 140

Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp  
145 150 155

<210> 107  
<211> 288  
<212> PRT  
<213> Homo sapiens

<400> 107

Met Val Gly Val Gly Gly Gly Asp Val Glu Asp Val Thr Pro Arg Pro  
1 5 10 15

Gly Gly Cys Gln Ile Ser Gly Arg Gly Ala Arg Gly Cys Asn Gly Ile  
20 25 30

Pro Gly Ala Ala Ala Trp Glu Ala Ala Leu Pro Arg Arg Arg Pro Arg  
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35

40

45

Arg His Pro Ser Val Asn Pro Arg Ser Arg Ala Ala Gly Ser Pro Arg  
50 55 60  
Thr Arg Gly Arg Arg Thr Glu Glu Arg Pro Ser Gly Ser Arg Leu Gly  
65 70 75 80  
Asp Arg Gly Arg Gly Arg Ala Leu Pro Gly Gly Arg Leu Gly Gly Arg  
85 90 95  
Gly Arg Gly Arg Ala Pro Glu Arg Val Gly Gly Arg Gly Arg Gly Arg  
100 105 110  
Gly Thr Ala Ala Pro Arg Ala Ala Pro Ala Ala Arg Gly Ser Arg Pro  
115 120 125  
Gly Pro Ala Gly Thr Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala  
130 135 140  
Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys  
145 150 155 160  
Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile  
165 170 175  
His Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His  
180 185 190  
Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys  
195 200 205  
Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu  
210 215 220  
Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu  
225 230 235 240  
Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp  
245 250 255  
Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr  
260 265 270  
Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser  
275 280 285

<210> 108  
<211> 390  
<212> PRT  
<213> Homo sapiens

## FAB-008PC-SequenceListing

&lt;400&gt; 108

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu  
 1 5 10 15  
 Trp Leu Leu Val Leu Thr Pro Gly Arg Pro Ala Ala Gly Leu Ser Thr  
 20 25 30  
 Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala  
 35 40 45  
 Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser  
 50 55 60  
 Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu  
 65 70 75 80  
 Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro Glu  
 85 90 95  
 Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu  
 100 105 110  
 Met Val Glu Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr  
 115 120 125  
 His Ser Ile Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val  
 130 135 140  
 Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Leu  
 145 150 155 160  
 Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser Asn  
 165 170 175  
 Asn Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp Ser  
 180 185 190  
 Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp Leu  
 195 200 205  
 Ser Arg Gly Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys Ser  
 210 215 220  
 Cys Asp Ser Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe Thr  
 225 230 235 240  
 Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg Pro  
 245 250 255  
 Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu Gln  
 260 265 270



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Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser  
275 280 285

Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys  
290 295 300

Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn  
305 310 315 320

Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr  
325 330 335

Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala  
340 345 350

Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr  
355 360 365

Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val  
370 375 380

Arg Ser Cys Lys Cys Ser  
385 390

<210> 109  
<211> 442  
<212> PRT  
<213> Homo sapiens

<400> 109

Met His Tyr Cys Val Leu Ser Ala Phe Leu Ile Leu His Leu Val Thr  
1 5 10 15

Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe  
20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu  
35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Glu Glu Val Pro  
50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu  
65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Asp Glu  
85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Pro Phe Phe  
100 105 110

# FAB-008PC-SequenceListing

Pro Ser Glu Thr Val Cys Pro Val Val Thr Thr Pro Ser Gly Ser Val  
 115 120 125  
 Gly Ser Leu Cys Ser Arg Gln Ser Gln Val Leu Cys Gly Tyr Leu Asp  
 130 135 140  
 Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg Ile Val Arg Phe  
 145 150 155 160  
 Asp Val Ser Ala Met Glu Lys Asn Ala Ser Asn Leu Val Lys Ala Glu  
 165 170 175  
 Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg Val Pro Glu Gln  
 180 185 190  
 Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp Leu Thr Ser Pro  
 195 200 205  
 Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr Arg Ala Glu Gly  
 210 215 220  
 Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val His Glu Trp Leu His  
 225 230 235 240  
 His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu His Cys Pro Cys  
 245 250 255  
 Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro Asn Lys Ser Glu  
 260 265 270  
 Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr Ser Thr Tyr Thr  
 275 280 285  
 Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys Lys Asn Ser Gly  
 290 295 300  
 Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser Tyr Arg Leu Glu  
 305 310 315 320  
 Ser Gln Gln Thr Asn Arg Arg Lys Lys Arg Ala Leu Asp Ala Ala Tyr  
 325 330 335  
 Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg Pro Leu Tyr Ile  
 340 345 350  
 Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly  
 355 360 365  
 Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp Ser Ser  
 370 375 380

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Asp Thr Gln His Ser Arg Val Leu Ser Leu Tyr Asn Thr Ile Asn Pro  
385 390 395 400

Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp Leu Glu Pro Leu  
405 410 415

Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro Lys Ile Glu Gln Leu Ser  
420 425 430

Asn Met Ile Val Lys Ser Cys Lys Cys Ser  
435 440

<210> 110  
<211> 414  
<212> PRT  
<213> Homo sapiens

<400> 110

Met His Tyr Cys Val Leu Ser Ala Phe Leu Ile Leu His Leu Val Thr  
1 5 10 15

Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe  
20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu  
35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Glu Glu Val Pro  
50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu  
65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Asp Glu  
85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Pro Phe Phe  
100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg  
115 120 125

Ile Val Arg Phe Asp Val Ser Ala Met Glu Lys Asn Ala Ser Asn Leu  
130 135 140

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

Val Pro Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp  
165 170 175

# FAB-008PC-SequenceListing

Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr  
 180 185 190  
 Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val His  
 195 200 205  
 Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu  
 210 215 220  
 His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro  
 225 230 235 240  
 Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Gly Ile Asp Gly Thr  
 245 250 255  
 Ser Thr Tyr Thr Ser Gly Asp Gln Lys Thr Ile Lys Ser Thr Arg Lys  
 260 265 270  
 Lys Asn Ser Gly Lys Thr Pro His Leu Leu Leu Met Leu Leu Pro Ser  
 275 280 285  
 Tyr Arg Leu Glu Ser Gln Gln Thr Asn Arg Arg Lys Lys Arg Ala Leu  
 290 295 300  
 Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp Asn Cys Cys Leu Arg  
 305 310 315 320  
 Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly Trp Lys Trp Ile His  
 325 330 335  
 Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr  
 340 345 350  
 Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu Tyr Asn  
 355 360 365  
 Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Ser Gln Asp  
 370 375 380  
 Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys Thr Pro Lys Ile  
 385 390 395 400  
 Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys Cys Ser  
 405 410

<210> 111  
 <211> 377  
 <212> PRT  
 <213> Homo sapiens

<400> 111

Met Cys Asp Glu Asp Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser  
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1 5 10 15

Gly Leu Val Lys<sub>20</sub> Ala Gly Phe Ala Gly<sub>25</sub> Asp Asp Ala Pro Arg Ala Val

Phe Pro Ser<sub>35</sub> Ile Val Gly Arg Pro<sub>40</sub> Arg His Gln Gly<sub>45</sub> Val Met Val Gly

Met Gly<sub>50</sub> Gln Lys Asp Ser Tyr<sub>55</sub> Val Gly Asp Glu Ala<sub>60</sub> Gln Ser Lys Arg

Gly<sub>65</sub> Ile Leu Thr Leu Lys<sub>70</sub> Tyr Pro Ile Glu His<sub>75</sub> Gly Ile Ile Thr Asn<sub>80</sub>

Trp Asp Asp Met Glu<sub>85</sub> Lys Ile Trp His His<sub>90</sub> Thr Phe Tyr Asn Glu<sub>95</sub> Leu

Arg Val Ala Pro<sub>100</sub> Glu Glu His Pro Thr<sub>105</sub> Leu Leu Thr Glu Ala<sub>110</sub> Pro Leu

Asn Pro Lys<sub>115</sub> Ala Asn Arg Glu Lys<sub>120</sub> Met Thr Gln Ile Met<sub>125</sub> Phe Glu Thr

Phe Asn Val Pro Ala Met Tyr<sub>135</sub> Val Ala Ile Gln Ala<sub>140</sub> Val Leu Ser Leu

Tyr<sub>145</sub> Ala Ser Gly Arg Thr<sub>150</sub> Thr Gly Ile Val Leu<sub>155</sub> Asp Ser Gly Asp Gly<sub>160</sub>

Val Thr His Asn Val<sub>165</sub> Pro Ile Tyr Glu Gly<sub>170</sub> Tyr Ala Leu Pro His<sub>175</sub> Ala

Ile Met Arg Leu<sub>180</sub> Asp Leu Ala Gly Arg<sub>185</sub> Asp Leu Thr Asp Tyr<sub>190</sub> Leu Met

Lys Ile Leu<sub>195</sub> Thr Glu Arg Gly Tyr<sub>200</sub> Ser Phe Val Thr Thr<sub>205</sub> Ala Glu Arg

Glu Ile Val Arg Asp Ile Lys<sub>215</sub> Glu Lys Leu Cys Tyr<sub>220</sub> Val Ala Leu Asp

Phe Glu Asn Glu Met Ala<sub>230</sub> Thr Ala Ala Ser Ser<sub>235</sub> Ser Ser Leu Glu Lys<sub>240</sub>

Ser Tyr Glu Leu Pro<sub>245</sub> Asp Gly Gln Val Ile<sub>250</sub> Thr Ile Gly Asn Glu<sub>255</sub> Arg

Phe Arg Cys Pro<sub>260</sub> Glu Thr Leu Phe Gln<sub>265</sub> Pro Ser Phe Ile Gly<sub>270</sub> Met Glu

Ser Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp

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275

280

285

Ile Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val Met Ser Gly Gly  
290 295 300

Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr  
305 310 315 320

Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu  
325 330 335

Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser  
340 345 350

Thr Phe Gln Gln Met Trp Ile Thr Lys Gln Glu Tyr Asp Glu Ala Gly  
355 360 365

Pro Ser Ile Val His Arg Lys Cys Phe  
370 375

<210> 112  
<211> 377  
<212> PRT  
<213> Homo sapiens

<400> 112

Met Cys Glu Glu Glu Asp Ser Thr Ala Leu Val Cys Asp Asn Gly Ser  
1 5 10 15

Gly Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val  
20 25 30

Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly  
35 40 45

Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg  
50 55 60

Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn  
65 70 75 80

Trp Asp Asp Met Glu Lys Ile Trp His His Ser Phe Tyr Asn Glu Leu  
85 90 95

Arg Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu  
100 105 110

Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr  
115 120 125

Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu  
130 135 140

# FAB-008PC-SequenceListing

Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly  
 145 150 155 160  
 Val Thr His Asn Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala  
 165 170 175  
 Ile Met Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met  
 180 185 190  
 Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Val Thr Thr Ala Glu Arg  
 195 200 205  
 Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp  
 210 215 220  
 Phe Glu Asn Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys  
 225 230 235 240  
 Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg  
 245 250 255  
 Phe Arg Cys Pro Glu Thr Leu Phe Gln Pro Ser Phe Ile Gly Met Glu  
 260 265 270  
 Ser Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp  
 275 280 285  
 Ile Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val Leu Ser Gly Gly  
 290 295 300  
 Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr  
 305 310 315 320  
 Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu  
 325 330 335  
 Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser  
 340 345 350  
 Thr Phe Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly  
 355 360 365  
 Pro Ser Ile Val His Arg Lys Cys Phe  
 370 375

<210> 113  
 <211> 375  
 <212> PRT  
 <213> Homo sapiens

<400> 113

FAB-008PC-SequenceListing

Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn Gly Ser Gly Met  
1 5 10 15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro  
20 25 30

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

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile  
50 55 60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp  
65 70 75 80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val  
85 90 95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro  
100 105 110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn  
115 120 125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala  
130 135 140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr  
145 150 155 160

His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu  
165 170 175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile  
180 185 190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile  
195 200 205

Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe Glu  
210 215 220

Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr  
225 230 235 240

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

Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys  
260 265 270



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Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp  
275 280 285

Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr  
290 295 300

Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu  
305 310 315 320

Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys  
325 330 335

Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe  
340 345 350

Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser  
355 360 365

Ile Val His Arg Lys Cys Phe  
370 375

<210> 114  
<211> 377  
<212> PRT  
<213> Homo sapiens

<400> 114

Met Cys Asp Asp Glu Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser  
1 5 10 15

Gly Leu Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val  
20 25 30

Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly  
35 40 45

Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg  
50 55 60

Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn  
65 70 75 80

Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu  
85 90 95

Arg Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu  
100 105 110

Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr  
115 120 125

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Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu  
 130 135 140  
 Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly  
 145 150 155 160  
 Val Thr His Asn Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala  
 165 170 175  
 Ile Met Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met  
 180 185 190  
 Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Val Thr Thr Ala Glu Arg  
 195 200 205  
 Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp  
 210 215 220  
 Phe Glu Asn Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys  
 225 230 235 240  
 Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg  
 245 250 255  
 Phe Arg Cys Pro Glu Thr Leu Phe Gln Pro Ser Phe Ile Gly Met Glu  
 260 265 270  
 Ser Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp  
 275 280 285  
 Ile Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val Leu Ser Gly Gly  
 290 295 300  
 Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr  
 305 310 315 320  
 Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu  
 325 330 335  
 Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser  
 340 345 350  
 Thr Phe Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly  
 355 360 365  
 Pro Ser Ile Val His Arg Lys Cys Phe  
 370 375

<210> 115  
 <211> 375  
 <212> PRT  
 <213> Homo sapiens

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<400> 115

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Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
1      5      10      15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
      20      25      30

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

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
      50      55      60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
65      70      75      80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
      85      90      95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
      100      105      110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
      115      120      125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
      130      135      140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
145      150      155      160

His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
      165      170      175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
      180      185      190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
      195      200      205

Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe Glu
      210      215      220

Gln Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr
225      230      235      240

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

Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys

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260

265

270

Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp  
275 280 285

Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr  
290 295 300

Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu  
305 310 315 320

Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys  
325 330 335

Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe  
340 345 350

Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser  
355 360 365

Ile Val His Arg Lys Cys Phe  
370 375

<210> 116  
<211> 376  
<212> PRT  
<213> Homo sapiens

<400> 116

Met Cys Glu Glu Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser Gly  
1 5 10 15

Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe  
20 25 30

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

Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly  
50 55 60

Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Ile Thr Asn Trp  
65 70 75 80

Asp Asp Met Glu Lys Ile Trp His His Ser Phe Tyr Asn Glu Leu Arg  
85 90 95

Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr Glu Ala Pro Leu Asn  
100 105 110

Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe  
115 120 125

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Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr  
130 135 140

Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly Val  
145 150 155 160

Thr His Asn Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile  
165 170 175

Met Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys  
180 185 190

Ile Leu Thr Glu Arg Gly Tyr Ser Phe Val Thr Thr Ala Glu Arg Glu  
195 200 205

Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe  
210 215 220

Glu Asn Glu Met Ala Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser  
225 230 235 240

Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe  
245 250 255

Arg Cys Pro Glu Thr Leu Phe Gln Pro Ser Phe Ile Gly Met Glu Ser  
260 265 270

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

Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val Leu Ser Gly Gly Thr  
290 295 300

Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala  
305 310 315 320

Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg  
325 330 335

Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr  
340 345 350

Phe Gln Gln Met Trp Ile Ser Lys Pro Glu Tyr Asp Glu Ala Gly Pro  
355 360 365

Ser Ile Val His Arg Lys Cys Phe  
370 375

<210> 117

<211> 333

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<212> PRT  
<213> Homo sapiens

<400> 117

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Met Cys Glu Glu Glu Thr Thr Ala Leu Val Cys Asp Asn Gly Ser Gly
1      5      10      15

Leu Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe
20     25     30

Pro Ser Ile Val Gly Arg Pro Arg His Gln Ile Trp His His Ser Phe
35     40     45

Tyr Asn Glu Leu Arg Val Ala Pro Glu Glu His Pro Thr Leu Leu Thr
50     55     60

Glu Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile
65     70     75     80

