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1997/09/17 (US60/059,122); 1997/09/17 (US60/059,121);
1997/09/17 (US60/059,113); 1997/09/17 (US60/059,117);
1997/09/17 (US60/059,115); 1997/09/17 (US60/059,119);
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1997/10/15 (US60/062,125); 1997/10/17 (US60/062,287);
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C07K 14/47 (2006.01), *C07K 14/705* (2006.01),
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C07K 19/00 (2006.01), *C12N 15/62* (2006.01),
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PENNICA, DIANE, US;
CHEN, JIAN, US;
YUAN, JEAN, US

(73) Propriétaire/Owner:

(54) Titre : ACIDE NUCLEIQUE ET POLYPEPTIDE CODANT SERVANT A INHIBER L'ANGIOGENESE TUMORALE

(54) Title: A NUCLEIC ACID AND ENCODING POLYPEPTIDE FOR USE IN INHIBITING TUMOR ANGIOGENESIS

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACCCG
CCATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCC
GCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTT
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TGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGC
CTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACAC
TGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCC
CAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTC
CTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCA
GCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGC
TCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGC
CTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCCTCCCTGCAGCGCTGCGCAGT
TCTGTAAGAACGCCAACGGCTCCTACACGTGCCAAGAGTGTGACTCCAGCTGTGTGGGCTGC
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GTGTGCAGATGTGGACGAGTGTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAAACT
GCTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCCTGACGGCTTCGAAGAAACGGAAGAT
GCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCCTC
CCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGGA
AAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTC
TCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGA
CTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAA
AAAAAA

(57) Abrégé/Abstract:

The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptides molecules comprising the

(30) **Priorités(suite)/Priorities(continued):** 1997/10/24 (US60/063,120); 1997/10/24 (US60/063,128); 1997/10/24 (US60/063,121); 1997/10/24 (US60/063,045); 1997/10/27 (US60/063,327); 1997/10/27 (US60/063,329); 1997/10/28 (US60/063,549); 1997/10/28 (US60/063,550); 1997/10/28 (US60/063,541); 1997/10/28 (US60/063,544); 1997/10/28 (US60/063,542); 1997/10/28 (US60/063,564); 1997/10/29 (US60/063,435); 1997/10/29 (US60/063,732); 1997/10/29 (US60/063,735); 1997/10/29 (US60/063,738); 1997/10/29 (US60/064,215); 1997/10/29 (US60/063,704); 1997/10/29 (US60/063,734); 1997/10/31 (US60/064,103); 1997/10/31 (US60/063,870); 1997/11/03 (US60/064,248); 1997/11/07 (US60/064,809); 1997/11/12 (US60/065,186); 1997/11/17 (US60/065,846); 1997/11/18 (US60/065,693); 1997/11/21 (US60/066,364); 1997/11/21 (US60/066,120); 1997/11/24 (US60/066,466); 1997/11/24 (US60/066,770); 1997/11/24 (US60/066,511); 1997/11/24 (US60/066,772); 1997/11/24 (US60/066,453); 1997/11/25 (US60/066,840)

(73) **Propriétaires(suite)/Owners(continued):** GENENTECH, INC., US

(74) **Agent:** DENNISON ASSOCIATES

(57) **Abrégé(suite)/Abstract(continued):**

polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(21) International Application Number: PCT/US98/19330 (22) International Filing Date: 16 September 1998 (16.09.98) (30) Priority Data: <table style="width: 100%; border-collapse: collapse;"> <tr><td style="width: 30%;">60/059,115</td><td style="width: 40%;">17 September 1997 (17.09.97)</td><td style="width: 30%;">US</td></tr> <tr><td>60/059,184</td><td>17 September 1997 (17.09.97)</td><td>US</td></tr> <tr><td>60/059,122</td><td>17 September 1997 (17.09.97)</td><td>US</td></tr> <tr><td>60/059,117</td><td>17 September 1997 (17.09.97)</td><td>US</td></tr> <tr><td>60/059,113</td><td>17 September 1997 (17.09.97)</td><td>US</td></tr> <tr><td>60/059,121</td><td>17 September 1997 (17.09.97)</td><td>US</td></tr> <tr><td>60/059,119</td><td>17 September 1997 (17.09.97)</td><td>US</td></tr> <tr><td>60/059,263</td><td>18 September 1997 (18.09.97)</td><td>US</td></tr> <tr><td>60/059,266</td><td>18 September 1997 (18.09.97)</td><td>US</td></tr> <tr><td>60/062,125</td><td>15 October 1997 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[US/US]; One DNA Way, South San Francisco, CA 94080 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): WOOD, William, I. [US/US]; 1400 Tarrytown Street, San Mateo, CA 94402 (US). GURNEY, Austin, L. [US/US]; One Debbie Lane, Belmont, CA 94002 (US). GODDARD, Audrey [CA/US]; 110 Congo Street, San Francisco, CA 94131 (US). PENNICA, Diane [US/US]; 2417 Hale Drive, Burlingame, CA 94010 (US). CHEN, Jian [CN/US]; 1860 Ogden Drive #14, Burlingame, CA 94010 (US). YUAN, Jean [CN/US]; 176 West 37th Avenue, San Mateo, CA 94403 (US). (74) Agents: DREGER, Walter, H. et al.; Flehr, Hohbach, Test, Albritton & Herbert LLP, Suite 3400, 4 Embarcadero Center, San Francisco, CA 94111-4187 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	60/066,770	24 November 1997 (24.11.97)	US	60/066,511	24 November 1997 (24.11.97)	US	60/066,453	24 November 1997 (24.11.97)	US	60/066,840	25 November 1997 (25.11.97)	US
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Published

Without international search report and to be republished upon receipt of that report.

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
(57) Abstract The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptides molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME 1 DE 2

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME 1 OF 2

NOTE: For additional volumes please contact the Canadian Patent Office.

WO 99/14328

PCT/US98/19330

A NUCLEIC ACID AND ENCODING POLYPEPTIDE FOR USE IN INHIBITING TUMOR ANGIOGENESIS

FIELD OF THE INVENTION

The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides encoded by that DNA.

BACKGROUND OF THE INVENTION

Extracellular and membrane-bound proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of action in the extracellular environment, usually at a membrane-bound receptor protein.

Secreted proteins have various industrial applications, including use as pharmaceuticals, diagnostics, biosensors and bioreactors. In fact, most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane-bound proteins, also have potential as therapeutic or diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interaction. Membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. Transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and nerve growth factor receptor.

Efforts are being undertaken by both industry and academia to identify new, native secreted and membrane-bound receptor proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound receptor proteins. Examples of screening methods and techniques are described in the literature (see, for example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Patent No. 5,536,637).

We herein describe the identification and characterization of novel secreted and transmembrane polypeptides and novel nucleic acids encoding those polypeptides.

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1. PRO211 and PRO217

Epidermal growth factor (EGF) is a conventional mitogenic factor that stimulates the proliferation of various types of cells including epithelial cells and fibroblasts. EGF binds to and activates the EGF receptor (EGFR), which initiates intracellular signaling and subsequent effects. The EGFR is expressed in neurons of the cerebral cortex, cerebellum, and hippocampus in addition to other regions of the central nervous system (CNS). In addition, EGF is also expressed in various regions of the CNS. Therefore, EGF acts not only on mitotic cells, but also on postmitotic neurons. In fact, many studies have indicated that EGF has neurotrophic or neuromodulatory effects on various types of neurons in the CNS. For example, EGF acts directly on cultured cerebral cortical and cerebellar neurons, enhancing neurite outgrowth and survival. On the other hand, EGF also acts on other cell types, including septal cholinergic and mesencephalic dopaminergic neurons, indirectly through glial cells. Evidence of the effects of EGF on neurons in the CNS is accumulating, but the mechanisms of action remain essentially unknown. EGF-induced signaling in mitotic cells is better understood than in postmitotic neurons. Studies of cloned pheochromocytoma PC12 cells and cultured cerebral cortical neurons have suggested that the EGF-induced neurotrophic actions are mediated by sustained activation of the EGFR and mitogen-activated protein kinase (MAPK) in response to EGF. The sustained intracellular signaling correlates with the decreased rate of EGFR down-regulation, which might determine the response of neuronal cells to EGF. It is likely that EGF is a multi-potent growth factor that acts upon various types of cells including mitotic cells and postmitotic neurons.

EGF is produced by the salivary and Brunner's glands of the gastrointestinal system, kidney, pancreas, thyroid gland, pituitary gland, and the nervous system, and is found in body fluids such as saliva, blood, cerebrospinal fluid (CSF), urine, amniotic fluid, prostatic fluid, pancreatic juice, and breast milk, Plata-Salaman, *Peptides* 12: 653-663 (1991).

EGF is mediated by its membrane specific receptor, which contains an intrinsic tyrosine kinase. Stoscheck *et al.*, *J. Cell Biochem.* 31: 135-152 (1986). EGF is believed to function by binding to the extracellular portion of its receptor which induces a transmembrane signal that activates the intrinsic tyrosine kinase.

Purification and sequence analysis of the EGF-like domain has revealed the presence of six conserved cysteine residues which cross-bind to create three peptide loops, Savage *et al.*, *J. Biol. Chem.* 248: 7669-7672 (1979). It is now generally known that several other peptides can react with the EGF receptor which share the same generalized motif $X_nCX_7CX_{4/5}CX_{10}CXCX_5GX_2CX_n$, where X represents any non-cysteine amino acid, and n is a variable repeat number. Non isolated peptides having this motif include TGF- α , amphiregulin, schwannoma-derived growth factor (SDGF), heparin-binding EGF-like growth factors and certain virally encoded peptides (e.g., Vaccinia virus, Reisner, *Nature* 313: 801-803 (1985), Shope fibroma virus, Chang *et al.*, *Mol Cell Biol.* 7: 535-540 (1987), Molluscum contagiosum, Porter and Archard, *J. Gen. Virol.* 68: 673-682 (1987), and Myxoma virus, Upton *et al.*, *J. Virol.* 61: 1271-1275 (1987), Prigent and Lemoine, *Prog. Growth Factor Res.* 4: 1-24 (1992).

EGF-like domains are not confined to growth factors but have been observed in a variety of cell-surface and extracellular proteins which have interesting properties in cell adhesion, protein-protein interaction and development, Laurence and Gusterson, *Tumor Biol.* 11: 229-261 (1990). These proteins include blood coagulation factors (factors VI, IX, X, XII, protein C, protein S, protein Z, tissue plasminogen activator, urokinase), extracellular matrix components (laminin, cytactin, entactin), cell surface receptors (LDL receptor, thrombomodulin receptor) and

immunity-related proteins (complement C1r, uromodulin).

Even more interesting, the general structure pattern of EGF-like precursors is preserved through lower organisms as well as in mammalian cells. A number of genes with developmental significance have been identified in invertebrates with EGF-like repeats. For example, the *notch* gene of *Drosophila* encodes 36 tandemly arranged 40 amino acid repeats which show homology to EGF, Wharton *et al.*, *Cell* **43**: 557-581 (1985). Hydropathy plots indicate a putative membrane spanning domain, with the EGF-related sequences being located on the extracellular side of the membrane. Other homeotic genes with EGF-like repeats include Delta, 95F and 5ZD which were identified using probes based on Notch, and the nematode gene *Lin-12* which encodes a putative receptor for a developmental signal transmitted between two specified cells.

Specifically, EGF has been shown to have potential in the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, Konturek *et al.*, *Eur. J. Gastroenterol Hepatol.* **7** (10), 933-37 (1995), including the treatment of necrotizing enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration gastrointestinal ulcerations and congenital microvillus atrophy, Guglietta and Sullivan, *Eur. J. Gastroenterol Hepatol.* **7**(10), 945-50 (1995). Additionally, EGF has been implicated in hair follicle differentiation; du Cros, *J. Invest. Dermatol.* **101** (1 Suppl.), 106S-113S (1993), Hillier, *Clin. Endocrinol.* **33**(4), 427-28 (1990); kidney function, Hamm *et al.*, *Semin. Nephrol.* **13** (1): 109-15 (1993), Harris, *Am. J. Kidney Dis.* **17**(6): 627-30 (1991); tear fluid, van Setten *et al.*, *Int. Ophthalmol* **15**(6): 359-62 (1991); vitamin K mediated blood coagulation, Stenflo *et al.*, *Blood* **78**(7): 1637-51 (1991). EGF is also implicated various skin disease characterized by abnormal keratinocyte differentiation, e.g., psoriasis, epithelial cancers such as squamous cell carcinomas of the lung, epidermoid carcinoma of the vulva and gliomas. King *et al.*, *Am. J. Med. Sci.* **296**: 154-158 (1988).

Of great interest is mounting evidence that genetic alterations in growth factors signaling pathways are closely linked to developmental abnormalities and to chronic diseases including cancer. Aaronson, *Science* **254**: 1146-1153 (1991). For example, c-erb-2 (also known as HER-2), a proto-oncogene with close structural similarity to EGF receptor protein, is overexpressed in human breast cancer. King *et al.*, *Science* **229**: 974-976 (1985); Gullick, *Hormones and their actions*, Cooke *et al.*, eds, Amsterdam, Elsevier, pp 349-360 (1986).

We herein describe the identification and characterization of novel polypeptides having homology to EGF, wherein those polypeptides are herein designated PRO211 and PRO217.

2. PRO230

Nephritis is a condition characterized by inflammation of the kidney affecting the structure and normal function of the kidney. This condition can be chronic or acute and is generally caused by infection, degenerative process or vascular disease. In all cases, early detection is desirable so that the patient with nephritis can begin treatment of the condition.

An approach to detecting nephritis is to determine the antigens associated with nephritis and antibodies thereto. In rabbit, a tubulointerstitial nephritis antigen (TIN-ag) has been reported in Nelson, T. R., et al., *J. Biol. Chem.*, **270**(27):16265-70 (July 1995) (GENBANK/U24270). This study reports that the rabbit TIN-ag is a basement membrane glycoprotein having a predicted amino acid sequence which has a carboxyl-terminal region exhibiting 30% homology with human preprocathepsin B, a member of the cystein proteinase family of proteins. It is also reported

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that the rabbit TIN-ag has a domain in the amino-terminal region containing an epidermal growth factor-like motif that shares homology with laminin A and S chains, alpha 1 chain of type I collagen, von Willebrand's factor and mucin, indicating structural and functional similarities. Studies have also been conducted in mice. However, it is desirable to identify tubulointerstitial nephritis antigens in humans to aid in the development of early detection methods and treatment of nephritis.

5 Proteins which have homology to tubulointerstitial nephritis antigens are of particular interest to the medical and industrial communities. Often, proteins having homology to each other have similar function. It is also of interest when proteins having homology do not have similar functions, indicating that certain structural motifs identify information other than function, such as locality of function. We herein describe the identification and characterization of a novel polypeptide, designated hgerein as PRO230, which has homology to tubulointerstitial
10 nephritis antigens.

3. PRO232

Stem cells are undifferentiated cells capable of (a) proliferation, (b) self maintenance, (c) the production of a large number of differentiated functional progeny, (d) regeneration of tissue after injury and/or (e) a flexibility in
15 the use of these options. Stem cells often express cell surface antigens which are capable of serving as cell specific markers that can be exploited to identify stem cells, thereby providing a means for identifying and isolating specific stem cell populations.

Having possession of different stem cell populations will allow for a number of important applications. For example, possessing a specific stem cell population will allow for the identification of growth factors and other
20 proteins which are involved in their proliferation and differentiation. In addition, there may be as yet undiscovered proteins which are associated with (1) the early steps of dedication of the stem cell to a particular lineage, (2) prevention of such dedication, and (3) negative control of stem cell proliferation, all of which may be identified if one has possession of the stem cell population. Moreover, stem cells are important and ideal targets for gene therapy where the inserted genes promote the health of the individual into whom the stem cells are transplanted. Finally, stem
25 cells may play important roles in transplantation of organs or tissues, for example liver regeneration and skin grafting.

Given the importance of stem cells in various different applications, efforts are currently being undertaken by both industry and academia to identify new, native stem cell antigen proteins so as to provide specific cell surface markers for identifying stem cell populations as well as for providing insight into the functional roles played by stem
30 cell antigens in cell proliferation and differentiation. We herein describe the identification and characterization of novel polypeptides having homology to a stem cell antigen, wherein those polypeptides are herein designated as PRO232 polypeptides..

4. PRO187

35 Growth factors are molecular signals or mediators that enhance cell growth or proliferation, alone or in concert, by binding to specific cell surface receptors. However, there are other cellular reactions than only growth upon expression to growth factors. As a result, growth factors are better characterized as multifunctional and potent

cellular regulators. Their biological effects include proliferation, chemotaxis and stimulation of extracellular matrix production. Growth factors can have both stimulatory and inhibitory effects. For example, transforming growth factor (TGF- β) is highly pleiotropic and can stimulate proliferation in some cells, especially connective tissue, while being a potent inhibitor of proliferation in others, such as lymphocytes and epithelial cells.

5 The physiological effect of growth stimulation or inhibition by growth factors depends upon the state of development and differentiation of the target tissue. The mechanism of local cellular regulation by classical endocrine molecules involves comprehends autocrine (same cell), juxtacrine (neighbor cell), and paracrine (adjacent cells) pathways. Peptide growth factors are elements of a complex biological language, providing the basis for intercellular communication. They permit cells to convey information between each other, mediate interaction between cells and change gene expression. The effect of these multifunctional and pluripotent factors is dependent on the presence or
10 absence of other peptides.

FGF-8 is a member of the fibroblast growth factors (FGFs) which are a family of heparin-binding, potent mitogens for both normal diploid fibroblasts and established cell lines, Gospodarowicz *et al.* (1984), *Proc. Natl. Acad. Sci. USA* 81:6963. The FGF family comprises acidic FGF (FGF-1), basic FGF (FGF-2), INT-2 (FGF-3), K-FGF/HST (FGF-4), FGF-5, FGF-6, KGF (FGF-7), AIGF (FGF-8) among others. All FGFs have two conserved
15 cysteine residues and share 30-50% sequence homology at the amino acid level. These factors are mitogenic for a wide variety of normal diploid mesoderm-derived and neural crest-derived cells, including granulosa cells, adrenal cortical cells, chondrocytes, myoblasts, corneal and vascular endothelial cells (bovine or human), vascular smooth muscle cells, lens, retina and prostatic epithelial cells, oligodendrocytes, astrocytes, chondrocytes, myoblasts and osteoblasts.

20 Fibroblast growth factors can also stimulate a large number of cell types in a non-mitogenic manner. These activities include promotion of cell migration into wound area (chemotaxis), initiation of new blood vessel formulation (angiogenesis), modulation of nerve regeneration and survival (neurotrophism), modulation of endocrine functions, and stimulation or suppression of specific cellular protein expression, extracellular matrix production and cell survival. Baird & Bohlen, *Handbook of Exp. Pharmacol.* 95(1): 369-418, Springer, (1990). These properties provide
25 a basis for using fibroblast growth factors in therapeutic approaches to accelerate wound healing, nerve repair, collateral blood vessel formation, and the like. For example, fibroblast growth factors have been suggested to minimize myocardium damage in heart disease and surgery (U.S.P. 4,378,347).

FGF-8, also known as androgen-induced growth factor (AIGF), is a 215 amino acid protein which shares 30-40% sequence homology with the other members of the FGF family. FGF-8 has been proposed to be under
30 androgenic regulation and induction in the mouse mammary carcinoma cell line SC3. Tanaka *et al.*, *Proc. Natl. Acad. Sci. USA* 89: 8928-8932 (1992); Sato *et al.*, *J. Steroid Biochem. Molec. Biol.* 47: 91-98 (1993). As a result, FGF-8 may have a local role in the prostate, which is known to be an androgen-responsive organ. FGF-8 can also be oncogenic, as it displays transforming activity when transfected into NIH-3T3 fibroblasts. Kouhara *et al.*, *Oncogene* 9 455-462 (1994). While FGF-8 has been detected in heart, brain, lung, kidney, testis, prostate and ovary,
35 expression was also detected in the absence of exogenous androgens. Schmitt *et al.*, *J. Steroid Biochem. Mol. Biol.* 57 (3-4): 173-78 (1996).

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FGF-8 shares the property with several other FGFs of being expressed at a variety of stages of murine embryogenesis, which supports the theory that the various FGFs have multiple and perhaps coordinated roles in differentiation and embryogenesis. Moreover, FGF-8 has also been identified as a protooncogene that cooperates with Wnt-1 in the process of mammary tumorigenesis (Shackleford *et al.*, *Proc. Natl. Acad. Sci. USA* **90**, 740-744 (1993); Heikinheimo *et al.*, *Mech. Dev.* **48**: 129-138 (1994)).

5 In contrast to the other FGFs, FGF-8 exists as three protein isoforms, as a result of alternative splicing of the primary transcript. Tanaka *et al.*, *supra*. Normal adult expression of FGF-8 is weak and confined to gonadal tissue, however northern blot analysis has indicated that FGF-8 mRNA is present from day 10 through day 12 or
10 murine gestation, which suggests that FGF-8 is important to normal development. Heikinheimo *et al.*, *Mech. Dev.* **48**(2): 129-38 (1994). Further *in situ* hybridization assays between day 8 and 16 of gestation indicated initial expression in the surface ectoderm of the first bronchial arches, the frontonasal process, the forebrain and the midbrain-hindbrain junction. At days 10-12, FGF-8 was expressed in the surface ectoderm of the forelimb and hindlimb buds, the nasal pits and nasopharynx, the infundibulum and in the telencephalon, diencephalon and metencephalon. Expression continues in the developing hindlimbs through day 13 of gestation, but is undetectable thereafter. The results suggest that FGF-8 has a unique temporal and spatial pattern in embryogenesis and suggests
15 a role for this growth factor in multiple regions of ectodermal differentiation in the post-gastrulation embryo.

We herein describe the identification of novel polypeptides having homology to FGF-8, wherein those polypeptides are herein designated PRO187 polypeptides.

5. PRO265

20 Protein-protein interactions include receptor and antigen complexes and signaling mechanisms. As more is known about the structural and functional mechanisms underlying protein-protein interactions, protein-protein interactions can be more easily manipulated to regulate the particular result of the protein-protein interaction. Thus, the underlying mechanisms of protein-protein interactions are of interest to the scientific and medical community.

All proteins containing leucine-rich repeats are thought to be involved in protein-protein interactions.
25 Leucine-rich repeats are short sequence motifs present in a number of proteins with diverse functions and cellular locations. The crystal structure of ribonuclease inhibitor protein has revealed that leucine-rich repeats correspond to beta-alpha structural units. These units are arranged so that they form a parallel beta-sheet with one surface exposed to solvent, so that the protein acquires an unusual, nonglobular shape. These two features have been indicated as responsible for the protein-binding functions of proteins containing leucine-rich repeats. See, Kobe and
30 Deisenhofer, *Trends Biochem. Sci.*, **19**(10):415-421 (Oct. 1994).

A study has been reported on leucine-rich proteoglycans which serve as tissue organizers, orienting and ordering collagen fibrils during ontogeny and are involved in pathological processes such as wound healing, tissue repair, and tumor stroma formation. Iozzo, R. V., *Crit. Rev. Biochem. Mol. Biol.*, **32**(2):141-174 (1997). Others studies implicating leucine rich proteins in wound healing and tissue repair are De La Salle, C., *et al.*, *Vouv. Rev. Fr. Hematol.* (Germany), **37**(4):215-222 (1995), reporting mutations in the leucine rich motif in a complex associated with the bleeding disorder Bernard-Soulier syndrome and Chlemetson, K. J., *Thromb. Haemost.* (Germany), **74**(1):111-116 (July 1995), reporting that platelets have leucine rich repeats. Another protein of particular interest
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which has been reported to have leucine-rich repeats is the SLIT protein which has been reported to be useful in treating neuro-degenerative diseases such as Alzheimer's disease, nerve damage such as in Parkinson's disease, and for diagnosis of cancer, see, Artavanistsakonas, S. and Rothberg, J. M., WO9210518-A1 by Yale University. Other studies reporting on the biological functions of proteins having leucine-rich repeats include: Tayar, N., et al., Mol. Cell Endocrinol., (Ireland), 125(1-2):65-70 (Dec. 1996) (gonadotropin receptor involvement); Miura, Y., et al., Nippon Rinsho (Japan), 54(7):1784-1789 (July 1996) (apoptosis involvement); Harris, P. C., et al., J. Am. Soc. Nephrol., 6(4):1125-1133 (Oct. 1995) (kidney disease involvement); and Ruoslahti, E. I., et al., WO9110727-A by La Jolla Cancer Research Foundation (decorin binding to transforming growth factor- β involvement for treatment for cancer, wound healing and scarring). Also of particular interest is fibromodulin and its use to prevent or reduce dermal scarring. A study of fibromodulin is found in U.S. Patent No. 5,654,270 to Ruoslahti, et al.

Efforts are therefore being undertaken by both industry and academia to identify new proteins having leucine rich repeats to better understand protein-protein interactions. Of particular interest are those proteins having leucine rich repeats and homology to known proteins having leucine rich repeats such as fibromodulin, the SLIT protein and platelet glycoprotein V. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound proteins having leucine rich repeats. We herein describe the identification and characterization of novel polypeptides having homology to fibromodulin, herein designated as PRO265 polypeptides.

6. PRO219

Human matrilin-2 polypeptide is a member of the von Willebrand factor type A-like module superfamily. von Willebrand factor is a protein which plays an important role in the maintenance of hemostasis. More specifically, von Willebrand factor is a protein which is known to participate in platelet-vessel wall interactions at the site of vascular injury via its ability to interact and form a complex with Factor VIII. The absence of von Willebrand factor in the blood causes an abnormality with the blood platelets that prevents platelet adhesion to the vascular wall at the site of the vascular injury. The result is the propensity for bruising, nose bleeds, intestinal bleeding, and the like comprising von Willebrand's disease.

Given the physiological importance of the blood clotting factors, efforts are currently being undertaken by both industry and academia to identify new, native proteins which may be involved in the coagulation process. We herein describe the identification of a novel full-length polypeptide which possesses homology to the human matrilin-2 precursor polypeptide.

7. PRO246

The cell surface protein HCAR is a membrane-bound protein that acts as a receptor for subgroup C of the adenoviruses and subgroup B of the coxsackieviruses. Thus, HCAR may provide a means for mediating viral infection of cells in that the presence of the HCAR receptor on the cellular surface provides a binding site for viral particles, thereby facilitating viral infection.

In light of the physiological importance of membrane-bound proteins and specifically those which serve a cell surface receptor for viruses, efforts are currently being undertaken by both industry and academia to identify

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new, native membrane-bound receptor proteins. Many of these efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor proteins. We herein describe a novel membrane-bound polypeptide (designated herein as PRO246) having homology to the cell surface protein HCAR and to various tumor antigens including A33 and carcinoembryonic antigen, wherein this polypeptide may be a novel cell surface virus receptor or tumor antigen.

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8. PRO228

There are a number of known seven transmembrane proteins and within this family is a group which includes CD97 and EMR1. CD97 is a seven-span transmembrane receptor which has a cellular ligand, CD55, DAF. Hamann, et al., J. Exp. Med. (U.S.), 184(3):1189 (1996). Additionally, CD97 has been reported as being a dedifferentiation marker in human thyroid carcinomas and as associated with inflammation. Aust, et al., Cancer Res. (U.S.), 57(9):1798 (1997); Gray, et al., J. Immunol. (U.S.), 157(12):5438 (1996). CD97 has also been reported as being related to the secretin receptor superfamily, but unlike known members of that family, CD97 and EMR1 have extended extracellular regions that possess several EGF domains at the N-terminus. Hamann, et al., Genomics, 32(1):144 (1996); Harmann, et al., J. Immunol., 155(4):1942 (1995). EMR1 is further described in Lin, et al., Genomics, 41(3):301 (1997) and Baud, et al., Genomics, 26(2):334 (1995). While CD97 and EMR1 appear to be related to the secretin receptors, a known member of the secretin family of G protein-coupled receptors includes the alpha-latroxin receptor, latrophilin, which has been described as calcium independent and abundant among neuronal tissues. Lelianaova, et al., J. Biol. Chem., 272(34), 21504 (1997); Davletov, et al., J. Biol. Chem. (U.S.), 271(38):23239 (1996). Both members of the secretin receptor superfamily and non-members which are related to the secretin receptor superfamily, or CRF and calcitonin receptors are of interest. In particular, new members of these families, identified by their homology to known proteins, are of interest.

Efforts are being undertaken by both industry and academia to identify new membrane-bound receptor proteins, particularly transmembrane proteins with EGF repeats and large N-terminuses which may belong to the family of seven-transmembrane proteins of which CD97 and EMR1 are members. We herein describe the identification and characterization of novel polypeptides having homology to CD97 and EMR1, designated herein as PRO228 polypeptides.

9. PRO533

Growth factors are molecular signals or mediators that enhance cell growth or proliferation, alone or in concert, by binding to specific cell surface receptors. However, there are other cellular reactions than only growth upon expression to growth factors. As a result, growth factors are better characterized as multifunctional and potent cellular regulators. Their biological effects include proliferation, chemotaxis and stimulation of extracellular matrix production. Growth factors can have both stimulatory and inhibitory effects. For example, transforming growth factors (TGF- β) is highly pleiotropic and can stimulate proliferation in some cells, especially connective tissues, while being a potent inhibitor of proliferation in others, such as lymphocytes and epithelial cells.

The physiological effect of growth stimulation or inhibition by growth factors depends upon the state of development and differentiation of the target tissue. The mechanism of local cellular regulation by classical endocrine

molecules comprehends autocrine (same cell), juxtacrine (neighbor cell), and paracrine (adjacent cell) pathways. Peptide growth factors are elements of a complex biological language, providing the basis for intercellular communication. They permit cells to convey information between each other, mediate interaction between cells and change gene expression. the effect of these multifunctional and pluripotent factors is dependent on the presence or absence of other peptides.

5 Fibroblast growth factors (FGFs) are a family of heparin-binding, potent mitogens for both normal diploid fibroblasts and established cell lines, Godpodarowicz, D. et al. (1984), Proc. Natl. Acad. Sci. USA 81: 6983. the FGF family comprises acidic FGF (FGF-1), basic FGF (FGF-2), INT-2 (FGF-3), K-FGF/HST (FGF-4), FGF-5, FGF-6, KGF (FGF-7), AIGF (FGF-8) among others. All FGFs have two conserved cysteine residues and share 30-50% sequence homology at the amino acid level. These factors are mitogenic for a wide variety of normal diploid mesoderm-derived
10 and neural crest-derived cells, inducing granulosa cells, adrenal cortical cells, chondrocytes, myoblasts, corneal and vascular endothelial cells (bovine or human), vascular smooth muscle cells, lens, retina and prostatic epithelial cells, oligodendrocytes, astrocytes, chondrocytes, myoblasts and osteoblasts.

Fibroblast growth factors can also stimulate a large number of cell types in a non-mitogenic manner. These activities include promotion of cell migration into a wound area (chemotaxis), initiation of new blood vessel formulation
15 (angiogenesis), modulation of nerve regeneration and survival (neurotrophism), modulation of endocrine functions, and stimulation or suppression of specific cellular protein expression, extracellular matrix production and cell survival. Baird, A. & Bohlen, P., *Handbook of Exp. Pharmacol.* 95(1): 369-418 (1990). These properties provide a basis for using fibroblast growth factors in therapeutic approaches to accelerate wound healing, nerve repair, collateral blood vessel formation, and the like. For example, fibroblast growth factors, have been suggested to minimize myocardium
20 damage in heart disease and surgery (U.S.P. 4,378,437).

We herein describe the identification and characterization of novel polypeptides having homology to FGF, herein designated PRO533 polypeptides.

10. PRO245

25 Some of the most important proteins involved in the above described regulation and modulation of cellular processes are the enzymes which regulate levels of protein phosphorylation in the cell. For example, it is known that the transduction of signals that regulate cell growth and differentiation is regulated at least in part by phosphorylation and dephosphorylation of various cellular proteins. The enzymes that catalyze these processes include the protein kinases, which function to phosphorylate various cellular proteins, and the protein phosphatases, which function to
30 remove phosphate residues from various cellular proteins. The balance of the level of protein phosphorylation in the cell is thus mediated by the relative activities of these two types of enzymes.

Although many protein kinase enzymes have been identified, the physiological role played by many of these catalytic proteins has yet to be elucidated. It is well known, however, that a number of the known protein kinases function to phosphorylate tyrosine residues in proteins, thereby leading to a variety of different effects. Perhaps most
35 importantly, there has been a great deal of interest in the protein tyrosine kinases since the discovery that many oncogene products and growth factors possess intrinsic protein tyrosine kinase activity. There is, therefore, a desire to identify new members of the protein tyrosine kinase family.