Met Phe Glu Thr Phe Asn Val Pro Ala Met Tyr Val Ala Ile Gln Ala
85     90     95

Val Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp
100    105    110

Ser Gly Asp Gly Val Thr His Asn Val Pro Ile Tyr Glu Gly Tyr Ala
115    120    125

Leu Pro His Ala Ile Met Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr
130    135    140

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

Thr Ala Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr
165    170    175

Val Ala Leu Asp Phe Glu Asn Glu Met Ala Thr Ala Ala Ser Ser Ser
180    185    190

Ser Leu Glu Lys Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile
195    200    205

Gly Asn Glu Arg Phe Arg Cys Pro Glu Thr Leu Phe Gln Pro Ser Phe
210    215    220

Ile Gly Met Glu Ser Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile
225    230    235    240

Met Lys Cys Asp Ile Asp Ile Arg Lys Asp Leu Tyr Ala Asn Asn Val
245    250    255

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Leu Ser Gly Gly Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln  
260 265 270

Lys Glu Ile Thr Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile  
275 280 285

Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu  
290 295 300

Ala Ser Leu Ser Thr Phe Gln Gln Met Trp Ile Ser Lys Pro Glu Tyr  
305 310 315 320

Asp Glu Ala Gly Pro Ser Ile Val His Arg Lys Cys Phe  
325 330

<210> 118  
<211> 207  
<212> PRT  
<213> Homo sapiens  
<400> 118

Met Ala Gly Pro Ala Thr Gln Ser Pro Met Lys Leu Met Ala Leu Gln  
1 5 10 15

Leu Leu Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro  
20 25 30

Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu  
35 40 45

Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys  
50 55 60

Leu Val Ser Glu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu  
65 70 75 80

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser  
85 90 95

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His  
100 105 110

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile  
115 120 125

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala  
130 135 140

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala  
145 150 155 160

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Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala  
165 170 175

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser  
180 185 190

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
195 200 205

<210> 119  
<211> 204  
<212> PRT  
<213> Homo sapiens

<400> 119

Met Ala Gly Pro Ala Thr Gln Ser Pro Met Lys Leu Met Ala Leu Gln  
1 5 10 15

Leu Leu Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro  
20 25 30

Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu  
35 40 45

Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys  
50 55 60

Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu  
65 70 75 80

Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser  
85 90 95

Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu  
100 105 110

Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu  
115 120 125

Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala  
130 135 140

Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu  
145 150 155 160

Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg  
165 170 175

Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu  
180 185 190

Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro



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200

195

<210> 120  
<211> 171  
<212> PRT  
<213> Homo sapiens

<400> 120

Met Ala Gly Pro Ala Thr Gln Ser Pro Met Lys Leu Met Ala Leu Gln  
1 5 10 15

Leu Leu Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro  
20 25 30

Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu  
35 40 45

Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys  
50 55 60

Leu Val Ser Glu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe  
65 70 75 80

Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu  
85 90 95

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

Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln  
115 120 125

Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg  
130 135 140

Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val  
145 150 155 160

Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
165 170

<210> 121  
<211> 168  
<212> PRT  
<213> Homo sapiens

<400> 121

Met Ala Gly Pro Ala Thr Gln Ser Pro Met Lys Leu Met Ala Leu Gln  
1 5 10 15

Leu Leu Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro  
20 25 30

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Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu  
35 40 45

Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys  
50 55 60

Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln  
65 70 75 80

Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr  
85 90 95

Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp  
100 105 110

Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln  
115 120 125

Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly  
130 135 140

Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg  
145 150 155 160

Val Leu Arg His Leu Ala Gln Pro  
165

<210> 122  
<211> 211  
<212> PRT  
<213> Homo sapiens

<400> 122

Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala  
1 5 10 15

His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg  
20 25 30

Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu  
35 40 45

Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg  
50 55 60

Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu  
65 70 75 80

Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys  
85 90 95

## FAB-008PC-SequenceListing

Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro  
100 105 110

Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg  
115 120 125

Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg  
130 135 140

Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys  
145 150 155 160

Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu  
165 170 175

Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp  
180 185 190

Thr Gly Arg Pro Arg Glu Ser Gly Lys Lys Arg Lys Arg Lys Arg Leu  
195 200 205

Lys Pro Thr  
210

<210> 123  
<211> 196  
<212> PRT  
<213> Homo sapiens

<400> 123

Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala  
1 5 10 15

His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg  
20 25 30

Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu  
35 40 45

Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg  
50 55 60

Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu  
65 70 75 80

Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys  
85 90 95

Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro  
100 105 110

Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg  
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115

120

125

Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg  
130 135 140

Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys  
145 150 155 160

Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu  
165 170 175

Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp  
180 185 190

Thr Asp Val Arg  
195

<210> 124  
<211> 241  
<212> PRT  
<213> Homo sapiens

<400> 124

Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg  
1 5 10 15

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

Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu  
35 40 45

His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met  
50 55 60

Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg  
65 70 75 80

Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu  
85 90 95

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

Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln  
115 120 125

Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr  
130 135 140

Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg  
145 150 155 160

# FAB-008PC-SequenceListing

Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu  
165 170 175

Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser  
180 185 190

Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val  
195 200 205

Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg  
210 215 220

Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly  
225 230 235 240

Ala

<210> 125  
<211> 226  
<212> PRT  
<213> Homo sapiens

<400> 125

Met Phe Ile Met Gly Leu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu  
1 5 10 15

Met Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu  
20 25 30

Leu His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn  
35 40 45

Met Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly  
50 55 60

Arg Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala  
65 70 75 80

Glu Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile  
85 90 95

Asp Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val  
100 105 110

Gln Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro  
115 120 125

Thr Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val  
130 135 140

FAB-008PC-SequenceListing

Arg Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His  
145 150 155 160

Leu Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg  
165 170 175

Ser Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg  
180 185 190

Val Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His  
195 200 205

Arg Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu  
210 215 220

Gly Ala  
225

<210> 126  
<211> 345  
<212> PRT  
<213> Homo sapiens  
  
<400> 126

Met Ser Leu Phe Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly Gln  
1 5 10 15

Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe  
20 25 30

Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg  
35 40 45

Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro  
50 55 60

His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val  
65 70 75 80

Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu  
85 90 95

Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu  
100 105 110

Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr  
115 120 125

Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe  
130 135 140

# FAB-008PC-SequenceListing

Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr  
145 150 155 160

Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu  
165 170 175

Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala  
180 185 190

Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp  
195 200 205

Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly  
210 215 220

Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu  
225 230 235 240

Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser  
245 250 255

Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro  
260 265 270

Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu  
275 280 285

His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys  
290 295 300

Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu  
305 310 315 320

His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp  
325 330 335

Cys Val Cys Arg Gly Ser Thr Gly Gly  
340 345

<210> 127  
<211> 370  
<212> PRT  
<213> Homo sapiens

<400> 127

Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys  
1 5 10 15

Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala  
20 25 30

Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp  
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35

40

45

Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val  
50 55 60  
Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr  
65 70 75 80  
Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp  
85 90 95  
Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp  
100 105 110  
Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly  
115 120 125  
Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr  
130 135 140  
Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys  
145 150 155 160  
Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala  
165 170 175  
Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly  
180 185 190  
Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp  
195 200 205  
Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu  
210 215 220  
Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr  
225 230 235 240  
Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser  
245 250 255  
Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys  
260 265 270  
Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala  
275 280 285  
Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly  
290 295 300  
Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser



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305 310 315 320

Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly  
325 330 335

His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile  
340 345 350

Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro  
355 360 365

Pro Arg  
370

<210> 128  
<211> 364  
<212> PRT  
<213> Homo sapiens  
<400> 128

Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys  
1 5 10 15

Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala  
20 25 30

Leu Arg Asn Ala Asn Leu Arg Arg Asp Asp Leu Tyr Arg Arg Asp Glu  
35 40 45

Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg Phe Pro  
50 55 60

Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His Ser Gln  
65 70 75 80

Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly Leu Glu  
85 90 95

Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Asp  
100 105 110

Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly His Lys  
115 120 125

Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys Ile Thr  
130 135 140

Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys Ile Tyr  
145 150 155 160

Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu Thr Asn  
165 170 175

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Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn Ser Pro  
180 185 190

Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys Lys Ile  
195 200 205

Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn Pro Glu  
210 215 220

Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro Arg Tyr  
225 230 235 240

Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg  
245 250 255

Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn Tyr Ser  
260 265 270

Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe Phe Pro  
275 280 285

Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr  
290 295 300

Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val Lys Lys  
305 310 315 320

Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg Arg Gly  
325 330 335

Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu  
340 345 350

Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg  
355 360

<210> 129  
<211> 469  
<212> PRT  
<213> Homo sapiens  
<400> 129

Met His Ser Phe Pro Pro Leu Leu Leu Leu Leu Phe Trp Gly Val Val  
1 5 10 15

Ser His Ser Phe Pro Ala Thr Leu Glu Thr Gln Glu Gln Asp Val Asp  
20 25 30

Leu Val Gln Lys Tyr Leu Glu Lys Tyr Tyr Asn Leu Lys Asn Asp Gly  
35 40 45

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Arg Gln Val Glu Lys Arg Arg Asn Ser Gly Pro Val Val Glu Lys Leu  
50 55 60

Lys Gln Met Gln Glu Phe Phe Gly Leu Lys Val Thr Gly Lys Pro Asp  
65 70 75 80

Ala Glu Thr Leu Lys Val Met Lys Gln Pro Arg Cys Gly Val Pro Asp  
85 90 95

Val Ala Gln Phe Val Leu Thr Glu Gly Asn Pro Arg Trp Glu Gln Thr  
100 105 110

His Leu Thr Tyr Arg Ile Glu Asn Tyr Thr Pro Asp Leu Pro Arg Ala  
115 120 125

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

Thr Pro Leu Thr Phe Thr Lys Val Ser Glu Gly Gln Ala Asp Ile Met  
145 150 155 160

Ile Ser Phe Val Arg Gly Asp His Arg Asp Asn Ser Pro Phe Asp Gly  
165 170 175

Pro Gly Gly Asn Leu Ala His Ala Phe Gln Pro Gly Pro Gly Ile Gly  
180 185 190

Gly Asp Ala His Phe Asp Glu Asp Glu Arg Trp Thr Asn Asn Phe Arg  
195 200 205

Glu Tyr Asn Leu His Arg Val Ala Ala His Glu Leu Gly His Ser Leu  
210 215 220

Gly Leu Ser His Ser Thr Asp Ile Gly Ala Leu Met Tyr Pro Ser Tyr  
225 230 235 240

Thr Phe Ser Gly Asp Val Gln Leu Ala Gln Asp Asp Ile Asp Gly Ile  
245 250 255

Gln Ala Ile Tyr Gly Arg Ser Gln Asn Pro Val Gln Pro Ile Gly Pro  
260 265 270

Gln Thr Pro Lys Ala Cys Asp Ser Lys Leu Thr Phe Asp Ala Ile Thr  
275 280 285

Thr Ile Arg Gly Glu Val Met Phe Phe Lys Asp Arg Phe Tyr Met Arg  
290 295 300

Thr Asn Pro Phe Tyr Pro Glu Val Glu Leu Asn Phe Ile Ser Val Phe  
305 310 315 320

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Trp Pro Gln Leu Pro Asn Gly Leu Glu Ala Ala Tyr Glu Phe Ala Asp  
325 330 335

Arg Asp Glu Val Arg Phe Phe Lys Gly Asn Lys Tyr Trp Ala Val Gln  
340 345 350

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

Gly Phe Pro Arg Thr Val Lys His Ile Asp Ala Ala Leu Ser Glu Glu  
370 375 380

Asn Thr Gly Lys Thr Tyr Phe Phe Val Ala Asn Lys Tyr Trp Arg Tyr  
385 390 395 400

Asp Glu Tyr Lys Arg Ser Met Asp Pro Gly Tyr Pro Lys Met Ile Ala  
405 410 415

His Asp Phe Pro Gly Ile Gly His Lys Val Asp Ala Val Phe Met Lys  
420 425 430

Asp Gly Phe Phe Tyr Phe Phe His Gly Thr Arg Gln Tyr Lys Phe Asp  
435 440 445

Pro Lys Thr Lys Arg Ile Leu Thr Leu Gln Lys Ala Asn Ser Trp Phe  
450 455 460

Asn Cys Arg Lys Asn  
465

<210> 130  
<211> 403  
<212> PRT  
<213> Homo sapiens

<400> 130

Met Gln Glu Phe Phe Gly Leu Lys Val Thr Gly Lys Pro Asp Ala Glu  
1 5 10 15

Thr Leu Lys Val Met Lys Gln Pro Arg Cys Gly Val Pro Asp Val Ala  
20 25 30

Gln Phe Val Leu Thr Glu Gly Asn Pro Arg Trp Glu Gln Thr His Leu  
35 40 45

Thr Tyr Arg Ile Glu Asn Tyr Thr Pro Asp Leu Pro Arg Ala Asp Val  
50 55 60

Asp His Ala Ile Glu Lys Ala Phe Gln Leu Trp Ser Asn Val Thr Pro  
65 70 75 80

## FAB-008PC-SequenceListing

Leu Thr Phe Thr Lys Val Ser Glu Gly Gln Ala Asp Ile Met Ile Ser  
 85 90 95  
 Phe Val Arg Gly Asp His Arg Asp Asn Ser Pro Phe Asp Gly Pro Gly  
 100 105 110  
 Gly Asn Leu Ala His Ala Phe Gln Pro Gly Pro Gly Ile Gly Gly Asp  
 115 120 125  
 Ala His Phe Asp Glu Asp Glu Arg Trp Thr Asn Asn Phe Arg Glu Tyr  
 130 135 140  
 Asn Leu His Arg Val Ala Ala His Glu Leu Gly His Ser Leu Gly Leu  
 145 150 155 160  
 Ser His Ser Thr Asp Ile Gly Ala Leu Met Tyr Pro Ser Tyr Thr Phe  
 165 170 175  
 Ser Gly Asp Val Gln Leu Ala Gln Asp Asp Ile Asp Gly Ile Gln Ala  
 180 185 190  
 Ile Tyr Gly Arg Ser Gln Asn Pro Val Gln Pro Ile Gly Pro Gln Thr  
 195 200 205  
 Pro Lys Ala Cys Asp Ser Lys Leu Thr Phe Asp Ala Ile Thr Thr Ile  
 210 215 220  
 Arg Gly Glu Val Met Phe Phe Lys Asp Arg Phe Tyr Met Arg Thr Asn  
 225 230 235 240  
 Pro Phe Tyr Pro Glu Val Glu Leu Asn Phe Ile Ser Val Phe Trp Pro  
 245 250 255  
 Gln Leu Pro Asn Gly Leu Glu Ala Ala Tyr Glu Phe Ala Asp Arg Asp  
 260 265 270  
 Glu Val Arg Phe Phe Lys Gly Asn Lys Tyr Trp Ala Val Gln Gly Gln  
 275 280 285  
 Asn Val Leu His Gly Tyr Pro Lys Asp Ile Tyr Ser Ser Phe Gly Phe  
 290 295 300  
 Pro Arg Thr Val Lys His Ile Asp Ala Ala Leu Ser Glu Glu Asn Thr  
 305 310 315 320  
 Gly Lys Thr Tyr Phe Phe Val Ala Asn Lys Tyr Trp Arg Tyr Asp Glu  
 325 330 335  
 Tyr Lys Arg Ser Met Asp Pro Gly Tyr Pro Lys Met Ile Ala His Asp  
 340 345 350

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Phe Pro Gly Ile Gly His Lys Val Asp Ala Val Phe Met Lys Asp Gly  
355 360 365

Phe Phe Tyr Phe Phe His Gly Thr Arg Gln Tyr Lys Phe Asp Pro Lys  
370 375 380

Thr Lys Arg Ile Leu Thr Leu Gln Lys Ala Asn Ser Trp Phe Asn Cys  
385 390 395 400