Given the physiological importance of the protein kinases, efforts are being undertaken by both industry and academia to identify new, native kinase proteins. Many of these efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel kinase proteins. We herein describe the identification and characterization of novel polypeptides having homology to tyrosine kinase proteins, designated herein as PRO245 polypeptides.

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11. PRO220, PRO221 and PRO227

Protein-protein interactions include receptor and antigen complexes and signaling mechanisms. As more is known about the structural and functional mechanisms underlying protein-protein interactions, protein-protein interactions can be more easily manipulated to regulate the particular result of the protein-protein interaction. Thus, the underlying mechanisms of protein-protein interactions are of interest to the scientific and medical community.

All proteins containing leucine-rich repeats are thought to be involved in protein-protein interactions. Leucine-rich repeats are short sequence motifs present in a number of proteins with diverse functions and cellular locations. The crystal structure of ribonuclease inhibitor protein has revealed that leucine-rich repeats correspond to beta-alpha structural units. These units are arranged so that they form a parallel beta-sheet with one surface exposed to solvent, so that the protein acquires an unusual, nonglobular shape. These two features have been indicated as responsible for the protein-binding functions of proteins containing leucine-rich repeats. See, Kobe and Deisenhofer, Trends Biochem. Sci., 19(10):415-421 (Oct. 1994).

A study has been reported on leucine-rich proteoglycans which serve as tissue organizers, orienting and ordering collagen fibrils during ontogeny and are involved in pathological processes such as wound healing, tissue repair, and tumor stroma formation. Iozzo, R. V., Crit. Rev. Biochem. Mol. Biol., 32(2):141-174 (1997). Others studies implicating leucine rich proteins in wound healing and tissue repair are De La Salle, C., et al., Vouv. Rev. Fr. Hematol. (Germany), 37(4):215-222 (1995), reporting mutations in the leucine rich motif in a complex associated with the bleeding disorder Bernard-Soulier syndrome and Chlemetson, K. J., Thromb. Haemost. (Germany), 74(1):111-116 (July 1995), reporting that platelets have leucine rich repeats. Another protein of particular interest which has been reported to have leucine-rich repeats is the SLIT protein which has been reported to be useful in treating neuro-degenerative diseases such as Alzheimer's disease, nerve damage such as in Parkinson's disease, and for diagnosis of cancer, see, Artavanistsakonas, S. and Rothberg, J. M., WO9210518-A1 by Yale University. Other studies reporting on the biological functions of proteins having leucine-rich repeats include: Tayar, N., et al., Mol. Cell Endocrinol., (Ireland), 125(1-2):65-70 (Dec. 1996) (gonadotropin receptor involvement); Miura, Y., et al., Nippon Rinsho (Japan), 54(7):1784-1789 (July 1996) (apoptosis involvement); Harris, P. C., et al., J. Am. Soc. Nephrol., 6(4):1125-1133 (Oct. 1995) (kidney disease involvement); and Ruoslahti, E. I., et al., WO9110727-A by La Jolla Cancer Research Foundation (decorin binding to transforming growth factor β involvement for treatment for cancer, wound healing and scarring).

Efforts are therefore being undertaken by both industry and academia to identify new proteins having leucine rich repeats to better understand protein-protein interactions. Of particular interest are those proteins having leucine rich repeats and homology to known proteins having leucine rich repeats such as the SLIT protein and platelet glycoprotein V.

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12. PRO258

Immunoglobulins are antibody molecules, the proteins that function both as receptors for antigen on the B-cell membrane and as the secreted products of the plasma cell. Like all antibody molecules, immunoglobulins perform two major functions: they bind specifically to an antigen and they participate in a limited number of biological effector functions. Therefore, new members of the Ig superfamily are always of interest. Molecules which
 5 act as receptors by various viruses and those which act to regulate immune function are of particular interest. Also of particular interest are those molecules which have homology to known Ig family members which act as virus receptors or regulate immune function. Thus, molecules having homology to poliovirus receptors, CRTAM and CD166 (a ligand for lymphocyte antigen CD6) are of particular interest.

Extracellular and membrane-bound proteins play important roles in the formation, differentiation and
 10 maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or
 15 signaling molecules normally pass through the cellular secretory pathway to reach their site of action in the extracellular environment, usually at a membrane-bound receptor protein.

We herein describe the identification and characterization of novel polypeptides having homology to CRTAM, designated herein as PRO258 polypeptides.

20 13. PRO266

Protein-protein interactions include receptor and antigen complexes and signaling mechanisms. As more is known about the structural and functional mechanisms underlying protein-protein interactions, protein-protein interactions can be more easily manipulated to regulate the particular result of the protein-protein interaction. Thus, the underlying mechanisms of protein-protein interactions are of interest to the scientific and medical community.

25 All proteins containing leucine-rich repeats are thought to be involved in protein-protein interactions. Leucine-rich repeats are short sequence motifs present in a number of proteins with diverse functions and cellular locations. The crystal structure of ribonuclease inhibitor protein has revealed that leucine-rich repeats correspond to beta-alpha structural units. These units are arranged so that they form a parallel beta-sheet with one surface exposed to solvent, so that the protein acquires an unusual, nonglobular shape. These two features have been
 30 indicated as responsible for the protein-binding functions of proteins containing leucine-rich repeats. See, Kobe and Deisenhofer, Trends Biochem. Sci., 19(10):415-421 (Oct. 1994).

A study has been reported on leucine-rich proteoglycans which serve as tissue organizers, orienting and ordering collagen fibrils during ontogeny and are involved in pathological processes such as wound healing, tissue repair, and tumor stroma formation. Iozzo, R. V., Crit. Rev. Biochem. Mol. Biol., 32(2):141-174 (1997). Others
 35 studies implicating leucine rich proteins in wound healing and tissue repair are De La Salle, C., et al., Vouv. Rev. Fr. Hematol. (Germany), 37(4):215-222 (1995), reporting mutations in the leucine rich motif in a complex associated with the bleeding disorder Bernard-Soulier syndrome and Chlemetson, K. J., Thromb. Haemost. (Germany),

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74(1):111-116 (July 1995), reporting that platelets have leucine rich repeats. Another protein of particular interest which has been reported to have leucine-rich repeats is the SLIT protein which has been reported to be useful in treating neuro-degenerative diseases such as Alzheimer's disease, nerve damage such as in Parkinson's disease, and for diagnosis of cancer, see, Artavanistsakonas, S. and Rothberg, J. M., WO9210518-A1 by Yale University. Other studies reporting on the biological functions of proteins having leucine-rich repeats include: Tayar, N., et al., Mol. Cell Endocrinol., (Ireland), 125(1-2):65-70 (Dec. 1996) (gonadotropin receptor involvement); Miura, Y., et al., Nippon Rinsho (Japan), 54(7):1784-1789 (July 1996) (apoptosis involvement); Harris, P. C., et al., J. Am. Soc. Nephrol., 6(4):1125-1133 (Oct. 1995) (kidney disease involvement); and Ruoslahti, E. I., et al., WO9110727-A by La Jolla Cancer Research Foundation (decorin binding to transforming growth factor β involvement for treatment for cancer, wound healing and scarring).

Efforts are therefore being undertaken by both industry and academia to identify new proteins having leucine rich repeats to better understand protein-protein interactions, neuronal development and adhesion molecules. Of particular interest are those proteins having leucine rich repeats and homology to known proteins having leucine rich repeats such as the SLIT protein. We herein describe novel polypeptides having homology to SLIT, designated herein as PRO266 polypeptides.

14. PRO269

Thrombomodulin binds to and regulates the activity of thrombin. It is important in the control of blood coagulation. Thrombomodulin functions as a natural anticoagulant by accelerating the activation of protein C by thrombin. Soluble thrombomodulin may have therapeutic use as an antithrombotic agent with reduced risk for hemorrhage as compared with heparin. Thrombomodulin is a cell surface trans-membrane glycoprotein, present on endothelial cells and platelets. A smaller, functionally active form of thrombomodulin circulates in the plasma and is also found in urine. (In Haeberli, A., Human Protein Data, VCH Oub., N.Y., 1992). Peptides having homology to thrombomodulin are particularly desirable.

We herein describe the identification and characterization of novel polypeptides having homology to thrombomodulin, designated herein as PRO269 polypeptides.

15. PRO287

Procollagen C-proteinase enhancer protein binds to and enhances the activity of bone morphogenic protein "BMP1"/procollagen C-proteinase (PCP). It plays a role in extracellular matrix deposition. BMP1 proteins may be used to induce bone and/or cartilage formation and in wound healing and tissue repair. Therefore, procollagen C-proteinase enhancer protein, BMP1 and proteins having homology thereto, are of interest to the scientific and medical communities.

We herein describe the identification and characterization of novel polypeptides having homology to procollagen C-proteinase enhancer protein precursor and procollagen C-proteinase enhancer protein, designated herein as PRO287 polypeptides.

16. **PRO214**

Growth factors are molecular signals or mediators that enhances cell growth or proliferation, alone or in concert, by binding to specific cell surface receptors. However, there are other cellular reactions than only growth upon expression to growth factors. As a result, growth factors are better characterized as multifunctional and potent cellular regulators. Their biological effects include proliferation, chemotaxis and stimulation of extracellular matrix production. Growth factors can have both stimulatory and inhibitory effects. For example, transforming growth factor β (TGF- β) is highly pleiotropic and can stimulate proliferation in some cells, especially connective tissue, while being a potent inhibitor of proliferation in others, such as lymphocytes and epithelial cells.

The physiological effect of growth stimulation or inhibition by growth factors depends upon the state of development and differentiation of the target tissue. The mechanism of local cellular regulation by classical endocrine molecules involves comprehends autocrine (same cell), juxtacrine (neighbor cell), and paracrine (adjacent cells) pathways. Peptide growth factors are elements of a complex biological language, providing the basis for intercellular communication. They permit cells to convey information between each other, mediate interaction between cells and change gene expression. The effect of these multifunctional and pluripotent factors is dependent on the presence or absence of other peptides.

Epidermal growth factor (EGF) is a conventional mitogenic factor that stimulates the proliferation of various types of cells including epithelial cells and fibroblasts. EGF binds to and activates the EGF receptor (EGFR), which initiates intracellular signaling and subsequent effects. The EGFR is expressed in neurons of the cerebral cortex, cerebellum, and hippocampus in addition to other regions of the central nervous system (CNS). In addition, EGF is also expressed in various regions of the CNS. Therefore, EGF acts not only on mitotic cells, but also on postmitotic neurons. In fact, many studies have indicated that EGF has neurotrophic or neuromodulatory effects on various types of neurons in the CNS. For example, EGF acts directly on cultured cerebral cortical and cerebellar neurons, enhancing neurite outgrowth and survival. On the other hand, EGF also acts on other cell types, including septal cholinergic and mesencephalic dopaminergic neurons, indirectly through glial cells. Evidence of the effects of EGF on neurons in the CNS is accumulating, but the mechanisms of action remain essentially unknown. EGF-induced signaling in mitotic cells is better understood than in postmitotic neurons. Studies of cloned pheochromocytoma PC12 cells and cultured cerebral cortical neurons have suggested that the EGF-induced neurotrophic actions are mediated by sustained activation of the EGFR and mitogen-activated protein kinase (MAPK) in response to EGF. The sustained intracellular signaling correlates with the decreased rate of EGFR down-regulation, which might determine the response of neuronal cells to EGF. It is likely that EGF is a multi-potent growth factor that acts upon various types of cells including mitotic cells and postmitotic neurons.

EGF is produced by the salivary and Brunner's glands of the gastrointestinal system, kidney, pancreas, thyroid gland, pituitary gland, and the nervous system, and is found in body fluids such as saliva, blood, cerebrospinal fluid (CSF), urine, amniotic fluid, prostatic fluid, pancreatic juice, and breast milk, Plata-Salaman, CR *Peptides* 12: 653-663 (1991).

EGF is mediated by its membrane specific receptor, which contains an intrinsic tyrosine kinase. Stoscheck CM *et al.*, *J. Cell Biochem.* 31: 135-152 (1986). EGF is believed to function by binding to the extracellular portion of its receptor which induces a transmembrane signal that activates the intrinsic tyrosine kinase.

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Purification and sequence analysis of the EGF-like domain has revealed the presence of six conserved cysteine residues which cross-bind to create three peptide loops, Savage *CR et al.*, *J. Biol. Chem.* **248**: 7669-7672 (1979). It is now generally known that several other peptides can react with the EGF receptor which share the same generalized motif $X_nCX_7CX_{4/5}CX_{10}CXCX_5GX_2CX_n$, where X represents any non-cysteine amino acid, and n is a variable repeat number. Non isolated peptides having this motif include TGF- α , amphiregulin, schwannoma-derived growth factor (SDGF), heparin-binding EGF-like growth factors and certain virally encoded peptides (e.g., Vaccinia virus, Reisner AH, *Nature* **313**: 801-803 (1985), Shope fibroma virus, Chang W., et al., *Mol Cell Biol.* **7**: 535-540 (1987), Molluscum contagiosum, Porter CD & Archard LC, *J. Gen. Virol.* **68**: 673-682 (1987), and Myxoma virus, Upton C *et al.*, *J. Virol.* **61**: 1271-1275 (1987). Prigent SA & Lemoine N.R., *Prog. Growth Factor Res.* **4**: 1-24 (1992).

- 10 EGF-like domains are not confined to growth factors but have been observed in a variety of cell-surface and extracellular proteins which have interesting properties in cell adhesion, protein-protein interaction and development, Laurence DJR & Gusterson BA, *Tumor Biol.* **11**: 229-261 (1990). These proteins include blood coagulation factors (factors VI, IX, X, XII, protein C, protein S, protein Z, tissue plasminogen activator, urokinase), extracellular matrix components (laminin, cytactin, entactin), cell surface receptors (LDL receptor, thrombomodulin receptor) and
- 15 immunity-related proteins (complement C1r, uromodulin).

Even more interesting, the general structure pattern of EGF-like precursors is preserved through lower organisms as well as in mammalian cells. A number of genes with developmental significance have been identified in invertebrates with EGF-like repeats. For example, the *notch* gene of *Drosophila* encodes 36 tandemly arranged 40 amino acid repeats which show homology to EGF, Wharton W *et al.*, *Cell* **43**: 557-581 (1985). Hydropathy plots

20 indicate a putative membrane spanning domain, with the EGF-related sequences being located on the extracellular side of the membrane. Other homeotic genes with EGF-like repeats include Delta, 95F and 5ZD which were identified using probes based on Notch, and the nematode gene *Lin-12* which encodes a putative receptor for a developmental signal transmitted between two specified cells.

Specifically, EGF has been shown to have potential in the preservation and maintenance of gastrointestinal

25 mucosa and the repair of acute and chronic mucosal lesions, Konturek, PC *et al.*, *Eur. J. Gastroenterol Hepatol.* **7** (10), 933-37 (1995), including the treatment of necrotizing enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration gastrointestinal ulcerations and congenital microvillus atrophy, A. Guglietta & PB Sullivan, *Eur. J. Gastroenterol Hepatol.* **7**(10), 945-50 (1995). Additionally, EGF has been implicated in hair follicle differentiation; C.L. du Cros, *J. Invest. Dermatol.* **101** (1 Suppl.), 106S-113S (1993), SG Hillier, *Clin. Endocrinol.*

30 **33**(4), 427-28 (1990); kidney function, L.L. Hamm *et al.*, *Semin. Nephrol.* **13** (1): 109-15 (1993), RC Harris, *Am. J. Kidney Dis.* **17**(6): 627-30 (1991); tear fluid, GB van Setten *et al.*, *Int. Ophthalmol* **15**(6); 359-62 (1991); vitamin K mediated blood coagulation, J. Stenflo *et al.*, *Blood* **78**(7): 1637-51 (1991). EGF is also implicated various skin disease characterized by abnormal keratinocyte differentiation, e.g., psoriasis, epithelial cancers such as squamous cell carcinomas of the lung, epidermoid carcinoma of the vulva and gliomas. King, LE *et al.*, *Am. J. Med. Sci.* **296**:

35 154-158 (1988).

Of great interest is mounting evidence that genetic alterations in growth factors signaling pathways are closely linked to developmental abnormalities and to chronic diseases including cancer. Aaronson SA, *Science* **254**:

1146-1153 (1991). For example, c-erb-2 (also known as HER-2), a proto-oncogene with close structural similarity to EGF receptor protein, is overexpressed in human breast cancer. King *et al.*, *Science* **229**: 974-976 (1985); Gullick, WJ, *Hormones and their actions*, Cooke BA *et al.*, eds, Amsterdam, Elsevier, pp 349-360 (1986).

17. PRO317

5 The TGF- β supergene family, or simply TGF- β superfamily, a group of secreted proteins, includes a large number of related growth and differentiation factors expressed in virtually all phyla. Superfamily members bind to specific cell surface receptors that activate signal transduction mechanisms to elicit their multifunctional cytokine effects. Kolodziejczyk and Hall, *Biochem. Cell. Biol.*, **74**: 299-314 (1996); Attisano and Wrana, *Cytokine Growth Factor Rev.*, **7**: 327-339 (1996); and Hill, *Cellular Signaling*, **8**: 533-544 (1996).

10 Members of this family include five distinct forms of TGF- β (Sporn and Roberts, in *Peptide Growth Factors and Their Receptors*, Sporn and Roberts, eds. (Springer-Verlag: Berlin, 1990) pp. 419-472), as well as the differentiation factors vgl (Weeks and Melton, *Cell*, **51**: 861-867 (1987)) and DPP-C polypeptide (Padgett *et al.*, *Nature*, **325**: 81-84 (1987)), the hormones activin and inhibin (Mason *et al.*, *Nature*, **318**: 659-663 (1985); Mason *et al.*, *Growth Factors*, **1**: 77-88 (1987)), the Mullerian-inhibiting substance (MIS) (Cate *et al.*, *Cell*, **45**: 685-698 (1986)), the bone morphogenetic proteins (BMPs) (Wozney *et al.*, *Science*, **242**: 1528-1534 (1988); PCT WO 88/00205 published January 14, 1988; U.S. 4,877,864 issued October 31, 1989), the developmentally regulated proteins Vgr-1 (Lyons *et al.*, *Proc. Natl. Acad. Sci. USA*, **86**: 4554-4558 (1989)) and Vgr-2 (Jones *et al.*, *Molec. Endocrinol.*, **6**: 1961-1968 (1992)), the mouse growth differentiation factor (GDF), such as GDF-3 and GDF-9 (Kingsley, *Genes Dev.*, **8**: 133-146 (1994); McPherron and Lee, *J. Biol. Chem.*, **268**: 3444-3449 (1993)), the mouse
20 leftry/Stral (Meno *et al.*, *Nature*, **381**: 151-155 (1996); Bouillet *et al.*, *Dev. Biol.*, **170**: 420-433 (1995)), glial cell line-derived neurotrophic factor (GDNF) (Lin *et al.*, *Science*, **260**: 1130-1132 (1993), neurturin (Kotzbauer *et al.*, *Nature*, **384**: 467-470 (1996)), and endometrial bleeding-associated factor (EBAF) (Kothapalli *et al.*, *J. Clin. Invest.*, **99**: 2342-2350 (1997)). The subset BMP-2A and BMP-2B is approximately 75% homologous in sequence to DPP-C and may represent the mammalian equivalent of that protein.

25 The proteins of the TGF- β superfamily are disulfide-linked homo- or heterodimers encoded by larger precursor polypeptide chains containing a hydrophobic signal sequence, a long and relatively poorly conserved N-terminal pro region of several hundred amino acids, a cleavage site (usually polybasic), and a shorter and more highly conserved C-terminal region. This C-terminal region corresponds to the processed mature protein and contains approximately 100 amino acids with a characteristic cysteine motif, *i.e.*, the conservation of seven of the nine cysteine
30 residues of TGF- β among all known family members. Although the position of the cleavage site between the mature and pro regions varies among the family members, the C-terminus of all of the proteins is in the identical position, ending in the sequence Cys-X-Cys-X, but differing in every case from the TGF- β consensus C-terminus of Cys-Lys-Cys-Ser. Sporn and Roberts, 1990, *supra*.

There are at least five forms of TGF- β currently identified, TGF- β 1, TGF- β 2, TGF- β 3, TGF- β 4, and TGF-
35 β 5. The activated form of TGF- β 1 is a homodimer formed by dimerization of the carboxy-terminal 112 amino acids of a 390 amino acid precursor. Recombinant TGF- β 1 has been cloned (Derynck *et al.*, *Nature*, **316**: 701-705 (1985)) and expressed in Chinese hamster ovary cells (Gentry *et al.*, *Mol. Cell. Biol.*, **7**: 3418-3427 (1987)). Additionally,

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recombinant human TGF- β 2 (deMartin *et al.*, EMBO J., 6: 3673 (1987)), as well as human and porcine TGF- β 3 (Derynck *et al.*, EMBO J., 7: 3737-3743 (1988); ten Dijke *et al.*, Proc. Natl. Acad. Sci. USA, 85: 4715 (1988)) have been cloned. TGF- β 2 has a precursor form of 414 amino acids and is also processed to a homodimer from the carboxy-terminal 112 amino acids that shares approximately 70% homology with the active form of TGF- β 1 (Marquardt *et al.*, J. Biol. Chem., 262: 12127 (1987)). See also EP 200,341; 169,016; 268,561; and 267,463; U.S. Pat. No. 4,774,322; Cheifetz *et al.*, Cell, 48: 409-415 (1987); Jakowlew *et al.*, Molecular Endocrin., 2: 747-755 (1988); Derynck *et al.*, J. Biol. Chem., 261: 4377-4379 (1986); Sharples *et al.*, DNA, 6: 239-244 (1987); Derynck *et al.*, Nucl. Acids. Res., 15: 3188-3189 (1987); Derynck *et al.*, Nucl. Acids. Res., 15: 3187 (1987); Seyedin *et al.*, J. Biol. Chem., 261: 5693-5695 (1986); Madisen *et al.*, DNA, 7: 1-8 (1988); and Hanks *et al.*, Proc. Natl. Acad. Sci. (U.S.A.), 85: 79-82 (1988).

10 TGF- β 4 and TGF- β 5 were cloned from a chicken chondrocyte cDNA library (Jakowlew *et al.*, Molec. Endocrinol., 2: 1186-1195 (1988)) and from a frog oocyte cDNA library, respectively.

The pro region of TGF- β associates non-covalently with the mature TGF- β dimer (Wakefield *et al.*, J. Biol. Chem., 263: 7646-7654 (1988); Wakefield *et al.*, Growth Factors, 1: 203-218 (1989)), and the pro regions are found to be necessary for proper folding and secretion of the active mature dimers of both TGF- β and activin (Gray and 15 Mason, Science, 247: 1328-1330 (1990)). The association between the mature and pro regions of TGF- β masks the biological activity of the mature dimer, resulting in formation of an inactive latent form. Latency is not a constant of the TGF- β superfamily, since the presence of the pro region has no effect on activin or inhibin biological activity.

A unifying feature of the biology of the proteins from the TGF- β superfamily is their ability to regulate developmental processes. TGF- β has been shown to have numerous regulatory actions on a wide variety of both 20 normal and neoplastic cells. TGF- β is multifunctional, as it can either stimulate or inhibit cell proliferation, differentiation, and other critical processes in cell function (Sporn and Roberts, *supra*).

One member of the TGF- β superfamily, EBAF, is expressed in endometrium only in the late secretory phase and during abnormal endometrial bleeding. Kothapalli *et al.*, J. Clin. Invest., 99: 2342-2350 (1997). Human endometrium is unique in that it is the only tissue in the body that bleeds at regular intervals. In addition, abnormal 25 endometrial bleeding is one of the most common manifestations of gynecological diseases, and is a prime indication for hysterectomy. *In situ* hybridization showed that the mRNA of EBAF was expressed in the stroma without any significant mRNA expression in the endometrial glands or endothelial cells.

The predicted protein sequence of EBAF showed a strong homology to the protein encoded by mouse *lefty/stra3* of the TGF- β superfamily. A motif search revealed that the predicted EBAF protein contains most of the 30 cysteine residues which are conserved among the TGF- β -related proteins and which are necessary for the formation of the cysteine knot structure. The EBAF sequence contains an additional cysteine residue, 12 amino acids upstream from the first conserved cysteine residue. The only other family members known to contain an additional cysteine residue are TGF- β s, inhibins, and GDF-3. EBAF, similar to LEFTY, GDF-3/Vgr2, and GDF-9, lacks the cysteine residue that is known to form the intermolecular disulfide bond. Therefore, EBAF appears to be an additional 35 member of the TGF- β superfamily with an unpaired cysteine residue that may not exist as a dimer. However, hydrophobic contacts between the two monomer subunits may promote dimer formation. Fluorescence *in situ* hybridization showed that the *ebaf* gene is located on human chromosome 1 at band q42.1.

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Additional members of the TGF- β superfamily, such as those related to EBAF, are being searched for by industry and academics. We herein describe the identification and characterization of novel polypeptides having homology to EBAF, designated herein as PRO317 polypeptides.

18. PRO301

5 The widespread occurrence of cancer has prompted the devotion of considerable resources and discovering new treatments of treatment. One particular method involves the creation of tumor or cancer specific monoclonal antibodies (mAbs) which are specific to tumor antigens. Such mAbs, which can distinguish between normal and cancerous cells are useful in the diagnosis, prognosis and treatment of the disease. Particular antigens are known to be associated with neoplastic diseases, such as colorectal cancer.

10 One particular antigen, the A33 antigen is expressed in more than 90% of primary or metastatic colon cancers as well as normal colon epithelium. Since colon cancer is a widespread disease, early diagnosis and treatment is an important medical goal. Diagnosis and treatment of colon cancer can be implemented using monoclonal antibodies (mAbs) specific therefore having fluorescent, nuclear magnetic or radioactive tags. Radioactive gene, toxins and/or drug tagged mAbs can be used for treatment *in situ* with minimal patient description. 15 mAbs can also be used to diagnose during the diagnosis and treatment of colon cancers. For example, when the serum levels of the A33 antigen are elevated in a patient, a drop of the levels after surgery would indicate the tumor resection was successful. On the other hand, a subsequent rise in serum A33 antigen levels after surgery would indicate that metastases of the original tumor may have formed or that new primary tumors may have appeared. Such monoclonal antibodies can be used in lieu of, or in conjunction with surgery and/or other chemotherapies. For example, U.S.P. 4,579,827 and U.S.S.N. 424,991 (E.P. 199,141) are directed to therapeutic administration of 20 monoclonal antibodies, the latter of which relates to the application of anti-A33 mAb.

Many cancers of epithelial origin have adenovirus receptors. In fact, adenovirus-derived vectors have been proposed as a means of inserting antisense nucleic acids into tumors (U.S.P. 5,518,885). Thus, the association of viral receptors with neoplastic tumors is not unexpected.

25 We herein describe the identification and characterization of novel polypeptides having homology to certain cancer-associated antigens, designated herein as PRO301 polypeptides.

19. PRO224

30 Cholesterol uptake can have serious implications on one's health. Cholesterol uptake provides cells with most of the cholesterol they require for membrane synthesis. If this uptake is blocked, cholesterol accumulates in the blood and can contribute to the formation of atherosclerotic plaques in blood vessel walls. Most cholesterol is transported in the blood bound to protein in the form of complexes known as low-density lipoproteins (LDLs). LDLs are endocytosed into cells via LDL receptor proteins. Therefore, LDL receptor proteins, and proteins having homology thereto, are of interest to the scientific and medical communities. Membrane-bound proteins and 35 receptors can play an important role in the formation, differentiation and maintenance of multicellular organisms. The LDL receptors are an example of membrane-bound proteins which are involved in the synthesis and formation of cell membranes, wherein the health of an individual is affected directly and indirectly by its function. Many

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membrane-bound proteins act as receptors such as the LDL receptor. These receptors can function to endocytose substrates or they can function as a receptor for a channel. Other membrane-bound proteins function as signals or antigens.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule regulators of the relevant receptor/ligand interaction. In the case of the LDL receptor, it is desirable to find molecules which enhance endocytosis so as to lower blood cholesterol levels and plaque formation. It is also desirable to identify molecules which inhibit endocytosis so that these molecules can be avoided or regulated by individuals having high blood cholesterol. Polypeptides which are homologous to lipoprotein receptors but which do not function as lipoprotein receptors are also of interest in the determination of the function of the fragments which show homology.

The following studies report on previously known low density lipoprotein receptors and related proteins including apolipoproteins: Sawamura, et al., Nippon Chemiphar Co, Japan patent application J09098787; Novak, S., et al., J. Biol. Chem., 271:(20)11732-6 (1996); Blaas, D., J. Virol., 69(11)7244-7 (Nov. 1995); Scott, J., J. Inherit. Metab. Dis. (UK), 9/Supp. 1 (3-16) (1986); Yamamoto, et al., Cell, 39:27-38 (1984); Rebecq, et al., Neurobiol. Aging, 15:5117 (1994); Novak, S., et al., J. Biol. Chemistry, 271:11732-11736 (1996); and Sestavel and Fruchart, Cell Mol. Biol., 40(4):461-81 (June 1994). These publications and others published prior to the filing of this application provide further background to peptides already known in the art.

Efforts are being undertaken by both industry and academia to identify new, native membrane-bound receptor proteins, particularly those having homology to lipoprotein receptors. We herein describe the identification and characterization of novel polypeptides having homology to lipoprotein receptors, designated herein as PRO224 polypeptides.

20. PRO222

Complement is a group of proteins found in the blood that are important in humoral immunity and inflammation. Complement proteins are sequentially activated by antigen-antibody complexes or by proteolytic enzymes. When activated, complement proteins kill bacteria and other microorganisms, affect vascular permeability, release histamine and attract white blood cells. Complement also enhances phagocytosis when bound to target cells. In order to prevent harm to autologous cells, the complement activation pathway is tightly regulated.

Deficiencies in the regulation of complement activation or in the complement proteins themselves may lead to immune-complex diseases, such as systemic lupus erythematosus, and may result in increased susceptibility to bacterial infection. In all cases, early detection of complement deficiency is desirable so that the patient can begin treatment. Thus, research efforts are currently directed toward identification of soluble and membrane proteins that regulate complement activation.

Proteins known to be important in regulating complement activation in humans include Factor H and Complement receptor type 1 (CR1). Factor H is a 150 kD soluble serum protein that interacts with complement protein C3b to accelerate the decay of C3 convertase and acts as a cofactor for Factor I-mediated cleavage of complement protein C4b. Complement receptor type 1 is a 190-280 kD membrane bound protein found in mast cells

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and most blood cells. CR1 interacts with complement proteins C3b, C4b, and iC3b to accelerate dissociation of C3 convertases, acts as a cofactor for Factor I-mediated cleavage of C3b and C4b, and binds immune complexes and promotes their dissolution and phagocytosis.

Proteins which have homology to complement proteins are of particular interest to the medical and industrial communities. Often, proteins having homology to each other have similar function. It is also of interest when proteins having homology do not have similar functions, indicating that certain structural motifs identify information other than function, such as locality of function.

Efforts are being undertaken by both industry and academia to identify new, native secreted and membrane-bound proteins, particularly those having homology to known proteins involved in the complement pathway. Proteins involved in the complement pathway were reviewed in Birmingham DJ (1995), *Critical Reviews in Immunology*, 15(2):133-154 and in Abbas AK, et al. (1994) *Cellular and Molecular Immunology*, 2nd Ed. W.B. Saunders Company, Philadelphia, pp 295-315.

We herein describe the identification and characterization of novel polypeptides having homology to complement receptors, designated herein as PRO222 polypeptides.

21. PRO234

The successful function of many systems within multicellular organisms is dependent on cell-cell interactions. Such interactions are affected by the alignment of particular ligands with particular receptors in a manner which allows for ligand-receptor binding and thus a cell-cell adhesion. While protein-protein interactions in cell recognition have been recognized for some time, only recently has the role of carbohydrates in physiologically relevant recognition been widely considered (see B.K. Brandley *et al.*, *J. Leuk. Biol.* 40: 97 (1986) and N. Sharon *et al.*, *Science* 246: 227 (1989). Oligosaccharides are well positioned to act as recognition novel lectins due to their cell surface location and structural diversity. Many oligosaccharide structures can be created through the differential activities of a smaller number of glycosyltransferases. The diverse structures of oligosaccharides can be generated by transcription of relatively few gene products, which suggests that the oligosaccharides are a plausible mechanism by which is directed a wide range of cell-cell interactions. Examples of differential expression of cell surface carbohydrates and putative carbohydrate binding proteins (lectins) on interacting cells have been described (J. Dodd & T.M. Jessel, *J. Neurosci.* 5: 3278 (1985); L.J. Regan *et al.*, *Proc. Natl. Acad. Sci. USA* 83: 2248 (1986); M. Constantine-Paton *et al.*, *Nature* 324: 459 (1986); and M. Tiemeyer *et al.*, *J. Biol. Chem.* 263: 1671 (1989). One interesting member of the lectin family are selectins.

The migration of leukocytes to sites of acute or chronic inflammation involves adhesive interactions between these cells and the endothelium. This specific adhesion is the initial event in the cascade that is initiated by inflammatory insults, and it is, therefore, of paramount importance to the regulated defense of the organism.

The types of cell adhesion molecules that are involved in the interaction between leukocytes and the endothelium during an inflammatory response currently stands at four: (1) selectins; (2) (carbohydrate and glycoprotein) ligands for selectins; (3) integrins; and (4) integrin ligands, which are members of the immunoglobulin gene superfamily.

The selectins are cell adhesion molecules that are unified both structurally and functionally. Structurally, selectins are characterized by the inclusion of a domain with homology to a calcium-dependent lectin (C-lectins), an epidermal growth factor (egf)-like domain and several complement binding-like domains, Bevilacqua, M.P. *et al.*, *Science* **243**: 1160-1165 (1989); Johnston *et al.*, *Cell* **56**: 1033-1044 (1989); Lasky *et al.*, *Cell* **56**: 1045-1055 (1989); Siegalman, M. *et al.*, *Science* **243**: 1165-1172 (1989); Stoolman, L.M., *Cell* **56**: 907-910 (1989). Functionally, selectins share the common property of their ability to mediate cell binding through interactions between their lectin domains and cell surface carbohydrate ligands (Brandley, B. *et al.*, *Cell* **63**, 861-863 (1990); Springer, T. and Lasky, L.A., *Nature* **349**, 19-197 (1991); Bevilacqua, M.P. and Nelson, R.M., *J. Clin. Invest.* **91** 379-387 (1993) and Tedder *et al.*, *J. Exp. Med.* **170**: 123-133 (1989).

There are three members identified so far in the selectin family of cell adhesion molecules: L-selectin (also called peripheral lymph node homing receptor (pnHR), LEC-CAM-1, LAM-1, gp90^{MEL}, gp100^{MEL}, gp110^{MEL}, MEL-14 antigen, Leu-8 antigen, TQ-1 antigen, DREG antigen), E-selectin (LEC-CAM-2, LECAM-2, ELAM-1) and P-selectin (LEC-CAM-3, LECAM-3, GMP-140, PADGEM).

The identification of the C-lectin domain has led to an intense effort to define carbohydrate binding ligands for proteins containing such domains. E-selectin is believed to recognize the carbohydrate sequence NeuNAc α 2-3Gal β 1-4(Fuc α 1-3)GlcNAc (sialyl-Lewis x, or sLe^x) and related oligosaccharides, Berg *et al.*, *J. Biol. Chem.* **265**: 14869-14872 (1991); Lowe *et al.*, *Cell* **63**: 475-484 (1990); Phillips *et al.*, *Science* **250**: 1130-1132 (1990); Tiemeyer *et al.*, *Proc. Natl. Acad. Sci. USA* **88**: 1138-1142 (1991).

L-selectin, which comprises a lectin domain, performs its adhesive function by recognizing carbohydrate-containing ligands on endothelial cells. L-selectin is expressed on the surface of leukocytes, such as lymphocytes, neutrophils, monocytes and eosinophils, and is involved with the trafficking of lymphocytes to peripheral lymphoid tissues (Gallatin *et al.*, *Nature* **303**: 30-34 (1983)) and with acute neutrophil-mediated inflammatory responses (Watson, S.R., *Nature* **349**: 164-167 (1991)). The amino acid sequence of L-selectin and the encoding nucleic acid sequence are, for example, disclosed in U.S. patent No. 5,098,833 issued 24 March 1992.

L-selectin (LEC-CAM-1) is particularly interesting because of its ability to block neutrophil influx (Watson *et al.*, *Nature* **349**: 164-167 (1991)). It is expressed in chronic lymphocytic leukemia cells which bind to HEV (Spertini *et al.*, *Nature* **349**: 691-694 (1991)). It is also believed that HEV structures at sites of chronic inflammation are associated with the symptoms of diseases such as rheumatoid arthritis, psoriasis and multiple sclerosis.

E-selectin (ELAM-1), is particularly interesting because of its transient expression on endothelial cells in response to IL-1 or TNF. Bevilacqua *et al.*, *Science* **243**: 1160 (1989). The time course of this induced expression (2-8 h) suggests a role for this receptor in initial neutrophil induced extravasation in response to infection and injury. It has further been reported that anti-ELAM-1 antibody blocks the influx of neutrophils in a primate asthma model and thus is beneficial for preventing airway obstruction resulting from the inflammatory response. Gundel *et al.*, *J. Clin. Invest.* **88**: 1407 (1991).

The adhesion of circulating neutrophils to stimulated vascular endothelium is a primary event of the inflammatory response. P-selectin has been reported to recognize the Lewis x structure (Gal β 1-4(Fuc α 1-3) GlcNAc), Larsen *et al.*, *Cell* **63**: 467-474(1990). Others report that an additional terminal linked sialic acid is required for high affinity binding, Moore *et al.*, *J. Cell. Biol.* **112**: 491-499 (1991). P-selectin has been shown to be significant in acute

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lung injury. Anti-P-selectin antibody has been shown to have strong protective effects in a rodent lung injury model. M.S. Mulligan *et al.*, *J. Clin. Invest.* 90: 1600 (1991).

We herein describe the identification and characterization of novel polypeptides having homology to lectin proteins, herein designated as PRO234 polypeptides.

5 22. PRO231

Some of the most important proteins involved in the above described regulation and modulation of cellular processes are the enzymes which regulate levels of protein phosphorylation in the cell. For example, it is known that the transduction of signals that regulate cell growth and differentiation is regulated at least in part by phosphorylation and dephosphorylation of various cellular proteins. The enzymes that catalyze these processes include the protein
10 kinases, which function to phosphorylate various cellular proteins, and the protein phosphatases, which function to remove phosphate residues from various cellular proteins. The balance of the level of protein phosphorylation in the cell is thus mediated by the relative activities of these two types of enzymes.

Protein phosphatases represent a growing family of enzymes that are found in many diverse forms, including both membrane-bound and soluble forms. While many protein phosphatases have been described, the functions of
15 only a very few are beginning to be understood (Tonks, *Semin. Cell Biol.* 4:373-453 (1993) and Dixon, *Recent Prog. Horm. Res.* 51:405-414 (1996)). However, in general, it appears that many of the protein phosphatases function to modulate the positive or negative signals induced by various protein kinases. Therefore, it is likely that protein phosphatases play critical roles in numerous and diverse cellular processes.

Given the physiological importance of the protein phosphatases, efforts are being undertaken by both
20 industry and academia to identify new, native phosphatase proteins. Many of these efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel phosphatase proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein *et al.*, *Proc. Natl. Acad. Sci.*, 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

We herein describe the identification and characterization of novel polypeptides having homology to acid
25 phosphatases, designated herein as PRO231 polypeptides.

23. PRO229

Scavenger receptors are known to protect IgG molecules from catabolic degradation. Riechmann and Hollinger, *Nature Biotechnology*, 15:617 (1997). In particular, studies of the CH2 and CH3 domains have shown
30 that specific sequences of these domains are important in determining the half-lives of antibodies. Ellerson, *et al.*, *J. Immunol.*, 116: 510 (1976); Yasmeen, *et al.*, *J. Immunol.* 116: 518 (1976; Pollock, *et al.*, *Eur. J. Immunol.*, 20: 2021 (1990). Scavenger receptor proteins and antibodies thereto are further reported in U.S. Patent No. 5,510,466 to Krieger, *et al.* Due to the ability of scavenger receptors to increase the half-life of polypeptides and their involvement in immune function, molecules having homology to scavenger receptors are of importance to the
35 scientific and medical community.

Efforts are being undertaken by both industry and academia to identify new, native secreted and membrane-bound receptor proteins, particularly those having homology to scavenger receptors. Many efforts are focused on

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the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound receptor proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., Proc. Natl. Acad. Sci., 93:7108-7113 (1996); U.S. Patent No. 5,536,637)].

We herein describe the identification and characterization of novel polypeptides having homology to scavenger receptors, designated herein as PRO229 polypeptides.

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24. PRO238

Oxygen free radicals and antioxidants appear to play an important role in the central nervous system after cerebral ischemia and reperfusion. Moreover, cardiac injury, related to ischaemia and reperfusion has been reported to be caused by the action of free radicals. Additionally, studies have reported that the redox state of the cell is a pivotal determinant of the fate of the cells. Furthermore, reactive oxygen species have been reported to be cytotoxic, causing inflammatory disease, including tissue necrosis, organ failure, atherosclerosis, infertility, birth defects, premature aging, mutations and malignancy. Thus, the control of oxidation and reduction is important for a number of reasons including for control and prevention of strokes, heart attacks, oxidative stress and hypertension. In this regard, reductases, and particularly, oxidoreductases, are of interest. Publications further describing this subject matter include Kelsey, et al., Br. J. Cancer, 76(7):852-4 (1997); Friedrich and Weiss, J. Theor. Biol., 187(4):529-40 (1997) and Pieulle, et al., J. Bacteriol., 179(18):5684-92 (1997).

Efforts are being undertaken by both industry and academia to identify new, native secreted and membrane-bound receptor proteins, particularly secreted proteins which have homology to reductase. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound receptor proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., Proc. Natl. Acad. Sci., 93:7108-7113 (1996); U.S. Patent No. 5,536,637)].

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We herein describe the identification and characterization of novel polypeptides having homology to reductase, designated herein as PRO238 polypeptides.

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25. PRO233

Studies have reported that the redox state of the cell is an important determinant of the fate of the cell. Furthermore, reactive oxygen species have been reported to be cytotoxic, causing inflammatory disease, including tissue necrosis, organ failure, atherosclerosis, infertility, birth defects, premature aging, mutations and malignancy. Thus, the control of oxidation and reduction is important for a number of reasons, including the control and prevention of strokes, heart attacks, oxidative stress and hypertension. Oxygen free radicals and antioxidants appear to play an important role in the central nervous system after cerebral ischemia and reperfusion. Moreover, cardiac injury, related to ischaemia and reperfusion has been reported to be caused by the action of free radicals. In this regard, reductases, and particularly, oxidoreductases, are of interest. In addition, the transcription factors, NF-kappa B and AP-1, are known to be regulated by redox state and to affect the expression of a large variety of genes thought to be involved in the pathogenesis of AIDS, cancer, atherosclerosis and diabetic complications. Publications further describing this subject matter include Kelsey, et al., Br. J. Cancer, 76(7):852-4 (1997); Friedrich and Weiss, J. Theor. Biol., 187(4):529-40 (1997) and Pieulle, et al., J. Bacteriol., 179(18):5684-92 (1997). Given the physiological

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importance of redox reactions *in vivo*, efforts are currently being under taken to identify new, native proteins which are involved in redox reactions. We describe herein the identification of novel polypeptides which have homology to reductase, designated herein as PRO233 polypeptides.

26. PRO223

5 The carboxypeptidase family of exopeptidases constitutes a diverse group of enzymes that hydrolyze carboxyl-terminal amide bonds in polypeptides, wherein a large number of mammalian tissues produce these enzymes. Many of the carboxypeptidase enzymes that have been identified to date exhibit rather strong cleavage specificities for certain amino acids in polypeptides. For example, carboxypeptidase enzymes have been identified which prefer lysine, arginine, serine or amino acids with either aromatic or branched aliphatic side chains as
10 substrates at the carboxyl terminus of the polypeptide.

With regard to the serine carboxypeptidases, such amino acid specific enzymes have been identified from a variety of different mammalian and non-mammalian organisms. The mammalian serine carboxypeptidase enzymes play important roles in many different biological processes including, for example, protein digestion, activation, inactivation, or modulation of peptide hormone activity, and alteration of the physical properties of proteins and
15 enzymes.

In light of the physiological importance of the serine carboxypeptidases, efforts are being undertaken by both industry and academia to identify new, native secreted and membrane-bound receptor proteins and specifically novel carboxypeptidases. Many of these efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound receptor proteins. We describe herein novel
20 polypeptides having homology to one or more serine carboxypeptidase polypeptides, designated herein as PRO223 polypeptides.

27. PRO235

Plexin was first identified in *Xenopus* tadpole nervous system as a membrane glycoprotein which was shown
25 to mediate cell adhesion via a homophilic binding mechanism in the presence of calcium ions. Strong evolutionary conservation between *Xenopus*, mouse and human homologs of plexin has been observed. [Kaneyama et al., Biochem. And Biophys. Res. Comm. 226: 524-529 (1996)]. Given the physiological importance of cell adhesion mechanisms *in vivo*, efforts are currently being under taken to identify new, native proteins which are involved in cell adhesion. We describe herein the identification of a novel polypeptide which has homology to plexin, designated
30 herein as PRO235.

28. PRO236 and PRO262

β -galactosidase is a well known enzymatic protein which functions to hydrolyze β -galactoside molecules. β -galactosidase has been employed for a variety of different applications, both *in vitro* and *in vivo* and has proven
35 to be an extremely useful research tool. As such, there is an interest in obtaining novel polypeptides which exhibit homology to the β -galactosidase polypeptide.

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Given the strong interest in obtaining novel polypeptides having homology to β -galactosidase, efforts are currently being undertaken by both industry and academia to identify new, native β -galactosidase homolog proteins. Many of these efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel β -galactosidase-like proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., Proc. Natl. Acad. Sci., 93:7108-7113 (1996); U.S. Patent No. 5,536,637]. We herein describe novel polypeptides having significant homology to the β -galactosidase enzyme, designated herein as PRO236 and PRO262 polypeptides.

29. PRO239

Densin is a glycoprotein which has been isolated from the brain which has all the hallmarks of an adhesion molecule. It is highly concentrated at synaptic sites in the brain and is expressed prominently in dendritic processes in developing neurons. Densin has been characterized as a member of the O-linked sialoglycoproteins. Densin has relevance to medically important processes such as regeneration. Given the physiological importance of synaptic processes and cell adhesion mechanisms *in vivo*, efforts are currently being undertaken to identify new, native proteins which are involved in synaptic machinery and cell adhesion. We describe herein the identification of novel polypeptides which have homology to densin, designated herein as PRO239 polypeptides.

30. PRO257

Ebnerin is a cell surface protein associated with von Ebner glands in mammals. Efforts are being undertaken by both industry and academia to identify new, native cell surface receptor proteins and specifically those which possess sequence homology to cell surface proteins such as ebnerin. Many of these efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor proteins. We herein describe the identification of novel polypeptides having significant homology to the von Ebner's gland-associated protein ebnerin, designated herein as PRO257 polypeptides.

31. PRO260

Fucosidases are enzymes that remove fucose residues from fucose containing proteoglycans. In some pathological conditions, such as cancer, rheumatoid arthritis, and diabetes, there is an abnormal fucosylation of serum proteins. Therefore, fucosidases, and proteins having homology to fucosidase, are of importance to the study and abrogation of these conditions. In particular, proteins having homology to the alpha-l-fucosidase precursor are of interest. Fucosidases and fucosidase inhibitors are further described in U.S. Patent Nos. 5,637,490, 5,382,709, 5,240,707, 5,153,325, 5,100,797, 5,096,909 and 5,017,704. Studies are also reported in Valk, et al., J. Virol., 71(9):6796 (1997), Aktogu, et al., Monaldi Arch. Chest Dis. (Italy), 52(2):118 (1997) and Focarelli, et al., Biochem. Biophys. Res. Commun. (U.S.), 234(1):54 (1997).

Efforts are being undertaken by both industry and academia to identify new, native secreted and membrane-bound receptor proteins. Of particular interest are proteins having homology to the alpha-l-fucosidase precursor. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound receptor proteins. Examples of screening methods and techniques are

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described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.*, 93:7108-7113 (1996); U.S. Patent No. 5,536,637)].

We herein describe the identification and characterization of novel polypeptides having homology to fucosidases, designated herein as PRO260 polypeptides.

5 32. PRO263

CD44 is a cell surface adhesion molecule involved in cell-cell and cell-matrix interactions. Hyaluronic acid, a component of the extracellular matrix is a major ligand. Other ligands include collagen, fibronectin, laminin, chondroitin sulfate, mucosal addressin, serglycin and osteopontin. CD44 is also important in regulating cell traffic, lymph node homing, transmission of growth signals, and presentation of chemokines and growth factors to traveling
10 cells. CD44 surface proteins are associated with metastatic tumors and CD44 has been used as a marker for HIV infection. Certain splice variants are associated with metastasis and poor prognosis of cancer patients. Therefore, molecules having homology with CD44 are of particular interest, as their homology indicates that they may have functions related to those functions of CD44. CD44 is further described in U.S. Patent Nos. 5,506,119, 5,504,194 and 5,108,904; Gerberick, et al., *Toxicol. Appl. Pharmacol.*, 146(1):1 (1997); Wittig, et al., *Immunol. Letters*
15 (Netherlands), 57(1-3):217 (1997); and Oliveira and Odell, *Oral Oncol.* (England), 33(4):260 (1997).

Efforts are being undertaken by both industry and academia to identify new, native secreted and membrane-bound receptor proteins, particularly transmembrane proteins with homology to CD44 antigen. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound receptor proteins. Examples of screening methods and techniques are described in
20 the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.*, 93:7108-7113 (1996); U.S. Patent No. 5,536,637)].

We herein describe the identification and characterization of novel polypeptides having homology to CD44 antigen, designated herein as PRO263 polypeptides.

25 33. PRO270

Thioredoxins effect reduction-oxidation (redox) state. Many diseases are potentially related to redox state and reactive oxygen species may play a role in many important biological processes. The transcription factors, NF-kappa B and AP-1, are regulated by redox state and are known to affect the expression of a large variety of genes thought to be involved in the pathogenesis of AIDS, cancer, atherosclerosis and diabetic complications. Such proteins may also
30 play a role in cellular antioxidant defense, and in pathological conditions involving oxidative stress such as stroke and inflammation in addition to having a role in apoptosis. Therefore, thioredoxins, and proteins having homology thereto, are of interest to the scientific and medical communities.

We herein describe the identification and characterization of novel polypeptides having homology to thioredoxin, designated herein as PRO270 polypeptides.

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34. PRO271

The proteoglycan link protein is a protein which is intimately associated with various extracellular matrix proteins and more specifically with proteins such as collagen. For example, one primary component of collagen is a large proteoglycan called aggrecan. This molecule is retained by binding to the glycosaminoglycan hyaluronan through the amino terminal G1 globular domain of the core protein. This binding is stabilized by the proteoglycan link protein which is a protein that is also associated with other tissues containing hyaluronan binding proteoglycans such as versican.

Link protein has been identified as a potential target for autoimmune antibodies in individuals who suffer from juvenile rheumatoid arthritis (see Guerassimov et al., *J. Rheumatology* 24(5):959-964 (1997)). As such, there is strong interest in identifying novel proteins having homology to link protein. We herein describe the identification and characterization of novel polypeptides having such homology, designated herein as PRO271 polypeptides.

35. PRO272

Reticulocalbin is an endoplasmic reticular protein which may be involved in protein transport and luminal protein processing. Reticulocalbin resides in the lumen of the endoplasmic reticulum, is known to bind calcium, and may be involved in a luminal retention mechanism of the endoplasmic reticulum. It contains six domains of the EF-hand motif associated with high affinity calcium binding. We describe herein the identification and characterization of a novel polypeptide which has homology to the reticulocalbin protein, designated herein as PRO272.

20 36. PRO294

Collagen, a naturally occurring protein, finds wide application in industry. Chemically hydrolyzed natural collagen can be denatured and renatured by heating and cooling to produce gelatin, which is used in photographic and medical, among other applications. Collagen has important properties such as the ability to form interchain aggregates having a conformation designated as a triple helix. We herein describe the identification and characterization of a novel polypeptide which has homology to portions of the collagen molecule, designated herein as PRO294.

37. PRO295

The integrins comprise a supergene family of cell-surface glycoprotein receptors that promote cellular adhesion. Each cell has numerous receptors that define its cell adhesive capabilities. Integrins are involved in a wide variety of interaction between cells and other cells or matrix components. The integrins are of particular importance in regulating movement and function of immune system cells. The platelet IIb/IIIa integrin complex is of particular importance in regulating platelet aggregation. A member of the integrin family, integrin β -6, is expressed on epithelial cells and modulates epithelial inflammation. Another integrin, leucocyte-associated antigen-1 (LFA-1) is important in the adhesion of lymphocytes during an immune response. The integrins are expressed as heterodimers of non-covalently associated alpha and beta subunits. Given the physiological importance of cell adhesion mechanisms *in vivo*, efforts are currently being under taken to identify new, native proteins which are involved in cell adhesion. We

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describe herein the identification and characterization of a novel polypeptide which has homology to integrin, designated herein as PRO295.

38. PRO293

Protein-protein interactions include receptor and antigen complexes and signaling mechanisms. As more is known about the structural and functional mechanisms underlying protein-protein interactions, protein-protein interactions can be more easily manipulated to regulate the particular result of the protein-protein interaction. Thus, the underlying mechanisms of protein-protein interactions are of interest to the scientific and medical community.

All proteins containing leucine-rich repeats are thought to be involved in protein-protein interactions. Leucine-rich repeats are short sequence motifs present in a number of proteins with diverse functions and cellular locations. The crystal structure of ribonuclease inhibitor protein has revealed that leucine-rich repeats correspond to beta-alpha structural units. These units are arranged so that they form a parallel beta-sheet with one surface exposed to solvent, so that the protein acquires an unusual, nonglobular shape. These two features have been indicated as responsible for the protein-binding functions of proteins containing leucine-rich repeats. See, Kobe and Deisenhofer, Trends Biochem. Sci., 19(10):415-421 (Oct. 1994).

A study has been reported on leucine-rich proteoglycans which serve as tissue organizers, orienting and ordering collagen fibrils during ontogeny and are involved in pathological processes such as wound healing, tissue repair, and tumor stroma formation. Iozzo, R. V., Crit. Rev. Biochem. Mol. Biol., 32(2):141-174 (1997). Others studies implicating leucine rich proteins in wound healing and tissue repair are De La Salle, C., et al., Vouv. Rev. Fr. Hematol. (Germany), 37(4):215-222 (1995), reporting mutations in the leucine rich motif in a complex associated with the bleeding disorder Bernard-Soulier syndrome and Chlemetson, K. J., Thromb. Haemost. (Germany), 74(1):111-116 (July 1995), reporting that platelets have leucine rich repeats. Another protein of particular interest which has been reported to have leucine-rich repeats is the SLIT protein which has been reported to be useful in treating neuro-degenerative diseases such as Alzheimer's disease, nerve damage such as in Parkinson's disease, and for diagnosis of cancer, see, Artavanistsakonas, S. and Rothberg, J. M., WO9210518-A1 by Yale University. Other studies reporting on the biological functions of proteins having leucine-rich repeats include: Tayar, N., et al., Mol. Cell Endocrinol., (Ireland), 125(1-2):65-70 (Dec. 1996) (gonadotropin receptor involvement); Miura, Y., et al., Nippon Rinsho (Japan), 54(7):1784-1789 (July 1996) (apoptosis involvement); Harris, P. C., et al., J. Am. Soc. Nephrol., 6(4):1125-1133 (Oct. 1995) (kidney disease involvement); and Ruoslahti, E. I., et al., WO9110727-A by La Jolla Cancer Research Foundation (decorin binding to transforming growth factor β involvement for treatment for cancer, wound healing and scarring).

Efforts are therefore being undertaken by both industry and academia to identify new proteins having leucine rich repeats to better understand protein-protein interactions. Of particular interest are those proteins having leucine rich repeats and homology to known neuronal leucine rich repeat proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound proteins having leucine rich repeats. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., Proc. Natl. Acad. Sci., 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

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We describe herein the identification and characterization of a novel polypeptide which has homology to leucine rich repeat proteins, designated herein as PRO293.

39. PRO247

Protein-protein interactions include receptor and antigen complexes and signaling mechanisms. As more is known about the structural and functional mechanisms underlying protein-protein interactions, protein-protein interactions can be more easily manipulated to regulate the particular result of the protein-protein interaction. Thus, the underlying mechanisms of protein-protein interactions are of interest to the scientific and medical community.

All proteins containing leucine-rich repeats are thought to be involved in protein-protein interactions. Leucine-rich repeats are short sequence motifs present in a number of proteins with diverse functions and cellular locations. The crystal structure of ribonuclease inhibitor protein has revealed that leucine-rich repeats correspond to beta-alpha structural units. These units are arranged so that they form a parallel beta-sheet with one surface exposed to solvent, so that the protein acquires an unusual, nonglobular shape. These two features have been indicated as responsible for the protein-binding functions of proteins containing leucine-rich repeats. See, Kobe and Deisenhofer, Trends Biochem. Sci., 19(10):415-421 (Oct. 1994).

A study has been reported on leucine-rich proteoglycans which serve as tissue organizers, orienting and ordering collagen fibrils during ontogeny and are involved in pathological processes such as wound healing, tissue repair, and tumor stroma formation. Iozzo, R. V., Crit. Rev. Biochem. Mol. Biol., 32(2):141-174 (1997). Others studies implicating leucine rich proteins in wound healing and tissue repair are De La Salle, C., et al., Vouv. Rev. Fr. Hematol. (Germany), 37(4):215-222 (1995), reporting mutations in the leucine rich motif in a complex associated with the bleeding disorder Bernard-Soulier syndrome and Chlemetson, K. J., Thromb. Haemost. (Germany), 74(1):111-116 (July 1995), reporting that platelets have leucine rich repeats. Another protein of particular interest which has been reported to have leucine-rich repeats is the SLIT protein which has been reported to be useful in treating neuro-degenerative diseases such as Alzheimer's disease, nerve damage such as in Parkinson's disease, and for diagnosis of cancer, see, Artavanistsakonas, S. and Rothberg, J. M., WO9210518-A1 by Yale University. Other studies reporting on the biological functions of proteins having leucine-rich repeats include: Tayar, N., et al., Mol. Cell Endocrinol., (Ireland), 125(1-2):65-70 (Dec. 1996) (gonadotropin receptor involvement); Miura, Y., et al., Nippon Rinsho (Japan), 54(7):1784-1789 (July 1996) (apoptosis involvement); Harris, P. C., et al., J. Am. Soc. Nephrol., 6(4):1125-1133 (Oct. 1995) (kidney disease involvement); and Ruoslahti, E. I., et al., WO9110727-A by La Jolla Cancer Research Foundation (decorin binding to transforming growth factor β involvement for treatment for cancer, wound healing and scarring).

Densin is a glycoprotein which has been isolated from the brain which has all the hallmarks of an adhesion molecule. It is highly concentrated at synaptic sites in the brain and is expressed prominently in dendritic processes in developing neurons. Densin has been characterized as a member of the O-linked sialoglycoproteins. Densin has relevance to medically important processes such as regeneration. Given the physiological importance of synaptic processes and cell adhesion mechanisms *in vivo*, efforts are currently being under taken to identify new, native proteins which are involved in synaptic machinery and cell adhesion. Densin is further described in Kennedy, M.B., Trends Neurosci. (England), 20(6):264 (1997) and Apperson, et al., J. Neurosci., 16(21):6839 (1996).

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Efforts are therefore being undertaken by both industry and academia to identify new proteins having leucine rich repeats to better understand protein-protein interactions. Of particular interest are those proteins having leucine rich repeats and homology to known proteins having leucine rich repeats such as KIAA0231 and densin. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound proteins having leucine rich repeats. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., Proc. Natl. Acad. Sci., 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

We describe herein the identification and characterization of a novel polypeptide which has homology to leucine rich repeat proteins, designated herein as PRO247.

40. PRO302, PRO303, PRO304, PRO307 and PRO343

Proteases are enzymatic proteins which are involved in a large number of very important biological processes in mammalian and non-mammalian organisms. Numerous different protease enzymes from a variety of different mammalian and non-mammalian organisms have been both identified and characterized. The mammalian protease enzymes play important roles in many different biological processes including, for example, protein digestion, activation, inactivation, or modulation of peptide hormone activity, and alteration of the physical properties of proteins and enzymes.

In light of the important physiological roles played by protease enzymes, efforts are currently being undertaken by both industry and academia to identify new, native protease homologs. Many of these efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound receptor proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., Proc. Natl. Acad. Sci., 93:7108-7113 (1996); U.S. Patent No. 5,536,637]. We herein describe the identification of novel polypeptides having homology to various protease enzymes, designated herein as PRO302, PRO303, PRO304, PRO307 and PRO343 polypeptides.

41. PRO328

The GLIP protein family has been characterized as comprising zinc-finger proteins which play important roles in embryogenesis. These proteins may function as transcriptional regulatory proteins and are known to be amplified in a subset of human tumors. Glioma pathogenesis protein is structurally related to a group of plant pathogenesis-related proteins. It is highly expressed in glioblastoma. See US Pat. Nos. 5,582,981 (issued Dec. 10, 1996) and 5,322,801 (issued June 21, 1996), Ellington, A.D. et al., Nature, 346:818 (1990), Grindley, J.C. et al., Dev. Biol., 188(2):337 (1997), Marine, J.C. et al., Mech. Dev., 63(2):211 (1997), The CRISP or cysteine rich secretory protein family are a group of proteins which are also structurally related to a group of plant pathogenesis proteins. [Schwidetzky, U., Biochem. J., 321:325 (1997), Pfisterer, P., Mol. Cell Biol., 16(11):6160 (1996), Kratzschmar, J., Eur. J. Biochem., 236(3):827 (1996)]. We describe herein the identification of a novel polypeptide which has homology to GLIP and CRISP, designated herein as PRO328 polypeptides.

42. PRO335, PRO331 and PRO326

Protein-protein interactions include receptor and antigen complexes and signaling mechanisms. As more is known about the structural and functional mechanisms underlying protein-protein interactions, protein-protein interactions can be more easily manipulated to regulate the particular result of the protein-protein interaction. Thus, the underlying mechanisms of protein-protein interactions are of interest to the scientific and medical community.

5 All proteins containing leucine-rich repeats are thought to be involved in protein-protein interactions. Leucine-rich repeats are short sequence motifs present in a number of proteins with diverse functions and cellular locations. The crystal structure of ribonuclease inhibitor protein has revealed that leucine-rich repeats correspond to beta-alpha structural units. These units are arranged so that they form a parallel beta-sheet with one surface exposed to solvent, so that the protein acquires an unusual, nonglobular shape. These two features have been
10 indicated as responsible for the protein-binding functions of proteins containing leucine-rich repeats. See, Kobe and Deisenhofer, Trends Biochem. Sci., 19(10):415-421 (Oct. 1994).

A study has been reported on leucine-rich proteoglycans which serve as tissue organizers, orienting and ordering collagen fibrils during ontogeny and are involved in pathological processes such as wound healing, tissue repair, and tumor stroma formation. Iozzo, R. V., Crit. Rev. Biochem. Mol. Biol., 32(2):141-174 (1997). Others
15 studies implicating leucine rich proteins in wound healing and tissue repair are De La Salle, C., et al., Vouv. Rev. Fr. Hematol. (Germany), 37(4):215-222 (1995), reporting mutations in the leucine rich motif in a complex associated with the bleeding disorder Bernard-Soulier syndrome, Chlemetson, K. J., Thromb. Haemost. (Germany), 74(1):111-116 (July 1995), reporting that platelets have leucine rich repeats and Ruoslahti, E. I., et al., WO9110727-A by La Jolla Cancer Research Foundation reporting that decorin binding to transforming growth factor β has involvement in
20 a treatment for cancer, wound healing and scarring. Related by function to this group of proteins is the insulin like growth factor (IGF), in that it is useful in wound-healing and associated therapies concerned with re-growth of tissue, such as connective tissue, skin and bone; in promoting body growth in humans and animals; and in stimulating other growth-related processes. The acid labile subunit of IGF (ALS) is also of interest in that it increases the half-life of IGF and is part of the IGF complex *in vivo*.