Arg Lys Asn

<210> 131  
<211> 467  
<212> PRT  
<213> Homo sapiens  
<400> 131

Met Phe Ser Leu Lys Thr Leu Pro Phe Leu Leu Leu Leu His Val Gln  
1 5 10 15

Ile Ser Lys Ala Phe Pro Val Ser Ser Lys Glu Lys Asn Thr Lys Thr  
20 25 30

Val Gln Asp Tyr Leu Glu Lys Phe Tyr Gln Leu Pro Ser Asn Gln Tyr  
35 40 45

Gln Ser Thr Arg Lys Asn Gly Thr Asn Val Ile Val Glu Lys Leu Lys  
50 55 60

Glu Met Gln Arg Phe Phe Gly Leu Asn Val Thr Gly Lys Pro Asn Glu  
65 70 75 80

Glu Thr Leu Asp Met Met Lys Lys Pro Arg Cys Gly Val Pro Asp Ser  
85 90 95

Gly Gly Phe Met Leu Thr Pro Gly Asn Pro Lys Trp Glu Arg Thr Asn  
100 105 110

Leu Thr Tyr Arg Ile Arg Asn Tyr Thr Pro Gln Leu Ser Glu Ala Glu  
115 120 125

Val Glu Arg Ala Ile Lys Asp Ala Phe Glu Leu Trp Ser Val Ala Ser  
130 135 140

Pro Leu Ile Phe Thr Arg Ile Ser Gln Gly Glu Ala Asp Ile Asn Ile  
145 150 155 160

Ala Phe Tyr Gln Arg Asp His Gly Asp Asn Ser Pro Phe Asp Gly Pro  
165 170 175

Asn Gly Ile Leu Ala His Ala Phe Gln Pro Gly Gln Gly Ile Gly Gly  
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180

185

190

Asp Ala His Phe Asp Ala Glu Glu Thr Trp Thr Asn Thr Ser Ala Asn  
 195 200 205  
 Tyr Asn Leu Phe Leu Val Ala Ala His Glu Phe Gly His Ser Leu Gly  
 210 215 220  
 Leu Ala His Ser Ser Asp Pro Gly Ala Leu Met Tyr Pro Asn Tyr Ala  
 225 230 235 240  
 Phe Arg Glu Thr Ser Asn Tyr Ser Leu Pro Gln Asp Asp Ile Asp Gly  
 245 250 255  
 Ile Gln Ala Ile Tyr Gly Leu Ser Ser Asn Pro Ile Gln Pro Thr Gly  
 260 265 270  
 Pro Ser Thr Pro Lys Pro Cys Asp Pro Ser Leu Thr Phe Asp Ala Ile  
 275 280 285  
 Thr Thr Leu Arg Gly Glu Ile Leu Phe Phe Lys Asp Arg Tyr Phe Trp  
 290 295 300  
 Arg Arg His Pro Gln Leu Gln Arg Val Glu Met Asn Phe Ile Ser Leu  
 305 310 315 320  
 Phe Trp Pro Ser Leu Pro Thr Gly Ile Gln Ala Ala Tyr Glu Asp Phe  
 325 330 335  
 Asp Arg Asp Leu Ile Phe Leu Phe Lys Gly Asn Gln Tyr Trp Ala Leu  
 340 345 350  
 Ser Gly Tyr Asp Ile Leu Gln Gly Tyr Pro Lys Asp Ile Ser Asn Tyr  
 355 360 365  
 Gly Phe Pro Ser Ser Val Gln Ala Ile Asp Ala Ala Val Phe Tyr Arg  
 370 375 380  
 Ser Lys Thr Tyr Phe Phe Val Asn Asp Gln Phe Trp Arg Tyr Asp Asn  
 385 390 395 400  
 Gln Arg Gln Phe Met Glu Pro Gly Tyr Pro Lys Ser Ile Ser Gly Ala  
 405 410 415  
 Phe Pro Gly Ile Glu Ser Lys Val Asp Ala Val Phe Gln Gln Glu His  
 420 425 430  
 Phe Phe His Val Phe Ser Gly Pro Arg Tyr Tyr Ala Phe Asp Leu Ile  
 435 440 445  
 Ala Gln Arg Val Thr Arg Val Ala Arg Gly Asn Lys Trp Leu Asn Cys

450

455

460

Arg Tyr Gly  
465

<210> 132  
 <211> 476  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 132

Met Met His Leu Ala Phe Leu Val Leu Leu Cys Leu Pro Val Cys Ser  
1 5 10 15Ala Tyr Pro Leu Ser Gly Ala Ala Lys Glu Glu Asp Ser Asn Lys Asp  
20 25 30Leu Ala Gln Gln Tyr Leu Glu Lys Tyr Tyr Asn Leu Glu Lys Asp Val  
35 40 45Lys Gln Phe Arg Arg Lys Asp Ser Asn Leu Ile Val Lys Lys Ile Gln  
50 55 60Gly Met Gln Lys Phe Leu Gly Leu Glu Val Thr Gly Lys Leu Asp Thr  
65 70 75 80Asp Thr Leu Glu Val Met Arg Lys Pro Arg Cys Gly Val Pro Asp Val  
85 90 95Gly His Phe Ser Ser Phe Pro Gly Met Pro Lys Trp Arg Lys Thr His  
100 105 110Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp Leu Pro Arg Asp Ala  
115 120 125Val Asp Ser Ala Ile Glu Lys Ala Leu Lys Val Trp Glu Glu Val Thr  
130 135 140Pro Leu Thr Phe Ser Arg Leu Tyr Glu Gly Glu Ala Asp Ile Met Ile  
145 150 155 160Ser Phe Ala Val Lys Glu His Gly Asp Phe Tyr Ser Phe Asp Gly Pro  
165 170 175Gly His Ser Leu Ala His Ala Tyr Pro Pro Gly Pro Gly Leu Tyr Gly  
180 185 190Asp Ile His Phe Asp Asp Asp Glu Lys Trp Thr Glu Asp Ala Ser Gly  
195 200 205Thr Asn Leu Phe Leu Val Ala Ala His Glu Leu Gly His Ser Leu Gly  
210 215 220



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Leu Phe His Ser Ala Asn Thr Glu Ala Leu Met Tyr Pro Leu Tyr Asn  
 225 230 235 240  
 Ser Phe Thr Glu Leu Ala Gln Phe Arg Leu Ser Gln Asp Asp Val Asn  
 245 250 255  
 Gly Ile Gln Ser Leu Tyr Gly Pro Pro Ala Ser Thr Glu Glu Pro  
 260 265 270  
 Leu Val Pro Thr Lys Ser Val Pro Ser Gly Ser Glu Met Pro Ala Lys  
 275 280 285  
 Cys Asp Pro Ala Leu Ser Phe Asp Ala Ile Ser Thr Leu Arg Gly Glu  
 290 295 300  
 Tyr Leu Phe Phe Lys Asp Arg Tyr Phe Trp Arg Arg Ser His Trp Asn  
 305 310 315 320  
 Pro Glu Pro Glu Phe His Leu Ile Ser Ala Phe Trp Pro Ser Leu Pro  
 325 330 335  
 Ser Tyr Leu Asp Ala Ala Tyr Glu Val Asn Ser Arg Asp Thr Val Phe  
 340 345 350  
 Ile Phe Lys Gly Asn Glu Phe Trp Ala Ile Arg Gly Asn Glu Val Gln  
 355 360 365  
 Ala Gly Tyr Pro Arg Gly Ile His Thr Leu Gly Phe Pro Pro Thr Ile  
 370 375 380  
 Arg Lys Ile Asp Ala Ala Val Ser Asp Lys Glu Lys Lys Lys Thr Tyr  
 385 390 395 400  
 Phe Phe Ala Ala Asp Lys Tyr Trp Arg Phe Asp Glu Asn Ser Gln Ser  
 405 410 415  
 Met Glu Gln Gly Phe Pro Arg Leu Ile Ala Asp Asp Phe Pro Gly Val  
 420 425 430  
 Glu Pro Lys Val Asp Ala Val Leu Gln Ala Phe Gly Phe Phe Tyr Phe  
 435 440 445  
 Phe Ser Gly Ser Ser Gln Phe Glu Phe Asp Pro Asn Ala Arg Met Val  
 450 455 460  
 Thr His Ile Leu Lys Ser Asn Ser Trp Leu His Cys  
 465 470

<210> 133

<211> 470

FAB-008PC-SequenceListing

<212> PRT  
 <213> Homo sapiens  
 <400> 133

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

Leu  Pro  Leu  Asn  Ser  Ser  Thr  Ser  Leu  Glu  Lys  Asn  Asn  Val  Leu  Phe
      20      25      30

Gly  Glu  Arg  Tyr  Leu  Glu  Lys  Phe  Tyr  Gly  Leu  Glu  Ile  Asn  Lys  Leu
      35      40      45

Pro  Val  Thr  Lys  Met  Lys  Tyr  Ser  Gly  Asn  Leu  Met  Lys  Glu  Lys  Ile
      50      55      60

Gln  Glu  Met  Gln  His  Phe  Leu  Gly  Leu  Lys  Val  Thr  Gly  Gln  Leu  Asp
65      70      75      80

Thr  Ser  Thr  Leu  Glu  Met  Met  His  Ala  Pro  Arg  Cys  Gly  Val  Pro  Asp
      85      90      95

Val  His  His  Phe  Arg  Glu  Met  Pro  Gly  Gly  Pro  Val  Trp  Arg  Lys  His
      100     105     110

Tyr  Ile  Thr  Tyr  Arg  Ile  Asn  Asn  Tyr  Thr  Pro  Asp  Met  Asn  Arg  Glu
      115     120     125

Asp  Val  Asp  Tyr  Ala  Ile  Arg  Lys  Ala  Phe  Gln  Val  Trp  Ser  Asn  Val
      130     135     140

Thr  Pro  Leu  Lys  Phe  Ser  Lys  Ile  Asn  Thr  Gly  Met  Ala  Asp  Ile  Leu
145     150     155     160

Val  Val  Phe  Ala  Arg  Gly  Ala  His  Gly  Asp  Phe  His  Ala  Phe  Asp  Gly
      165     170     175

Lys  Gly  Gly  Ile  Leu  Ala  His  Ala  Phe  Gly  Pro  Gly  Ser  Gly  Ile  Gly
      180     185     190

Gly  Asp  Ala  His  Phe  Asp  Glu  Asp  Glu  Phe  Trp  Thr  Thr  His  Ser  Gly
      195     200     205

Gly  Thr  Asn  Leu  Phe  Leu  Thr  Ala  Val  His  Glu  Ile  Gly  His  Ser  Leu
210     215     220

Gly  Leu  Gly  His  Ser  Ser  Asp  Pro  Lys  Ala  Val  Met  Phe  Pro  Thr  Tyr
225     230     235     240

Lys  Tyr  Val  Asp  Ile  Asn  Thr  Phe  Arg  Leu  Ser  Ala  Asp  Asp  Ile  Arg
      245     250     255
    
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Gly Ile Gln Ser Leu Tyr Gly Asp Pro Lys Glu Asn Gln Arg Leu Pro  
260 265 270

Asn Pro Asp Asn Ser Glu Pro Ala Leu Cys Asp Pro Asn Leu Ser Phe  
275 280 285

Asp Ala Val Thr Thr Val Gly Asn Lys Ile Phe Phe Phe Lys Asp Arg  
290 295 300

Phe Phe Trp Leu Lys Val Ser Glu Arg Pro Lys Thr Ser Val Asn Leu  
305 310 315 320

Ile Ser Ser Leu Trp Pro Thr Leu Pro Ser Gly Ile Glu Ala Ala Tyr  
325 330 335

Glu Ile Glu Ala Arg Asn Gln Val Phe Leu Phe Lys Asp Asp Lys Tyr  
340 345 350

Trp Leu Ile Ser Asn Leu Arg Pro Glu Pro Asn Tyr Pro Lys Ser Ile  
355 360 365

His Ser Phe Gly Phe Pro Asn Phe Val Lys Lys Ile Asp Ala Ala Val  
370 375 380

Phe Asn Pro Arg Phe Tyr Arg Thr Tyr Phe Phe Val Asp Asn Gln Tyr  
385 390 395 400

Trp Arg Tyr Asp Glu Arg Arg Gln Met Met Asp Pro Gly Tyr Pro Lys  
405 410 415

Leu Ile Thr Lys Asn Phe Gln Gly Ile Gly Pro Lys Ile Asp Ala Val  
420 425 430

Phe Tyr Ser Lys Asn Lys Tyr Tyr Tyr Phe Phe Gln Gly Ser Asn Gln  
435 440 445

Phe Glu Tyr Asp Phe Leu Leu Gln Arg Ile Thr Lys Thr Leu Lys Ser  
450 455 460

Asn Ser Trp Phe Gly Cys  
465 470

<210> 134  
<211> 2871  
<212> PRT  
<213> Homo sapiens

<400> 134

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

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Leu Ala Ser Tyr Thr Ser His Gly Ala Asp Ala Asn Leu Glu Ala Gly  
20 25 30

Asn Val Lys Glu Thr Arg Ala Ser Arg Ala Lys Arg Arg Gly Gly Gly  
35 40 45

Gly His Asp Ala Leu Lys Gly Pro Asn Val Cys Gly Ser Arg Tyr Asn  
50 55 60

Ala Tyr Cys Cys Pro Gly Trp Lys Thr Leu Pro Gly Gly Asn Gln Cys  
65 70 75 80

Ile Val Pro Ile Cys Arg His Ser Cys Gly Asp Gly Phe Cys Ser Arg  
85 90 95

Pro Asn Met Cys Thr Cys Pro Ser Gly Gln Ile Ala Pro Ser Cys Gly  
100 105 110

Ser Arg Ser Ile Gln His Cys Asn Ile Arg Cys Met Asn Gly Gly Ser  
115 120 125

Cys Ser Asp Asp His Cys Leu Cys Gln Lys Gly Tyr Ile Gly Thr His  
130 135 140

Cys Gly Gln Pro Val Cys Glu Ser Gly Cys Leu Asn Gly Gly Arg Cys  
145 150 155 160

Val Ala Pro Asn Arg Cys Ala Cys Thr Tyr Gly Phe Thr Gly Pro Gln  
165 170 175

Cys Glu Arg Asp Tyr Arg Thr Gly Pro Cys Phe Thr Val Ile Ser Asn  
180 185 190

Gln Met Cys Gln Gly Gln Leu Ser Gly Ile Val Cys Thr Lys Thr Leu  
195 200 205

Cys Cys Ala Thr Val Gly Arg Ala Trp Gly His Pro Cys Glu Met Cys  
210 215 220

Pro Ala Gln Pro His Pro Cys Arg Arg Gly Phe Ile Pro Asn Ile Arg  
225 230 235 240