25 Another protein which has been reported to have leucine-rich repeats is the SLIT protein which has been reported to be useful in treating neuro-degenerative diseases such as Alzheimer's disease, nerve damage such as in Parkinson's disease, and for diagnosis of cancer, see, Artavanistsakonas, S. and Rothberg, J. M., WO9210518-A1 by Yale University. Of particular interest is LIG-1, a membrane glycoprotein that is expressed specifically in glial cells in the mouse brain, and has leucine rich repeats and immunoglobulin-like domains. Suzuki, et al., J. Biol.
30 Chem. (U.S.), 271(37):22522 (1996). Other studies reporting on the biological functions of proteins having leucine rich repeats include: Tayar, N., et al., Mol. Cell Endocrinol., (Ireland), 125(1-2):65-70 (Dec. 1996) (gonadotropin receptor involvement); Miura, Y., et al., Nippon Rinsho (Japan), 54(7):1784-1789 (July 1996) (apoptosis involvement); Harris, P. C., et al., J. Am. Soc. Nephrol., 6(4):1125-1133 (Oct. 1995) (kidney disease involvement).

Efforts are therefore being undertaken by both industry and academia to identify new proteins having leucine
35 rich repeats to better understand protein-protein interactions. Of particular interest are those proteins having leucine rich repeats and homology to known proteins having leucine rich repeats such as LIG-1, ALS and decorin. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for

novel secreted and membrane-bound proteins having leucine rich repeats. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.*, 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

We describe herein the identification and characterization of novel polypeptides which have homology to proteins of the leucine rich repeat superfamily, designated herein as PRO335, PRO331 and PRO326 polypeptides.

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43. PRO332

Secreted proteins comprising a repeat characterized by an arrangement of conserved leucine residues (leucine-rich repeat motif) have diverse biological roles. Certain proteoglycans, such as biglycan, fibromodulin and decorin, are, for example, characterized by the presence of a leucine-rich repeat of about 24 amino acids [Ruoslahti, *Ann. Rev. Cell. Biol.* 4 229-255 (1988); Oldberg et al., *EMBO J.* 8, 2601-2604 (1989)]. In general, proteoglycans are believed to play a role in regulating extracellular matrix, cartilage or bone function. The proteoglycan decorin binds to collagen type I and II and affects the rate of fibril formation. Fibromodulin also binds collagen and delays fibril formation. Both fibromodulin and decorin inhibit the activity of transforming growth factor beta (TGF- β) (U.S. Patent No. 5,583,103 issued December 10, 1996). TGF- β is known to play a key role in the induction of extracellular matrix and has been implicated in the development of fibrotic diseases, such as cancer and glomerulonephritis. Accordingly, proteoglycans have been proposed for the treatment of fibrotic cancer, based upon their ability to inhibit TGF- β 's growth stimulating activity on the cancer cell. Proteoglycans have also been described as potentially useful in the treatment of other proliferative pathologies, including rheumatoid arthritis, arteriosclerosis, adult respiratory distress syndrome, cirrhosis of the liver, fibrosis of the lungs, post-myocardial infarction, cardiac fibrosis, post-angioplasty restenosis, renal interstitial fibrosis and certain dermal fibrotic conditions, such as keloids and scarring, which might result from burn injuries, other invasive skin injuries, or cosmetic or reconstructive surgery (U.S. Patent No. 5,654,270, issued August 5, 1997).

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We describe herein the identification and characterization of novel polypeptides which have homology to proteins of the leucine rich repeat superfamily, designated herein as PRO332 polypeptides.

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44. PRO334

Microfibril bundles and proteins found in association with these bundles, particularly attachment molecules, are of interest in the field of dermatology, particularly in the study of skin which has been damaged from aging, injuries or the sun. Fibrillin microfibrils define the continuous elastic network of skin, and are present in dermis as microfibril bundles devoid of measurable elastin extending from the dermal-epithelial junction and as components of the thick elastic fibres present in the deep reticular dermis. Moreover, Marfan syndrome has been linked to mutations which interfere with multimerization of fibrillin monomers or other connective tissue elements.

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Fibulin-1 is a modular glycoprotein with amino-terminal anaphylatoxin-like modules followed by nine epidermal growth factor (EGF)-like modules and, depending on alternative splicing, four possible carboxyl termini. Fibulin-2 is a novel extracellular matrix protein frequently found in close association with microfibrils containing either fibronectin or fibrillin. Thus, fibrillin, fibulin, and molecules related thereto are of interest, particularly for the use of preventing skin from being damaged from aging, injuries or the sun, or for restoring skin damaged from

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same. Moreover, these molecules are generally of interest in the study of connective tissue and attachment molecules and related mechanisms. Fibrillin, fibulin and related molecules are further described in Adams, et al., *J. Mol. Biol.*, 272(2):226-36 (1997); Kielty and Shuttleworth, *Microsc. Res. Tech.*, 38(4):413-27 (1997); and *Child. J. Card. Surg.*, 12(2Supp.):131-5 (1997).

Currently, efforts are being undertaken by both industry and academia to identify new, native secreted and membrane-bound receptor proteins, particularly secreted proteins which have homology to fibulin and fibrillin. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound receptor proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.*, 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

We herein describe the identification and characterization of novel polypeptides having homology to fibulin and fibrillin, designated herein as PRO334 polypeptides.

45. PRO346

The widespread occurrence of cancer has prompted the devotion of considerable resources and discovering new treatments of treatment. One particular method involves the creation of tumor or cancer specific monoclonal antibodies (mAbs) which are specific to tumor antigens. Such mAbs, which can distinguish between normal and cancerous cells are useful in the diagnosis, prognosis and treatment of the disease. Particular antigens are known to be associated with neoplastic diseases, such as colorectal and breast cancer. Since colon cancer is a widespread disease, early diagnosis and treatment is an important medical goal. Diagnosis and treatment of cancer can be implemented using monoclonal antibodies (mAbs) specific therefore having fluorescent, nuclear magnetic or radioactive tags. Radioactive genes, toxins and/or drug tagged mAbs can be used for treatment *in situ* with minimal patient description.

Carcinoembryonic antigen (CEA) is a glycoprotein found in human colon cancer and the digestive organs of a 2-6 month human embryos. CEA is a known human tumor marker and is widely used in the diagnosis of neoplastic diseases, such as colon cancer. For example, when the serum levels of CEA are elevated in a patient, a drop of CEA levels after surgery would indicate the tumor resection was successful. On the other hand, a subsequent rise in serum CEA levels after surgery would indicate that metastases of the original tumor may have formed or that new primary tumors may have appeared. CEA may also be a target for mAb, antisense nucleotides

46. PRO268

Protein disulfide isomerase is an enzymatic protein which is involved in the promotion of correct refolding of proteins through the establishment of correct disulfide bond formation. Protein disulfide isomerase was initially identified based upon its ability to catalyze the renaturation of reduced denatured RNase (Goldberger et al., *J. Biol. Chem.* 239:1406-1410 (1964) and Epstein et al., *Cold Spring Harbor Symp. Quant. Biol.* 28:439-449 (1963)). Protein disulfide isomerase has been shown to be a resident enzyme of the endoplasmic reticulum which is retained in the endoplasmic reticulum via a -KDEL or -HDEL amino acid sequence at its C-terminus.

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Given the importance of disulfide bond-forming enzymes and their potential uses in a number of different applications, for example in increasing the yield of correct refolding of recombinantly produced proteins, efforts are currently being undertaken by both industry and academia to identify new, native proteins having homology to protein disulfide isomerase. Many of these efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel protein disulfide isomerase homologs. We herein describe a novel polypeptide having homology to protein disulfide isomerase, designated herein as PRO268.

47. PRO330

Prolyl 4-hydroxylase is an enzyme which functions to post-translationally hydroxylate proline residues at the Y position of the amino acid sequence Gly-X-Y, which is a repeating three amino acid sequence found in both collagen and procollagen. Hydroxylation of proline residues at the Y position of the Gly-X-Y amino acid triplet to form 4-hydroxyproline residues at those positions is required before newly synthesized collagen polypeptide chains may fold into their proper three-dimensional triple-helical conformation. If hydroxylation does not occur, synthesized collagen polypeptides remain non-helical, are poorly secreted by cells and cannot assemble into stable functional collagen fibrils. Vuorio et al., *Proc. Natl. Acad. Sci. USA* 89:7467-7470 (1992). Prolyl 4-hydroxylase is comprised of at least two different polypeptide subunits, alpha and beta.

Efforts are being undertaken by both industry and academia to identify new, native secreted and membrane-bound receptor proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted and membrane-bound receptor proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.*, 93:7108-7113 (1996); U.S. Patent No. 5,536,637]. Based upon these efforts, Applicants have herein identified and describe a novel polypeptide having homology to the alpha subunit of prolyl 4-hydroxylase, designated herein as PRO330.

48. PRO339 and PRO310

Fringe is a protein which specifically blocks serrate-mediated activation of notch in the dorsal compartment of the *Drosophila* wing imaginal disc. Fleming, et al., *Development*, 124(15):2973-81 (1997). Therefore, fringe is of interest for both its role in development as well as its ability to regulate serrate, particularly serrate's signaling abilities. Also of interest are novel polypeptides which may have a role in development and/or the regulation of serrate-like molecules. Of particular interest are novel polypeptides having homology to fringe as identified and described herein, designated herein as PRO339 and PRO310 polypeptides.

49. PRO244

Lectins are a class of proteins comprising a region that binds carbohydrates specifically and non-covalently. Numerous lectins have been identified in higher animals, both membrane-bound and soluble, and have been implicated in a variety of cell-recognition phenomena and tumor metastasis.

Most lectins can be classified as either C-type (calcium-dependent) or S-type (thiol-dependent).

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Lectins are thought to play a role in regulating cellular events that are initiated at the level of the plasma membrane. For example, plasma membrane associated molecules are involved in the activation of various subsets of lymphoid cells, e.g. T-lymphocytes, and it is known that cell surface molecules are responsible for activation of these cells and consequently their response during an immune reaction.

A particular group of cell adhesion molecules, selectins, belong in the superfamily of C-type lectins. This group includes L-selectin (peripheral lymph node homing receptor (pnHR), LEC-CAM-1, LAM-1, gp90^{MEL}, gp100^{MEL}, gp110^{MEL}, MEL-14 antigen, Leu-8 antigen, TQ-1 antigen, DREG antigen), E-selectin (LEC-CAM-2, LECAM-2, ELAM-1), and P-selectin (LEC-CAM-3, LECAM-3, GMP-140, PADGEM). The structure of selectins consists of a C-type lectin (carbohydrate binding) domain, an epidermal growth factor-like (EGF-like) motif, and variable numbers of complement regulatory (CR) motifs. Selectins are associated with leukocyte adhesion, e.g. the attachment of neutrophils to venular endothelial cells adjacent to inflammation (E-selectin), or with the trafficking of lymphocytes from blood to secondary lymphoid organs, e.g. lymph nodes and Peyer's patches (L-selectin).

Another exemplary lectin is the cell-associated macrophage antigen, Mac-2 that is believed to be involved in cell adhesion and immune responses. Macrophages also express a lectin that recognizes Tn Ag, a human carcinoma-associated epitope.

Another C-type lectin is CD95 (Fas antigen/APO-1) that is an important mediator of immunologically relevant regulated or programmed cell death (apoptosis). "Apoptosis" is a non-necrotic cell death that takes place in metazoan animal cells following activation of an intrinsic cell suicide program. The cloning of Fas antigen is described in PCT publication WO 91/10448, and European patent application EP510691. The mature Fas molecule consists of 319 amino acids of which 157 are extracellular, 17 constitute the transmembrane domain, and 145 are intracellular. Increased levels of Fas expression at T cell surface have been associated with tumor cells and HIV-infected cells. Ligation of CD95 triggers apoptosis in the presence of interleukin-1 (IL-2).

C-type lectins also include receptors for oxidized low-density lipoprotein (LDL). This suggests a possible role in the pathogenesis of atherosclerosis.

We herein describe the identification and characterization of novel polypeptides having homology to C-type lectins, designated herein as PRO244 polypeptides.

SUMMARY OF THE INVENTION

1. PRO211 and PRO217

Applicants have identified cDNA clones that encode novel polypeptides having homology to EGF, designated in the present application as "PRO211" and "PRO217" polypeptides.

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO211 or PRO217 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding EGF-like homologue PRO211 and PRO217 polypeptides of Fig. 2 (SEQ ID NO:2) and/or 4 (SEQ ID NO:4) indicated in Fig. 1 (SEQ ID NO: 1) and/or Fig. 3 (SEQ ID NO:3), respectively, or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO211 and PRO217 EGF-like homologue PRO211 and PRO217 polypeptides. In particular, the invention provides isolated native sequence PRO211 and PRO217 EGF-

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like homologue polypeptides, which in one embodiment, includes an amino acid sequence comprising residues: 1 to 353 of Fig. 2 (SEQ ID NO:2) or (2) 1 to 379 of Fig. 4 (SEQ ID NO: 4).

2. PRO230

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO230".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO230 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO230 polypeptide having amino acid residues 1 through 467 of Figure 6 (SEQ ID NO:12), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO230 polypeptide. In particular, the invention provides isolated native sequence PRO230 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 467 of Figure 6 (SEQ ID NO:12).

In another embodiment, the invention provides an expressed sequence tag (EST) comprising the nucleotide sequence of SEQ ID NO:13 (Figure 7) which is herein designated as DNA20088.

3. PRO232

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO232".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO232 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO232 polypeptide having amino acid residues 1 to 114 of Figure 9 (SEQ ID NO:18), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO232 polypeptide. In particular, the invention provides isolated native sequence PRO232 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 114 of Figure 9 (SEQ ID NO:18).

4. PRO187

Applicants have identified a cDNA clone that encodes a novel polypeptide, designated in the present application as "PRO187".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO187 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO187 polypeptide of Figure 11 (SEQ ID NO:23), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. In another aspect, the invention provides a nucleic acid comprising the coding sequence of Figure 10 (SEQ ID NO:22) or its complement. In another aspect, the invention provides a nucleic acid of the full length protein of clone DNA27864-1155, deposited with the ATCC under accession number ATCC 209375, alternatively the coding sequence of clone DNA27864-1155,

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deposited under accession number ATCC 209375.

In yet another embodiment, the invention provides isolated PRO187 polypeptide. In particular, the invention provides isolated native sequence PRO187 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 205 of Figure 11 (SEQ ID NO:23). Alternatively, the invention provides a polypeptide encoded by the nucleic acid deposited under accession number ATCC 209375.

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5. PRO265

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO265".

10 In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO265 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO265 polypeptide having amino acid residues 1 to 660 of Figure 13 (SEQ ID NO:28), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

15 In another embodiment, the invention provides isolated PRO265 polypeptide. In particular, the invention provides isolated native sequence PRO265 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 660 of Figure 13 (SEQ ID NO:28). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO265 polypeptide.

6. PRO219

20 Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO219".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO219 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO219 polypeptide having amino acid residues 1 to 915 of Figure 15 (SEQ ID NO:34), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO219 polypeptide. In particular, the invention provides isolated native sequence PRO219 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 915 of Figure 15 (SEQ ID NO:34).

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7. PRO246

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO246".

35 In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO246 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO246 polypeptide having amino acid residues 1 to 390 of Figure 17 (SEQ ID NO:39), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency

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conditions.

In another embodiment, the invention provides isolated PRO246 polypeptide. In particular, the invention provides isolated native sequence PRO246 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 390 of Figure 17 (SEQ ID NO:39). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO246 polypeptide.

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8. PRO228

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to CD97, EMR1 and latrophilin, wherein the polypeptide is designated in the present application as "PRO228".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO228 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO228 polypeptide having amino acid residues 1 to 690 of Figure 19 (SEQ ID NO:49), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO228 polypeptide. In particular, the invention provides isolated native sequence PRO228 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 690 of Figure 19 (SEQ ID NO:49). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO228 polypeptide.

In another embodiment, the invention provides an expressed sequence tag (EST) comprising the nucleotide sequence of SEQ ID NO:50, designated herein as DNA21951.

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9. PRO533

Applicants have identified a cDNA clone (DNA49435-1219) that encodes a novel polypeptide, designated in the present application as PRO533.

In one embodiment, the invention provides an isolated nucleic acid molecule having at least about 80% sequence identity to (a) a DNA molecule encoding a PRO533 polypeptide comprising the sequence of amino acids 23 to 216 of Figure 22 (SEQ ID NO:59), or (b) the complement of the DNA molecule of (a). The sequence identity preferably is about 85%, more preferably about 90%, most preferably about 95%. In one aspect, the isolated nucleic acid has at least about 80%, preferably at least about 85%, more preferably at least about 90%, and most preferably at least about 95% sequence identity with a polypeptide having amino acid residues 23 to 216 of Figure 22 (SEQ ID NO:59). Preferably, the highest degree of sequence identity occurs within the secreted portion (amino acids 23 to 216 of Figure 22, SEQ ID NO:59). In a further embodiment, the isolated nucleic acid molecule comprises DNA encoding a PRO533 polypeptide having amino acid residues 1 to 216 of Figure 22 (SEQ ID NO:59), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. In another aspect, the invention provides a nucleic acid of the full length protein of clone DNA49435-1219, deposited with the ATCC under accession number ATCC 209480.

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In yet another embodiment, the invention provides isolated PRO533 polypeptide. In particular, the invention provides isolated native sequence PRO533 polypeptide, which in one embodiment, includes an amino acid sequence

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comprising residues 23 to 216 of Figure 22 (SEQ ID NO:59). Native PRO533 polypeptides with or without the native signal sequence (amino acids 1 to 22 in Figure 22 (SEQ ID NO:59)), and with or without the initiating methionine are specifically included. Alternatively, the invention provides a PRO533 polypeptide encoded by the nucleic acid deposited under accession number ATCC 209480.

5 10. **PRO245**

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO245".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO245 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO245 polypeptide
10 having amino acid residues 1 to 312 of Fig. 24 (SEQ ID NO:64), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO245 polypeptide. In particular, the invention provides isolated native sequence PRO245 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 312 of Figure 24 (SEQ ID NO:64).

15 11. **PRO220, PRO221 and PRO227**

Applicants have identified cDNA clones that each encode novel polypeptides, all having leucine rich repeats. These polypeptides are designated in the present application as PRO220, PRO221 and PRO227.

In one embodiment, the invention provides isolated nucleic acid molecules comprising DNA respectively
20 encoding PRO220, PRO221 and PRO227, respectively. In one aspect, provided herein is an isolated nucleic acid comprises DNA encoding the PRO220 polypeptide having amino acid residues 1 through 708 of Figure 26 (SEQ ID NO:69), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. Also provided herein is an isolated nucleic acid comprises DNA encoding the PRO221 polypeptide having amino acid residues 1 through 259 of Figure 28 (SEQ ID
25 NO:71), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. Moreover, also provided herein is an isolated nucleic acid comprises DNA encoding the PRO227 polypeptide having amino acid residues 1 through 620 of Figure 30 (SEQ ID NO:73), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

30 In another embodiment, the invention provides isolated PRO220, PRO221 and PRO227 polypeptides. In particular, provided herein is the isolated native sequence for the PRO220 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 708 of Figure 26 (SEQ ID NO:69). Additionally provided herein is the isolated native sequence for the PRO221 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 259 of Figure 28 (SEQ ID NO:71). Moreover, provided herein is the isolated
35 native sequence for the PRO227 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 620 of Figure 30 (SEQ ID NO:73).

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12. PRO258

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to CRTAM and poliovirus receptor precursors, wherein the polypeptide is designated in the present application as "PRO258".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO258 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO258 polypeptide
5 having amino acid residues 1 to 398 of Figure 32 (SEQ ID NO:84), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO258 polypeptide. In particular, the invention provides isolated native sequence PRO258 polypeptide, which in one embodiment, includes an amino acid sequence
10 comprising residues 1 to 398 of Figure 32 (SEQ ID NO:84). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO258 polypeptide.

13. PRO266

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is
15 designated in the present application as "PRO266".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO266 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO266 polypeptide having amino acid residues 1 to 696 of Figure 34 (SEQ ID NO:91), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency
20 conditions.

In another embodiment, the invention provides isolated PRO266 polypeptide. In particular, the invention provides isolated native sequence PRO266 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 696 of Figure 34 (SEQ ID NO:91).

25 14. PRO269

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as PRO269.

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO269 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO269 polypeptide
30 having amino acid residues 1 to 490 of Fig. 36 (SEQ ID NO:96), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO269 polypeptide. In particular, the invention provides isolated native sequence PRO269 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 490 of Figure 36 (SEQ ID NO:96). An additional embodiment of the present invention is
35 directed to an isolated extracellular domain of a PRO269 polypeptide.

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15. PRO287

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO287".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO287 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO287 polypeptide
5 having amino acid residues 1 to 415 of Fig. 38 (SEQ ID NO:104), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO287 polypeptide. In particular, the invention provides isolated native sequence PRO287 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 415 of Figure 38 (SEQ ID NO:104).

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16. PRO214

Applicants have identified a cDNA clone that encodes a novel polypeptide, designated in the present application as "PRO214".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a
15 PRO214 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO214 polypeptide of Fig. 40 (SEQ ID NO:109), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. In another aspect, the invention provides a nucleic acid comprising the coding sequence of Fig. 39 (SEQ ID NO:108) or its complement. In another aspect, the invention provides a nucleic acid of the full length protein of clone DNA32286-1191, deposited with
20 ATCC under accession number ATCC 209385.

In yet another embodiment, the invention provides isolated PRO214 polypeptide. In particular, the invention provides isolated native sequence PRO214 polypeptide, which in one embodiment, includes an amino acid sequence comprising the residues of Figure 40 (SEQ ID NO:109). Alternatively, the invention provides a polypeptide encoded by the nucleic acid deposited under accession number ATCC 209385.

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17. PRO317

Applicants have identified a cDNA clone that encodes a novel polypeptide, designated in the present application as "PRO317".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding
30 PRO317 polypeptide. In one aspect, the isolated nucleic acid comprises DNA (SEQ ID NO:113) encoding PRO317 polypeptide having amino acid residues 1 to 366 of Fig. 42, or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO317 polypeptide. In particular, the invention provides isolated native-sequence PRO317 polypeptide, which in one embodiment, includes an amino acid sequence
35 comprising residues 1 to 366 of Figure 42 (SEQ ID NO:114).

In yet another embodiment, the invention supplies a method of detecting the presence of PRO317 in a sample, the method comprising:

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- a) contacting a detectable anti-PRO317 antibody with a sample suspected of containing PRO317; and
- b) detecting binding of the antibody to the sample; wherein the sample is selected from the group consisting of a body fluid, a tissue sample, a cell extract, and a cell culture medium.

In a still further embodiment a method is provided for determining the presence of PRO317 mRNA in a sample, the method comprising:

- 5 a) contacting a sample suspected of containing PRO317 mRNA with a detectable nucleic acid probe that hybridizes under moderate to stringent conditions to PRO317 mRNA; and
- b) detecting hybridization of the probe to the sample.

Preferably, in this method the sample is a tissue sample and the detecting step is by *in situ* hybridization, or the sample is a cell extract and detection is by Northern analysis.

- 10 Further, the invention provides a method for treating a PRO317-associated disorder comprising administering to a mammal an effective amount of the PRO317 polypeptide or a composition thereof containing a carrier, or with an effective amount of a PRO317 agonist or PRO317 antagonist, such as an antibody which binds specifically to PRO317.

15 18. PRO301

Applicants have identified a cDNA clone (DNA40628-1216) that encodes a novel polypeptide, designated in the present application as "PRO301".

- In one embodiment, the invention provides an isolated nucleic acid molecule having at least about 80% sequence identity to (a) a DNA molecule encoding a PRO301 polypeptide comprising the sequence of amino acids 28 to 258 of Fig. 44 (SEQ ID NO:119), or (b) the complement of the DNA molecule of (a). The sequence identity preferably is about 85%, more preferably about 90%, most preferably about 95%. In one aspect, the isolated nucleic acid has at least about 80%, preferably at least about 85%, more preferably at least about 90%, and most preferably at least about 95% sequence identity with a polypeptide having amino acid residues 28 to 258 of Fig. 44 (SEQ ID NO:119). Preferably, the highest degree of sequence identity occurs within the extracellular domains (amino acids 28 to 258 of Fig. 44, SEQ ID NO:119). In a further embodiment, the isolated nucleic acid molecule comprises DNA encoding a PRO301 polypeptide having amino acid residues 28 to 299 of Fig. 44 (SEQ ID NO:119), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. In another aspect, the invention provides a nucleic acid of the full length protein of clone DNA40628-1216, deposited with the ATCC under accession number ATCC 209432, alternatively the coding sequence of clone DNA40628-1216, deposited under accession number ATCC 209432.

- In yet another embodiment, the invention provides isolated PRO301 polypeptide. In particular, the invention provides isolated native sequence PRO301 polypeptide, which in one embodiment, includes an amino acid sequence comprising the extracellular domain residues 28 to 258 of Figure 44 (SEQ ID NO:119). Native PRO301 polypeptides with or without the native signal sequence (amino acids 1 to 27 in Figure 44 (SEQ ID NO:119), and with or without the initiating methionine are specifically included. Additionally, the sequences of the invention may also comprise the transmembrane domain (residues 236 to about 258 in Figure 44; SEQ ID NO:119) and/or the intracellular domain (about residue 259 to 299 in Figure 44; SEQ ID NO:119). Alternatively, the invention provides a PRO301

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polypeptide encoded by the nucleic acid deposited under accession number ATCC 209432.

19. PRO224

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO224".

5 In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO224 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO224 polypeptide having amino acid residues 1 to 282 of Figure 46 (SEQ ID NO:127), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

10 In another embodiment, the invention provides isolated PRO224 polypeptide. In particular, the invention provides isolated native sequence PRO224 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 282 of Figure 46 (SEQ ID NO:127).

20. PRO222

15 Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO222".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO222 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO222 polypeptide having amino acid residues 1 to 490 of Fig. 48 (SEQ ID NO:132), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

20 In another embodiment, the invention provides isolated PRO222 polypeptide. In particular, the invention provides isolated native sequence PRO222 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 490 of Figure 48 (SEQ ID NO:132).

21. PRO234

25 Applicants have identified a cDNA clone that encodes a novel lectin polypeptide molecule, designated in the present application as "PRO234".

In one embodiment, the invention provides an isolated nucleic acid encoding a novel lectin comprising DNA encoding a PRO234 polypeptide. In one aspect, the isolated nucleic acid comprises the DNA encoding PRO234 polypeptides having amino acid residues 1 to 382 of Fig. 50 (SEQ ID NO:137), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. In another aspect, the invention provides an isolated nucleic acid molecule comprising the nucleotide sequence of Fig. 49 (SEQ ID NO:136).

30 In another embodiment, the invention provides isolated novel PRO234 polypeptides. In particular, the invention provides isolated native sequence PRO234 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 382 of Figure 50 (SEQ ID NO:137).

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In yet another embodiment, the invention provides oligonucleotide probes useful for isolating genomic and cDNA nucleotide sequences.

22. PRO231

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to a putative acid phosphatase, wherein the polypeptide is designated in the present application as "PRO231".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO231 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO231 polypeptide having amino acid residues 1 to 428 of Fig. 52 (SEQ ID NO:142), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO231 polypeptide. In particular, the invention provides isolated native sequence PRO231 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 428 of Figure 52 (SEQ ID NO:142).

23. PRO229

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to scavenger receptors wherein the polypeptide is designated in the present application as "PRO229".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO229 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO229 polypeptide having amino acid residues 1 to 347 of Figure 54 (SEQ ID NO:148), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO229 polypeptide. In particular, the invention provides isolated native sequence PRO229 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 347 of Figure 54 (SEQ ID NO:148).

24. PRO238

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to reductase, wherein the polypeptide is designated in the present application as "PRO238".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO238 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO238 polypeptide having amino acid residues 1 to 310 of Figure 56 (SEQ ID NO:153), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO238 polypeptide. In particular, the invention provides isolated native sequence PRO238 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 310 of Figure 56 (SEQ ID NO:153).

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25. PRO233

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO233".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO233 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO233 polypeptide
5 having amino acid residues 1 to 300 of Figure 58 (SEQ ID NO:159), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO233 polypeptide. In particular, the invention provides isolated native sequence PRO233 polypeptide, which in one embodiment, includes an amino acid sequence
10 comprising residues 1 to 300 of Figure 58 (SEQ ID NO:159).

26. PRO223

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to serine carboxypeptidase polypeptides, wherein the polypeptide is designated in the present application as "PRO223".

15 In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO223 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO223 polypeptide having amino acid residues 1 to 476 of Figure 60 (SEQ ID NO:164), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

20 In another embodiment, the invention provides isolated PRO223 polypeptide. In particular, the invention provides isolated native sequence PRO223 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 476 of Figure 60 (SEQ ID NO:164).

27. PRO235

25 Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO235".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO235 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO235 polypeptide
30 having amino acid residues 1 to 552 of Figure 62 (SEQ ID NO:170), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO235 polypeptide. In particular, the invention provides isolated native sequence PRO235 polypeptide, which in one embodiment, includes an amino acid sequence
35 comprising residues 1 to 552 of Figure 62 (SEQ ID NO:170).

28. PRO236 and PRO262

Applicants have identified cDNA clones that encode novel polypeptides having homology to β -galactosidase, wherein those polypeptides are designated in the present application as "PRO236" and "PRO262".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO236 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO236 polypeptide
5 having amino acid residues 1 to 636 of Figure 64 (SEQ ID NO:175), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO262 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO262 polypeptide
10 having amino acid residues 1 to 654 of Figure 66 (SEQ ID NO:177), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO236 polypeptide. In particular, the invention provides isolated native sequence PRO236 polypeptide, which in one embodiment, includes an amino acid sequence
15 comprising residues 1 to 636 of Figure 64 (SEQ ID NO:175).

In another embodiment, the invention provides isolated PRO262 polypeptide. In particular, the invention provides isolated native sequence PRO262 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 654 of Figure 66 (SEQ ID NO:177).

20 29. PRO239

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO239".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO239 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO239 polypeptide
25 having amino acid residues 1 to 501 of Figure 68 (SEQ ID NO:185), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO239 polypeptide. In particular, the invention provides isolated native sequence PRO239 polypeptide, which in one embodiment, includes an amino acid sequence
30 comprising residues 1 to 501 of Figure 68 (SEQ ID NO:185).

30. PRO257

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO257".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO257 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO257 polypeptide
35 having amino acid residues 1 to 607 of Figure 70 (SEQ ID NO:190), or is complementary to such encoding nucleic

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acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO257 polypeptide. In particular, the invention provides isolated native sequence PRO257 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 607 of Figure 70 (SEQ ID NO:190). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO257 polypeptide.

31. PRO260

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO260".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO260 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO260 polypeptide having amino acid residues 1 to 467 of Figure 72 (SEQ ID NO:195), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO260 polypeptide. In particular, the invention provides isolated native sequence PRO260 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 467 of Figure 72 (SEQ ID NO:195).

32. PRO263

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to CD44 antigen, wherein the polypeptide is designated in the present application as "PRO263".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO263 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO263 polypeptide having amino acid residues 1 to 322 of Figure 74 (SEQ ID NO:201), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO263 polypeptide. In particular, the invention provides isolated native sequence PRO263 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 322 of Figure 74 (SEQ ID NO:201). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO263 polypeptide.

33. PRO270

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO270".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO270 polypeptide. In one aspect, the isolated nucleic acid comprises DNA which includes the sequence encoding the PRO270 polypeptide having amino acid residues 1 to 296 of Fig. 76 (SEQ ID NO:207), or is complementary to

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such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO270 polypeptide. In particular, the invention provides isolated native sequence PRO270 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 296 of Figure 76 (SEQ ID NO:207).

5

34. PRO271

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to the proteoglycan link protein, wherein the polypeptide is designated in the present application as "PRO271".

10 In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO271 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO271 polypeptide having amino acid residues 1 to 360 of Figure 78 (SEQ ID NO:213), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

15 In another embodiment, the invention provides isolated PRO271 polypeptide. In particular, the invention provides isolated native sequence PRO271 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 360 of Figure 78 (SEQ ID NO:213).

35. PRO272

20 Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO272".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO272 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO272 polypeptide having amino acid residues 1 to 328 of Figure 80 (SEQ ID NO:221), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO272 polypeptide. In particular, the invention provides isolated native sequence PRO272 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 328 of Figure 80 (SEQ ID NO:211).

30

36. PRO294

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO294".

35 In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO294 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO294 polypeptide having amino acid residues 1 to 550 of Figure 82 (SEQ ID NO:227), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO294 polypeptide. In particular, the invention provides isolated native sequence PRO294 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 550 of Figure 82 (SEQ ID NO:227).

37. PRO295

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is designated in the present application as "PRO295".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO295 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO295 polypeptide having amino acid residues 1 to 350 of Figure 84 (SEQ ID NO:236), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO295 polypeptide. In particular, the invention provides isolated native sequence PRO295 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 350 of Figure 84 (SEQ ID NO:236).

38. PRO293

Applicants have identified a cDNA clone that encodes a novel human neuronal leucine rich repeat polypeptide, wherein the polypeptide is designated in the present application as "PRO293".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO293 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO293 polypeptide having amino acid residues 1 to 713 of Figure 86 (SEQ ID NO:244), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO293 polypeptide. In particular, the invention provides isolated native sequence PRO293 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 713 of Figure 86 (SEQ ID NO:244). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO293 polypeptide.

39. PRO247

Applicants have identified a cDNA clone that encodes a novel polypeptide having leucine rich repeats wherein the polypeptide is designated in the present application as "PRO247".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO247 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO247 polypeptide having amino acid residues 1 to 546 of Figure 88 (SEQ ID NO:249), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO247 polypeptide. In particular, the invention provides isolated native sequence PRO247 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 546 of Figure 88 (SEQ ID NO:249). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO247 polypeptide.

5 40. PRO302, PRO303, PRO304, PRO307 and PRO343

Applicants have identified cDNA clones that encode novel polypeptides having homology to various proteases, wherein those polypeptide are designated in the present application as "PRO302", "PRO303", "PRO304", "PRO307" and "PRO343" polypeptides.

10 In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO302 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO302 polypeptide having amino acid residues 1 to 452 of Figure 90 (SEQ ID NO:254), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

15 In another embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO303 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO303 polypeptide having amino acid residues 1 to 314 of Figure 92 (SEQ ID NO:256), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

20 In yet another embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO304 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO304 polypeptide having amino acid residues 1 to 556 of Figure 94 (SEQ ID NO:258), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

25 In another embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO307 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO307 polypeptide having amino acid residues 1 to 383 of Figure 96 (SEQ ID NO:260), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

30 In another embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO343 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO343 polypeptide having amino acid residues 1 to 317 of Figure 98 (SEQ ID NO:262), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

35 In another embodiment, the invention provides isolated PRO302 polypeptide. In particular, the invention provides isolated native sequence PRO302 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 452 of Figure 90 (SEQ ID NO:254).

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In another embodiment, the invention provides isolated PRO303 polypeptide. In particular, the invention provides isolated native sequence PRO303 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 314 of Figure 92 (SEQ ID NO:256).

In another embodiment, the invention provides isolated PRO304 polypeptide. In particular, the invention provides isolated native sequence PRO304 polypeptide, which in one embodiment, includes an amino acid sequence
5 comprising residues 1 to 556 of Figure 94 (SEQ ID NO:258).

In another embodiment, the invention provides isolated PRO307 polypeptide. In particular, the invention provides isolated native sequence PRO307 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 383 of Figure 96 (SEQ ID NO:260).

In another embodiment, the invention provides isolated PRO343 polypeptide. In particular, the invention
10 provides isolated native sequence PRO343 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 317 of Figure 98 (SEQ ID NO:262).

41. PRO328

Applicants have identified a cDNA clone that encodes a novel polypeptide, wherein the polypeptide is
15 designated in the present application as "PRO328".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO328 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO328 polypeptide having amino acid residues 1 to 463 of Figure 100 (SEQ ID NO:284), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency
20 conditions.

In another embodiment, the invention provides isolated PRO328 polypeptide. In particular, the invention provides isolated native sequence PRO328 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 463 of Figure 100 (SEQ ID NO:284). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO306 polypeptide.
25

42. PRO335, PRO331 and PRO326

Applicants have identified three cDNA clones that respectively encode three novel polypeptides, each having leucine rich repeats and homology to LIG-1 and ALS. These polypeptides are designated in the present application as PRO335, PRO331 and PRO326, respectively.

In one embodiment, the invention provides three isolated nucleic acid molecules comprising DNA respectively encoding PRO335, PRO331 and PRO326, respectively. In one aspect, herein is provided an isolated nucleic acid comprising DNA encoding the PRO335 polypeptide having amino acid residues 1 through 1059 of Figure 102 (SEQ ID NO:289), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. Also provided herein is an isolated
30 nucleic acid comprising DNA encoding the PRO331 polypeptide having amino acid residues 1 through 640 of Figure 104 (SEQ ID NO:291), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions. Additionally provided herein is an
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isolated nucleic acid comprises DNA encoding the PRO326 polypeptide having amino acid residues 1 through 1119 of Figure 106 (SEQ ID NO:293), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO335, PRO331 and PRO326 polypeptides or extracellular domains thereof. In particular, the invention provides isolated native sequence for the PRO335 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 1059 of Figure 102 (SEQ ID NO:289). Also provided herein is the isolated native sequence for the PRO331 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 640 of Figure 104 (SEQ ID NO:291). Also provided herein is the isolated native sequence for the PRO326 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 through 1119 of Figure 106 (SEQ ID NO:293).

43. PRO332

Applicants have identified a cDNA clone (DNA40982-1235) that encodes a novel polypeptide, designated in the present application as "PRO332."

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA having at least about 80% sequence identity to (a) a DNA molecule encoding a PRO358 polypeptide comprising the sequence of amino acids 49 to 642 of Fig. 108 (SEQ ID NO:309), or (b) the complement of the DNA molecule of (a). The sequence identity preferably is about 85%, more preferably about 90%, most preferably about 95%. In one aspect, the isolated nucleic acid has at least about 80%, preferably at least about 85%, more preferably at least about 90%, and most preferably at least about 95% sequence identity with a polypeptide having amino acid residues 1 to 642 of Fig. 108 (SEQ ID NO:309). Preferably, the highest degree of sequence identity occurs within the leucine-rich repeat domains (amino acids 116 to 624 of Fig. 108, SEQ ID NO:309). In a further embodiment, the isolated nucleic acid molecule comprises DNA encoding a PRO332 polypeptide having amino acid residues 49 to 642 of Fig. 108 (SEQ ID NO:309), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO332 polypeptides. In particular, the invention provides isolated native sequence PRO332 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 49 to 624 of Figure 108 (SEQ ID NO:309). Native PRO332 polypeptides with or without the native signal sequence (amino acids 1 to 48 in Figure 108, SEQ ID NO:309), and with or without the initiating methionine are specifically included.

44. PRO334

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to fibulin and fibrillin, wherein the polypeptide is designated in the present application as "PRO334".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO334 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO334 polypeptide having amino acid residues 1 to 509 of Figure 110 (SEQ ID NO:314), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency

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conditions.

In another embodiment, the invention provides isolated PRO334 polypeptide. In particular, the invention provides isolated native sequence PRO334 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 509 of Figure 110 (SEQ ID NO:314).

5 45. **PRO346**

Applicants have identified a cDNA clone (DNA44167-1243) that encodes a novel polypeptide, designated in the present application as "PRO346."

In one embodiment, the invention provides an isolated nucleic acid molecule having at least about 80% sequence identity to (a) a DNA molecule encoding a PRO346 polypeptide comprising the sequence of amino acids
10 19 to 339 of Fig. 112 (SEQ ID NO:319), or (b) the complement of the DNA molecule of (a). The sequence identity preferably is about 85%, more preferably about 90%, most preferably about 95%. In one aspect, the isolated nucleic acid has at least about 80%, preferably at least about 85%, more preferably at least about 90%, and most preferably at least about 95% sequence identity with a polypeptide having amino acid residues 19 to 339 of Fig. 112 (SEQ ID NO:319). Preferably, the highest degree of sequence identity occurs within the extracellular domains (amino acids
15 19 to 339 of Fig. 112, SEQ ID NO:319). In alternative embodiments, the polypeptide by which the homology is measured comprises the residues 1-339, 19-360 or 19-450 of Fig. 112, SEQ ID NO:319). In a further embodiment, the isolated nucleic acid molecule comprises DNA encoding a PRO346 polypeptide having amino acid residues 19 to 339 of Fig. 112 (SEQ ID NO:319), alternatively residues 1-339, 19-360 or 19-450 of Fig. 112 (SEQ ID NO:319) or is complementary to such encoding nucleic acid sequence; and remains stably bound to it under at least moderate,
20 and optionally, under high stringency conditions. In another aspect, the invention provides a nucleic acid of the full length protein of clone DNA44167-1243, deposited with the ATCC under accession number ATCC 209434, alternatively the coding sequence of clone DNA44167-1243, deposited under accession number ATCC 209434.

In yet another embodiment, the invention provides isolated PRO346 polypeptide. In particular, the invention provides isolated native sequence PRO346 polypeptide, which in one embodiment, includes an amino acid sequence
25 comprising residues 19 to 339 of Figure 112 (SEQ ID NO:319). Native PRO346 polypeptides with or without the native signal sequence (residues 1 to 18 in Figure 112 (SEQ ID NO:319), with or without the initiating methionine, with or without the transmembrane domain (residues 340 to 360) and with or without the intracellular domain (residues 361 to 450) are specifically included. Alternatively, the invention provides a PRO346 polypeptide encoded by the nucleic acid deposited under accession number ATCC 209434.

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 46. **PRO268**

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to protein disulfide isomerase, wherein the polypeptide is designated in the present application as "PRO268".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a
35 PRO268 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO268 polypeptide having amino acid residues 1 to 280 of Figure 114 (SEQ ID NO:324), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency

conditions.

In another embodiment, the invention provides isolated PRO268 polypeptide. In particular, the invention provides isolated native sequence PRO268 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 280 of Figure 114 (SEQ ID NO:324). An additional embodiment of the present invention is directed to an isolated extracellular domain of a PRO268 polypeptide.

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47. PRO330

Applicants have identified a cDNA clone that encodes a novel polypeptide having homology to the alpha subunit of prolyl 4-hydroxylase, wherein the polypeptide is designated in the present application as "PRO330".

10 In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding a PRO330 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO330 polypeptide having amino acid residues 1 to 533 of Figure 116 (SEQ ID NO:331), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

15 In another embodiment, the invention provides isolated PRO330 polypeptide. In particular, the invention provides isolated native sequence PRO330 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 533 of Figure 116 (SEQ ID NO:331).

48. PRO339 and PRO310

20 Applicants have identified two cDNA clones wherein each clone encodes a novel polypeptide having homology to fringe, wherein the polypeptides are designated in the present application as "PRO339" and "PRO310".

In one embodiment, the invention provides isolated nucleic acid molecules comprising DNA encoding a PRO339 and/or a PRO310 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding the PRO339 polypeptide having amino acid residues 1 to 772 of Figure 118 (SEQ ID NO:338), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under 25 high stringency conditions. In another aspect, the isolated nucleic acid comprises DNA encoding the PRO310 polypeptide having amino acid residues 1 to 318 of Figure 120 (SEQ ID NO:340), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

30 In another embodiment, the invention provides isolated PRO339 as well as isolated PRO310 polypeptides. In particular, the invention provides isolated native sequence PRO339 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 772 of Figure 118 (SEQ ID NO:338). The invention further provides isolated native sequence PRO310 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 318 of Figure 120 (SEQ ID NO:340).

35

49. PRO244

Applicants have identified a cDNA clone that encodes a novel polypeptide, designated in the present application as "PRO244".

In one embodiment, the invention provides an isolated nucleic acid molecule comprising DNA encoding PRO244 polypeptide. In one aspect, the isolated nucleic acid comprises DNA encoding PRO244 polypeptide having amino acid residues 1 to 219 of Fig. 122 (SEQ ID NO:376), or is complementary to such encoding nucleic acid sequence, and remains stably bound to it under at least moderate, and optionally, under high stringency conditions.

In another embodiment, the invention provides isolated PRO244 polypeptide. In particular, the invention provides isolated native sequence PRO244 polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 219 of Figure 122 (SEQ ID NO:376).

50. Additional Embodiments

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the above or below described polypeptides. A host cell comprising any such vector is also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the above or below described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the above or below described polypeptides fused to a heterologous polypeptide or amino acid sequence. An example of such a chimeric molecule comprises any of the above or below described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which specifically binds to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody.

In yet other embodiments, the invention provides oligonucleotide probes useful for isolating genomic and cDNA nucleotide sequences, wherein those probes may be derived from any of the above or below described nucleotide sequences.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO211 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "UNQ185" and/or "DNA32292-1131".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO217 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "UNQ191" and/or "DNA33094-1131".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO230 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "UNQ204" and/or "DNA33223-1136".

Figure 6 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 5.

Figure 7 shows a nucleotide sequence designated herein as DNA20088 (SEQ ID NO:13).

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Figure 8 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO232 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "UNQ206" and/or "DNA34435-1140".

Figure 9 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 8.

Figure 10 shows a nucleotide sequence (SEQ ID NO:22) of a native sequence PRO187 cDNA, wherein SEQ ID NO:22 is a clone designated herein as "UNQ161" and/or "DNA27864-1155".

Figure 11 shows the amino acid sequence (SEQ ID NO:23) derived from the coding sequence of SEQ ID NO:22 shown in Figure 10.

Figure 12 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO265 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "UNQ232" and/or "DNA36350-1158".

Figure 13 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 12.

Figures 14A-B show a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO219 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "UNQ193" and/or "DNA32290-1164".

Figure 15 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figures 14A-B.

Figure 16 shows a nucleotide sequence (SEQ ID NO:38) of a native sequence PRO246 cDNA, wherein SEQ ID NO:38 is a clone designated herein as "UNQ220" and/or "DNA35639-1172".

Figure 17 shows the amino acid sequence (SEQ ID NO:39) derived from the coding sequence of SEQ ID NO:38 shown in Figure 16.

Figure 18 shows a nucleotide sequence (SEQ ID NO:48) of a native sequence PRO228 cDNA, wherein SEQ ID NO:48 is a clone designated herein as "UNQ202" and/or "DNA33092-1202".

Figure 19 shows the amino acid sequence (SEQ ID NO:49) derived from the coding sequence of SEQ ID NO:48 shown in Figure 18.

Figure 20 shows a nucleotide sequence designated herein as DNA21951 (SEQ ID NO:50).

Figure 21 shows a nucleotide sequence (SEQ ID NO:58) of a native sequence PRO533 cDNA, wherein SEQ ID NO:58 is a clone designated herein as "UNQ344" and/or "DNA49435-1219".

Figure 22 shows the amino acid sequence (SEQ ID NO:59) derived from the coding sequence of SEQ ID NO:58 shown in Figure 21.

Figure 23 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO245 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "UNQ219" and/or "DNA35638-1141".

Figure 24 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:68) of a native sequence PRO220 cDNA, wherein SEQ ID NO:68 is a clone designated herein as "UNQ194" and/or "DNA32298-1132".

Figure 26 shows the amino acid sequence (SEQ ID NO:69) derived from the coding sequence of SEQ ID NO:68 shown in Figure 25.

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Figure 27 shows a nucleotide sequence (SEQ ID NO:70) of a native sequence PRO221 cDNA, wherein SEQ ID NO:70 is a clone designated herein as "UNQ195" and/or "DNA33089-1132".

Figure 28 shows the amino acid sequence (SEQ ID NO:71) derived from the coding sequence of SEQ ID NO:70 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:72) of a native sequence PRO227 cDNA, wherein SEQ ID NO:72 is a clone designated herein as "UNQ201" and/or "DNA33786-1132".

Figure 30 shows the amino acid sequence (SEQ ID NO:73) derived from the coding sequence of SEQ ID NO:72 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO258 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "UNQ225" and/or "DNA35918-1174".

Figure 32 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:90) of a native sequence PRO266 cDNA, wherein SEQ ID NO:90 is a clone designated herein as "UNQ233" and/or "DNA37150-1178".

Figure 34 shows the amino acid sequence (SEQ ID NO:91) derived from the coding sequence of SEQ ID NO:90 shown in Figure 33.

Figure 35 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO269 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "UNQ236" and/or "DNA38260-1180".

Figure 36 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 35.

Figure 37 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO287 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "UNQ250" and/or "DNA39969-1185".

Figure 38 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:108) of a native sequence PRO214 cDNA, wherein SEQ ID NO:108 is a clone designated herein as "UNQ188" and/or "DNA32286-1191".

Figure 40 shows the amino acid sequence (SEQ ID NO:109) derived from the coding sequence of SEQ ID NO:108 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO317 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "UNQ278" and/or "DNA33461-1199".

Figure 42 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 41.

Figure 43 shows a nucleotide sequence (SEQ ID NO:118) of a native sequence PRO301 cDNA, wherein SEQ ID NO:118 is a clone designated herein as "UNQ264" and/or "DNA40628-1216".

Figure 44 shows the amino acid sequence (SEQ ID NO:119) derived from the coding sequence of SEQ ID NO:118 shown in Figure 43.

Figure 45 shows a nucleotide sequence (SEQ ID NO:126) of a native sequence PRO224 cDNA, wherein SEQ ID NO:126 is a clone designated herein as "UNQ198" and/or "DNA33221-1133".

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Figure 46 shows the amino acid sequence (SEQ ID NO:127) derived from the coding sequence of SEQ ID NO:126 shown in Figure 45.

Figure 47 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO222 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "UNQ196" and/or "DNA33107-1135".

Figure 48 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:136) of a native sequence PRO234 cDNA, wherein SEQ ID NO:136 is a clone designated herein as "UNQ208" and/or "DNA35557-1137".

Figure 50 shows the amino acid sequence (SEQ ID NO:137) derived from the coding sequence of SEQ ID NO:136 shown in Figure 49.

Figure 51 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO231 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "UNQ205" and/or "DNA34434-1139".

Figure 52 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO229 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "UNQ203" and/or "DNA33100-1159".

Figure 54 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:152) of a native sequence PRO238 cDNA, wherein SEQ ID NO:152 is a clone designated herein as "UNQ212" and/or "DNA35600-1162".

Figure 56 shows the amino acid sequence (SEQ ID NO:153) derived from the coding sequence of SEQ ID NO:152 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:158) of a native sequence PRO233 cDNA, wherein SEQ ID NO:158 is a clone designated herein as "UNQ207" and/or "DNA34436-1238".

Figure 58 shows the amino acid sequence (SEQ ID NO:159) derived from the coding sequence of SEQ ID NO:158 shown in Figure 57.

Figure 59 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO223 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "UNQ197" and/or "DNA33206-1165".

Figure 60 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 59.

Figure 61 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO235 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "UNQ209" and/or "DNA35558-1167".

Figure 62 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:174) of a native sequence PRO236 cDNA, wherein SEQ ID NO:174 is a clone designated herein as "UNQ210" and/or "DNA35599-1168".

Figure 64 shows the amino acid sequence (SEQ ID NO:175) derived from the coding sequence of SEQ ID NO:174 shown in Figure 63.

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Figure 65 shows a nucleotide sequence (SEQ ID NO:176) of a native sequence PRO262 cDNA, wherein SEQ ID NO:176 is a clone designated herein as "UNQ229" and/or "DNA36992-1168".

Figure 66 shows the amino acid sequence (SEQ ID NO:177) derived from the coding sequence of SEQ ID NO:176 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:184) of a native sequence PRO239 cDNA, wherein
5 SEQ ID NO:184 is a clone designated herein as "UNQ213" and/or "DNA34407-1169".

Figure 68 shows the amino acid sequence (SEQ ID NO:185) derived from the coding sequence of SEQ ID NO:184 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO257 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "UNQ224" and/or "DNA35841-1173".

10 Figure 70 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 69.

Figure 71 shows a nucleotide sequence (SEQ ID NO:194) of a native sequence PRO260 cDNA, wherein SEQ ID NO:194 is a clone designated herein as "UNQ227" and/or "DNA33470-1175".

15 Figure 72 shows the amino acid sequence (SEQ ID NO:195) derived from the coding sequence of SEQ ID NO:194 shown in Figure 71.

Figure 73 shows a nucleotide sequence (SEQ ID NO:200) of a native sequence PRO263 cDNA, wherein SEQ ID NO:200 is a clone designated herein as "UNQ230" and/or "DNA34431-1177".

Figure 74 shows the amino acid sequence (SEQ ID NO:201) derived from the coding sequence of SEQ ID NO:200 shown in Figure 73.

20 Figure 75 shows a nucleotide sequence (SEQ ID NO:206) of a native sequence PRO270 cDNA, wherein SEQ ID NO:206 is a clone designated herein as "UNQ237" and/or "DNA39510-1181".

Figure 76 shows the amino acid sequence (SEQ ID NO:207) derived from the coding sequence of SEQ ID NO:206 shown in Figure 75.

Figure 77 shows a nucleotide sequence (SEQ ID NO:212) of a native sequence PRO271 cDNA, wherein
25 SEQ ID NO:212 is a clone designated herein as "UNQ238" and/or "DNA39423-1182".

Figure 78 shows the amino acid sequence (SEQ ID NO:213) derived from the coding sequence of SEQ ID NO:212 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:220) of a native sequence PRO272 cDNA, wherein SEQ ID NO:220 is a clone designated herein as "UNQ239" and/or "DNA40620-1183".

30 Figure 80 shows the amino acid sequence (SEQ ID NO:221) derived from the coding sequence of SEQ ID NO:220 shown in Figure 79.

Figure 81 shows a nucleotide sequence (SEQ ID NO:226) of a native sequence PRO294 cDNA, wherein SEQ ID NO:226 is a clone designated herein as "UNQ257" and/or "DNA40604-1187".

35 Figure 82 shows the amino acid sequence (SEQ ID NO:227) derived from the coding sequence of SEQ ID NO:226 shown in Figure 81.

Figure 83 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO295 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "UNQ258" and/or "DNA38268-1188".

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Figure 84 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 83.

Figures 85A-B show a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO293 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "UNQ256" and/or "DNA37151-1193".

Figure 86 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figures 85A-B.

Figures 89A-B show a nucleotide sequence (SEQ ID NO:248) of a native sequence PRO247 cDNA, wherein SEQ ID NO:248 is a clone designated herein as "UNQ221" and/or "DNA35673-1201".

Figure 88 shows the amino acid sequence (SEQ ID NO:249) derived from the coding sequence of SEQ ID NO:248 shown in Figure 87.

Figure 89 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO302 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "UNQ265" and/or "DNA40370-1217".

Figure 90 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO303 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "UNQ266" and/or "DNA42551-1217".

Figure 92 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO304 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "UNQ267" and/or "DNA39520-1217".

Figure 94 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in Figure 93.

Figure 95 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO307 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "UNQ270" and/or "DNA41225-1217".

Figure 96 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in Figure 95.

Figure 97 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO343 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "UNQ302" and/or "DNA43318-1217".

Figure 98 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in Figure 97.

Figure 99 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO328 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "UNQ289" and/or "DNA40587-1231".

Figure 100 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in Figure 99.

Figures 101A-B show a nucleotide sequence (SEQ ID NO:288) of a native sequence PRO335 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "UNQ287" and/or "DNA41388-1234".

Figure 102 shows the amino acid sequence (SEQ ID NO:289) derived from the coding sequence of SEQ ID NO:288 shown in Figures 103A-B.

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Figure 103 shows a nucleotide sequence (SEQ ID NO:290) of a native sequence PRO331 cDNA, wherein SEQ ID NO:290 is a clone designated herein as "UNQ292" and/or "DNA40981-1234".

Figure 104 shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:290 shown in Figure 103.

Figures 105A-B show a nucleotide sequence (SEQ ID NO:292) of a native sequence PRO326 cDNA, wherein SEQ ID NO:292 is a clone designated herein as "UNQ287" and/or "DNA37140-1234".

Figure 106 shows the amino acid sequence (SEQ ID NO:293) derived from the coding sequence of SEQ ID NO:292 shown in Figures 105A-B.

Figures 107A-B show a nucleotide sequence (SEQ ID NO:308) of a native sequence PRO332 cDNA, wherein SEQ ID NO:308 is a clone designated herein as "UNQ293" or "DNA40982-1235".

Figure 108 shows the amino acid sequence (SEQ ID NO:309) derived from the coding sequence of SEQ ID NO:308 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO334 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "UNQ295" or "DNA41379-1236".

Figure 110 shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in Figure 109.

Figure 111 shows a nucleotide sequence (SEQ ID NO:318) of a native sequence PRO346 cDNA, wherein SEQ ID NO:318 is a clone designated herein as "UNQ305" or "DNA44167-1243".

Figure 112 shows the amino acid sequence (SEQ ID NO:319) derived from the coding sequence of SEQ ID NO:318 shown in Figure 111.

Figure 113 shows a nucleotide sequence (SEQ ID NO:323) of a native sequence PRO268 cDNA, wherein SEQ ID NO:323 is a clone designated herein as "UNQ235" or "DNA39427-1179".

Figure 114 shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323 shown in Figure 113.

Figure 115 shows a nucleotide sequence (SEQ ID NO:330) of a native sequence PRO330 cDNA, wherein SEQ ID NO:330 is a clone designated herein as "UNQ290" or "DNA40603-1232".

Figure 116 shows the amino acid sequence (SEQ ID NO:331) derived from the coding sequence of SEQ ID NO:330 shown in Figure 115.

Figure 117 shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO339 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "UNQ229" or "DNA43466-1225".

Figure 118 shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO310 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "UNQ273" or "DNA43046-1225".

Figure 120 shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in Figure 119.

Figure 121 shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO244 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "UNQ218" or "DNA35668-1171".

Figure 122 shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in Figure 121.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

5 The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from
10 another source, or prepared by recombinant or synthetic methods.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (e.g., an
15 extracellular domain sequence), naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO211 is a mature or full-length native sequence PRO211 polypeptide comprising amino acids 1 to 353 of Figure 2 (SEQ ID NO:2), the native sequence PRO217 is a mature or full-length native sequence PRO217 polypeptide comprising amino acids 1 to 379 of Figure 4 (SEQ ID NO:4), the native sequence PRO230 is a mature or full-length native
20 sequence PRO230 polypeptide comprising amino acids 1 to 467 of Figure 6 (SEQ ID NO:12), the native sequence PRO232 polypeptide is a mature or full-length native sequence PRO232 polypeptide comprising amino acids 1 to 114 of Figure 9 (SEQ ID NO:18), the native sequence PRO187 is a mature or full-length native sequence PRO187 comprising amino acids 1 to 205 of Figure 11 (SEQ ID NO:23), the native sequence PRO265 polypeptide is a mature or full-length native sequence PRO265 polypeptide comprising amino acids 1 to 660 of Figure 13 (SEQ ID NO:28)
25 or the native sequence PRO265 polypeptide is an extracellular domain of the full-length PRO265 protein, wherein the putative transmembrane domain of the full-length PRO265 protein is encoded by nucleotides beginning at nucleotide 1969 of SEQ ID NO:31, the native sequence PRO219 polypeptide is a mature or full-length native sequence PRO219 polypeptide comprising amino acids 1 to 915 of Figure 15 (SEQ ID NO:34), the native sequence PRO246 polypeptide is a mature or full-length native sequence PRO246 polypeptide comprising amino acids 1 to 390
30 of Figure 17 (SEQ ID NO:39) or the native sequence PRO246 polypeptide is an extracellular domain of the full-length PRO246 protein, wherein the putative transmembrane domain of the full-length PRO246 protein is encoded by nucleotides beginning at nucleotide 855 as shown in Figure 16, the native sequence PRO228 polypeptide is a mature or full-length native sequence PRO228 polypeptide comprising amino acids 1 to 690 of Figure 19 (SEQ ID NO:49) or the native sequence PRO228 polypeptide is an extracellular domain of the full-length PRO228 protein, the native
35 sequence PRO533 is a mature or full-length native sequence PRO533 comprising amino acids 1 to 216 of Figure 22 (SEQ ID NO:59), with or without the N-terminal signal sequence, and with or without the initiating methionine at position 1, the native sequence PRO245 polypeptide is a mature or full-length native sequence PRO245 polypeptide

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comprising amino acids 1 to 312 of Figure 24 (SEQ ID NO:64), the native sequence of each PRO220, PRO221 and PRO227 polypeptides is a mature or full-length native sequence PRO220, PRO221 and PRO227 polypeptide comprising amino acids 1 through 708 of Figure 26 (SEQ ID NO:69), 1 through 259 of Figure 28 (SEQ ID NO:71), and 1 through 620 of Figure 30 (SEQ ID NO:73), the native sequence PRO258 polypeptide is a mature or full-length native sequence PRO258 polypeptide comprising amino acids 1 to 398 of Figure 32 (SEQ ID NO:84) or the native sequence PRO258 polypeptide is an extracellular domain of the full-length PRO258 protein, wherein the putative transmembrane domain of the full-length PRO258 protein is encoded by nucleotides beginning at nucleotide 1134 of SEQ ID NO:83, the native sequence PRO266 polypeptide is a mature or full-length native sequence PRO266 polypeptide comprising amino acids 1 to 696 of Figure 34 (SEQ ID NO:91) or the native sequence PRO266 polypeptide is an extracellular domain of the full-length PRO266 protein, wherein the putative transmembrane domain of the full-length PRO266 protein is encoded by nucleotides beginning at about nucleotide 2009 of SEQ ID NO:104, the native sequence PRO269 polypeptide is a mature or full-length native sequence PRO269 polypeptide comprising amino acids 1 to 490 of Figure 36 (SEQ ID NO:96) or the native sequence PRO269 polypeptide is an extracellular domain of the full-length PRO269 protein, wherein the putative transmembrane domain of the full-length PRO269 protein is encoded by nucleotides beginning at nucleotide 1502 as shown in Figure 35, the native sequence PRO287 polypeptide is a mature or full-length native sequence PRO287 polypeptide comprising amino acids 1 to 415 of Figure 38 (SEQ ID NO:104), the native sequence PRO214 is a mature or full-length native sequence PRO214 comprising amino acids 1 to 420 of Fig. 40 (SEQ ID NO:109), the native-sequence PRO317 is a full-length native-pre-sequence PRO317 comprising amino acids 1 to 366 of Fig. 42 (SEQ ID NO:114) or a mature native-sequence PRO317 comprising amino acids 19 to 366 of Fig. 42 (SEQ ID NO:114), the native sequence PRO301 is a mature or full-length native sequence PRO301 comprising amino acids 1 to 299 of Fig. 44 (SEQ ID NO:119), with or without the N-terminal signal sequence, with or without the initiating methionine at position 1, with or without the potential transmembrane domain at position 236 to about 258, and with or without the intracellular domain at about position 259 to 299, the native sequence PRO224 polypeptide is a mature or full-length native sequence PRO224 polypeptide comprising amino acids 1 to 282 of Figure 46 (SEQ ID NO:127), the native sequence PRO222 polypeptide is a mature or full-length native sequence PRO222 polypeptide comprising amino acids 1 to 490 of Figure 48 (SEQ ID NO:132), the native sequence PRO234 is a mature or full-length native sequence novel lectin comprising amino acids 1 to 382 of Fig. 50 (SEQ ID NO:137), the native sequence PRO231 polypeptide is a mature or full-length native sequence PRO231 polypeptide comprising amino acids 1 to 428 of Figure 52 (SEQ ID NO:142), the native sequence PRO229 polypeptide is a mature or full-length native sequence PRO229 polypeptide comprising amino acids 1 to 347 of Figure 54 (SEQ ID NO:148), the native sequence PRO238 polypeptide is a mature or full-length native sequence PRO238 polypeptide comprising amino acids 1 to 310 of Figure 56 (SEQ ID NO:153), the native sequence PRO233 polypeptide is a mature or full-length native sequence PRO233 polypeptide comprising amino acids 1 to 300 of Figure 58 (SEQ ID NO:159), the native sequence PRO223 polypeptide is a mature or full-length native sequence PRO223 polypeptide comprising amino acids 1 to 476 of Figure 60 (SEQ ID NO:164), the native sequence PRO235 polypeptide is a mature or full-length native sequence PRO235 polypeptide comprising amino acids 1 to 552 of Figure 62 (SEQ ID NO:170), the native sequence PRO236 polypeptide is a mature or full-length native sequence PRO236 polypeptide comprising amino acids 1 to 636 of Figure 64 (SEQ ID NO:175), the native sequence PRO262

polypeptide is a mature or full-length native sequence PRO262 polypeptide comprising amino acids 1 to 654 of Figure 66 (SEQ ID NO:177), the native sequence PRO239 polypeptide is a mature or full-length native sequence PRO239 polypeptide comprising amino acids 1 to 501 of Figure 68 (SEQ ID NO:185), the native sequence PRO257 polypeptide is a mature or full-length native sequence PRO257 polypeptide comprising amino acids 1 to 607 of Figure 70 (SEQ ID NO:190) or the native sequence PRO257 polypeptide is an extracellular domain of the full-length PRO257 protein, wherein the putative transmembrane domain of the full-length PRO257 protein is encoded by nucleotides beginning at nucleotide 2668 as shown in Figure 69, the native sequence PRO260 polypeptide is a mature or full-length native sequence PRO260 polypeptide comprising amino acids 1 to 467 of Figure 72 (SEQ ID NO:195), the native sequence PRO263 polypeptide is a mature or full-length native sequence PRO263 polypeptide comprising amino acids 1 to 322 of Figure 74 (SEQ ID NO:201) or the native sequence PRO263 polypeptide is an extracellular domain of the full-length PRO263 protein, wherein the putative transmembrane domain of the full-length PRO263 protein is encoded by nucleotides beginning at nucleotide 868 of SEQ ID NO:200, the native sequence PRO270 polypeptide is a mature or full-length native sequence PRO270 polypeptide comprising amino acids 1 to 296 of Figure 76 (SEQ ID NO:207), the native sequence PRO271 polypeptide is a mature or full-length native sequence PRO271 polypeptide comprising amino acids 1 to 360 of Figure 78 (SEQ ID NO:213), the native sequence PRO272 polypeptide is a mature or full-length native sequence PRO272 polypeptide comprising amino acids 1 to 328 of Figure 80 (SEQ ID NO:221), the native sequence PRO294 polypeptide is a mature or full-length native sequence PRO294 polypeptide comprising amino acids 1 to 550 of Figure 82 (SEQ ID NO:227), the native sequence PRO295 polypeptide is a mature or full-length native sequence PRO295 polypeptide comprising amino acids 1 to 350 of Figure 84 (SEQ ID NO:236), the native sequence PRO293 polypeptide is a mature or full-length native sequence PRO293 polypeptide comprising amino acids 1 to 713 of Figure 86 (SEQ ID NO:244) or the native sequence PRO293 polypeptide is an extracellular domain of the full-length PRO293 protein, wherein the putative transmembrane domain of the full-length PRO293 protein is encoded by nucleotides beginning at nucleotide 2771 of SEQ ID NO:243, the native sequence PRO247 polypeptide is a mature or full-length native sequence PRO247 polypeptide comprising amino acids 1 to 546 of Figure 88 (SEQ ID NO:249), the native sequence PRO302 polypeptide is a mature or full-length native sequence PRO302 polypeptide comprising amino acids 1 to 452 of Figure 90 (SEQ ID NO:254), the native sequence PRO303 polypeptide is a mature or full-length native sequence PRO303 polypeptide comprising amino acids 1 to 314 of Figure 92 (SEQ ID NO:256), the native sequence PRO304 polypeptide is a mature or full-length native sequence PRO304 polypeptide comprising amino acids 1 to 556 of Figure 94 (SEQ ID NO:258), the native sequence PRO307 polypeptide is a mature or full-length native sequence PRO307 polypeptide comprising amino acids 1 to 383 of Figure 96 (SEQ ID NO:260), the native sequence PRO343 polypeptide is a mature or full-length native sequence PRO343 polypeptide comprising amino acids 1 to 317 of Figure 98 (SEQ ID NO:262), the native sequence PRO328 polypeptide is a mature or full-length native sequence PRO328 polypeptide comprising amino acids 1 to 463 of Figure 100 (SEQ ID NO:284) or the native sequence PRO306 polypeptide is an extracellular domain of the full-length PRO306 protein, wherein the putative extracellular domain of the full-length PRO306 protein, the native sequence PRO335 polypeptide is a mature or full-length native sequence PRO335 polypeptide comprising amino acids 1 through 1059 of Figure 102 (SEQ ID NO:289), the native sequence PRO331 polypeptide is a mature or full-length native sequence PRO331 polypeptide comprising amino acids 1 through 640 of Figure 104