Thr Gly Ala Cys Gln Asp Val Asp Glu Cys Gln Ala Ile Pro Gly Leu  
245 250 255

Cys Gln Gly Gly Asn Cys Ile Asn Thr Val Gly Ser Phe Glu Cys Lys  
260 265 270

Cys Pro Ala Gly His Lys Leu Asn Glu Val Ser Gln Lys Cys Glu Asp  
275 280 285

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Ile Asp Glu Cys Ser Thr Ile Pro Gly Ile Cys Glu Gly Gly Glu Cys  
 290 295 300  
 Thr Asn Thr Val Ser Ser Tyr Phe Cys Lys Cys Pro Pro Gly Phe Tyr  
 305 310 315 320  
 Thr Ser Pro Asp Gly Thr Arg Cys Ile Asp Val Arg Pro Gly Tyr Cys  
 325 330 335  
 Tyr Thr Ala Leu Thr Asn Gly Arg Cys Ser Asn Gln Leu Pro Gln Ser  
 340 345 350  
 Ile Thr Lys Met Gln Cys Cys Cys Asp Ala Gly Arg Cys Trp Ser Pro  
 355 360 365  
 Gly Val Thr Val Ala Pro Glu Met Cys Pro Ile Arg Ala Thr Glu Asp  
 370 375 380  
 Phe Asn Lys Leu Cys Ser Val Pro Met Val Ile Pro Gly Arg Pro Glu  
 385 390 395 400  
 Tyr Pro Pro Pro Pro Leu Gly Pro Ile Pro Pro Val Leu Pro Val Pro  
 405 410 415  
 Pro Gly Phe Pro Pro Gly Pro Gln Ile Pro Val Pro Arg Pro Pro Val  
 420 425 430  
 Glu Tyr Leu Tyr Pro Ser Arg Glu Pro Pro Arg Val Leu Pro Val Asn  
 435 440 445  
 Val Thr Asp Tyr Cys Gln Leu Val Arg Tyr Leu Cys Gln Asn Gly Arg  
 450 455 460  
 Cys Ile Pro Thr Pro Gly Ser Tyr Arg Cys Glu Cys Asn Lys Gly Phe  
 465 470 475 480  
 Gln Leu Asp Leu Arg Gly Glu Cys Ile Asp Val Asp Glu Cys Glu Lys  
 485 490 495  
 Asn Pro Cys Ala Gly Gly Glu Cys Ile Asn Asn Gln Gly Ser Tyr Thr  
 500 505 510  
 Cys Gln Cys Arg Ala Gly Tyr Gln Ser Thr Leu Thr Arg Thr Glu Cys  
 515 520 525  
 Arg Asp Ile Asp Glu Cys Leu Gln Asn Gly Arg Ile Cys Asn Asn Gly  
 530 535 540  
 Arg Cys Ile Asn Thr Asp Gly Ser Phe His Cys Val Cys Asn Ala Gly  
 545 550 555 560

## FAB-008PC-SequenceListing

Phe His Val Thr Arg<sub>565</sub> Asp Gly Lys Asn Cys<sub>570</sub> Glu Asp Met Asp Glu<sub>575</sub> Cys  
 Ser Ile Arg Asn<sub>580</sub> Met Cys Leu Asn Gly<sub>585</sub> Met Cys Ile Asn Glu<sub>590</sub> Asp Gly  
 Ser Phe Lys<sub>595</sub> Cys Ile Cys Lys Pro<sub>600</sub> Gly Phe Gln Leu Ala<sub>605</sub> Ser Asp Gly  
 Arg Tyr<sub>610</sub> Cys Lys Asp Ile Asn<sub>615</sub> Glu Cys Glu Thr Pro<sub>620</sub> Gly Ile Cys Met  
 Asn Gly Arg Cys Val Asn<sub>630</sub> Thr Asp Gly Ser Tyr<sub>635</sub> Arg Cys Glu Cys Phe<sub>640</sub>  
 Pro Gly Leu Ala Val<sub>645</sub> Gly Leu Asp Gly Arg<sub>650</sub> Val Cys Val Asp Thr His<sub>655</sub>  
 Met Arg Ser Thr<sub>660</sub> Cys Tyr Gly Gly Tyr<sub>665</sub> Lys Arg Gly Gln Cys<sub>670</sub> Ile Lys  
 Pro Leu Phe<sub>675</sub> Gly Ala Val Thr Lys<sub>680</sub> Ser Glu Cys Cys Cys<sub>685</sub> Ala Ser Thr  
 Glu Tyr<sub>690</sub> Ala Phe Gly Glu Pro<sub>695</sub> Cys Gln Pro Cys Pro<sub>700</sub> Ala Gln Asn Ser  
 Ala Glu Tyr Gln Ala Leu<sub>710</sub> Cys Ser Ser Gly Pro<sub>715</sub> Gly Met Thr Ser Ala<sub>720</sub>  
 Gly Ser Asp Ile Asn<sub>725</sub> Glu Cys Ala Leu Asp<sub>730</sub> Pro Asp Ile Cys Pro<sub>735</sub> Asn  
 Gly Ile Cys Glu<sub>740</sub> Asn Leu Arg Gly Thr<sub>745</sub> Tyr Lys Cys Ile Cys<sub>750</sub> Asn Ser  
 Gly Tyr Glu<sub>755</sub> Val Asp Ser Thr Gly<sub>760</sub> Lys Asn Cys Val Asp<sub>765</sub> Ile Asn Glu  
 Cys Val<sub>770</sub> Leu Asn Ser Leu Leu<sub>775</sub> Cys Asp Asn Gly Gln<sub>780</sub> Cys Arg Asn Thr  
 Pro Gly Ser Phe Val Cys<sub>790</sub> Thr Cys Pro Lys Gly<sub>795</sub> Phe Ile Tyr Lys Pro<sub>800</sub>  
 Asp Leu Lys Thr Cys<sub>805</sub> Glu Asp Ile Asp Glu<sub>810</sub> Cys Glu Ser Ser Pro<sub>815</sub> Cys  
 Ile Asn Gly Val<sub>820</sub> Cys Lys Asn Ser Pro<sub>825</sub> Gly Ser Phe Ile Cys<sub>830</sub> Glu Cys

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Ser Ser Glu Ser Thr Leu Asp Pro Thr Lys Thr Ile Cys Ile Glu Thr  
835 840 845

Ile Lys Gly Thr Cys Trp Gln Thr Val Ile Asp Gly Arg Cys Glu Ile  
850 855 860

Asn Ile Asn Gly Ala Thr Leu Lys Ser Gln Cys Cys Ser Ser Leu Gly  
865 870 875 880

Ala Ala Trp Gly Ser Pro Cys Thr Leu Cys Gln Val Asp Pro Ile Cys  
885 890 895

Gly Lys Gly Tyr Ser Arg Ile Lys Gly Thr Gln Cys Glu Asp Ile Asp  
900 905 910

Glu Cys Glu Val Phe Pro Gly Val Cys Lys Asn Gly Leu Cys Val Asn  
915 920 925

Thr Arg Gly Ser Phe Lys Cys Gln Cys Pro Ser Gly Met Thr Leu Asp  
930 935 940

Ala Thr Gly Arg Ile Cys Leu Asp Ile Arg Leu Glu Thr Cys Phe Leu  
945 950 955 960

Arg Tyr Glu Asp Glu Glu Cys Thr Leu Pro Ile Ala Gly Arg His Arg  
965 970 975

Met Asp Ala Cys Cys Cys Ser Val Gly Ala Ala Trp Gly Thr Glu Glu  
980 985 990

Cys Glu Glu Cys Pro Met Arg Asn Thr Pro Glu Tyr Glu Glu Leu Cys  
995 1000 1005

Pro Arg Gly Pro Gly Phe Ala Thr Lys Glu Ile Thr Asn Gly Lys  
1010 1015 1020

Pro Phe Phe Lys Asp Ile Asn Glu Cys Lys Met Ile Pro Ser Leu  
1025 1030 1035

Cys Thr His Gly Lys Cys Arg Asn Thr Ile Gly Ser Phe Lys Cys  
1040 1045 1050

Arg Cys Asp Ser Gly Phe Ala Leu Asp Ser Glu Glu Arg Asn Cys  
1055 1060 1065

Thr Asp Ile Asp Glu Cys Arg Ile Ser Pro Asp Leu Cys Gly Arg  
1070 1075 1080

Gly Gln Cys Val Asn Thr Pro Gly Asp Phe Glu Cys Lys Cys Asp  
1085 1090 1095

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Glu	Gly	Tyr	Glu	Ser	Gly	Phe	Met	Met	Met	Lys	Asn	Cys	Met	Asp
	1100					1105					1110			
Ile	Asp	Glu	Cys	Gln	Arg	Asp	Pro	Leu	Leu	Cys	Arg	Gly	Gly	Val
	1115					1120					1125			
Cys	His	Asn	Thr	Glu	Gly	Ser	Tyr	Arg	Cys	Glu	Cys	Pro	Pro	Gly
	1130					1135					1140			
His	Gln	Leu	Ser	Pro	Asn	Ile	Ser	Ala	Cys	Ile	Asp	Ile	Asn	Glu
	1145					1150					1155			
Cys	Glu	Leu	Ser	Ala	His	Leu	Cys	Pro	Asn	Gly	Arg	Cys	Val	Asn
	1160					1165					1170			
Leu	Ile	Gly	Lys	Tyr	Gln	Cys	Ala	Cys	Asn	Pro	Gly	Tyr	His	Ser
	1175					1180					1185			
Thr	Pro	Asp	Arg	Leu	Phe	Cys	Val	Asp	Ile	Asp	Glu	Cys	Ser	Ile
	1190					1195					1200			
Met	Asn	Gly	Gly	Cys	Glu	Thr	Phe	Cys	Thr	Asn	Ser	Glu	Gly	Ser
	1205					1210					1215			
Tyr	Glu	Cys	Ser	Cys	Gln	Pro	Gly	Phe	Ala	Leu	Met	Pro	Asp	Gln
	1220					1225					1230			
Arg	Ser	Cys	Thr	Asp	Ile	Asp	Glu	Cys	Glu	Asp	Asn	Pro	Asn	Ile
	1235					1240					1245			
Cys	Asp	Gly	Gly	Gln	Cys	Thr	Asn	Ile	Pro	Gly	Glu	Tyr	Arg	Cys
	1250					1255					1260			
Leu	Cys	Tyr	Asp	Gly	Phe	Met	Ala	Ser	Glu	Asp	Met	Lys	Thr	Cys
	1265					1270					1275			
Val	Asp	Val	Asn	Glu	Cys	Asp	Leu	Asn	Pro	Asn	Ile	Cys	Leu	Ser
	1280					1285					1290			
Gly	Thr	Cys	Glu	Asn	Thr	Lys	Gly	Ser	Phe	Ile	Cys	His	Cys	Asp
	1295					1300					1305			
Met	Gly	Tyr	Ser	Gly	Lys	Lys	Gly	Lys	Thr	Gly	Cys	Thr	Asp	Ile
	1310					1315					1320			
Asn	Glu	Cys	Glu	Ile	Gly	Ala	His	Asn	Cys	Gly	Lys	His	Ala	Val
	1325					1330					1335			
Cys	Thr	Asn	Thr	Ala	Gly	Ser	Phe	Lys	Cys	Ser	Cys	Ser	Pro	Gly
	1340					1345					1350			



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Trp Ile Gly Asp Gly Ile Lys Cys Thr Asp Leu Asp Glu Cys Ser  
 1355 1360 1365  
 Asn Gly Thr His Met Cys Ser Gln His Ala Asp Cys Lys Asn Thr  
 1370 1375 1380  
 Met Gly Ser Tyr Arg Cys Leu Cys Lys Glu Gly Tyr Thr Gly Asp  
 1385 1390 1395  
 Gly Phe Thr Cys Thr Asp Leu Asp Glu Cys Ser Glu Asn Leu Asn  
 1400 1405 1410  
 Leu Cys Gly Asn Gly Gln Cys Leu Asn Ala Pro Gly Gly Tyr Arg  
 1415 1420 1425  
 Cys Glu Cys Asp Met Gly Phe Val Pro Ser Ala Asp Gly Lys Ala  
 1430 1435 1440  
 Cys Glu Asp Ile Asp Glu Cys Ser Leu Pro Asn Ile Cys Val Phe  
 1445 1450 1455  
 Gly Thr Cys His Asn Leu Pro Gly Leu Phe Arg Cys Glu Cys Glu  
 1460 1465 1470  
 Ile Gly Tyr Glu Leu Asp Arg Ser Gly Gly Asn Cys Thr Asp Val  
 1475 1480 1485  
 Asn Glu Cys Leu Asp Pro Thr Thr Cys Ile Ser Gly Asn Cys Val  
 1490 1495 1500  
 Asn Thr Pro Gly Ser Tyr Ile Cys Asp Cys Pro Pro Asp Phe Glu  
 1505 1510 1515  
 Leu Asn Pro Thr Arg Val Gly Cys Val Asp Thr Arg Ser Gly Asn  
 1520 1525 1530  
 Cys Tyr Leu Asp Ile Arg Pro Arg Gly Asp Asn Gly Asp Thr Ala  
 1535 1540 1545  
 Cys Ser Asn Glu Ile Gly Val Gly Val Ser Lys Ala Ser Cys Cys  
 1550 1555 1560  
 Cys Ser Leu Gly Lys Ala Trp Gly Thr Pro Cys Glu Met Cys Pro  
 1565 1570 1575  
 Ala Val Asn Thr Ser Glu Tyr Lys Ile Leu Cys Pro Gly Gly Glu  
 1580 1585 1590  
 Gly Phe Arg Pro Asn Pro Ile Thr Val Ile Leu Glu Asp Ile Asp  
 1595 1600 1605

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Glu	Cys	Gln	Glu	Leu	Pro	Gly	Leu	Cys	Gln	Gly	Gly	Lys	Cys	Ile
	1610					1615					1620			
Asn	Thr	Phe	Gly	Ser	Phe	Gln	Cys	Arg	Cys	Pro	Thr	Gly	Tyr	Tyr
	1625					1630					1635			
Leu	Asn	Glu	Asp	Thr	Arg	Val	Cys	Asp	Asp	Val	Asn	Glu	Cys	Glu
	1640					1645					1650			
Thr	Pro	Gly	Ile	Cys	Gly	Pro	Gly	Thr	Cys	Tyr	Asn	Thr	Val	Gly
	1655					1660					1665			
Asn	Tyr	Thr	Cys	Ile	Cys	Pro	Pro	Asp	Tyr	Met	Gln	Val	Asn	Gly
	1670					1675					1680			
Gly	Asn	Asn	Cys	Met	Asp	Met	Arg	Arg	Ser	Leu	Cys	Tyr	Arg	Asn
	1685					1690					1695			
Tyr	Tyr	Ala	Asp	Asn	Gln	Thr	Cys	Asp	Gly	Glu	Leu	Leu	Phe	Asn
	1700					1705					1710			
Met	Thr	Lys	Lys	Met	Cys	Cys	Cys	Ser	Tyr	Asn	Ile	Gly	Arg	Ala
	1715					1720					1725			
Trp	Asn	Lys	Pro	Cys	Glu	Gln	Cys	Pro	Ile	Pro	Ser	Thr	Asp	Glu
	1730					1735					1740			
Phe	Ala	Thr	Leu	Cys	Gly	Ser	Gln	Arg	Pro	Gly	Phe	Val	Ile	Asp
	1745					1750					1755			
Ile	Tyr	Thr	Gly	Leu	Pro	Val	Asp	Ile	Asp	Glu	Cys	Arg	Glu	Ile
	1760					1765					1770			
Pro	Gly	Val	Cys	Glu	Asn	Gly	Val	Cys	Ile	Asn	Met	Val	Gly	Ser
	1775					1780					1785			
Phe	Arg	Cys	Glu	Cys	Pro	Val	Gly	Phe	Phe	Tyr	Asn	Asp	Lys	Leu
	1790					1795					1800			
Leu	Val	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Gln	Asn	Gly	Pro	Val	Cys
	1805					1810					1815			
Gln	Arg	Asn	Ala	Glu	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Arg	Cys
	1820					1825					1830			
Asp	Cys	Lys	Pro	Gly	Tyr	Arg	Phe	Thr	Ser	Thr	Gly	Gln	Cys	Asn
	1835					1840					1845			
Asp	Arg	Asn	Glu	Cys	Gln	Glu	Ile	Pro	Asn	Ile	Cys	Ser	His	Gly
	1850					1855					1860			