(SEQ ID NO:291), the native sequence PRO326 polypeptide is a mature or full-length native sequence PRO326 polypeptide comprising amino acids 1 through 1119 of Figure 106 (SEQ ID NO:293), wherein additional embodiments include wherein the transmembrane regions are deleted or the peptides are truncated, so as to not include the transmembrane regions for each of PRO335, PRO331, and PRO326, the native sequence PRO332 is a mature or full-length native sequence PRO332 comprising amino acids 49 to 642 of Fig. 180 (SEQ ID NO:309),

5 without or without the N-terminal signal sequence, and with or without the initiating methionine at position 1, the native sequence PRO334 polypeptide is a mature or full-length native sequence PRO334 polypeptide comprising amino acids 1 to 509 of Figure 110 (SEQ ID NO:314), the native sequence PRO346 is a mature or full-length native sequence PRO346 comprising amino acids 19 to 339 of Fig. 112 (SEQ ID NO:319), with or without the N-terminal signal sequence, with or without the initiating methionine, with or without the transmembrane domain at positions

10 340 to 360 and with or without the intracellular domain at positions 361 to 450, the native sequence PRO268 polypeptide is a mature or full-length native sequence PRO268 polypeptide comprising amino acids 1 to 280 of Figure 114 (SEQ ID NO:324) or the native sequence PRO268 polypeptide is an extracellular domain of the full-length PRO268 protein, wherein the putative transmembrane domain of the full-length PRO268 protein is encoded by nucleotides beginning at nucleotide 559 as shown in Figure 113, the native sequence PRO330 polypeptide is a mature

15 or full-length native sequence PRO330 polypeptide comprising amino acids 1 to 533 of Figure 116 (SEQ ID NO:331), the native sequence PRO339 polypeptide is a mature or full-length native sequence PRO339 polypeptide comprising amino acids 1 to 772 of Figure 118 (SEQ ID NO:338), the native sequence PRO310 polypeptide is a mature or full-length native sequence PRO310 polypeptide comprising amino acids 1 to 318 of Figure 120 (SEQ ID NO:340) and the native sequence PRO244 is a mature or full-length native sequence PRO244 comprising amino acids 1 to 219 of

20 Fig. 122 (SEQ ID NO:376), wherein the mature, full-length native-sequence PRO244 protein comprises a cytoplasmic domain (about amino acid positions 1 to 20), a transmembrane domain (about amino acid positions 21 to 46), and an extracellular domain (about amino acid positions 47 to 219). Within the extracellular domain, the C-lectin domain is between about amino acid position 55 and about amino acid position 206. Native sequence PRO244 as shown in Figure 122 maps to chromosome 12, bands p12-p13.

25 "PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with the full-length native sequence PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, more preferably at least about 90%

30 amino acid sequence identity, and even more preferably at least about 95% amino acid sequence identity with the amino acid sequence of the full-length native amino acid sequence as disclosed herein.

"PRO317 variants" or "PRO317 sequence variants" as defined herein mean biologically active PRO317s as defined below having less than 100% sequence identity with the PRO317 isolated from recombinant cell culture or from mammalian fetal kidney tissue having the deduced sequence described in Figure 42. Ordinarily, a

35 biologically active PRO317 variant will have an amino acid sequence having at least about 70% amino acid sequence identity with the PRO317 of Figure 42, preferably at least about 75%, more preferably at least about 80%, still more preferably at least about 85%, even more preferably, at least about 90%, and most preferably at least about 95% (*i.e.*,

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70-100%, 75-100%, 80-100%, 85-100%, 90-100%, and 95-100% sequence identity, respectively). These variants include covalently modified polypeptides, as well as PRO317 fragments and glycosylation variants thereof. PRO317 fragments have a consecutive sequence of at least 10, 15, 20, 25, 30, or 40 amino acid residues, preferably about 10-150 residues, that is identical to the sequence of the PRO317 shown in Figure 42. Other preferred PRO317 fragments include those produced as a result of chemical or enzymatic hydrolysis or digestion of the purified
 5 PRO317.

A "chimeric PRO317" is a polypeptide comprising full-length PRO317 or one or more fragments thereof fused or bonded to a second protein or one or more fragments thereof. The chimera will typically share at least one biological property in common with PRO317. The second protein will typically be a cytokine, growth factor, or hormone such as a neurotrophic or angiogenic factor such as GDNF or VEGF, or another member of the TGF-
 10 superfamily such as EBAF-1. Another exemplary preferred PRO317 chimera is a "domain chimera" that consists of the N-terminal residues substituted with one or more, but not all, of the residues of the human EBAF-1. In this embodiment, the PRO317 chimera would have individual or blocks of residues from the human EBAF-1 sequence added or substituted into the PRO317 sequence. For example, one or more of those segments of EBAF-1 that are not homologous could be substituted into the corresponding segments of PRO317. It is contemplated that this
 15 "PRO317-EBAF-1 domain chimera" will have an agonist biological activity.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the
 20 sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, ALIGN or Megalign (DNASTAR) software. The preferred software alignment program is BLAST. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

25 "Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available
 30 computer software such as BLAST, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components
 35 of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal

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or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the PRO polypeptide nucleic acid. An isolated PRO polypeptide nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated PRO polypeptide nucleic acid molecules therefore are distinguished from the specific PRO polypeptide nucleic acid molecule as it exists in natural cells. However, an isolated PRO polypeptide nucleic acid molecule includes PRO polypeptide nucleic acid molecules contained in cells that ordinarily express the PRO polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

"Southern analysis" or "Southern blotting" is a method by which the presence of DNA sequences in a restriction endonuclease digest of DNA or a DNA-containing composition is confirmed by hybridization to a known, labeled oligonucleotide or DNA fragment. Southern analysis typically involves electrophoretic separation of DNA digests on agarose gels, denaturation of the DNA after electrophoretic separation, and transfer of the DNA to nitrocellulose, nylon, or another suitable membrane support for analysis with a radiolabeled, biotinylated, or enzyme-labeled probe as described in sections 9.37-9.52 of Sambrook *et al.*, Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989).

"Northern analysis" or "Northern blotting" is a method used to identify RNA sequences that hybridize to a known probe such as an oligonucleotide, DNA fragment, cDNA or fragment thereof, or RNA fragment. The probe is labeled with a radioisotope such as ^{32}P , or by biotinylation, or with an enzyme. The RNA to be analyzed is usually electrophoretically separated on an agarose or polyacrylamide gel, transferred to nitrocellulose, nylon, or other suitable membrane, and hybridized with the probe, using standard techniques well known in the art such as those described in sections 7.39-7.52 of Sambrook *et al.*, *supra*.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

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The term "antibody" is used in the broadest sense and specifically covers single anti-PRO polypeptide monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies) and anti-PRO polypeptide antibody compositions with polyepitopic specificity. The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

5 "Active" or "activity" for the purposes herein refers to form(s) of PRO polypeptide which retain the biologic and/or immunologic activities of the specific native or naturally-occurring PRO polypeptide. The activity of a PRO332 polypeptide preferably involves the regulation of extracellular matrix, cartilage, or bone function.

"PRO317-associated disorder" refers to a pathological condition or disease wherein PRO317 is over- or underexpressed. Such disorders include diseases of the female genital tract or of the endometrium of a mammal, 10 including hyperplasia, endometritis, endometriosis, wherein the patient is at risk for infertility due to endometrial factor, endometrioma, and endometrial cancer, especially those diseases involving abnormal bleeding such as a gynecological disease. They also include diseases involving angiogenesis, wherein the angiogenesis results in a pathological condition, such as cancer involving solid tumors (the therapy for the disorder would result in decreased vascularization and a decline in growth and metastasis of a variety of tumors). Alternatively, the angiogenesis may 15 be beneficial, such as for ischemia, especially coronary ischemia. Hence, these disorders include those found in patients whose hearts are functioning but who have a blocked blood supply due to atherosclerotic coronary artery disease, and those with a functioning but underperfused heart, including patients with coronary arterial disease who are not optimal candidates for angioplasty and coronary artery by-pass surgery. The disorders also include diseases involving the kidney or originating from the kidney tissue, such as polycystic kidney disease and chronic and acute 20 renal failure.

"Treatment" or "treating" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in which the disorder is to be prevented.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, 25 domestic and farm animals, and zoo, sports, or pet animals, such as sheep, dogs, horses, cats, cows, and the like. Preferably, the mammal herein is a human.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable 30 carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions 35 such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

The term "agonist" is used to refer to peptide and non-peptide analogs of the native PRO polypeptides (where native PRO polypeptide refers to pro-PRO polypeptide, pre-PRO polypeptide, prepro-PRO polypeptide, or

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mature PRO polypeptide) of the present invention and to antibodies specifically binding such native PRO polypeptides, provided that they retain at least one biological activity of a native PRO polypeptide. Preferably, the agonists of the present invention retain the qualitative binding recognition properties and receptor activation properties of the native PRO polypeptide.

The term "antagonist" is used to refer to a molecule inhibiting a biological activity of a native PRO polypeptide of the present invention wherein native PRO polypeptide refers to pro-PRO polypeptide, pre-PRO polypeptide, prepro-PRO polypeptide, or mature PRO polypeptide. Preferably, the antagonists herein inhibit the binding of a native PRO polypeptide of the present invention. Preferred antagonists essentially completely block the binding of a native PRO317 polypeptide to a PRO317 polypeptide receptor to which it otherwise binds. Such receptors may include the Type I and Type II, and possibly Type III receptors identified for the TGF- superfamily. Kolodziejczyk and Hall, *supra*. A PRO polypeptide "antagonist" is a molecule which prevents, or interferes with, a PRO antagonist effector function (e.g. a molecule which prevents or interferes with binding and/or activation of a PRO polypeptide receptor by PRO polypeptide). Such molecules can be screened for their ability to competitively inhibit PRO polypeptide receptor activation by monitoring binding of native PRO polypeptide in the presence and absence of the test antagonist molecule, for example. Examples of PRO317 polypeptide antagonists include neutralizing antibodies against F-2. An antagonist of the invention also encompasses an antisense polynucleotide against the PRO polypeptide gene, which antisense polynucleotide blocks transcription or translation of the PRO polypeptide gene, thereby inhibiting its expression and biological activity.

"Stringent conditions" means (1) employing low ionic strength and high temperature for washing, for example, 0.015 sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C, or (2) employing during hybridization a denaturing agent, such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 nM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C. Another example is use of 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6/8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC and 0.1% SDS. Yet another example is hybridization using a buffer of 10% dextran sulfate, 2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" are described in Sambrook *et al.*, *supra*, and include the use of a washing solution and hybridization conditions (e.g., temperature, ionic strength, and %SDS) less stringent than described above. An example of moderately stringent conditions is a condition such as overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/mL denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, *etc.*, as necessary to accommodate factors such as probe length and the like.

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* - trademark

II. Compositions and Methods of the Invention

1. Full-length PRO211 and PRO217 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO211 and PRO217. In particular, Applicants have identified and isolated cDNA encoding PRO211 and PRO217 polypeptides, as disclosed in further detail in the Examples below. Using
 5 BLAST (FastA format) sequence alignment computer programs, Applicants found that cDNA sequences encoding full-length native sequence PRO211 and PRO217 have homologies to known proteins having EGF-like domains. Specifically, the cDNA sequence DNA32292-1131 (Figure 1, SEQ ID NO:1) has 36% identity and a Blast score of 209 with PAC6_RAT and 31% identity and a Blast score of 206 with Fibulin-1, isoform c precursor. The cDNA
 10 sequence DNA33094-1131 (Figure 3, SEQ ID NO:3) has 36% identity and a Blast score of 336 with eastern newt tenascin, and 37% identity and a Blast score of 331 with human tenascin-X precursor. Accordingly, it is presently believed that PRO211 and PRO217 polypeptides disclosed in the present application are newly identified members of the EGF-like family and possesses properties typical of the EGF-like protein family.

2. Full-length PRO230 Polypeptides

15 The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO230. In particular, Applicants have identified and isolated cDNA encoding a PRO230 polypeptide, as disclosed in further detail in the Examples below. Using known programs such as BLAST and FastA sequence alignment computer programs, Applicants found that a cDNA sequence encoding full-length native sequence PRO230 has 48% amino acid identity with the rabbit tubulointerstitial nephritis antigen
 20 precursor. Accordingly, it is presently believed that PRO230 polypeptide disclosed in the present application is a newly identified member of the tubulointerstitial nephritis antigen family and possesses the ability to be recognized by human autoantibodies in certain forms of tubulointerstitial nephritis.

3. Full-length PRO232 Polypeptides

25 The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO232. In particular, Applicants have identified and isolated cDNA encoding a PRO232 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that a portion of the full-length native sequence PRO232 (shown in Figure 9 and SEQ ID NO:18) has 35% sequence identity with a stem cell surface antigen from Gallus
 30 gallus. Accordingly, it is presently believed that the PRO232 polypeptide disclosed in the present application may be a newly identified stem cell antigen.

4. Full-length PRO187 Polypeptides

35 The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO187. In particular, Applicants have identified and isolated cDNA encoding a PRO187 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that a full-length native sequence PRO187 (shown in Figure

5. Full-length PRO265 Polypeptides

6. Full-length PRO219 Polypeptides

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7. **Full-length PRO246 Polypeptides**

8. Full-length PRO228 Polypeptides

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encoding a PRO228 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO228 polypeptide have significant homology with the EMR1 protein. Applicants have also found that the DNA encoding the PRO228 polypeptide has significant homology with latrophilin, macrophage-restricted cell surface glycoprotein, B0457.1 and leucocyte antigen CD97 precursor. Accordingly, it is presently believed that PRO228 polypeptide disclosed in the present application is a newly identified member of the seven transmembrane superfamily and possesses characteristics and functional properties typical of this family. In particular, it is believed that PRO228 is a new member of the subgroup within this family to which CD97 and EMR1 belong.

9. Full-length PRO533 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO533. In particular, Applicants have identified and isolated cDNA encoding a PRO533 polypeptide, as disclosed in further detail in the Examples below. Using BLAST-2 and FastA sequence alignment computer programs, Applicants found that a full-length native sequence PRO533 (shown in Figure 22 and SEQ ID NO:59) has a Blast score of 509 and 53% amino acid sequence identity with fibroblast growth factor (FGF). Accordingly, it is presently believed that PRO533 disclosed in the present application is a newly identified member of the fibroblast growth factor family and may possess activity typical of such polypeptides.

10. Full-length PRO245 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO245. In particular, Applicants have identified and isolated cDNA encoding a PRO245 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that a portion of the amino acid sequence of the PRO245 polypeptide has 60% amino acid identity with the human c-myc protein. Accordingly, it is presently believed that the PRO245 polypeptide disclosed in the present application may be a newly identified member of the transmembrane protein tyrosine kinase family.

11. Full-length PRO220, PRO221 and PRO227 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO220, PRO221 and PRO227. In particular, Applicants have identified and isolated cDNAs encoding a PRO220, PRO221 and PRO227 polypeptide, respectively, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, PRO220 has amino acid identity with the amino acid sequence of a leucine rich protein wherein the identity is 87%. PRO220 additionally has amino acid identity with the neuronal leucine rich protein wherein the identity is 55%. The neuronal leucine rich protein is further described in Taguchi, *et al.*, Mol. Brain Res., 35:31-40 (1996).

PRO221 has amino acid identity with the SLIT protein precursor, wherein different portions of these two proteins have the respective percent identities of 39%, 38%, 34%, 31%, and 30%.

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PRO227 has amino acid identity with the amino acid sequence of platelet glycoprotein V precursor. The same results were obtained for human glycoprotein V. Different portions of these two proteins show the following percent identities of 30 %, 28 %, 28 %, 31 %, 35 %, 39 % and 27 %.

Accordingly, it is presently believed that PRO220, PRO221 and PRO227 polypeptides disclosed in the present application are newly identified members of the leucine rich repeat protein superfamily and that each possesses protein-protein binding capabilities typical of the leucine rich repeat protein superfamily. It is also believed that they have capabilities similar to those of SLIT, the leucine rich repeat protein and human glycoprotein V.

12. Full-length PRO258 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO258. In particular, Applicants have identified and isolated cDNA encoding a PRO258 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO258 polypeptide have significant homology with the CRTAM and poliovirus receptors. Accordingly, it is presently believed that PRO258 polypeptide disclosed in the present application is a newly identified member of the Ig superfamily and possesses virus receptor capabilities or regulates immune function as typical of this family.

13. Full-length PRO266 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO266. In particular, Applicants have identified and isolated cDNA encoding a PRO266 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO266 polypeptide have significant homology with the SLIT protein from *Drosophila*. Accordingly, it is presently believed that PRO266 polypeptide disclosed in the present application is a newly identified member of the leucine rich repeat family and possesses ligand-ligand binding activity and neuronal development typical of this family. SLIT has been shown to be useful in the study and treatment of Alzheimer's disease, *supra*, and thus, PRO266 may have involvement in the study and cure of this disease.

14. Full-length PRO269 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO269. In particular, Applicants have identified and isolated cDNA encoding a PRO269 polypeptide, as disclosed in further detail in the Examples below. Using BLAST, FastA and sequence alignment computer programs, Applicants found that the amino acid sequence encoded by nucleotides 314 to 1783 of the full-length native sequence PRO269 (shown in Figure 35 and SEQ ID NO:95) has significant homology to human urinary thrombomodulin and various thrombomodulin analogues respectively, to which it was aligned. Accordingly, it is presently believed that PRO269 polypeptide disclosed in the present application is a newly identified member of the thrombomodulin family.

15. Full-length PRO287 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO287. In particular, Applicants have identified and isolated cDNA encoding a PRO287 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO287 polypeptide have
 5 significant homology with the type 1 procollagen C-proteinase enhancer protein precursor and type 1 procollagen C-proteinase enhancer protein. Accordingly, it is presently believed that PRO287 polypeptide disclosed in the present application is a newly identified member of the C-proteinase enhancer protein family.

16. Full-length PRO214 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO214. In particular, Applicants have identified and isolated cDNA encoding a PRO214 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that a full-length native sequence PRO214 polypeptide (shown in Figure 40 and SEQ ID NO:109) has 49% amino acid sequence identity with HT protein, a known member
 15 of the EGF-family. The comparison resulted in a BLAST score of 920, with 150 matching nucleotides. Accordingly, it is presently believed that the PRO214 polypeptide disclosed in the present application is a newly identified member of the family comprising EGF domains and may possess activities or properties typical of the EGF-domain containing family.

20 17. Full-length PRO317 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO317. In particular, cDNA encoding a PRO317 polypeptide has been identified and isolated, as disclosed in further detail in the Examples below. Using BLASTTM and FastATM sequence alignment computer programs, it was found that a full-length native-sequence PRO317 (shown in Figure 42 and SEQ
 25 ID NO:114) has 92% amino acid sequence identity with EBAF-1. Further, it is closely aligned with many other members of the TGF- superfamily.

Accordingly, it is presently believed that PRO317 disclosed in the present application is a newly identified member of the TGF- superfamily and may possess properties that are therapeutically useful in conditions of uterine bleeding, etc. Hence, PRO317 may be useful in diagnosing or treating abnormal bleeding involved in gynecological
 30 diseases, for example, to avoid or lessen the need for a hysterectomy. PRO317 may also be useful as an agent that affects angiogenesis in general, so PRO317 may be useful in anti-tumor indications, or conversely, in treating coronary ischemic conditions.

Library sources reveal that ESTs used to obtain the consensus DNA for generating PRO317 primers and probes were found in normal tissues (uterus, prostate, colon, and pancreas), in several tumors (colon, brain (twice),
 35 pancreas, and mullerian cell), and in a heart with ischemia. PRO317 has shown up in several tissues as well, but it does look to have a greater concentration in uterus. Hence, PRO317 may have a broader use by the body than EBAF-1. It is contemplated that, at least for some indications, PRO317 may have opposite effects from EBAF-1.

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18. Full-length PRO301 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO301. In particular, Applicants have identified and isolated cDNA encoding a PRO301 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that a full-length native sequence PRO301 (shown in Figure 44 and SEQ ID NO:119) has a Blast score of 246 corresponding to 30% amino acid sequence identity with human A33 antigen precursor. Accordingly, it is presently believed that PRO301 disclosed in the present application is a newly identified member of the A33 antigen protein family and may be expressed in human neoplastic diseases such as colorectal cancer.

19. Full-length PRO224 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO224. In particular, Applicants have identified and isolated cDNA encoding a PRO224 polypeptide, as disclosed in further detail in the Examples below. Using known programs such as BLAST and FastA sequence alignment computer programs, Applicants found that full-length native PRO224 (Figure 46, SEQ ID NO:127) has amino acid identity with apolipoprotein E receptor 2906 from homo sapiens. The alignments of different portions of these two polypeptides show amino acid identities of 37%, 36%, 30%, 44%, 44% and 28% respectively. Full-length native PRO224 (Figure 46, SEQ ID NO:127) also has amino acid identity with very low-density lipoprotein receptor precursor from gall. The alignments of different portions of these two polypeptides show amino acid identities of 38%, 37%, 42%, 33%, and 37% respectively. Additionally, full-length native PRO224 (Figure 46, SEQ ID NO:127) has amino acid identity with the chicken oocyte receptor P95 from Gallus gallus. The alignments of different portions of these two polypeptides show amino acid identities of 38%, 37%, 42%, 33%, and 37% respectively. Moreover, full-length native PRO224 (Figure 46, SEQ ID NO:127) has amino acid identity with very low density lipoprotein receptor short form precursor from humans. The alignments of different portions of these two polypeptides show amino acid identities of 32%, 38%, 34%, 45%, and 31%, respectively. Accordingly, it is presently believed that PRO224 polypeptide disclosed in the present application is a newly identified member of the low density lipoprotein receptor family and possesses the structural characteristics required to have the functional ability to recognize and endocytose low density lipoproteins typical of the low density lipoprotein receptor family. (The alignments described above used the following scoring parameters: T=7, S+65, S2=36, Matrix: BLOSUM62.)

20. Full-length PRO222 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO222. In particular, Applicants have identified and isolated cDNA encoding a PRO222 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that a sequence encoding full-length native sequence PRO222 (shown in Figure 48 and SEQ ID NO:132) has 25-26% amino acid identity with mouse complement factor h precursor, has 27-29% amino acid identity with complement receptor, has 25-47% amino acid identity with mouse

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complement C3b receptor type 2 long form precursor, has 40% amino acid identity with human hypothetical protein k1aa0247. Accordingly, it is presently believed that PRO222 polypeptide disclosed in the present application is a newly identified member of the complement receptor family and possesses activity typical of the complement receptor family.

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21. Full-length PRO234 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO234. In particular, Applicants have identified and isolated cDNA encoding a PRO234 polypeptide, as disclosed in further detail in the Examples below. Using BLAST (FastA-format) sequence alignment computer programs, Applicants found that a cDNA sequence encoding full-length native sequence PRO234 has 31% identity and Blast score of 134 with E-selectin precursor. Accordingly, it is presently believed that the PRO234 polypeptides disclosed in the present application are newly identified members of the lectin/selectin family and possess activity typical of the lectin/selectin family.

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22. Full-length PRO231 Polypeptides

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The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO231. In particular, Applicants have identified and isolated cDNA encoding a PRO231 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the full-length native sequence PRO231 polypeptide (shown in Figure 52 and SEQ ID NO:142) has 30% and 31% amino acid identity with human and rat prostatic acid phosphatase precursor proteins, respectively. Accordingly, it is presently believed that the PRO231 polypeptide disclosed in the present application may be a newly identified member of the acid phosphatase protein family.

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23. Full-length PRO229 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO229. In particular, Applicants have identified and isolated cDNA encoding a PRO229 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO229 polypeptide have significant homology with antigen wcl.1, M130 antigen, T cell surface glycoprotein CD6 and CD6. It also is related to Sp-alpha. Accordingly, it is presently believed that PRO229 polypeptide disclosed in the present application is a newly identified member of the family containing scavenger receptor homology, a sequence motif found in a number of proteins involved in immune function and thus possesses immune function and /or segments which resist degradation, typical of this family.

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24. Full-length PRO238 Polypeptides

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The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO238. In particular, Applicants have identified and isolated cDNA encoding a PRO238 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA

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sequence alignment computer programs, Applicants found that various portions of the PRO238 polypeptide have significant homology with reductases, including oxidoreductase and fatty acyl-CoA reductase. Accordingly, it is presently believed that PRO238 polypeptide disclosed in the present application is a newly identified member of the reductase family and possesses reducing activity typical of the reductase family.

5 **25. Full-length PRO233 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO233. In particular, Applicants have identified and isolated cDNA encoding a PRO233 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO233 polypeptide have
10 significant homology with the reductase protein. Applicants have also found that the DNA encoding the PRO233 polypeptide has significant homology with proteins from *Caenorhabditis elegans*. Accordingly, it is presently believed that PRO233 polypeptide disclosed in the present application is a newly identified member of the reductase family and possesses the ability to effect the redox state of the cell typical of the reductase family.

15 **26. Full-length PRO223 Polypeptides**

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO223. In particular, Applicants have identified and isolated cDNA encoding a PRO223 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO223 polypeptide has significant homology with
20 various serine carboxypeptidase polypeptides. Accordingly, it is presently believed that PRO223 polypeptide disclosed in the present application is a newly identified serine carboxypeptidase.

27. Full-length PRO235 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO235. In particular, Applicants have identified and isolated cDNA encoding a PRO235 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO235 polypeptide have
25 significant homology with the various plexin proteins. Accordingly, it is presently believed that PRO235 polypeptide disclosed in the present application is a newly identified member of the plexin family and possesses cell adhesion
30 properties typical of the plexin family.

28. Full-length PRO236 and PRO262 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO236 and PRO262. In particular, Applicants have identified and isolated
35 cDNA encoding PRO236 and PRO262 polypeptides, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO236 and PRO262 polypeptides have significant homology with various β -galactosidase and β -galactosidase precursor

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polypeptides. Accordingly, it is presently believed that the PRO236 and PRO262 polypeptides disclosed in the present application are newly identified β -galactosidase homologs.

29. Full-length PRO239 Polypeptides

5 The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO239. In particular, Applicants have identified and isolated cDNA encoding a PRO239 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO239 polypeptide have significant homology with densin proteins. Accordingly, it is presently believed that PRO239 polypeptide disclosed in the present application is a newly identified member of the densin family and possesses cell adhesion and the ability
10 to effect synaptic processes as is typical of the densin family.

30. Full-length PRO257 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO257. In particular, Applicants have identified and isolated cDNA
15 encoding a PRO257 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO257 polypeptide have significant homology with the ebnerin precursor and ebnerin protein. Accordingly, it is presently believed that PRO257 polypeptide disclosed in the present application is a newly identified protein member which is related to the ebnerin protein.

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31. Full-length PRO260 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO260. In particular, Applicants have identified and isolated cDNA encoding a PRO260 polypeptide, as disclosed in further detail in the Examples below. Using programs such as
25 BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO260 polypeptide have significant homology with the alpha-l-fucosidase precursor. Accordingly, it is presently believed that PRO260 polypeptide disclosed in the present application is a newly identified member of the fucosidase family and possesses enzymatic activity related to fucose residues typical of the fucosidase family.

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32. Full-length PRO263 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO263. In particular, Applicants have identified and isolated cDNA encoding a PRO263 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO263 polypeptide have
35 significant homology with the CD44 antigen and related proteins. Accordingly, it is presently believed that PRO263 polypeptide disclosed in the present application is a newly identified member of the CD44 antigen family and possesses at least one of the properties associated with these antigens, i.e., cancer and HIV marker, cell-cell or cell-

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matrix interactions, regulating cell traffic, lymph node homing, transmission of growth signals, and presentation of chemokines and growth factors to traveling cells.

33. Full-length PRO270 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO270. In particular, Applicants have identified and isolated cDNA encoding a PRO270 polypeptide, as disclosed in further detail in the Examples below. Using BLAST, FastA and sequence alignment computer programs, Applicants found that various portions of the PRO270 polypeptide have significant homology with various thioredoxin proteins. Accordingly, it is presently believed that PRO270 polypeptide disclosed in the present application is a newly identified member of the thioredoxin family and possesses the ability to effect reduction-oxidation (redox) state typical of the thioredoxin family.

34. Full-length PRO271 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO271. In particular, Applicants have identified and isolated cDNA encoding a PRO271 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO271 polypeptide has significant homology with various link proteins and precursors thereof. Accordingly, it is presently believed that PRO271 polypeptide disclosed in the present application is a newly identified link protein homolog.

35. Full-length PRO272 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO272. In particular, Applicants have identified and isolated cDNA encoding a PRO272 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO272 polypeptide have significant homology with the human reticulocalbin protein and its precursors. Applicants have also found that the DNA encoding the PRO272 polypeptide has significant homology with the mouse reticulocalbin precursor protein. Accordingly, it is presently believed that PRO272 polypeptide disclosed in the present application is a newly identified member of the reticulocalbin family and possesses the ability to bind calcium typical of the reticulocalbin family.

36. Full-length PRO294 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO294. In particular, Applicants have identified and isolated cDNA encoding a PRO294 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO294 polypeptide have significant homology with the various portions of a number of collagen proteins. Accordingly, it is presently believed that PRO294 polypeptide disclosed in the present application is a newly identified member of the collagen family.

37. Full-length PRO295 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO295. In particular, Applicants have identified and isolated cDNA encoding a PRO295 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO295 polypeptide have significant homology with integrin proteins. Accordingly, it is presently believed that PRO295 polypeptide disclosed in the present application is a newly identified member of the integrin family and possesses cell adhesion typical of the integrin family.