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Gln	Cys	Ile	Asp	Thr	Val	Gly	Ser	Phe	Tyr	Cys	Leu	Cys	His	Thr
	1865					1870					1875			
Gly	Phe	Lys	Thr	Asn	Asp	Asp	Gln	Thr	Met	Cys	Leu	Asp	Ile	Asn
	1880					1885					1890			
Glu	Cys	Glu	Arg	Asp	Ala	Cys	Gly	Asn	Gly	Thr	Cys	Arg	Asn	Thr
	1895					1900					1905			
Ile	Gly	Ser	Phe	Asn	Cys	Arg	Cys	Asn	His	Gly	Phe	Ile	Leu	Ser
	1910					1915					1920			
His	Asn	Asn	Asp	Cys	Ile	Asp	Val	Asp	Glu	Cys	Ala	Ser	Gly	Asn
	1925					1930					1935			
Gly	Asn	Leu	Cys	Arg	Asn	Gly	Gln	Cys	Ile	Asn	Thr	Val	Gly	Ser
	1940					1945					1950			
Phe	Gln	Cys	Gln	Cys	Asn	Glu	Gly	Tyr	Glu	Val	Ala	Pro	Asp	Gly
	1955					1960					1965			
Arg	Thr	Cys	Val	Asp	Ile	Asn	Glu	Cys	Leu	Leu	Glu	Pro	Arg	Lys
	1970					1975					1980			
Cys	Ala	Pro	Gly	Thr	Cys	Gln	Asn	Leu	Asp	Gly	Ser	Tyr	Arg	Cys
	1985					1990					1995			
Ile	Cys	Pro	Pro	Gly	Tyr	Ser	Leu	Gln	Asn	Glu	Lys	Cys	Glu	Asp
	2000					2005					2010			
Ile	Asp	Glu	Cys	Val	Glu	Glu	Pro	Glu	Ile	Cys	Ala	Leu	Gly	Thr
	2015					2020					2025			
Cys	Ser	Asn	Thr	Glu	Gly	Ser	Phe	Lys	Cys	Leu	Cys	Pro	Glu	Gly
	2030					2035					2040			
Phe	Ser	Leu	Ser	Ser	Ser	Gly	Arg	Arg	Cys	Gln	Asp	Leu	Arg	Met
	2045					2050					2055			
Ser	Tyr	Cys	Tyr	Ala	Lys	Phe	Glu	Gly	Gly	Lys	Cys	Ser	Ser	Pro
	2060					2065					2070			
Lys	Ser	Arg	Asn	His	Ser	Lys	Gln	Glu	Cys	Cys	Cys	Ala	Leu	Lys
	2075					2080					2085			
Gly	Glu	Gly	Trp	Gly	Asp	Pro	Cys	Glu	Leu	Cys	Pro	Thr	Glu	Pro
	2090					2095					2100			
Asp	Glu	Ala	Phe	Arg	Gln	Ile	Cys	Pro	Tyr	Gly	Ser	Gly	Ile	Ile
	2105					2110					2115			

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Val	Gly	Pro	Asp	Asp	Ser	Ala	Val	Asp	Met	Asp	Glu	Cys	Lys	Glu
	2120					2125					2130			
Pro	Asp	Val	Cys	Lys	His	Gly	Gln	Cys	Ile	Asn	Thr	Asp	Gly	Ser
	2135					2140					2145			
Tyr	Arg	Cys	Glu	Cys	Pro	Phe	Gly	Tyr	Ile	Leu	Ala	Gly	Asn	Glu
	2150					2155					2160			
Cys	Val	Asp	Thr	Asp	Glu	Cys	Ser	Val	Gly	Asn	Pro	Cys	Gly	Asn
	2165					2170					2175			
Gly	Thr	Cys	Lys	Asn	Val	Ile	Gly	Gly	Phe	Glu	Cys	Thr	Cys	Glu
	2180					2185					2190			
Glu	Gly	Phe	Glu	Pro	Gly	Pro	Met	Met	Thr	Cys	Glu	Asp	Ile	Asn
	2195					2200					2205			
Glu	Cys	Ala	Gln	Asn	Pro	Leu	Leu	Cys	Ala	Phe	Arg	Cys	Val	Asn
	2210					2215					2220			
Thr	Tyr	Gly	Ser	Tyr	Glu	Cys	Lys	Cys	Pro	Val	Gly	Tyr	Val	Leu
	2225					2230					2235			
Arg	Glu	Asp	Arg	Arg	Met	Cys	Lys	Asp	Glu	Asp	Glu	Cys	Glu	Glu
	2240					2245					2250			
Gly	Lys	His	Asp	Cys	Thr	Glu	Lys	Gln	Met	Glu	Cys	Lys	Asn	Leu
	2255					2260					2265			
Ile	Gly	Thr	Tyr	Met	Cys	Ile	Cys	Gly	Pro	Gly	Tyr	Gln	Arg	Arg
	2270					2275					2280			
Pro	Asp	Gly	Glu	Gly	Cys	Val	Asp	Glu	Asn	Glu	Cys	Gln	Thr	Lys
	2285					2290					2295			
Pro	Gly	Ile	Cys	Glu	Asn	Gly	Arg	Cys	Leu	Asn	Thr	Arg	Gly	Ser
	2300					2305					2310			
Tyr	Thr	Cys	Glu	Cys	Asn	Asp	Gly	Phe	Thr	Ala	Ser	Pro	Asn	Gln
	2315					2320					2325			
Asp	Glu	Cys	Leu	Asp	Asn	Arg	Glu	Gly	Tyr	Cys	Phe	Thr	Glu	Val
	2330					2335					2340			
Leu	Gln	Asn	Met	Cys	Gln	Ile	Gly	Ser	Ser	Asn	Arg	Asn	Pro	Val
	2345					2350					2355			
Thr	Lys	Ser	Glu	Cys	Cys	Cys	Asp	Gly	Gly	Arg	Gly	Trp	Gly	Pro
	2360					2365					2370			

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His	Cys	Glu	Ile	Cys	Pro	Phe	Gln	Gly	Thr	Val	Ala	Phe	Lys	Lys
	2375					2380					2385			
Leu	Cys	Pro	His	Gly	Arg	Gly	Phe	Met	Thr	Asn	Gly	Ala	Asp	Ile
	2390					2395					2400			
Asp	Glu	Cys	Lys	Val	Ile	His	Asp	Val	Cys	Arg	Asn	Gly	Glu	Cys
	2405					2410					2415			
Val	Asn	Asp	Arg	Gly	Ser	Tyr	His	Cys	Ile	Cys	Lys	Thr	Gly	Tyr
	2420					2425					2430			
Thr	Pro	Asp	Ile	Thr	Gly	Thr	Ser	Cys	Val	Asp	Leu	Asn	Glu	Cys
	2435					2440					2445			
Asn	Gln	Ala	Pro	Lys	Pro	Cys	Asn	Phe	Ile	Cys	Lys	Asn	Thr	Glu
	2450					2455					2460			
Gly	Ser	Tyr	Gln	Cys	Ser	Cys	Pro	Lys	Gly	Tyr	Ile	Leu	Gln	Glu
	2465					2470					2475			
Asp	Gly	Arg	Ser	Cys	Lys	Asp	Leu	Asp	Glu	Cys	Ala	Thr	Lys	Gln
	2480					2485					2490			
His	Asn	Cys	Gln	Phe	Leu	Cys	Val	Asn	Thr	Ile	Gly	Gly	Phe	Thr
	2495					2500					2505			
Cys	Lys	Cys	Pro	Pro	Gly	Phe	Thr	Gln	His	His	Thr	Ser	Cys	Ile
	2510					2515					2520			
Asp	Asn	Asn	Glu	Cys	Thr	Ser	Asp	Ile	Asn	Leu	Cys	Gly	Ser	Lys
	2525					2530					2535			
Gly	Ile	Cys	Gln	Asn	Thr	Pro	Gly	Ser	Phe	Thr	Cys	Glu	Cys	Gln
	2540					2545					2550			
Arg	Gly	Phe	Ser	Leu	Asp	Gln	Thr	Gly	Ser	Ser	Cys	Glu	Asp	Val
	2555					2560					2565			
Asp	Glu	Cys	Glu	Gly	Asn	His	Arg	Cys	Gln	His	Gly	Cys	Gln	Asn
	2570					2575					2580			
Ile	Ile	Gly	Gly	Tyr	Arg	Cys	Ser	Cys	Pro	Gln	Gly	Tyr	Leu	Gln
	2585					2590					2595			
His	Tyr	Gln	Trp	Asn	Gln	Cys	Val	Asp	Glu	Asn	Glu	Cys	Leu	Ser
	2600					2605					2610			
Ala	His	Ile	Cys	Gly	Gly	Ala	Ser	Cys	His	Asn	Thr	Leu	Gly	Ser
	2615					2620					2625			

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Tyr	Lys	Cys	Met	Cys	Pro	Ala	Gly	Phe	Gln	Tyr	Glu	Gln	Phe	Ser
	2630					2635					2640			
Gly	Gly	Cys	Gln	Asp	Ile	Asn	Glu	Cys	Gly	Ser	Ala	Gln	Ala	Pro
	2645					2650					2655			
Cys	Ser	Tyr	Gly	Cys	Ser	Asn	Thr	Glu	Gly	Gly	Tyr	Leu	Cys	Gly
	2660					2665					2670			
Cys	Pro	Pro	Gly	Tyr	Phe	Arg	Ile	Gly	Gln	Gly	His	Cys	Val	Ser
	2675					2680					2685			
Gly	Met	Gly	Met	Gly	Arg	Gly	Asn	Pro	Glu	Pro	Pro	Val	Ser	Gly
	2690					2695					2700			
Glu	Met	Asp	Asp	Asn	Ser	Leu	Ser	Pro	Glu	Ala	Cys	Tyr	Glu	Cys
	2705					2710					2715			
Lys	Ile	Asn	Gly	Tyr	Pro	Lys	Arg	Gly	Arg	Lys	Arg	Arg	Ser	Thr
	2720					2725					2730			
Asn	Glu	Thr	Asp	Ala	Ser	Asn	Ile	Glu	Asp	Gln	Ser	Glu	Thr	Glu
	2735					2740					2745			
Ala	Asn	Val	Ser	Leu	Ala	Ser	Trp	Asp	Val	Glu	Lys	Thr	Ala	Ile
	2750					2755					2760			
Phe	Ala	Phe	Asn	Ile	Ser	His	Val	Ser	Asn	Lys	Val	Arg	Ile	Leu
	2765					2770					2775			
Glu	Leu	Leu	Pro	Ala	Leu	Thr	Thr	Leu	Thr	Asn	His	Asn	Arg	Tyr
	2780					2785					2790			
Leu	Ile	Glu	Ser	Gly	Asn	Glu	Asp	Gly	Phe	Phe	Lys	Ile	Asn	Gln
	2795					2800					2805			
Lys	Glu	Gly	Ile	Ser	Tyr	Leu	His	Phe	Thr	Lys	Lys	Lys	Pro	Val
	2810					2815					2820			
Ala	Gly	Thr	Tyr	Ser	Leu	Gln	Ile	Ser	Ser	Thr	Pro	Leu	Tyr	Lys
	2825					2830					2835			
Lys	Lys	Glu	Leu	Asn	Gln	Leu	Glu	Asp	Lys	Tyr	Asp	Lys	Asp	Tyr
	2840					2845					2850			
Leu	Ser	Gly	Glu	Leu	Gly	Asp	Asn	Leu	Lys	Met	Lys	Ile	Gln	Val
	2855					2860					2865			
Leu	Leu	His												
	2870													

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<210> 135  
 <211> 2912  
 <212> PRT  
 <213> Homo sapiens

<400> 135

Met Gly Arg Arg Arg Arg Leu Cys Leu Gln Leu Tyr Phe Leu Trp Leu  
 1 5 10 15

Gly Cys Val Val Leu Trp Ala Gln Gly Thr Ala Gly Gln Pro Gln Pro  
 20 25 30

Pro Pro Pro Lys Pro Pro Arg Pro Gln Pro Pro Pro Gln Gln Val Arg  
 35 40 45

Ser Ala Thr Ala Gly Ser Glu Gly Gly Phe Leu Ala Pro Glu Tyr Arg  
 50 55 60

Glu Glu Gly Ala Ala Val Ala Ser Arg Val Arg Arg Arg Gly Gln Gln  
 65 70 75 80

Asp Val Leu Arg Gly Pro Asn Val Cys Gly Ser Arg Phe His Ser Tyr  
 85 90 95

Cys Cys Pro Gly Trp Lys Thr Leu Pro Gly Gly Asn Gln Cys Ile Val  
 100 105 110

Pro Ile Cys Arg Asn Ser Cys Gly Asp Gly Phe Cys Ser Arg Pro Asn  
 115 120 125

Met Cys Thr Cys Ser Ser Gly Gln Ile Ser Ser Thr Cys Gly Ser Lys  
 130 135 140

Ser Ile Gln Gln Cys Ser Val Arg Cys Met Asn Gly Gly Thr Cys Ala  
 145 150 155 160

Asp Asp His Cys Gln Cys Gln Lys Gly Tyr Ile Gly Thr Tyr Cys Gly  
 165 170 175

Gln Pro Val Cys Glu Asn Gly Cys Gln Asn Gly Gly Arg Cys Ile Gly  
 180 185 190

Pro Asn Arg Cys Ala Cys Val Tyr Gly Phe Thr Gly Pro Gln Cys Glu  
 195 200 205

Arg Asp Tyr Arg Thr Gly Pro Cys Phe Thr Gln Val Asn Asn Gln Met  
 210 215 220

Cys Gln Gly Gln Leu Thr Gly Ile Val Cys Thr Lys Thr Leu Cys Cys  
 225 230 235 240

Ala Thr Ile Gly Arg Ala Trp Gly His Pro Cys Glu Met Cys Pro Ala

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245

250

255

Gln Pro Gln Pro Cys Arg Arg Gly Phe Ile Pro Asn Ile Arg Thr Gly  
260 265 270

Ala Cys Gln Asp Val Asp Glu Cys Gln Ala Ile Pro Gly Ile Cys Gln  
275 280 285

Gly Gly Asn Cys Ile Asn Thr Val Gly Ser Phe Glu Cys Arg Cys Pro  
290 295 300

Ala Gly His Lys Gln Ser Glu Thr Thr Gln Lys Cys Glu Asp Ile Asp  
305 310 315 320

Glu Cys Ser Ile Ile Pro Gly Ile Cys Glu Thr Gly Glu Cys Ser Asn  
325 330 335

Thr Val Gly Ser Tyr Phe Cys Val Cys Pro Arg Gly Tyr Val Thr Ser  
340 345 350

Thr Asp Gly Ser Arg Cys Ile Asp Gln Arg Thr Gly Met Cys Phe Ser  
355 360 365

Gly Leu Val Asn Gly Arg Cys Ala Gln Glu Leu Pro Gly Arg Met Thr  
370 375 380

Lys Met Gln Cys Cys Cys Glu Pro Gly Arg Cys Trp Gly Ile Gly Thr  
385 390 395 400

Ile Pro Glu Ala Cys Pro Val Arg Gly Ser Glu Glu Tyr Arg Arg Leu  
405 410 415

Cys Met Asp Gly Leu Pro Met Gly Gly Ile Pro Gly Ser Ala Gly Ser  
420 425 430

Arg Pro Gly Gly Thr Gly Gly Asn Gly Phe Ala Pro Ser Gly Asn Gly  
435 440 445

Asn Gly Tyr Gly Pro Gly Gly Thr Gly Phe Ile Pro Ile Pro Gly Gly  
450 455 460

Asn Gly Phe Ser Pro Gly Val Gly Gly Ala Gly Val Gly Ala Gly Gly  
465 470 475 480

Gln Gly Pro Ile Ile Thr Gly Leu Thr Ile Leu Asn Gln Thr Ile Asp  
485 490 495

Ile Cys Lys His His Ala Asn Leu Cys Leu Asn Gly Arg Cys Ile Pro  
500 505 510

Thr Val Ser Ser Tyr Arg Cys Glu Cys Asn Met Gly Tyr Lys Gln Asp



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515

520

525

Ala Asn Gly Asp Cys Ile Asp Val Asp Glu Cys Thr Ser Asn Pro Cys  
530 535 540

Thr Asn Gly Asp Cys Val Asn Thr Pro Gly Ser Tyr Tyr Cys Lys Cys  
545 550 555 560