38. Full-length PRO293 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO293. In particular, Applicants have identified and isolated cDNA encoding a PRO293 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that portions of the PRO293 polypeptide have significant homology with the neuronal leucine rich repeat proteins 1 and 2, (NLRR-1 and NLRR-2), particularly NLRR-2. Accordingly, it is presently believed that PRO293 polypeptide disclosed in the present application is a newly identified member of the neuronal leucine rich repeat protein family and possesses ligand-ligand binding activity typical of the NRLL protein family.

39. Full-length PRO247 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO247. In particular, Applicants have identified and isolated cDNA encoding a PRO247 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO247 polypeptide have significant homology with densin. Applicants have also found that the DNA encoding the PRO247 polypeptide has significant homology with a number of other proteins, including KIAA0231. Accordingly, it is presently believed that PRO247 polypeptide disclosed in the present application is a newly identified member of the leucine rich repeat family and possesses ligand binding abilities typical of this family.

40. Full-length PRO302, PRO303, PRO304, PRO307 and PRO343 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO302, PRO303, PRO304, PRO307 and PRO343. In particular, Applicants have identified and isolated cDNA encoding PRO302, PRO303, PRO304, PRO307 and PRO343 polypeptides, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO302, PRO303, PRO304, PRO307 and PRO343 polypeptides have significant homology with various protease proteins. Accordingly, it is presently believed that the PRO302, PRO303, PRO304, PRO307 and PRO343 polypeptides disclosed in the present application are newly identified protease proteins.

41. Full-length PRO328 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO328. In particular, Applicants have identified and isolated cDNA encoding a PRO328 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO328 polypeptide have significant homology with the human glioblastoma protein ("GLIP"). Further, Applicants found that various portions of the PRO328 polypeptide have significant homology with the cysteine rich secretory protein ("CRISP") as identified by BLAST homology [ECCRISP3_1, S68683, and CRS3_HUMAN]. Accordingly, it is presently believed that PRO328 polypeptide disclosed in the present application is a newly identified member of the GLIP or CRISP families and possesses transcriptional regulatory activity typical of the GLIP or CRISP families.

42. Full-length PRO335, PRO331 and PRO326 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO335, PRO331 or PRO326. In particular, Applicants have identified and isolated cDNA encoding a PRO335, PRO331 or PRO326 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO335, PRO331 or PRO326 polypeptide have significant homology with LIG-1, ALS and in the case of PRO331, additionally, decorin. Accordingly, it is presently believed that the PRO335, PRO331 and PRO326 polypeptides disclosed in the present application are newly identified members of the leucine rich repeat superfamily, and particularly, are related to LIG-1 and possess the biological functions of this family as discussed and referenced herein.

43. Full-length PRO332 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO332. In particular, Applicants have identified and isolated cDNA encoding PRO332 polypeptides, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that a full-length native sequence PRO332 (shown in Figure 108 and SEQ ID NO:309) has about 30-40% amino acid sequence identity with a series of known proteoglycan sequences, including, for example, fibromodulin and fibromodulin precursor sequences of various species (FMOD_BOVIN, FMOD_CHICK, FMOD_RAT, FMOD_MOUSE, FMOD_HUMAN, P_R36773), osteomodulin sequences (AB000114_1, AB007848_1), decorin sequences (CFU83141_1, OCU03394_1, P_R42266, P_R42267, P_R42260, P_R89439), keratan sulfate proteoglycans (BTU48360_1, AF022890_1), corneal proteoglycan (AF022256_1), and bone/cartilage proteoglycans and proteoglycan precursors (PGS1_BOVIN, PGS2_MOUSE, PGS2_HUMAN). Accordingly, it is presently believed that PRO332 disclosed in the present application is a new proteoglycan-type molecule, and may play a role in regulating extracellular matrix, cartilage, and/or bone function.

44. Full-length PRO334 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO334. In particular, Applicants have identified and isolated cDNA encoding a PRO334 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO334 polypeptide have significant homology with fibulin and fibrillin. Accordingly, it is presently believed that PRO334 polypeptide disclosed in the present application is a newly identified member of the epidermal growth factor family and possesses properties and activities typical of this family.

45. Full-length PRO346 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO346. In particular, Applicants have identified and isolated cDNA encoding a PRO346 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that a full-length native sequence PRO346 (shown in Figure 112 and SEQ ID NO:319) has 28 % amino acid sequence identity with carcinoembryonic antigen. Accordingly, it is presently believed that PRO346 disclosed in the present application is a newly identified member of the carcinoembryonic protein family and may be expressed in association with neoplastic tissue disorders.

46. Full-length PRO268 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO268. In particular, Applicants have identified and isolated cDNA encoding a PRO268 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that portions of the PRO268 polypeptide have significant homology with the various protein disulfide isomerase proteins. Accordingly, it is presently believed that PRO268 polypeptide disclosed in the present application is a homolog of the protein disulfide isomerase p5 protein.

47. Full-length PRO330 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO330. In particular, Applicants have identified and isolated cDNA encoding a PRO330 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO330 polypeptide have significant homology with the murine prolyl 4-hydroxylase alpha-II subunit protein. Accordingly, it is presently believed that PRO330 polypeptide disclosed in the present application is a novel prolyl 4-hydroxylase subunit polypeptide.

48. Full-length PRO339 and PRO310 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO339 and PRO310. In particular, Applicants have identified and isolated

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cDNA encoding a PRO339 polypeptide, as disclosed in further detail in the Examples below. Applicants have also identified and isolated cDNA encoding a PRO310 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that various portions of the PRO339 and PRO310 polypeptides have significant homology with small secreted proteins from *C. elegans* and are distantly related to fringe. PRO339 also shows homology to collagen-like polymers. Sequences which were used to identify PRO310, designated herein as DNA40533 and DNA42267, also show homology to proteins from *C. elegans*. Accordingly, it is presently believed that the PRO339 and PRO310 polypeptides disclosed in the present application are newly identified member of the family of proteins involved in development, and which may have regulatory abilities similar to the capability of fringe to regulate serrate.

49. Full Length PRO244 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding C-type lectins referred to in the present application as PRO244. In particular, applicants have identified and isolated cDNA encoding PRO244 polypeptides, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that a full-length native sequence PRO244 (shown in Figure 122 and SEQ ID NO:376) has 43% amino acid sequence identity with the hepatic lectin gallus gallus (LECH-CHICK), and 42% amino acid sequence identity with an HIV gp120 binding C-type lectin (A46274). Accordingly, it is presently believed that PRO244 disclosed in the present application is a newly identified member of the C-lectin superfamily and may play a role in immune function, apoptosis, or in the pathogenesis of atherosclerosis. In addition, PRO244 may be useful in identifying tumor-associated epitopes.

50. PRO Polypeptide Variants

In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO polypeptide variants can be prepared. PRO polypeptide variants can be prepared by introducing appropriate nucleotide changes into the PRO polypeptide DNA, or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO polypeptides, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence PRO polypeptides or in various domains of the PRO polypeptides described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO polypeptide that results in a change in the amino acid sequence of the PRO polypeptide as compared with the native sequence PRO polypeptide. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO polypeptide. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO polypeptide with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e.,

conservative amino acid replacements. Insertions or deletions may optionally be in the range of 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity in the *in vitro* assay described in the Examples below.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the desired PRO polypeptide variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

51. Modifications of PRO Polypeptides

Covalent modifications of PRO polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of the PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking a PRO polypeptide to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO polypeptide antibodies, and vice-versa. Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutamyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptides included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in a native sequence PRO polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence PRO polypeptide.

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Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO polypeptide (for O-linked glycosylation sites). The PRO polypeptide amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO polypeptides of the invention comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO polypeptides of the present invention may also be modified in a way to form a chimeric molecule comprising a PRO polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of the PRO polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO polypeptide. The presence of such epitope-tagged forms of the PRO polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-

6397 (1990)].

52. Modification of PRO317

Amino acid sequence variants of PRO317 are prepared by introducing appropriate nucleotide changes into the PRO317 DNA, or by *in vitro* synthesis of the desired PRO317 polypeptide. Such variants include, for example, deletions from, or insertions or substitutions of, residues within the amino acid sequence shown for human PRO317 in Figure 42. Any combination of deletion, insertion, and substitution is made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the PRO317, such as changing the number or position of glycosylation sites. Moreover, like most mammalian genes, PRO317 is presumably encoded by multi-exon genes. Alternative mRNA constructs which may be attributed to different mRNA splicing events following transcription, and which share large regions of identity with the cDNAs claimed herein, are considered to be within the scope of the present invention.

For the design of amino acid sequence variants of PRO317, the location of the mutation site and the nature of the mutation will depend on the PRO317 characteristic(s) to be modified. For example, candidate PRO317 antagonists or agonists will be initially selected by locating sites that are identical or highly conserved among PRO317, EBAF-1, LEFTY, and other members of the TGF- superfamily. The sites for mutation can be modified individually or in series, *e.g.*, by (1) substituting first with conservative amino acid choices and then with more radical selections depending upon the results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

A useful method for identification of certain residues or regions of the PRO317 polypeptide that are preferred locations for mutagenesis is called "alanine scanning mutagenesis," as described by Cunningham and Wells, *Science*, 244: 1081-1085 (1989). Here, a residue or group of target residues are identified (*e.g.*, charged residues such as arg, asp, his, lys, and glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine) to affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions then are refined by introducing further or other variants at or for the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation *per se* need not be predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis is conducted at the target codon or region and the PRO317 variants produced are screened for the optimal combination of desired activity.

There are two principal variables in the construction of amino acid sequence variants: the location of the mutation site and the nature of the mutation. These are variants from the Figure 42 sequence, and may represent naturally occurring alleles (which will not require manipulation of the PRO317 DNA) or predetermined mutant forms made by mutating the DNA, either to arrive at an allele or a variant not found in nature. In general, the location and nature of the mutation chosen will depend upon the PRO317 characteristic to be modified.

Amino acid sequence deletions generally range from about 1 to 30 residues, more preferably about 1 to 10 residues, and typically are contiguous. Contiguous deletions ordinarily are made in even numbers of residues, but single or odd numbers of deletions are within the scope hereof. Deletions may be introduced into regions of low

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homology among PRO317, EBAF-1, and other members of the TGF- superfamily which share the most sequence identity to the human PRO317 amino acid sequence to modify the activity of PRO317. Deletions from PRO317 in areas of substantial homology with one of the receptor binding sites of other members of the TGF- superfamily will be more likely to modify the biological activity of PRO317 more significantly. The number of consecutive deletions will be selected so as to preserve the tertiary structure of PRO317 in the affected domain, *e.g.*, beta-pleated sheet or alpha helix.

Amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from one residue to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions (*i.e.*, insertions within the mature PRO317 sequence) may range generally from about 1 to 10 residues, more preferably 1 to 5, most preferably 1 to 3. Insertions are preferably made in even numbers of residues, but this is not required. Examples of terminal insertions include mature PRO317 with an N-terminal methionyl residue, an artifact of the direct production of mature PRO317 in recombinant cell culture, and fusion of a heterologous N-terminal signal sequence to the N-terminus of the mature PRO317 molecule to facilitate the secretion of mature PRO317 from recombinant hosts. Such signal sequences may be obtained from, and thus homologous to, the intended host cell species, but also may be from other members of the TGF- superfamily. Suitable sequences include STII or lpp for *E. coli*, alpha factor for yeast, and viral signals such as herpes gD or the native EBAF-1 sequence for mammalian cells.

Other insertional variants of the PRO317 molecule include the fusion to the N- or C-terminus of PRO317 of immunogenic polypeptides, *e.g.*, bacterial polypeptides such as beta-lactamase or an enzyme encoded by the *E. coli trp* locus, or yeast protein, and C-terminal fusions with proteins having a long half-life such as immunoglobulin constant regions (or other immunoglobulin regions), albumin, or ferritin, as described in WO 89/02922 published 6 April 1989.

A third group of variants are amino acid substitution variants. These variants have at least one amino acid residue in the PRO317 molecule removed and a different residue inserted in its place. The sites of greatest interest for substitutional mutagenesis include sites identified as the active site(s) of PRO317 and sites where the amino acids found in the known analogs are substantially different in terms of side-chain bulk, charge, or hydrophobicity, but where there is also a high degree of sequence identity at the selected site within various animal PRO317 species, or where the amino acids found in known members of the TGF- superfamily and novel PRO317 are substantially different in terms of side-chain bulk, charge, or hydrophobicity, but where there also is a high degree of sequence identity at the selected site within various animal analogues of such members (*e.g.*, among all the animal EBAF-1 molecules). This analysis will highlight residues that may be involved in the modulation of endometrial tissue or angiogenesis, and therefore, variations at these sites may affect such activities.

Other sites of interest are those in which particular residues of the PRO317 obtained from various species are identical among all animal species of PRO317 and other members of the TGF- superfamily, this degree of conservation suggesting importance in achieving biological activity common to these cytokines. These sites, especially those falling within a sequence of at least three other identically conserved sites, are substituted in a relatively conservative manner. Such conservative substitutions are shown in Table 1 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes,

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denominated exemplary substitutions in Table 1, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 1

5	<u>Original Residue</u>	<u>Exemplary Substitutions</u>	<u>Preferred Substitutions</u>
	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
10	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
	Gln (Q)	asn	asn
	Glu (E)	asp	asp
15	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe; norleucine	leu
	Leu (L)	norleucine; ile; val; met; ala; phe	ile
20	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
25	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe; ala; norleucine	leu
30			

Substantial modifications in function or immunological identity of the PRO317 are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- (2) neutral hydrophilic: cys, ser, thr;
- (3) acidic: asp, glu;
- 40 (4) basic: asn, gln, his, lys, arg;
- (5) residues that influence chain orientation: gly, pro; and
- (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

In one embodiment of the invention, it is desirable to inactivate one or more protease cleavage sites that are present in the molecule. These sites are identified by inspection of the encoded amino acid sequence, in the case of

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trypsin, *e.g.*, for an arginyl or lysinyl residue. When protease cleavage sites are identified, they are rendered inactive to proteolytic cleavage by substituting the targeted residue with another residue, preferably a basic residue such as glutamine or a hydrophilic residue such as serine; by deleting the residue; or by inserting a prolyl residue immediately after the residue.

In another embodiment, any methionyl residues other than the starting methionyl residue of the signal sequence, or any residue located within about three residues N- or C-terminal to each such methionyl residue, is substituted by another residue (preferably in accord with Table 1) or deleted. Alternatively, about 1-3 residues are inserted adjacent to such sites.

Any cysteine residues not involved in maintaining the proper conformation of PRO317 also may be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking.

Nucleic acid molecules encoding amino acid sequence variants of PRO317 are prepared by a variety of methods known in the art. These methods include, but are not limited to, isolation from a natural source (in the case of naturally occurring amino acid sequence variants) or preparation by oligonucleotide-mediated (or site-directed) mutagenesis, PCR mutagenesis, and cassette mutagenesis of an earlier prepared variant or a non-variant version of PRO317.

Oligonucleotide-mediated mutagenesis is a preferred method for preparing substitution, deletion, and insertion variants of PRO317 DNA. This technique is well known in the art as described by Adelman *et al.*, DNA, 2: 183 (1983). Briefly, PRO317 DNA is altered by hybridizing an oligonucleotide encoding the desired mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of PRO317. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the PRO317 DNA.

Generally, oligonucleotides of at least 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea *et al.*, Proc. Natl. Acad. Sci. USA, 75: 5765 (1978).

The DNA template can be generated by those vectors that are either derived from bacteriophage M13 vectors (the commercially available M13mp18 and M13mp19 vectors are suitable), or those vectors that contain a single-stranded phage origin of replication as described by Viera *et al.* Meth. Enzymol., 153: 3 (1987). Thus, the DNA that is to be mutated may be inserted into one of these vectors to generate single-stranded template. Production of the single-stranded template is described in Sections 4.21-4.41 of Sambrook *et al.*, *supra*.

Alternatively, single-stranded DNA template may be generated by denaturing double-stranded plasmid (or other) DNA using standard techniques.

For alteration of the native DNA sequence (to generate amino acid sequence variants, for example), the oligonucleotide is hybridized to the single-stranded template under suitable hybridization conditions. A DNA polymerizing enzyme, usually the Klenow fragment of DNA polymerase I, is then added to synthesize the complementary strand of the template using the oligonucleotide as a primer for synthesis. A heteroduplex molecule

is thus formed such that one strand of DNA encodes the mutated form of PRO317, and the other strand (the original template) encodes the native, unaltered sequence of PRO317. This heteroduplex molecule is then transformed into a suitable host cell, usually a prokaryote such as *E. coli* JM101. After the cells are grown, they are plated onto agarose plates and screened using the oligonucleotide primer radiolabeled with ³²P to identify the bacterial colonies that contain the mutated DNA. The mutated region is then removed and placed in an appropriate vector for protein production, generally an expression vector of the type typically employed for transformation of an appropriate host.

The method described immediately above may be modified such that a homoduplex molecule is created wherein both strands of the plasmid contain the mutation(s). The modifications are as follows: The single-stranded oligonucleotide is annealed to the single-stranded template as described above. A mixture of three deoxyribonucleotides, deoxyriboadenosine (dATP), deoxyriboguanosine (dGTP), and deoxyribothymidine (dTTP), is combined with a modified thio-deoxyribocytosine called dCTP-(aS) (which can be obtained from the Amersham Corporation). This mixture is added to the template-oligonucleotide complex. Upon addition of DNA polymerase to this mixture, a strand of DNA identical to the template except for the mutated bases is generated. In addition, this new strand of DNA will contain dCTP-(aS) instead of dCTP, which serves to protect it from restriction endonuclease digestion.

After the template strand of the double-stranded heteroduplex is nicked with an appropriate restriction enzyme, the template strand can be digested with *ExoIII* nuclease or another appropriate nuclease past the region that contains the site(s) to be mutagenized. The reaction is then stopped to leave a molecule that is only partially single-stranded. A complete double-stranded DNA homoduplex is then formed using DNA polymerase in the presence of all four deoxyribonucleotide triphosphates, ATP, and DNA ligase. This homoduplex molecule can then be transformed into a suitable host cell such as *E. coli* JM101, as described above.

DNA encoding PRO317 mutants with more than one amino acid to be substituted may be generated in one of several ways. If the amino acids are located close together in the polypeptide chain, they may be mutated simultaneously using one oligonucleotide that codes for all of the desired amino acid substitutions. If, however, the amino acids are located some distance from each other (separated by more than about ten amino acids), it is more difficult to generate a single oligonucleotide that encodes all of the desired changes. Instead, one of two alternative methods may be employed.

In the first method, a separate oligonucleotide is generated for each amino acid to be substituted. The oligonucleotides are then annealed to the single-stranded template DNA simultaneously, and the second strand of DNA that is synthesized from the template will encode all of the desired amino acid substitutions.

The alternative method involves two or more rounds of mutagenesis to produce the desired mutant. The first round is as described for the single mutants: wild-type DNA is used for the template, an oligonucleotide encoding the first desired amino acid substitution(s) is annealed to this template, and the heteroduplex DNA molecule is then generated. The second round of mutagenesis utilizes the mutated DNA produced in the first round of mutagenesis as the template. Thus, this template already contains one or more mutations. The oligonucleotide encoding the additional desired amino acid substitution(s) is then annealed to this template, and the resulting strand of DNA now encodes mutations from both the first and second rounds of mutagenesis. This resultant DNA can be used as a template in a third round of mutagenesis, and so on.

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PCR mutagenesis is also suitable for making amino acid variants of PRO317. While the following discussion refers to DNA, it is understood that the technique also finds application with RNA. The PCR technique generally refers to the following procedure (see Erlich, PCR Technology, (Stockton Press, NY, 1989), the chapter by R. Higuchi, p. 61-70): When small amounts of template DNA are used as starting material in a PCR, primers that differ slightly in sequence from the corresponding region in a template DNA can be used to generate relatively large quantities of a specific DNA fragment that differs from the template sequence only at the positions where the primers differ from the template. For introduction of a mutation into a plasmid DNA, one of the primers is designed to overlap the position of the mutation and to contain the mutation; the sequence of the other primer must be identical to a stretch of sequence of the opposite strand of the plasmid, but this sequence can be located anywhere along the plasmid DNA. It is preferred, however, that the sequence of the second primer is located within 200 nucleotides from that of the first, such that in the end the entire amplified region of DNA bounded by the primers can be easily sequenced. PCR amplification using a primer pair like the one just described results in a population of DNA fragments that differ at the position of the mutation specified by the primer, and possibly at other positions, as template copying is somewhat error-prone.

Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells *et al.*, Gene, **34**: 315 (1985). The starting material is the plasmid (or other vector) comprising the PRO317 DNA to be mutated. The codon(s) in the PRO317 DNA to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the PRO317 DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are compatible with the ends of the linearized plasmid, such that it can be directly ligated to the plasmid. This plasmid now contains the mutated PRO317 DNA sequence.

Covalent modifications of PRO317 are also included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of the PRO317 with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO317. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO317 to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO317 antibodies, and vice-versa. Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis-(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane, and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains (T.E.

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Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO317 polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native-sequence PRO polypeptide, and/or adding one or more glycosylation sites that are not present in the native-sequence PRO polypeptide. The deduced amino acid sequence of PRO317 shown in Figure 42 (SEQ ID NO:114) has one predicted N-linked glycosylation site at residue 160.

Addition of glycosylation sites to the PRO317 polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native-sequence PRO317 (for O-linked glycosylation sites). The PRO317 amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO317 polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO317 polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, *e.g.*, in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO317 polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, *et al.*, Arch. Biochem. Biophys., 259:52 (1987) and by Edge *et al.*, Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura *et al.*, Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO317 comprises linking the PRO317 polypeptide to one of a variety of nonproteinaceous polymers, *e.g.*, polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO317 of the present invention may also be modified in a way to form a chimeric molecule comprising PRO317 fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of the PRO317 with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO317. The presence of such epitope-tagged forms of the PRO317 can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO317 to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO317 with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5

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(Field *et al.*, Mol. Cell. Biol., 8:2159-2165 (1988)); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan *et al.*, Molecular and Cellular Biology, 5:3610-3616 (1985)); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky *et al.*, Protein Engineering, 3(6):547-553 (1990)). Other tag polypeptides include the Flag-peptide (Hopp *et al.*, Bio/Technology, 6:1204-1210 (1988)); the KT3 epitope peptide (Martin *et al.*, Science, 255:192-194 (1992)); an α -tubulin epitope peptide (Skinner *et al.*, J. Biol. Chem., 266:15163-15166 (1991)); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth *et al.*, Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)).

53. Preparation of PRO Polypeptides

The description below relates primarily to production of PRO polypeptides by culturing cells transformed or transfected with a vector containing the desired PRO polypeptide nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare the PRO polypeptide. For instance, the PRO polypeptide sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart *et al.*, Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the desired PRO polypeptide may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO polypeptide.

A. Isolation of DNA Encoding PRO Polypeptides

DNA encoding PRO polypeptides may be obtained from a cDNA library prepared from tissue believed to possess the desired PRO polypeptide mRNA and to express it at a detectable level. Accordingly, human PRO polypeptide DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO polypeptide-encoding gene may also be obtained from a genomic library or by oligonucleotide synthesis.

Libraries can be screened with probes (such as antibodies to the desired PRO polypeptide or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding the desired PRO polypeptide is to use PCR methodology [Sambrook *et al.*, *supra*; Dieffenbach *et al.*, PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ³²P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are

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provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank* or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined through sequence alignment using computer software programs such as

5 BLAST, ALIGN, DNASTar*, and INHERIT which employ various algorithms to measure homology.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

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B. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO polypeptide production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as

15 media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of transfection are known to the ordinarily skilled artisan, for example, CaPO_4 and electroporation.

20 Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate

25 precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transformations have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g.,

30 polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly

35 available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*,

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Serratia, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325); and K5 772 (ATCC 53,635). These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan^r*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan^r*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO polypeptide-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer *et al.*, Bio/Technology, 9: 968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt *et al.*, J. Bacteriol., 737 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg *et al.*, Bio/Technology, 8: 135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna *et al.*, J. Basic Microbiol., 28: 265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case *et al.*, Proc. Natl. Acad. Sci. USA, 76: 5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolytocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance *et al.*, Biochem. Biophys. Res. Commun., 112: 284-289 [1983]; Tilburn *et al.*, Gene, 26: 205-221 [1983]; Yelton *et al.*, Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4: 475-479 [1985]). Methylotropic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

Suitable host cells for the expression of glycosylated PRO polypeptides are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham *et al.*, J. Gen Virol.,

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36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

5 C. Selection and Use of a Replicable Vector

The nucleic acid (*e.g.*, cDNA or genomic DNA) encoding a desired PRO polypeptide may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The PRO polypeptide of interest may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO polypeptide DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, *e.g.*, the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, *e.g.*, the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO polypeptide nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene

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for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the PRO polypeptide nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the desired PRO polypeptide.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

PRO polypeptide transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the desired PRO polypeptide by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO polypeptide coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated

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regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO polypeptides.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO polypeptides in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

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D. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to a PRO polypeptide DNA and encoding a specific antibody epitope.

20

E. Purification of Polypeptide

Forms of PRO polypeptides may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (*e.g.* Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO polypeptides can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO polypeptides from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex^{*} G-75; protein A Sepharose^{*} columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO polypeptide. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO polypeptide produced.

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*-trademark

54. Uses for PRO Polypeptides

Nucleotide sequences (or their complement) encoding the PRO polypeptides of the present invention have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO polypeptide-encoding nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

5 The full-length native sequence PRO polypeptide-encoding nucleic acid or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO polypeptide gene or to isolate still other genes (for instance, those encoding naturally-occurring variants of the PRO polypeptide or PRO polypeptides from other species) which have a desired sequence identity to the PRO polypeptide nucleic acid sequences. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from the
10 nucleotide sequence of any of the DNA molecules disclosed herein or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO polypeptide encoding DNA. By way of example, a screening method will comprise isolating the coding region of the PRO polypeptide gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ³²P or ³⁵S, or enzymatic labels such as alkaline phosphatase coupled to the probe via
15 avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the specific PRO polypeptide gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

20 The ESTs disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO polypeptide sequences.

25 Nucleotide sequences encoding a PRO polypeptide can also be used to construct hybridization probes for mapping the gene which encodes that PRO polypeptide and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

30 The PRO polypeptide can be used in assays to identify its ligands. Similarly, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO polypeptide or a ligand for the PRO polypeptide. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of
35 formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

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Nucleic acids which encode a PRO polypeptide or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal
 5 develops. In one embodiment, cDNA encoding a PRO polypeptide of interest can be used to clone genomic DNA encoding the PRO polypeptide in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding the PRO polypeptide. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO
 10 polypeptide transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding a PRO polypeptide introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding the PRO polypeptide. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced
 15 incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO polypeptides can be used to construct a PRO polypeptide "knock out" animal which has a defective or altered gene encoding the PRO polypeptide of interest as a result of homologous recombination between the endogenous gene encoding the PRO polypeptide and altered genomic DNA
 20 encoding the PRO polypeptide introduced into an embryonic cell of the animal. For example, cDNA encoding a PRO polypeptide can be used to clone genomic DNA encoding the PRO polypeptide in accordance with established techniques. A portion of the genomic DNA encoding a PRO polypeptide can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and
 25 Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987),
 30 pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence
 35 of the PRO polypeptide.

With regard to the PRO211 and PRO217 polypeptide, therapeutic indications include disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions

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(e.g., enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g., psoriasis, epithelial cancers such as lung squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).

Since the PRO232 polypeptide and nucleic acid encoding it possess sequence homology to a cell surface stem cell antigen and its encoding nucleic acid, probes based upon the PRO232 nucleotide sequence may be employed to identify other novel stem cell surface antigen proteins. Soluble forms of the PRO232 polypeptide may be employed as antagonists of membrane bound PRO232 activity both *in vitro* and *in vivo*. PRO232 polypeptides may be employed in screening assays designed to identify agonists or antagonists of the native PRO232 polypeptide, wherein such assays may take the form of any conventional cell-type or biochemical binding assay. Moreover, the PRO232 polypeptide may serve as a molecular marker for the tissues in which the polypeptide is specifically expressed.

With regard to the PRO187 polypeptides disclosed herein, FGF-8 has been implicated in cellular differentiation and embryogenesis, including the patterning which appears during limb formation. FGF-8 and the PRO187 molecules of the invention therefore are likely to have potent effects on cell growth and development. Diseases which relate to cellular growth and differentiation are therefore suitable targets for therapeutics based on functionality similar to FGF-8. For example, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies. Additionally, disease related to uncontrolled cell growth, e.g., cancer, would also be expected therapeutic targets.

With regard to the PRO265 polypeptides disclosed herein, other methods for use with PRO265 are described in U.S. Patent 5,654,270 to Ruoslahti et al. In particular, PRO265 can be used in comparison with the fibromodulin disclosed therein to compare its effects on reducing dermal scarring and other properties of the fibromodulin described therein including where it is located and with what it binds and does not.

The PRO219 polypeptides of the present invention which play a regulatory role in the blood coagulation cascade may be employed *in vivo* for therapeutic purposes as well as for *in vitro* purposes. Those of ordinary skill in the art will well know how to employ PRO219 polypeptides for such uses.

The PRO246 polypeptides of the present invention which serve as cell surface receptors for one or more viruses will find other uses. For example, extracellular domains derived from these PRO246 polypeptides may be employed therapeutically *in vivo* for lessening the effects of viral infection. Those PRO246 polypeptides which serves as tumor specific antigens may be exploited as therapeutic targets for anti-tumor drugs, and the like. Those of ordinary skill in the art will well know how to employ PRO246 polypeptides for such uses.

Assays in which connective growth factor and other growth factors are usually used should be performed with PRO261. An assay to determine whether TGF beta induces PRO261, indicating a role in cancer is performed as known in the art. Wound repair and tissue growth assays are also performed with PRO261. The results are applied accordingly.

PRO228 polypeptides should be used in assays in which EMR1, CD97 and latrophilin would be used in to determine their relative activities. The results can be applied accordingly. For example, a competitive binding assay with PRO228 and CD97 can be performed with the ligand for CD97, CD55.

Native PRO533 is a 216 amino acid polypeptide of which residues 1-22 are the signal sequence. Residues 3 to 216 have a Blast score of 509, corresponding to 53% homology to fibroblast growth factor. At the nucleotide

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level, DNA47412, the EST from which PCR oligos were generated to isolate the full length DNA49435-1219, has been observed to map to 11p15. Sequence homology to the 11p15 locus would indicate that PRO533 may have utility in the treatment of Usher Syndrome or Atrophia areata.

As mentioned previously, fibroblast growth factors can act upon cells in both a mitogenic and non-mitogenic manner. These factors are mitogenic for a wide variety of normal diploid mesoderm-derived and neural crest-derived cells, inducing granulosa cells, adrenal cortical cells, chondrocytes, myoblasts, corneal and vascular endothelial cells (bovine or human), vascular smooth muscle cells, lens, retina and prostatic epithelial cells, oligodendrocytes, astrocytes, chondrocytes, myoblasts and osteoblasts.

Non-mitogenic actions of fibroblast growth factors include promotion of cell migration into a wound area (chemotaxis), initiation of new blood vessel formulation (angiogenesis), modulation of nerve regeneration and survival (neurotrophism), modulation of endocrine functions, and stimulation or suppression of specific cellular protein expression, extracellular matrix production and cell survival. Baird, A. & Bohlen, P., *Handbook of Exp. Pharmacol.* 95(1): 369-418 (1990). These properties provide a basis for using fibroblast growth factors in therapeutic approaches to accelerate wound healing, nerve repair, collateral blood vessel formation, and the like. For example, fibroblast growth factors, have been suggested to minimize myocardium damage in heart disease and surgery (U.S.P. 4,378,437).

Since the PRO245 polypeptide and nucleic acid encoding it possess sequence homology to a transmembrane protein tyrosine kinase protein and its encoding nucleic acid, probes based upon the PRO245 nucleotide sequence may be employed to identify other novel transmembrane tyrosine kinase proteins. Soluble forms of the PRO245 polypeptide may be employed as antagonists of membrane bound PRO245 activity both *in vitro* and *in vivo*. PRO245 polypeptides may be employed in screening assays designed to identify agonists or antagonists of the native PRO245 polypeptide, wherein such assays may take the form of any conventional cell-type or biochemical binding assay. Moreover, the PRO245 polypeptide may serve as a molecular marker for the tissues in which the polypeptide is specifically expressed.