His Ala Gly Phe Gln Arg Thr Pro Thr Lys Gln Ala Cys Ile Asp Ile  
565 570 575

Asp Glu Cys Ile Gln Asn Gly Val Leu Cys Lys Asn Gly Arg Cys Val  
580 585 590

Asn Thr Asp Gly Ser Phe Gln Cys Ile Cys Asn Ala Gly Phe Glu Leu  
595 600 605

Thr Thr Asp Gly Lys Asn Cys Val Asp His Asp Glu Cys Thr Thr Thr  
610 615 620

Asn Met Cys Leu Asn Gly Met Cys Ile Asn Glu Asp Gly Ser Phe Lys  
625 630 635 640

Cys Ile Cys Lys Pro Gly Phe Val Leu Ala Pro Asn Gly Arg Tyr Cys  
645 650 655

Thr Asp Val Asp Glu Cys Gln Thr Pro Gly Ile Cys Met Asn Gly His  
660 665 670

Cys Ile Asn Ser Glu Gly Ser Phe Arg Cys Asp Cys Pro Pro Gly Leu  
675 680 685

Ala Val Gly Met Asp Gly Arg Val Cys Val Asp Thr His Met Arg Ser  
690 695 700

Thr Cys Tyr Gly Gly Ile Lys Lys Gly Val Cys Val Arg Pro Phe Pro  
705 710 715 720

Gly Ala Val Thr Lys Ser Glu Cys Cys Cys Ala Asn Pro Asp Tyr Gly  
725 730 735

Phe Gly Glu Pro Cys Gln Pro Cys Pro Ala Lys Asn Ser Ala Glu Phe  
740 745 750

His Gly Leu Cys Ser Ser Gly Val Gly Ile Thr Val Asp Gly Arg Asp  
755 760 765

Ile Asn Glu Cys Ala Leu Asp Pro Asp Ile Cys Ala Asn Gly Ile Cys  
770 775 780

Glu Asn Leu Arg Gly Ser Tyr Arg Cys Asn Cys Asn Ser Gly Tyr Glu



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1055															
Pro	Phe	Tyr	Lys	Asp	Ile	Asn	Glu	Cys	Lys	Ala	Phe	Pro	Gly	Met	
	1070					1075					1080				
Cys	Thr	Tyr	Gly	Lys	Cys	Arg	Asn	Thr	Ile	Gly	Ser	Phe	Lys	Cys	
	1085					1090					1095				
Arg	Cys	Asn	Ser	Gly	Phe	Ala	Leu	Asp	Met	Glu	Glu	Arg	Asn	Cys	
	1100					1105					1110				
Thr	Asp	Ile	Asp	Glu	Cys	Arg	Ile	Ser	Pro	Asp	Leu	Cys	Gly	Ser	
	1115					1120					1125				
Gly	Ile	Cys	Val	Asn	Thr	Pro	Gly	Ser	Phe	Glu	Cys	Glu	Cys	Phe	
	1130					1135					1140				
Glu	Gly	Tyr	Glu	Ser	Gly	Phe	Met	Met	Met	Lys	Asn	Cys	Met	Asp	
	1145					1150					1155				
Ile	Asp	Glu	Cys	Glu	Arg	Asn	Pro	Leu	Leu	Cys	Arg	Gly	Gly	Thr	
	1160					1165					1170				
Cys	Val	Asn	Thr	Glu	Gly	Ser	Phe	Gln	Cys	Asp	Cys	Pro	Leu	Gly	
	1175					1180					1185				
His	Glu	Leu	Ser	Pro	Ser	Arg	Glu	Asp	Cys	Val	Asp	Ile	Asn	Glu	
	1190					1195					1200				
Cys	Ser	Leu	Ser	Asp	Asn	Leu	Cys	Arg	Asn	Gly	Lys	Cys	Val	Asn	
	1205					1210					1215				
Met	Ile	Gly	Thr	Tyr	Gln	Cys	Ser	Cys	Asn	Pro	Gly	Tyr	Gln	Ala	
	1220					1225					1230				
Thr	Pro	Asp	Arg	Gln	Gly	Cys	Thr	Asp	Ile	Asp	Glu	Cys	Met	Ile	
	1235					1240					1245				
Met	Asn	Gly	Gly	Cys	Asp	Thr	Gln	Cys	Thr	Asn	Ser	Glu	Gly	Ser	
	1250					1255					1260				
Tyr	Glu	Cys	Ser	Cys	Ser	Glu	Gly	Tyr	Ala	Leu	Met	Pro	Asp	Gly	
	1265					1270					1275				
Arg	Ser	Cys	Ala	Asp	Ile	Asp	Glu	Cys	Glu	Asn	Asn	Pro	Asp	Ile	
	1280					1285					1290				
Cys	Asp	Gly	Gly	Gln	Cys	Thr	Asn	Ile	Pro	Gly	Glu	Tyr	Arg	Cys	
	1295					1300					1305				
Leu	Cys	Tyr	Asp	Gly	Phe	Met	Ala	Ser	Met	Asp	Met	Lys	Thr	Cys	

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1310														
Ile	Asp	Val	Asn	Glu	Cys	Asp	Leu	Asn	Ser	Asn	Ile	Cys	Met	Phe
	1325					1330					1335			
Gly	Glu	Cys	Glu	Asn	Thr	Lys	Gly	Ser	Phe	Ile	Cys	His	Cys	Gln
	1340					1345					1350			
Leu	Gly	Tyr	Ser	Val	Lys	Lys	Gly	Thr	Thr	Gly	Cys	Thr	Asp	Val
	1355					1360					1365			
Asp	Glu	Cys	Glu	Ile	Gly	Ala	His	Asn	Cys	Asp	Met	His	Ala	Ser
	1370					1375					1380			
Cys	Leu	Asn	Ile	Pro	Gly	Ser	Phe	Lys	Cys	Ser	Cys	Arg	Glu	Gly
	1385					1390					1395			
Trp	Ile	Gly	Asn	Gly	Ile	Lys	Cys	Ile	Asp	Leu	Asp	Glu	Cys	Ser
	1400					1405					1410			
Asn	Gly	Thr	His	Gln	Cys	Ser	Ile	Asn	Ala	Gln	Cys	Val	Asn	Thr
	1415					1420					1425			
Pro	Gly	Ser	Tyr	Arg	Cys	Ala	Cys	Ser	Glu	Gly	Phe	Thr	Gly	Asp
	1430					1435					1440			
Gly	Phe	Thr	Cys	Ser	Asp	Val	Asp	Glu	Cys	Ala	Glu	Asn	Ile	Asn
	1445					1450					1455			
Leu	Cys	Glu	Asn	Gly	Gln	Cys	Leu	Asn	Val	Pro	Gly	Ala	Tyr	Arg
	1460					1465					1470			
Cys	Glu	Cys	Glu	Met	Gly	Phe	Thr	Pro	Ala	Ser	Asp	Ser	Arg	Ser
	1475					1480					1485			
Cys	Gln	Asp	Ile	Asp	Glu	Cys	Ser	Phe	Gln	Asn	Ile	Cys	Val	Phe
	1490					1495					1500			
Gly	Thr	Cys	Asn	Asn	Leu	Pro	Gly	Met	Phe	His	Cys	Ile	Cys	Asp
	1505					1510					1515			
Asp	Gly	Tyr	Glu	Leu	Asp	Arg	Thr	Gly	Gly	Asn	Cys	Thr	Asp	Ile
	1520					1525					1530			
Asp	Glu	Cys	Ala	Asp	Pro	Ile	Asn	Cys	Val	Asn	Gly	Leu	Cys	Val
	1535					1540					1545			
Asn	Thr	Pro	Gly	Arg	Tyr	Glu	Cys	Asn	Cys	Pro	Pro	Asp	Phe	Gln
	1550					1555					1560			
Leu	Asn	Pro	Thr	Gly	Val	Gly	Cys	Val	Asp	Asn	Arg	Val	Gly	Asn

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1565														
						1570								1575
Cys	Tyr	Leu	Lys	Phe	Gly	Pro	Arg	Gly	Asp	Gly	Ser	Leu	Ser	Cys
1580						1585					1590			
Asn	Thr	Glu	Ile	Gly	Val	Gly	Val	Ser	Arg	Ser	Ser	Cys	Cys	Cys
1595						1600					1605			
Ser	Leu	Gly	Lys	Ala	Trp	Gly	Asn	Pro	Cys	Glu	Thr	Cys	Pro	Pro
1610						1615					1620			
Val	Asn	Ser	Thr	Glu	Tyr	Tyr	Thr	Leu	Cys	Pro	Gly	Gly	Glu	Gly
1625						1630					1635			
Phe	Arg	Pro	Asn	Pro	Ile	Thr	Ile	Ile	Leu	Glu	Asp	Ile	Asp	Glu
1640						1645					1650			
Cys	Gln	Glu	Leu	Pro	Gly	Leu	Cys	Gln	Gly	Gly	Asn	Cys	Ile	Asn
1655						1660					1665			
Thr	Phe	Gly	Ser	Phe	Gln	Cys	Glu	Cys	Pro	Gln	Gly	Tyr	Tyr	Leu
1670						1675					1680			
Ser	Glu	Asp	Thr	Arg	Ile	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Phe	Ala
1685						1690					1695			
His	Pro	Gly	Val	Cys	Gly	Pro	Gly	Thr	Cys	Tyr	Asn	Thr	Leu	Gly
1700						1705					1710			
Asn	Tyr	Thr	Cys	Ile	Cys	Pro	Pro	Glu	Tyr	Met	Gln	Val	Asn	Gly
1715						1720					1725			
Gly	His	Asn	Cys	Met	Asp	Met	Arg	Lys	Ser	Phe	Cys	Tyr	Arg	Ser
1730						1735					1740			
Tyr	Asn	Gly	Thr	Thr	Cys	Glu	Asn	Glu	Leu	Pro	Phe	Asn	Val	Thr
1745						1750					1755			
Lys	Arg	Met	Cys	Cys	Cys	Thr	Tyr	Asn	Val	Gly	Lys	Ala	Trp	Asn
1760						1765					1770			
Lys	Pro	Cys	Glu	Pro	Cys	Pro	Thr	Pro	Gly	Thr	Ala	Asp	Phe	Lys
1775						1780					1785			
Thr	Ile	Cys	Gly	Asn	Ile	Pro	Gly	Phe	Thr	Phe	Asp	Ile	His	Thr
1790						1795					1800			
Gly	Lys	Ala	Val	Asp	Ile	Asp	Glu	Cys	Lys	Glu	Ile	Pro	Gly	Ile
1805						1810					1815			
Cys	Ala	Asn	Gly	Val	Cys	Ile	Asn	Gln	Ile	Gly	Ser	Phe	Arg	Cys

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1820						1825						1830			
Glu	Cys	Pro	Thr	Gly	Phe	Ser	Tyr	Asn	Asp	Leu	Leu	Leu	Val	Cys	
	1835					1840					1845				
Glu	Asp	Ile	Asp	Glu	Cys	Ser	Asn	Gly	Asp	Asn	Leu	Cys	Gln	Arg	
	1850					1855					1860				
Asn	Ala	Asp	Cys	Ile	Asn	Ser	Pro	Gly	Ser	Tyr	Arg	Cys	Glu	Cys	
	1865					1870					1875				
Ala	Ala	Gly	Phe	Lys	Leu	Ser	Pro	Asn	Gly	Ala	Cys	Val	Asp	Arg	
	1880					1885					1890				
Asn	Glu	Cys	Leu	Glu	Ile	Pro	Asn	Val	Cys	Ser	His	Gly	Leu	Cys	
	1895					1900					1905				
Val	Asp	Leu	Gln	Gly	Ser	Tyr	Gln	Cys	Ile	Cys	His	Asn	Gly	Phe	
	1910					1915					1920				
Lys	Ala	Ser	Gln	Asp	Gln	Thr	Met	Cys	Met	Asp	Val	Asp	Glu	Cys	
	1925					1930					1935				
Glu	Arg	His	Pro	Cys	Gly	Asn	Gly	Thr	Cys	Lys	Asn	Thr	Val	Gly	
	1940					1945					1950				
Ser	Tyr	Asn	Cys	Leu	Cys	Tyr	Pro	Gly	Phe	Glu	Leu	Thr	His	Asn	
	1955					1960					1965				
Asn	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ser	Ser	Phe	Phe	Gly	Gln	
	1970					1975					1980				
Val	Cys	Arg	Asn	Gly	Arg	Cys	Phe	Asn	Glu	Ile	Gly	Ser	Phe	Lys	
	1985					1990					1995				
Cys	Leu	Cys	Asn	Glu	Gly	Tyr	Glu	Leu	Thr	Pro	Asp	Gly	Lys	Asn	
	2000					2005					2010				
Cys	Ile	Asp	Thr	Asn	Glu	Cys	Val	Ala	Leu	Pro	Gly	Ser	Cys	Ser	
	2015					2020					2025				
Pro	Gly	Thr	Cys	Gln	Asn	Leu	Glu	Gly	Ser	Phe	Arg	Cys	Ile	Cys	
	2030					2035					2040				
Pro	Pro	Gly	Tyr	Glu	Val	Lys	Ser	Glu	Asn	Cys	Ile	Asp	Ile	Asn	
	2045					2050					2055				
Glu	Cys	Asp	Glu	Asp	Pro	Asn	Ile	Cys	Leu	Phe	Gly	Ser	Cys	Thr	
	2060					2065					2070				
Asn	Thr	Pro	Gly	Gly	Phe	Gln	Cys	Leu	Cys	Pro	Pro	Gly	Phe	Val	

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2075														
Leu	Ser	Asp	Asn	Gly	Arg	Arg	Cys	Phe	Asp	Thr	Arg	Gln	Ser	Phe
2090						2095					2100			
Cys	Phe	Thr	Asn	Phe	Glu	Asn	Gly	Lys	Cys	Ser	Val	Pro	Lys	Ala
2105						2110					2115			
Phe	Asn	Thr	Thr	Lys	Ala	Lys	Cys	Cys	Cys	Ser	Lys	Met	Pro	Gly
2120						2125					2130			
Glu	Gly	Trp	Gly	Asp	Pro	Cys	Glu	Leu	Cys	Pro	Lys	Asp	Asp	Glu
2135						2140					2145			
Val	Ala	Phe	Gln	Asp	Leu	Cys	Pro	Tyr	Gly	His	Gly	Thr	Val	Pro
2150						2155					2160			
Ser	Leu	His	Asp	Thr	Arg	Glu	Asp	Val	Asn	Glu	Cys	Leu	Glu	Ser
2165						2170					2175			
Pro	Gly	Ile	Cys	Ser	Asn	Gly	Gln	Cys	Ile	Asn	Thr	Asp	Gly	Ser
2180						2185					2190			
Phe	Arg	Cys	Glu	Cys	Pro	Met	Gly	Tyr	Asn	Leu	Asp	Tyr	Thr	Gly
2195						2200					2205			
Val	Arg	Cys	Val	Asp	Thr	Asp	Glu	Cys	Ser	Ile	Gly	Asn	Pro	Cys
2210						2215					2220			
Gly	Asn	Gly	Thr	Cys	Thr	Asn	Val	Ile	Gly	Ser	Phe	Glu	Cys	Asn
2225						2230					2235			
Cys	Asn	Glu	Gly	Phe	Glu	Pro	Gly	Pro	Met	Met	Asn	Cys	Glu	Asp
2240						2245					2250			
Ile	Asn	Glu	Cys	Ala	Gln	Asn	Pro	Leu	Leu	Cys	Ala	Phe	Arg	Cys
2255						2260					2265			
Met	Asn	Thr	Phe	Gly	Ser	Tyr	Glu	Cys	Thr	Cys	Pro	Ile	Gly	Tyr
2270						2275					2280			
Ala	Leu	Arg	Glu	Asp	Gln	Lys	Met	Cys	Lys	Asp	Leu	Asp	Glu	Cys
2285						2290					2295			
Ala	Glu	Gly	Leu	His	Asp	Cys	Glu	Ser	Arg	Gly	Met	Met	Cys	Lys
2300						2305					2310			
Asn	Leu	Ile	Gly	Thr	Phe	Met	Cys	Ile	Cys	Pro	Pro	Gly	Met	Ala
2315						2320					2325			
Arg	Arg	Pro	Asp	Gly	Glu	Gly	Cys	Val	Asp	Glu	Asn	Glu	Cys	Arg

## 2340

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2585														
Cys	Gln	Arg	Gly	Phe	Ser	Leu	Asp	Ala	Thr	Gly	Leu	Asn	Cys	Glu
2600						2605					2610			
Asp	Val	Asp	Glu	Cys	Asp	Gly	Asn	His	Arg	Cys	Gln	His	Gly	Cys
2615						2620					2625			
Gln	Asn	Ile	Leu	Gly	Gly	Tyr	Arg	Cys	Gly	Cys	Pro	Gln	Gly	Tyr
2630						2635					2640			
Ile	Gln	His	Tyr	Gln	Trp	Asn	Gln	Cys	Val	Asp	Glu	Asn	Glu	Cys
2645						2650					2655			
Ser	Asn	Pro	Asn	Ala	Cys	Gly	Ser	Ala	Ser	Cys	Tyr	Asn	Thr	Leu
2660						2665					2670			
Gly	Ser	Tyr	Lys	Cys	Ala	Cys	Pro	Ser	Gly	Phe	Ser	Phe	Asp	Gln
2675						2680					2685			
Phe	Ser	Ser	Ala	Cys	His	Asp	Val	Asn	Glu	Cys	Ser	Ser	Ser	Lys
2690						2695					2700			
Asn	Pro	Cys	Asn	Tyr	Gly	Cys	Ser	Asn	Thr	Glu	Gly	Gly	Tyr	Leu
2705						2710					2715			
Cys	Gly	Cys	Pro	Pro	Gly	Tyr	Tyr	Arg	Val	Gly	Gln	Gly	His	Cys
2720						2725					2730			
Val	Ser	Gly	Met	Gly	Phe	Asn	Lys	Gly	Gln	Tyr	Leu	Ser	Leu	Asp
2735						2740					2745			
Thr	Glu	Val	Asp	Glu	Glu	Asn	Ala	Leu	Ser	Pro	Glu	Ala	Cys	Tyr
2750						2755					2760			
Glu	Cys	Lys	Ile	Asn	Gly	Tyr	Ser	Lys	Lys	Asp	Ser	Arg	Gln	Lys
2765						2770					2775			
Arg	Ser	Ile	His	Glu	Pro	Asp	Pro	Thr	Ala	Val	Glu	Gln	Ile	Ser
2780						2785					2790			
Leu	Glu	Ser	Val	Asp	Met	Asp	Ser	Pro	Val	Asn	Met	Lys	Phe	Asn
2795						2800					2805			
Leu	Ser	His	Leu	Gly	Ser	Lys	Glu	His	Ile	Leu	Glu	Leu	Arg	Pro
2810						2815					2820			
Ala	Ile	Gln	Pro	Leu	Asn	Asn	His	Ile	Arg	Tyr	Val	Ile	Ser	Gln
2825						2830					2835			
Gly	Asn	Asp	Asp	Ser	Val	Phe	Arg	Ile	His	Gln	Arg	Asn	Gly	Leu

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2840

2845

2850

Ser Tyr Leu His Thr Ala Lys Lys Lys Leu Met Pro Gly Thr Tyr  
2855 2860 2865

Thr Leu Glu Ile Thr Ser Ile Pro Leu Tyr Lys Lys Lys Glu Leu  
2870 2875 2880

Lys Lys Leu Glu Glu Ser Asn Glu Asp Asp Tyr Leu Leu Gly Glu  
2885 2890 2895

Leu Gly Glu Ala Leu Arg Met Arg Leu Gln Ile Gln Leu Tyr  
2900 2905 2910

<210> 136  
<211> 574  
<212> PRT  
<213> Homo sapiens

<400> 136

Met Ala Leu Ala Arg Gly Ser Arg Gln Leu Gly Ala Leu Val Trp Gly  
1 5 10 15

Ala Cys Leu Cys Val Leu Val His Gly Gln Gln Ala Gln Pro Gly Gln  
20 25 30

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

Gly Gln Val Tyr Ser Leu Leu Asn Ser Gly Ser Glu Tyr Val Pro Ala  
50 55 60

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

Pro Gln Ala Gln Gln Arg Arg Ser His Gly Ser Pro Arg Arg Arg Gln  
85 90 95

Ala Pro Ser Leu Pro Leu Pro Gly Arg Val Gly Ser Asp Thr Val Arg  
100 105 110

Gly Gln Ala Arg His Pro Phe Gly Phe Gly Gln Val Pro Asp Asn Trp  
115 120 125

Arg Glu Val Ala Val Gly Asp Ser Thr Gly Met Ala Arg Ala Arg Thr  
130 135 140

Ser Val Ser Gln Gln Arg His Gly Gly Ser Ala Ser Ser Val Ser Ala  
145 150 155 160

Ser Ala Phe Ala Ser Thr Tyr Arg Gln Gln Pro Ser Tyr Pro Gln Gln  
165 170 175

# FAB-008PC-SequenceListing

Phe Pro Tyr Pro Gln Ala Pro Phe Val Ser Gln Tyr Glu Asn Tyr Asp  
 180 185 190  
 Pro Ala Ser Arg Thr Tyr Asp Gln Gly Phe Val Tyr Tyr Arg Pro Ala  
 195 200 205  
 Gly Gly Gly Val Gly Ala Gly Ala Ala Ala Val Ala Ser Ala Gly Val  
 210 215 220  
 Ile Tyr Pro Tyr Gln Pro Arg Ala Arg Tyr Glu Glu Tyr Gly Gly Gly  
 225 230 235 240  
 Glu Glu Leu Pro Glu Tyr Pro Pro Gln Gly Phe Tyr Pro Ala Pro Glu  
 245 250 255  
 Arg Pro Tyr Val Pro Pro Pro Pro Pro Pro Pro Asp Gly Leu Asp Arg  
 260 265 270  
 Arg Tyr Ser His Ser Leu Tyr Ser Glu Gly Thr Pro Gly Phe Glu Gln  
 275 280 285  
 Ala Tyr Pro Asp Pro Gly Pro Glu Ala Ala Gln Ala His Gly Gly Asp  
 290 295 300  
 Pro Arg Leu Gly Trp Tyr Pro Pro Tyr Ala Asn Pro Pro Pro Glu Ala  
 305 310 315 320  
 Tyr Gly Pro Pro Arg Ala Leu Glu Pro Pro Tyr Leu Pro Val Arg Ser  
 325 330 335  
 Ser Asp Thr Pro Pro Pro Gly Gly Glu Arg Asn Gly Ala Gln Gln Gly  
 340 345 350  
 Arg Leu Ser Val Gly Ser Val Tyr Arg Pro Asn Gln Asn Gly Arg Gly  
 355 360 365  
 Leu Pro Asp Leu Val Pro Asp Pro Asn Tyr Val Gln Ala Ser Thr Tyr  
 370 375 380  
 Val Gln Arg Ala His Leu Tyr Ser Leu Arg Cys Ala Ala Glu Glu Lys  
 385 390 395 400  
 Cys Leu Ala Ser Thr Ala Tyr Ala Pro Glu Ala Thr Asp Tyr Asp Val  
 405 410 415  
 Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln Gly Thr Ala  
 420 425 430  
 Asp Phe Leu Pro Asn Arg Pro Arg His Thr Trp Glu Trp His Ser Cys  
 435 440 445

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His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr Asp Leu Leu  
450 455 460

Asp Ala Ala Thr Gly Lys Lys Val Ala Glu Gly His Lys Ala Ser Phe  
465 470 475 480

Cys Leu Glu Asp Ser Thr Cys Asp Phe Gly Asn Leu Lys Arg Tyr Ala  
485 490 495

Cys Thr Ser His Thr Gln Gly Leu Ser Pro Gly Cys Tyr Asp Thr Tyr  
500 505 510

Asn Ala Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Gln Pro  
515 520 525

Gly Asn Tyr Ile Leu Lys Val His Val Asn Pro Lys Tyr Ile Val Leu  
530 535 540

Glu Ser Asp Phe Thr Asn Asn Val Val Arg Cys Asn Ile His Tyr Thr  
545 550 555 560

Gly Arg Tyr Val Ser Ala Thr Asn Cys Lys Ile Val Gln Ser  
565 570

<210> 137  
<211> 774  
<212> PRT  
<213> Homo sapiens

<400> 137

Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu  
1 5 10 15

Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro His  
20 25 30

Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu Tyr His Gln Pro Gln  
35 40 45

Ala Pro Ala Asn Val Ala Lys Ile Gln Leu Arg Leu Ala Gly Gln Lys  
50 55 60

Arg Lys His Ser Glu Gly Arg Val Glu Val Tyr Tyr Asp Gly Gln Trp  
65 70 75 80

Gly Thr Val Cys Asp Asp Asp Phe Ser Ile His Ala Ala His Val Val  
85 90 95

Cys Arg Glu Leu Gly Tyr Val Glu Ala Lys Ser Trp Thr Ala Ser Ser  
100 105 110

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Ser Tyr Gly Lys Gly Glu Gly Pro Ile Trp Leu Asp Asn Leu His Cys  
115 120 125

Thr Gly Asn Glu Ala Thr Leu Ala Ala Cys Thr Ser Asn Gly Trp Gly  
130 135 140

Val Thr Asp Cys Lys His Thr Glu Asp Val Gly Val Val Cys Ser Asp  
145 150 155 160

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

Glu Asn Leu Asn Ile Gln Val Glu Asp Ile Arg Ile Arg Ala Ile Leu  
180 185 190

Ser Thr Tyr Arg Lys Arg Thr Pro Val Met Glu Gly Tyr Val Glu Val  
195 200 205

Lys Glu Gly Lys Thr Trp Lys Gln Ile Cys Asp Lys His Trp Thr Ala  
210 215 220

Lys Asn Ser Arg Val Val Cys Gly Met Phe Gly Phe Pro Gly Glu Arg  
225 230 235 240

Thr Tyr Asn Thr Lys Val Tyr Lys Met Phe Ala Ser Arg Arg Lys Gln  
245 250 255

Arg Tyr Trp Pro Phe Ser Met Asp Cys Thr Gly Thr Glu Ala His Ile  
260 265 270

Ser Ser Cys Lys Leu Gly Pro Gln Val Ser Leu Asp Pro Met Lys Asn  
275 280 285

Val Thr Cys Glu Asn Gly Leu Pro Ala Val Val Ser Cys Val Pro Gly  
290 295 300

Gln Val Phe Ser Pro Asp Gly Pro Ser Arg Phe Arg Lys Ala Tyr Lys  
305 310 315 320

Pro Glu Gln Pro Leu Val Arg Leu Arg Gly Gly Ala Tyr Ile Gly Glu  
325 330 335

Gly Arg Val Glu Val Leu Lys Asn Gly Glu Trp Gly Thr Val Cys Asp  
340 345 350

Asp Lys Trp Asp Leu Val Ser Ala Ser Val Val Cys Arg Glu Leu Gly  
355 360 365

Phe Gly Ser Ala Lys Glu Ala Val Thr Gly Ser Arg Leu Gly Gln Gly  
370 375 380

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Ile Gly Pro Ile His Leu Asn Glu Ile Gln Cys Thr Gly Asn Glu Lys  
385 390 395 400

Ser Ile Ile Asp Cys Lys Phe Asn Ala Glu Ser Gln Gly Cys Asn His  
405 410 415

Glu Glu Asp Ala Gly Val Arg Cys Asn Thr Pro Ala Met Gly Leu Gln  
420 425 430

Lys Lys Leu Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu Gly Arg Val  
435 440 445

Glu Val Leu Val Glu Arg Asn Gly Ser Leu Val Trp Gly Met Val Cys  
450 455 460

Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys Arg Gln Leu  
465 470 475 480

Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp Tyr Trp His  
485 490 495

Gly Asp Val Asn Ser Asn Lys Val Val Met Ser Gly Val Lys Cys Ser  
500 505 510

Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Gly Glu Asp Val  
515 520 525

Ala Cys Pro Gln Gly Gly Val Gln Tyr Gly Ala Gly Val Ala Cys Ser  
530 535 540

Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Met Val Gln Gln Thr  
545 550 555 560

Thr Tyr Leu Glu Asp Arg Pro Met Phe Met Leu Gln Cys Ala Met Glu  
565 570 575

Glu Asn Cys Leu Ser Ala Ser Ala Ala Gln Thr Asp Pro Thr Thr Gly  
580 585 590

Tyr Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn Gly Gln  
595 600 605

Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp His Asp  
610 615 620

Cys His Arg His Tyr His Ser Met Glu Val Phe Thr His Tyr Asp Leu  
625 630 635 640

Leu Asn Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe  
645 650 655

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Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Asn Tyr Glu  
660 665 670

Cys Ala Asn Phe Gly Asp Gln Gly Ile Thr Met Gly Cys Trp Asp Met  
675 680 685

Tyr Arg His Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp Val Pro  
690 695 700

Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn Pro Asn Phe Glu Val  
705 710 715 720

Ala Glu Ser Asp Tyr Ser Asn Asn Ile Met Lys Cys Arg Ser Arg Tyr  
725 730 735

Asp Gly His Arg Ile Trp Met Tyr Asn Cys His Ile Gly Gly Ser Phe  
740 745 750

Ser Glu Glu Thr Glu Lys Lys Phe Glu His Phe Ser Gly Leu Leu Asn  
755 760 765

Asn Gln Leu Ser Pro Gln  
770

<210> 138  
<211> 753  
<212> PRT  
<213> Homo sapiens  
<400> 138

Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu  
1 5 10 15

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly  
20 25 30

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly  
35 40 45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly  
50 55 60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His  
65 70 75 80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His  
85 90 95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu  
100 105 110

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Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly  
 115 120 125  
 Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys  
 130 135 140  
 Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val  
 145 150 155 160  
 Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly  
 165 170 175  
 Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg  
 180 185 190  
 Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His  
 195 200 205  
 Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg  
 210 215 220  
 Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser  
 225 230 235 240  
 Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser  
 245 250 255  
 Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro  
 260 265 270  
 Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala  
 275 280 285  
 Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu  
 290 295 300  
 Ala Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val  
 305 310 315 320  
 Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp Arg Lys Trp  
 325 330 335  
 Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser  
 340 345 350  
 Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala  
 355 360 365  
 Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp  
 370 375 380



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Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln  
 385 390 395 400  
 Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg  
 405 410 415  
 Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val  
 420 425 430  
 Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp  
 435 440 445  
 Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu  
 450 455 460  
 Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly  
 465 470 475 480  
 Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu  
 485 490 495  
 Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys  
 500 505 510  
 Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala  
 515 520 525  
 Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile  
 530 535 540  
 Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys  
 545 550 555 560  
 Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg  
 565 570 575  
 Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe  
 580 585 590  
 Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly  
 595 600 605  
 His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr Pro  
 610 615 620  
 Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu  
 625 630 635 640  
 Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn  
 645 650 655

# FAB-008PC-SequenceListing

Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His  
660 665 670

Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn  
675 680 685

Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser  
690 695 700

Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His  
705 710 715 720

Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu  
725 730 735

Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile  
740 745 750

Ile

<210> 139  
<211> 608  
<212> PRT  
<213> Homo sapiens

<400> 139

Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu  
1 5 10 15

Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly  
20 25 30

Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly  
35 40 45

Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly  
50 55 60

Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His  
65 70 75 80

Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His  
85 90 95

Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu  
100 105 110

Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly  
115 120 125

Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys

## FAB-008PC-SequenceListing

130

135

140

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

Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val Glu  
 165 170 175

Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp Arg Lys Trp Asp  
 180 185 190

Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser Ala  
 195 200 205

Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala Ile  
 210 215 220

His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp Lys  
 225 230 235 240

Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln Asp  
 245 250 255

Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg Ile  
 260 265 270

Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val Gln  
 275 280 285

Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp Asp  
 290 295 300

Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu Gly  
 305 310 315 320

Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly Asn  
 325 330 335

Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu Leu  
 340 345 350

Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys Arg  
 355 360 365

Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala Ser  
 370 375 380

Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile Glu  
 385 390 395 400

Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys Leu  
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405

410

415

Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg Leu  
420 425 430

Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe Arg  
435 440 445

Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly His  
450 455 460

Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr Pro Asn  
465 470 475 480

Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu Asp  
485 490 495

Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn Phe  
500 505 510

Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His Asp  
515 520 525

Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn Tyr  
530 535 540

Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser Asp  
545 550 555 560

Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His Arg  
565 570 575

Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu Ala  
580 585 590

Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile Ile  
595 600 605

<210> 140  
<211> 392  
<212> PRT  
<213> Homo sapiens

<400> 140

Met Gly Gln Gly Met Gly Ala Ile His Leu Ser Glu Val Arg Cys Ser  
1 5 10 15

Gly Gln Glu Leu Ser Leu Trp Lys Cys Pro His Lys Asn Ile Thr Ala  
20 25 30

Glu Asp Cys Ser His Ser Gln Asp Ala Gly Val Arg Cys Asn Leu Pro  
35 40 45

FAB-008PC-SequenceListing

Tyr Thr Gly Ala Glu Thr Arg Ile Arg Leu Ser Gly Gly Arg Ser Gln  
 50 55 60  
 His Glu Gly Arg Val Glu Val Gln Ile Gly Gly Pro Gly Pro Leu Arg  
 65 70 75 80  
 Trp Gly Leu Ile Cys Gly Asp Asp Trp Gly Thr Leu Glu Ala Met Val  
 85 90 95  
 Ala Cys Arg Gln Leu Gly Leu Gly Tyr Ala Asn His Gly Leu Gln Glu  
 100 105 110  
 Thr Trp Tyr Trp Asp Ser Gly Asn Ile Thr Glu Val Val Met Ser Gly  
 115 120 125  
 Val Arg Cys Thr Gly Thr Glu Leu Ser Leu Asp Gln Cys Ala His His  
 130 135 140  
 Gly Thr His Ile Thr Cys Lys Arg Thr Gly Thr Arg Phe Thr Ala Gly  
 145 150 155 160  
 Val Ile Cys Ser Glu Thr Ala Ser Asp Leu Leu Leu His Ser Ala Leu  
 165 170 175  
 Val Gln Glu Thr Ala Tyr Ile Glu Asp Arg Pro Leu His Met Leu Tyr  
 180 185 190  
 Cys Ala Ala Glu Glu Asn Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn  
 195 200 205  
 Trp Pro Tyr Gly His Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His  
 210 215 220  
 Asn Leu Gly Arg Ala Asp Phe Arg Pro Lys Ala Gly Arg His Ser Trp  
 225 230 235 240  
 Val Trp His Glu Cys His Gly His Tyr His Ser Met Asp Ile Phe Thr  
 245 250 255  
 His Tyr Asp Ile Leu Thr Pro Asn Gly Thr Lys Val Ala Glu Gly His  
 260 265 270  
 Lys Ala Ser Phe Cys Leu Glu Asp Thr Glu Cys Gln Glu Asp Val Ser  
 275 280 285  
 Lys Arg Tyr Glu Cys Ala Asn Phe Gly Glu Gln Gly Ile Thr Val Gly  
 290 295 300  
 Cys Trp Asp Leu Tyr Arg His Asp Ile Asp Cys Gln Trp Ile Asp Ile  
 305 310 315 320

# FAB-008PC-SequenceListing

Thr Asp Val Lys Pro Gly Asn Tyr Ile Leu Gln Val Val Ile Asn Pro  
325 330 335

Asn Phe Glu Val Ala Glu Ser Asp Phe Thr Asn Asn Ala Met Lys Cys  
340 345 350

Asn Cys Lys Tyr Asp Gly His Arg Ile Trp Val His Asn Cys His Ile  
355 360 365

Gly Asp Ala Phe Ser Glu Glu Ala Asn Arg Arg Phe Glu Arg Tyr Pro  
370 375 380

Gly Gln Thr Ser Asn Gln Ile Ile  
385 390

<210> 141  
<211> 756  
<212> PRT  
<213> Homo sapiens

<400> 141

Met Ala Trp Ser Pro Pro Ala Thr Leu Phe Leu Phe Leu Leu Leu Leu  
1 5 10 15

Gly Gln Pro Pro Pro Ser Arg Pro Gln Ser Leu Gly Thr Thr Lys Leu  
20 25 30

Arg Leu Val Gly Pro Glu Ser Lys Pro Glu Glu Gly Arg Leu Glu Val  
35 40 45

Leu His Gln Gly Gln Trp Gly Thr Val Cys Asp Asp Asn Phe Ala Ile  
50 55 60

Gln Glu Ala Thr Val Ala Cys Arg Gln Leu Gly Phe Glu Ala Ala Leu  
65 70 75 80

Thr Trp Ala His Ser Ala Lys Tyr Gly Gln Gly Glu Gly Pro Ile Trp  
85 90 95

Leu Asp Asn Val Arg Cys Val Gly Thr Glu Ser Ser Leu Asp Gln Cys  
100 105 110

Gly Ser Asn Gly Trp Gly Val Ser Asp Cys Ser His Ser Glu Asp Val  
115 120 125

Gly Val Ile Cys His Pro Arg Arg His Arg Gly Tyr Leu Ser Glu Thr  
130 135 140

Val Ser Asn Ala Leu Gly Pro Gln Gly Arg Arg Leu Glu Glu Val Arg  
145 150 155 160

FAB-008PC-SequenceListing

Leu Lys Pro Ile Leu Ala Ser Ala Lys Gln His Ser Pro Val Thr Glu  
 165 170 175  
 Gly Ala Val Glu Val Lys Tyr Glu Gly His Trp Arg Gln Val Cys Asp  
 180 185 190  
 Gln Gly Trp Thr Met Asn Asn Ser Arg Val Val Cys Gly Met Leu Gly  
 195 200 205  
 Phe Pro Ser Glu Val Pro Val Asp Ser His Tyr Tyr Arg Lys Val Trp  
 210 215 220  
 Asp Leu Lys Met Arg Asp Pro Lys Ser Arg Leu Lys Ser Leu Thr Asn  
 225 230 235 240  
 Lys Asn Ser Phe Trp Ile His Gln Val Thr Cys Leu Gly Thr Glu Pro  
 245 250 255  
 His Met Ala Asn Cys Gln Val Gln Val Ala Pro Ala Arg Gly Lys Leu  
 260 265 270  
 Arg Pro Ala Cys Pro Gly Gly Met His Ala Val Val Ser Cys Val Ala  
 275 280 285  
 Gly Pro His Phe Arg Pro Pro Lys Thr Lys Pro Gln Arg Lys Gly Ser  
 290 295 300  
 Trp Ala Glu Glu Pro Arg Val Arg Leu Arg Ser Gly Ala Gln Val Gly  
 305 310 315 320  
 Glu Gly Arg Val Glu Val Leu Met Asn Arg Gln Trp Gly Thr Val Cys  
 325 330 335  
 Asp His Arg Trp Asn Leu Ile Ser Ala Ser Val Val Cys Arg Gln Leu  
 340 345 350  
 Gly Phe Gly Ser Ala Arg Glu Ala Leu Phe Gly Ala Arg Leu Gly Gln  
 355 360 365  
 Gly Leu Gly Pro Ile His Leu Ser Glu Val Arg Cys Arg Gly Tyr Glu  
 370 375 380  
 Arg Thr Leu Ser Asp Cys Pro Ala Leu Glu Gly Ser Gln Asn Gly Cys  
 385 390 395 400  
 Gln His Glu Asn Asp Ala Ala Val Arg Cys Asn Val Pro Asn Met Gly  
 405 410 415  
 Phe Gln Asn Gln Val Arg Leu Ala Gly Gly Arg Ile Pro Glu Glu Gly  
 420 425 430

# FAB-008PC-SequenceListing

Leu Leu Glu Val Gln Val Glu Val Asn Gly Val Pro Arg Trp Gly Ser  
 435 440 445  
 Val Cys Ser Glu Asn Trp Gly Leu Thr Glu Ala Met Val Ala Cys Arg  
 450 455 460  
 Gln Leu Gly Leu Gly Phe Ala Ile His Ala Tyr Lys Glu Thr Trp Phe  
 465 470 475 480  
 Trp Ser Gly Thr Pro Arg Ala Gln Glu Val Val Met Ser Gly Val Arg  
 485 490 495  
 Cys Ser Gly Thr Glu Leu Ala Leu Gln Gln Cys Gln Arg His Gly Pro  
 500 505 510  
 Val His Cys Ser His Gly Gly Gly Arg Phe Leu Ala Gly Val Ser Cys  
 515 520 525  
 Met Asp Ser Ala Pro Asp Leu Val Met Asn Ala Gln Leu Val Gln Glu  
 530 535 540  
 Thr Ala Tyr Leu Glu Asp Arg Pro Leu Ser Gln Leu Tyr Cys Ala His  
 545 550 555 560  
 Glu Glu Asn Cys Leu Ser Lys Ser Ala Asp His Met Asp Trp Pro Tyr  
 565 570 575  
 Gly Tyr Arg Arg Leu Leu Arg Phe Ser Thr Gln Ile Tyr Asn Leu Gly  
 580 585 590  
 Arg Thr Asp Phe Arg Pro Lys Thr Gly Arg Asp Ser Trp Val Trp His  
 595 600 605  
 Gln Cys His Arg His Tyr His Ser Ile Glu Val Phe Thr His Tyr Asp  
 610 615 620  
 Leu Leu Thr Leu Asn Gly Ser Lys Val Ala Glu Gly His Lys Ala Ser  
 625 630 635 640  
 Phe Cys Leu Glu Asp Thr Asn Cys Pro Thr Gly Leu Gln Arg Arg Tyr  
 645 650 655  
 Ala Cys Ala Asn Phe Gly Glu Gln Gly Val Thr Val Gly Cys Trp Asp  
 660 665 670  
 Thr Tyr Arg His Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp Val  
 675 680 685  
 Gly Pro Gly Asn Tyr Ile Phe Gln Val Ile Val Asn Pro His Tyr Glu  
 690 695 700



FAB-008PC-SequenceListing

Val Ala Glu Ser Asp Phe Ser Asn Asn Met Leu Gln Cys Arg Cys Lys  
705 710 715 720

Tyr Asp Gly His Arg Val Trp Leu His Asn Cys His Thr Gly Asn Ser  
725 730 735

Tyr Pro Ala Asn Ala Glu Leu Ser Leu Glu Gln Glu Gln Arg Leu Arg  
740 745 750

Asn Asn Leu Ile  
755

<210> 142  
<211> 183  
<212> PRT  
<213> Homo sapiens

<400> 142

Met Arg Ala Ala Tyr Leu Phe Leu Leu Phe Leu Pro Ala Gly Leu Leu  
1 5 10 15

Ala Gln Gly Gln Tyr Asp Leu Asp Pro Leu Pro Pro Phe Pro Asp His  
20 25 30

Val Gln Tyr Thr His Tyr Ser Asp Gln Ile Asp Asn Pro Asp Tyr Tyr  
35 40 45

Asp Tyr Gln Glu Val Thr Pro Arg Pro Ser Glu Glu Gln Phe Gln Phe  
50 55 60

Gln Ser Gln Gln Gln Val Gln Gln Glu Val Ile Pro Ala Pro Thr Pro  
65 70 75 80

Glu Pro Gly Asn Ala Glu Leu Glu Pro Thr Glu Pro Gly Pro Leu Asp  
85 90 95

Cys Arg Glu Glu Gln Tyr Pro Cys Thr Arg Leu Tyr Ser Ile His Arg  
100 105 110

Pro Cys Lys Gln Cys Leu Asn Glu Val Cys Phe Tyr Ser Leu Arg Arg  
115 120 125

Val Tyr Val Ile Asn Lys Glu Ile Cys Val Arg Thr Val Cys Ala His  
130 135 140

Glu Glu Leu Leu Arg Ala Asp Leu Cys Arg Asp Lys Phe Ser Lys Cys  
145 150 155 160

Gly Val Met Ala Ser Ser Gly Leu Cys Gln Ser Val Ala Ala Ser Cys  
165 170 175

## FAB-008PC-SequenceListing

Ala Arg Ser Cys Gly Ser Cys  
180

<210> 143  
<211> 182  
<212> PRT  
<213> Homo sapiens

<400> 143

Met Arg Ala Ala Tyr Leu Phe Leu Leu Phe Leu Pro Gly Leu Leu Ala  
1 5 10 15

Gln Gly Gln Tyr Asp Leu Asp Pro Leu Pro Pro Phe Pro Asp His Val  
20 25 30

Gln Tyr Thr His Tyr Ser Asp Gln Ile Asp Asn Pro Asp Tyr Tyr Asp  
35 40 45

Tyr Gln Glu Val Thr Pro Arg Pro Ser Glu Glu Gln Phe Gln Phe Gln  
50 55 60

Ser Gln Gln Gln Val Gln Gln Glu Val Ile Pro Ala Pro Thr Pro Glu  
65 70 75 80

Pro Gly Asn Ala Glu Leu Glu Pro Thr Glu Pro Gly Pro Leu Asp Cys  
85 90 95

Arg Glu Glu Gln Tyr Pro Cys Thr Arg Leu Tyr Ser Ile His Arg Pro  
100 105 110

Cys Lys Gln Cys Leu Asn Glu Val Cys Phe Tyr Ser Leu Arg Arg Val  
115 120 125

Tyr Val Ile Asn Lys Glu Ile Cys Val Arg Thr Val Cys Ala His Glu  
130 135 140

Glu Leu Leu Arg Ala Asp Leu Cys Arg Asp Lys Phe Ser Lys Cys Gly  
145 150 155 160

Val Met Ala Ser Ser Gly Leu Cys Gln Ser Val Ala Ala Ser Cys Ala  
165 170 175

Arg Ser Cys Gly Ser Cys  
180

<210> 144  
<211> 173  
<212> PRT  
<213> Homo sapiens

<400> 144

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

# FAB-008PC-SequenceListing

Ile Thr Ser Asp Trp Ile Pro Leu Gly Val Asn Ser Gln Arg Gly Asp  
20 25 30

Asp Val Thr Gln Ala Thr Pro Glu Thr Phe Thr Glu Asp Pro Asn Leu  
35 40 45

Val Asn Asp Pro Ala Thr Asp Glu Thr Val Leu Ala Val Leu Ala Asp  
50 55 60

Ile Ala Pro Ser Thr Asp Asp Leu Ala Ser Leu Ser Glu Lys Asn Thr  
65 70 75 80

Thr Ala Glu Cys Trp Asp Glu Lys Phe Thr Cys Thr Arg Leu Tyr Ser  
85 90 95

Val His Arg Pro Val Lys Gln Cys Ile His Gln Leu Cys Phe Thr Ser  
100 105 110

Leu Arg Arg Met Tyr Ile Val Asn Lys Glu Ile Cys Ser Arg Leu Val  
115 120 125

Cys Lys Glu His Glu Ala Met Lys Asp Glu Leu Cys Arg Gln Met Ala  
130 135 140

Gly Leu Pro Pro Arg Arg Leu Arg Arg Ser Asn Tyr Phe Arg Leu Pro  
145 150 155 160

Pro Cys Glu Asn Val Asp Leu Gln Arg Pro Asn Gly Leu  
165 170