PRO220, PRO221 and PRO227 all have leucine rich repeats. Additionally, PRO220 and PRO221 have homology to SLIT and leucine rich repeat protein. Therefore, these proteins are useful in assays described in the literature, *supra*, wherein the SLIT and leucine rich repeat protein are used. Regarding the SLIT protein, PRO227 can be used in an assay to determine the affect of PRO227 on neurodegenerative disease. Additionally, PRO227 has homology to human glycoprotein V. In the case of PRO227, this polypeptide is used in an assay to determine its affect on bleeding, clotting, tissue repair and scarring.

The PRO266 polypeptide can be used in assays to determine if it has a role in neurodegenerative diseases or their reversal.

PRO269 polypeptides and portions thereof which effect the activity of thrombin may also be useful for *in vivo* therapeutic purposes, as well as for various *in vitro* applications. In addition, PRO269 polypeptides and portions thereof may have therapeutic use as an antithrombotic agent with reduced risk for hemorrhage as compared with heparin. Peptides having homology to thrombomodulin are particularly desirable.

PRO287 polypeptides and portions thereof which effect the activity of bone morphogenic protein "BMP1"/procollagen C-proteinase (PCP) may also be useful for *in vivo* therapeutic purposes, as well as for various

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in vitro applications. In addition, PRO287 polypeptides and portions thereof may have therapeutic applications in wound healing and tissue repair. Peptides having homology to procollagen C-proteinase enhancer protein and its precursor may also be used to induce bone and/or cartilage formation and are therefore of particular interest to the scientific and medical communities.

Therapeutic indications for PRO214 polypeptides include disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g., enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g., psoriasis, epithelial cancers such as lung squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas.

Studies on the generation and analysis of mice deficient in members of the TGF- superfamily are reported in Matzuk, Trends in Endocrinol. and Metabol., 6: 120-127 (1995).

The PRO317 polypeptide, as well as PRO317-specific antibodies, inhibitors, agonists, receptors, or their analogs, herein are useful in treating PRO317-associated disorders. Hence, for example, they may be employed in modulating endometrial bleeding angiogenesis, and may also have an effect on kidney tissue. Endometrial bleeding can occur in gynecological diseases such as endometrial cancer as abnormal bleeding. Thus, the compositions herein may find use in diagnosing and treating abnormal bleeding conditions in the endometrium, as by reducing or eliminating the need for a hysterectomy. The molecules herein may also find use in angiogenesis applications such as anti-tumor indications for which the antibody against vascular endothelial growth factor is used, or, conversely, ischemic indications for which vascular endothelial growth factor is employed.

Bioactive compositions comprising PRO317 or agonists or antagonists thereof may be administered in a suitable therapeutic dose determined by any of several methodologies including clinical studies on mammalian species to determine maximal tolerable dose and on normal human subjects to determine safe dose. Additionally, the bioactive agent may be complexed with a variety of well established compounds or compositions which enhance stability or pharmacological properties such as half-life. It is contemplated that the therapeutic, bioactive composition may be delivered by intravenous infusion into the bloodstream or any other effective means which could be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g., in the heart or genital tract.

Dosages and administration of PRO317, PRO317 agonist, or PRO317 antagonist in a pharmaceutical composition may be determined by one of ordinary skill in the art of clinical pharmacology or pharmacokinetics. See, for example, Mordenti and Rescigno, Pharmaceutical Research, 9:17-25 (1992); Morenti *et al.*, Pharmaceutical Research, 8:1351-1359 (1991); and Mordenti and Chappell, "The use of interspecies scaling in toxicokinetics" in Toxicokinetics and New Drug Development, Yacobi *et al.* (eds) (Pergamon Press: NY, 1989), pp. 42-96. An effective amount of PRO317, PRO317 agonist, or PRO317 antagonist to be employed therapeutically will depend, for example, upon the therapeutic objectives, the route of administration, and the condition of the mammal. Accordingly, it will be necessary for the therapist to titer the dosage and modify the route of administration as required to obtain the optimal therapeutic effect. A typical daily dosage might range from about 10 ng/kg to up to 100 mg/kg of the mammal's body weight or more per day, preferably about 1 µg/kg/day to 10 mg/kg/day. Typically, the clinician will administer PRO317, PRO317 agonist, or PRO317 antagonist, until a dosage is reached that achieves

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the desired effect for treatment of the above mentioned disorders.

PRO317 or an PRO317 agonist or PRO317 antagonist may be administered alone or in combination with another to achieve the desired pharmacological effect. PRO317 itself, or agonists or antagonists of PRO317 can provide different effects when administered therapeutically. Such compounds for treatment will be formulated in a nontoxic, inert, pharmaceutically acceptable aqueous carrier medium preferably at a pH of about 5 to 8, more preferably 6 to 8, although the pH may vary according to the characteristics of the PRO317, agonist, or antagonist being formulated and the condition to be treated. Characteristics of the treatment compounds include solubility of the molecule, half-life, and antigenicity/immunogenicity; these and other characteristics may aid in defining an effective carrier.

PRO317 or PRO317 agonists or PRO317 antagonists may be delivered by known routes of administration including but not limited to topical creams and gels; transmucosal spray and aerosol, transdermal patch and bandage; injectable, intravenous, and lavage formulations; and orally administered liquids and pills, particularly formulated to resist stomach acid and enzymes. The particular formulation, exact dosage, and route of administration will be determined by the attending physician and will vary according to each specific situation.

Such determinations of administration are made by considering multiple variables such as the condition to be treated, the type of mammal to be treated, the compound to be administered, and the pharmacokinetic profile of the particular treatment compound. Additional factors which may be taken into account include disease state (*e.g.* severity) of the patient, age, weight, gender, diet, time of administration, drug combination, reaction sensitivities, and tolerance/response to therapy. Long-acting treatment compound formulations (such as liposomally encapsulated PRO317 or PEGylated PRO317 or PRO317 polymeric microspheres, such as polylactic acid-based microspheres) might be administered every 3 to 4 days, every week, or once every two weeks depending on half-life and clearance rate of the particular treatment compound.

Normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 μ g/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting the uterus, for example, may necessitate delivery in a manner different from that to another organ or tissue, such as cardiac tissue.

Where sustained-release administration of PRO317 is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of PRO317, microencapsulation of PRO317 is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon- (γ), interleukin-2, and MN rgp120. Johnson *et al.*, *Nat. Med.*, 2: 795-799 (1996); Yasuda, *Biomed. Ther.*, 27: 1221-1223 (1993); Hora *et al.*, *Bio/Technology*, 8: 755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in *Vaccine Design: The Subunit and Adjuvant Approach*, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S Pat. No. 5,654,010.

The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products

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of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), Biodegradable Polymers as Drug Delivery Systems (Marcel Dekker: New York, 1990), pp. 1-41.

For example, for a formulation that can provide a dosing of approximately 80 g/kg/day in mammals with a maximum body weight of 85 kg, the largest dosing would be approximately 6.8 mg PRO317 per day. In order to achieve this dosing level, a sustained-release formulation which contains a maximum possible protein loading (15-20% w/w PRO317) with the lowest possible initial burst (<20%) is necessary. A continuous (zero-order) release of PRO317 from microparticles for 1-2 weeks is also desirable. In addition, the encapsulated protein to be released should maintain its integrity and stability over the desired release period.

It is contemplated that conditions or diseases of the uterus, endometrial tissue, or other genital tissues or cardiac tissues may precipitate damage that is treatable with PRO317 or PRO317 agonist where PRO317 expression is reduced in the diseased state; or with antibodies to PRO317 or other PRO317 antagonists where the expression of PRO317 is increased in the diseased state. These conditions or diseases may be specifically diagnosed by the probing tests discussed above for physiologic and pathologic problems which affect the function of the organ.

The PRO317, PRO317 agonist, or PRO317 antagonist may be administered to a mammal with another biologically active agent, either separately or in the same formulation to treat a common indication for which they are appropriate. For example, it is contemplated that PRO317 can be administered together with EBAF-1 for those indications on which they demonstrate the same qualitative biological effects. Alternatively, where they have opposite effects, EBAF-1 may be administered together with an antagonist to PRO317, such as an anti-PRO317 antibody. Further, PRO317 may be administered together with VEGF for coronary ischemia where such indication is warranted, or with an anti-VEGF for cancer as warranted, or, conversely, an antagonist to PRO317 may be administered with VEGF for coronary ischemia or with anti-VEGF to treat cancer as warranted. These administrations would be in effective amounts for treating such disorders.

Native PRO301 (SEQ ID NO:119) has a Blast score of 246 and 30% homology at residues 24 to 282 of Figure 44 with A33_HUMAN, an A33 antigen precursor. A33 antigen precursor, as explained in the Background is a tumor-specific antigen, and as such, is a recognized marker and therapeutic target for the diagnosis and treatment of colon cancer. The expression of tumor-specific antigens is often associated with the progression of neoplastic tissue disorders. Native PRO301 (SEQ ID NO:119) and A33_HUMAN also show a Blast score of 245 and 30% homology at residues 21 to 282 of Fig. 44 with A33_HUMAN, the variation dependent upon how spaces are inserted into the compared sequences. Native PRO301 (SEQ ID NO:119) also has a Blast score of 165 and 29% homology at residues 60 to 255 of Fig. 44 with HS46KDA_1, a human coxsackie and adenovirus receptor protein, also known as cell surface protein HCAR. This region of PRO301 also shows a similar Blast score and homology with HSU90716_1. Expression of such proteins is usually associated with viral infection and therapeutics for the prevention of such infection may be accordingly conceived. As mentioned in the Background, the expression of viral receptors is often associated with neoplastic tumors.

Therapeutic uses for the PRO234 polypeptides of the invention includes treatments associated with leukocyte homing or the interaction between leukocytes and the endothelium during an inflammatory response. Examples

include asthma, rheumatoid arthritis, psoriasis and multiple sclerosis.

Since the PRO231 polypeptide and nucleic acid encoding it possess sequence homology to a putative acid phosphatase and its encoding nucleic acid, probes based upon the PRO231 nucleotide sequence may be employed to identify other novel phosphatase proteins. Soluble forms of the PRO231 polypeptide may be employed as antagonists of membrane bound PRO231 activity both *in vitro* and *in vivo*. PRO231 polypeptides may be employed in screening assays designed to identify agonists or antagonists of the native PRO231 polypeptide, wherein such assays may take the form of any conventional cell-type or biochemical binding assay. Moreover, the PRO231 polypeptide may serve as a molecular marker for the tissues in which the polypeptide is specifically expressed.

PRO229 polypeptides can be fused with peptides of interest to determine whether the fusion peptide has an increased half-life over the peptide of interest. The PRO229 polypeptides can be used accordingly to increase the half-life of polypeptides of interest. Portions of PRO229 which cause the increase in half-life are an embodiment of the invention herein.

PRO238 can be used in assays which measure its ability to reduce substrates, including oxygen and Acetyl-CoA, and particularly, measure PRO238's ability to produce oxygen free radicals. This is done by using assays which have been previously described. PRO238 can further be used to assay for candidates which block, reduce or reverse its reducing abilities. This is done by performing side by side assays where candidates are added in one assay having PRO238 and a substrate to reduce, and not added in another assay, being the same but for the lack of the presence of the candidate.

PRO233 polypeptides and portions thereof which have homology to reductase may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel reductase proteins and related molecules may be relevant to a number of human disorders such as inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications and mutations in general. Given that oxygen free radicals and antioxidants appear to play important roles in a number of disease processes, the identification of new reductase proteins and reductase-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research, as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO233.

The PRO223 polypeptides of the present invention which exhibit serine carboxypeptidase activity may be employed *in vivo* for therapeutic purposes as well as for *in vitro* purposes. Those of ordinary skill in the art will well know how to employ PRO223 polypeptides for such uses.

PRO235 polypeptides and portions thereof which may be involved in cell adhesion are also useful for *in vivo* therapeutic purposes, as well as for various *in vitro* applications. In addition, PRO235 polypeptides and portions thereof may have therapeutic applications in disease states which involve cell adhesion. Given the physiological importance of cell adhesion mechanisms *in vivo*, efforts are currently being under taken to identify new, native proteins which are involved in cell adhesion. Therefore, peptides having homology to plexin are of particular interest to the scientific and medical communities.

Because the PRO236 and PRO262 polypeptides disclosed herein are homologous to various known β -galactosidase proteins, the PRO236 and PRO262 polypeptides disclosed herein will find use in conjugates of

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monoclonal antibodies and the polypeptide for specific killing of tumor cells by generation of active drug from a galactosylated prodrug (e.g., the generation of 5-fluorouridine from the prodrug β -D-galactosyl-5-fluorouridine). The PRO236 and PRO262 polypeptides disclosed herein may also find various uses both *in vivo* and *in vitro*, wherein those uses will be similar or identical to uses for which β -galactosidase proteins are now employed. Those of ordinary skill in the art will well know how to employ PRO236 and PRO262 polypeptides for such uses.

5 PRO239 polypeptides and portions thereof which have homology to densin may also be useful for *in vivo* therapeutic purposes, as well as for various *in vitro* applications. In addition, PRO239 polypeptides and portions thereof may have therapeutic applications in disease states which involve synaptic mechanisms, regeneration or cell adhesion. Given the physiological importance of synaptic processes, regeneration and cell adhesion mechanisms *in vivo*, efforts are currently being under taken to identify new, native proteins which are involved in synaptic machinery and cell
10 adhesion. Therefore, peptides having homology to densin are of particular interest to the scientific and medical communities.

The PRO260 polypeptides described herein can be used in assays to determine their relation to fucosidase. In particular, the PRO260 polypeptides can be used in assays in determining their ability to remove fucose or other sugar residues from proteoglycans. The PRO260 polypeptides can be assayed to determine if they have any
15 functional or locational similarities as fucosidase. The PRO260 polypeptides can then be used to regulate the systems in which they are integral.

PRO263 can be used in assays wherein CD44 antigen is generally used to determine PRO263 activity relative to that of CD44. The results can be used accordingly.

PRO270 polypeptides and portions thereof which effect reduction-oxidation (redox) state may also be useful
20 for *in vivo* therapeutic purposes, as well as for various *in vitro* applications. More specifically, PRO270 polypeptides may affect the expression of a large variety of genes thought to be involved in the pathogenesis of AIDS, cancer, atherosclerosis, diabetic complications and in pathological conditions involving oxidative stress such as stroke and inflammation. In addition, PRO270 polypeptides and portions thereof may affect the expression of a genes which have a role in apoptosis. Therefore, peptides having homology to thioredoxin are particularly desirable to the scientific and
25 medical communities.

PRO272 polypeptides and portions thereof which possess the ability to bind calcium may also have numerous *in vivo* therapeutic uses, as well as various *in vitro* applications. Therefore, peptides having homology to reticulocalbin are particularly desirable. Those with ordinary skill in the art will know how to employ PRO272 polypeptides and portions thereof for such purposes.

30 PRO294 polypeptides and portions thereof which have homology to collagen may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel collagens and collage-like molecules may have relevance to a number of human disorders. Thus, the identification of new collagens and collage-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical
35 research as well as various industrial applications. Given the large number of uses for collagen, there is substantial interest in polypeptides with homology to the collagen molecule.

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PRO295 polypeptides and portions thereof which have homology to integrin may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel integrins and integrin-like molecules may have relevance to a number of human disorders such as modulating the binding or activity of cells of the immune system. Thus, the identification of new integrins and integrin-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO295.

As the PRO293 polypeptide is clearly a leucine rich repeat polypeptide homologue, the peptide can be used in all applications that the known NLRR-1 and NLRR-2 polypeptides are used. The activity can be compared between these peptides and thus applied accordingly.

The PRO247 polypeptides described herein can be used in assays in which densin is used to determine the activity of PRO247 relative to densin or these other proteins. The results can be used accordingly in diagnostics and/or therapeutic applications with PRO247.

PRO302, PRO303, PRO304, PRO307 and PRO343 polypeptides of the present invention which possess protease activity may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO302, PRO303, PRO304, PRO307 and PRO343 polypeptides of the present invention for such purposes.

PRO328 polypeptides and portions thereof which have homology to GLIP and CRISP may also be useful for *in vivo* therapeutic purposes, as well as for various other applications. The identification of novel GLIP and CRISP-like molecules may have relevance to a number of human disorders which involve transcriptional regulation or are over expressed in human tumors. Thus, the identification of new GLIP and CRISP-like molecules is of special importance in that such proteins may serve as potential therapeutics for a variety of different human disorders. Such polypeptides may also play important roles in biotechnological and medical research as well as in various industrial applications. As a result, there is particular scientific and medical interest in new molecules, such as PRO328.

Uses for PRO335, PRO331 or PRO326 including uses in competitive assays with LIG-1, ALS and decorin to determine their relative activities. The results can be used accordingly. PRO335, PRO331 or PRO326 can also be used in assays where LIG-1 would be used to determine if the same effects are incurred.

PRO332 contains GAG repeat (GKEK) at amino acid positions 625-628 in Fig. 108 (SEQ ID NO:309). Slippage in such repeats can be associated with human disease. Accordingly, PRO332 can use useful for the treatment of such disease conditions by gene therapy, i.e. by introduction of a gene containing the correct GKEK sequence motif.

Other uses of PRO334 include use in assays in which fibrillin or fibulin would be used to determine the relative activity of PRO334 to fibrillin or fibulin. In particular, PRO334 can be used in assays which require the mechanisms imparted by epidermal growth factor repeats.

Native PRO346 (SEQ ID NO:319) has a Blast score of 230, corresponding to 27% homology between amino acid residues 21 to 343 with residues 35 to 1040 CGM6_HUMAN, a carcinoembryonic antigen cgm6 precursor. This homology region includes nearly all but 2 N-terminal extracellular domain residues, including an immunoglobulin superfamily homology at residues 148 to 339 of PRO346 in addition to several transmembrane

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residues (340-343). Carcinoembryonic antigen precursor, as explained in the Background is a tumor-specific antigen, and as such, is a recognized marker and therapeutic target for the diagnosis and treatment of colon cancer. The expression of tumor-specific antigens is often associated with the progression of neoplastic tissue disorders. Native PRO346 (SEQ ID NO:319) and P_W06874, a human carcinoembryonic antigen CEA-d have a Blast score of 224 and homology of 28% between residues 2 to 343 and 67 to 342, respectively. This homology includes the entire
5 extracellular domain residues of native PRO346, minus the initiator methionine (residues 2 to 18) as well as several transmembrane residues (340-343).

PRO268 polypeptides which have protein disulfide isomerase activity will be useful for many applications where protein disulfide isomerase activity is desirable including, for example, for use in promoting proper disulfide bond formation in recombinantly produced proteins so as to increase the yield of correctly folded protein. Those of
10 ordinary skill in the art will readily know how to employ such PRO268 polypeptides for such purposes.

PRO330 polypeptides of the present invention which possess biological activity related to that of the prolyl 4-hydroxylase alpha subunit protein may be employed both *in vivo* for therapeutic purposes and *in vitro*. Those of ordinary skill in the art will well know how to employ the PRO330 polypeptides of the present invention for such purposes.

55. Anti-PRO Polypeptide Antibodies

The present invention further provides anti-PRO polypeptide antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

20 A. Polyclonal Antibodies

The anti-PRO polypeptide antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent
25 may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be
30 selected by one skilled in the art without undue experimentation.

B. Monoclonal Antibodies

The anti-PRO polypeptide antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975).
35 In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

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The immunizing agent will typically include the PRO polypeptide of interest or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are
5 usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine
10 ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Rockville,
15 Maryland. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur *et al.*, *Monoclonal Antibody Production Techniques and Applications*, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the PRO polypeptide of interest. Preferably, the binding specificity of
20 monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures
25 and grown by standard methods [Goding, *supra*]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose,
30 hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention
35 serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the

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recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

C. Humanized Antibodies

The anti-PRO polypeptide antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321: 522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321: 522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeyen et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In

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practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks *et al.*, *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human monoclonal antibodies
 5 (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner *et al.*, *J. Immunol.*, 147(1):86-95 (1991)].

D. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding
 10 specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO polypeptide, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where
 15 the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, *EMBO J.*, 10:3655-3659 (1991).

20 Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted
 25 into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

E. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies
 30 are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents
 35 for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

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56. Uses for Anti-Pro Polypeptide Antibodies

The anti-PRO polypeptide antibodies of the invention have various utilities. For example, anti-PRO polypeptide antibodies may be used in diagnostic assays for a PRO polypeptide, *e.g.*, detecting its expression in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either
 5 heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase,
 10 beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter *et al.*, *Nature*, **144**:945 (1962); David *et al.*, *Biochemistry*, **13**:1014 (1974); Pain *et al.*, *J. Immunol. Meth.*, **40**:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, **30**:407 (1982).

Anti-PRO polypeptide antibodies also are useful for the affinity purification of PRO polypeptide from
 15 recombinant cell culture or natural sources. In this process, the antibodies against the PRO polypeptide are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO polypeptide to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO polypeptide, which is bound to the immobilized antibody. Finally, the support is washed with another suitable
 20 solvent that will release the PRO polypeptide from the antibody.

With regard to PRO211 and PRO217, therapeutic indications include disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (*e.g.*, enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (*e.g.*, psoriasis, epithelial cancers such as lung squamous cell
 25 carcinoma, epidermoid carcinoma of the vulva and gliomas).

With regard to anti-PRO187 antibodies, FGF-8 has been implicated in cellular differentiation and embryogenesis, including the patterning which appears during limb formation. FGF-8 and the PRO187 molecules of the invention therefore are likely to have potent effects on cell growth and development. Diseases which relate to cellular growth and differentiation are therefore suitable targets for therapeutics based on functionality similar to
 30 FGF-8. For example, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies. Additionally, disease related to uncontrolled cell growth, *e.g.*, cancer, would also be expected therapeutic targets.

Native PRO533 is a 216 amino acid polypeptide of which residues 1-22 are the signal sequence. Residues 3 to 216 have a Blast score of 509, corresponding to 53% homology to fibroblast growth factor. At the nucleotide
 35 level, DNA47412, the EST from which PCR oligos were generated to isolate the full length DNA49435-1219, has been observed to map to 11p15. Sequence homology to the 11p15 locus would indicate that PRO533 may have utility in the treatment of Usher Syndrome or Atrophia areata.

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As mentioned previously, fibroblast growth factors can act upon cells in both a mitogenic and non-mitogenic manner. These factors are mitogenic for a wide variety of normal diploid mesoderm-derived and neural crest-derived cells, inducing granulosa cells, adrenal cortical cells, chondrocytes, myoblasts, corneal and vascular endothelial cells (bovine or human), vascular smooth muscle cells, lens, retina and prostatic epithelial cells, oligodendrocytes, astrocytes, chondrocytes, myoblasts and osteoblasts. Antibodies to these factors can be generated to modulate such effects.

Non-mitogenic actions of fibroblast growth factors include promotion of cell migration into a wound area (chemotaxis), initiation of new blood vessel formation (angiogenesis), modulation of nerve regeneration and survival (neurotrophism), modulation of endocrine functions, and stimulation or suppression of specific cellular protein expression, extracellular matrix production and cell survival. Baird, A. & Bohlen, P., *Handbook of Exp. Pharmacol.* 95(1): 369-418 (1990). These properties provide a basis for using fibroblast growth factors in therapeutic approaches to accelerate wound healing, nerve repair, collateral blood vessel formation, and the like. For example, fibroblast growth factors, have been suggested to minimize myocardium damage in heart disease and surgery (U.S.P. 4,378,437). Antibodies to these factors can be generated to modulate such effects.

Therapeutic indications for PRO214 polypeptides include disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g., enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g., psoriasis, epithelial cancers such as lung squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).

Anti-PRO317 antibodies find use in anti-tumor indications if they are angiostatic, or in coronary ischemic indications if they are angiogenic.

Native PRO301 (SEQ ID NO:119) has a Blast score of 246 and 30% homology at residues 24 to 282 of Fig. 44 with A33_HUMAN, an A33 antigen precursor. A33 antigen precursor, as explained in the Background is a tumor-specific antigen, and as such, is a recognized marker and therapeutic target for the diagnosis and treatment of colon cancer. The expression of tumor-specific antigens is often associated with the progression of neoplastic tissue disorders. Native PRO301 (SEQ ID NO:119) and A33_HUMAN also show a Blast score of 245 and 30% homology at residues 21 to 282 of Fig. 44 with A33_HUMAN, the variation dependent upon how spaces are inserted into the compared sequences. Native PRO301 (SEQ ID NO:119) also has a Blast score of 165 and 29% homology at residues 60 to 255 of Fig. 44 with HS46KDA_1, a human coxsackie and adenovirus receptor protein, also known as cell surface protein HCAR. This region of PRO301 also shows a similar Blast score and homology with HSU90716_1. Expression of such proteins is usually associated with viral infection and therapeutics for the prevention of such infection may be accordingly conceived. Accordingly, antibodies to the above identified antigens and receptors have therapeutic potential as diagnostic and treatment techniques.

Therapeutic uses for the PRO234 polypeptides of the invention includes treatments associated with leukocyte homing or the interaction between leukocytes and the endothelium during an inflammatory response. Examples include asthma, rheumatoid arthritis, psoriasis and multiple sclerosis.

Cancer-associated or specific antigens permit the creation of tumor or cancer specific monoclonal antibodies (mAbs) which are specific to such tumor antigens. Such mAbs, which can distinguish between normal and cancerous

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cells are useful in the diagnosis, prognosis and treatment of the disease.

Cancer specific monoclonal antibodies (mAbs) which are specific to tumor antigens. Such mAbs, which can distinguish between normal and cancerous cells are useful in the diagnosis, prognosis and treatment of the disease. Particular antigens are known to be associated with neoplastic diseases, such as colorectal and breast cancer. Since colon cancer is a widespread disease, early diagnosis and treatment is an important medical goal. Diagnosis and treatment of cancer can be implemented using monoclonal antibodies (mAbs) specific therefore having fluorescent, nuclear magnetic or radioactive tags. Radioactive genes, toxins and/or drug tagged mAbs can be used for treatment *in situ* with minimal patient description.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Rockville, Maryland.

EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g. LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altschul, and Gish, Methods in Enzymology 266: 460-80 (1996); <http://blast.wustl.edu/blast/README.html>) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a Blast score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA; (<http://bozeman.mbt.washington.edu/phrap.docs/phrap.html>)).

Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward (.f) and reverse (.r) PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe (.p) sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are

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synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

10

EXAMPLE 2: Isolation of cDNA Clones Encoding PRO211 and PRO217

Consensus DNA sequences were assembled as described in Example 1 above and were designated as DNA28730 and DNA28760, respectively. Based on these consensus sequences, oligonucleotides were synthesized and used to identify by PCR a cDNA library that contained the sequences of interest and for use as probes to isolate a clone of the full-length coding sequence for the PRO211 and PRO217 polypeptides. The libraries used to isolate DNA32292-1131 and DNA33094-1131 were fetal lung libraries.

cDNA clones were sequenced in their entirety. The entire nucleotide sequences of PRO211 (DNA32292-1131; UNQ185) and PRO217 (UNQ191; DNA33094-1131) are shown in Figure 1 (SEQ ID NO: 1) and Figure 3 (SEQ ID NO:3), respectively. The predicted polypeptides are 353 and 379 amino acid in length, respectively, with respective molecular weights of approximately 38,190 and 41,520 daltons.

The oligonucleotide sequences used in the above procedures were the following:

28730.p (OLI 516) (SEQ ID NO:5)
 5'-AGGGAGCACGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCA-3'
 28730.f (OLI 517) (SEQ ID NO:6)
 5'-AGAGTGTATCTCTGGCTACGC-3'
 28730.r (OLI 518) (SEQ ID NO:7)
 5'-TAAGTCCGGCACATTACAGGTC-3'
 28760.p (OLI 617) (SEQ ID NO:8)
 5'-CCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATC-3'
 28760.f (OLI 618) (SEQ ID NO:9)
 5'-AAAGACGCATCTGCGAGTGTCC-3'
 28760.r (OLI 619) (SEQ ID NO:10)
 5'-TGCTGATTTCACACTGCTCTCCC-3'

EXAMPLE 3: Isolation of cDNA Clones Encoding Human PRO230

A consensus DNA sequence was assembled relative to the other identified EST sequences as described in Example 1 above, wherein the consensus sequence is designated herein as DNA30837. An EST proprietary to

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Genentech was employed in the consensus assembly. The EST is designated as DNA20088 and has the nucleotide sequence shown in Figure 7 (SEQ ID NO:13).

Based on the DNA30857 consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO230.

5 A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TTCGAGGCCTCTGAGAAGTGGCCC-3' (SEQ ID NO:14)

reverse PCR primer 5'-GGCGGTATCTCTCTGGCCTCCC-3' (SEQ ID NO:15)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30857 sequence which had the following nucleotide sequence

10 hybridization probe

5'-TTCTCCACAGCAGCTGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGG-3' (SEQ ID NO:16)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO230 gene using the probe oligonucleotide and one of the PCR primers.

15 RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO230 (herein designated as UNQ204 (DNA33223-1136)) and the derived protein sequence for PRO230.

The entire nucleotide sequence of UNQ204 (DNA33223-1136) is shown in Figure 5 (SEQ ID NO:11). Clone UNQ204 (DNA33223-1136) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 100-103 and ending at the stop codon at nucleotide positions 1501-1503 (Figure 5; SEQ ID NO:11). The predicted polypeptide precursor is 467 amino acids long (Figure 6).

EXAMPLE 4: Isolation of cDNA Clones Encoding Human PRO232

25 A consensus DNA sequence was assembled relative to the other identified EST sequences as described in Example 1 above, wherein the consensus sequence is designated herein as DNA30935. Based on the DNA30935 consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO232.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TGCTGTGCTACTCCTGCAAAGCCC-3' (SEQ ID NO:19)

30 reverse PCR primer 5'-TGCACAAGTCGGTGTACAGCACG-3' (SEQ ID NO:20)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30935 sequence which had the following nucleotide sequence

hybridization probe

5'-AGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGG-3' (SEQ ID NO:21)

35 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO232 gene using the probe oligonucleotide and one of the PCR primers.

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RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO232 [herein designated as UNQ206 (DNA34435-1140)] and the derived protein sequence for PRO232.

The entire nucleotide sequence of UNQ206 (DNA34435-1140) is shown in Figure 8 (SEQ ID NO:17). Clone UNQ206 (DNA34435-1140) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 17-19 and ending at the stop codon at nucleotide positions 359-361 (Fig. 8; SEQ ID NO:17). The predicted polypeptide precursor is 114 amino acids long (Fig. 9). Clone UNQ206 (DNA34435-1140) has been deposited with ATCC on September 16, 1997 and is assigned ATCC deposit no. ATCC 209250.

Analysis of the amino acid sequence of the full-length PRO232 suggests that it possesses 35% sequence identity with a stem cell surface antigen from *Gallus gallus*.

EXAMPLE 5: Isolation of cDNA Clones Encoding PRO187

A proprietary expressed sequence tag (EST) DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) was searched and an EST (#843193) was identified which showed homology to fibroblast growth factor (FGF-8) also known as androgen-induced growth factor. mRNA was isolated from human fetal lung tissue using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents (e.g., Invitrogen, San Diego, CA, Life Technologies, Gaithersburg, MD). The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into the cloning vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). The double-stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linked cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

Several libraries from various tissue sources were screened by PCR amplification with the following oligonucleotide probes:

IN843193.f (OLI315) (SEQ ID NO:24)
5'-CAGTACGTGAGGGACCAGGGCGCCATGA-3'

IN843193.r (OLI 317) (SEQ ID NO:25)
5'-CCGGTGACCTGCACGTGCTTGCCA-3'

A positive library was then used to isolate clones encoding the PRO187 gene using one of the above oligonucleotides and the following oligonucleotide probe:

IN843193.p (OLI 316) (SEQ ID NO:26)
5'-GCGGATCTGCCGCTGCTCANCTGGTCGGTCATGGCGCCCT-3'

A cDNA clone was sequenced in entirety. The entire nucleotide sequence of PRO187 (DNA27864-1155) is shown in Figure 10 (SEQ ID NO:22). Clone DNA27864-1155 contains a single open reading frame with an apparent translational initiation site at nucleotide position 1 (Figure 10; SEQ ID NO:22). The predicted polypeptide precursor is 205 amino acids long. Clone DNA27864-1155 has been deposited with the ATCC (designation: DNA27864-1155) and is assigned ATCC deposit no. ATCC 209375.

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Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence, the PRO187 polypeptide shows 74% amino acid sequence identity (Blast score 310) to human fibroblast growth factor-8 (androgen-induced growth factor).

EXAMPLE 6: Isolation of cDNA Clones Encoding PRO265

5 A consensus DNA sequence was assembled relative to other EST sequences as described in Example 1 above using phrap. This consensus sequence is herein designated DNA33679. Based on the DNA33679 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO265.

PCR primers (two forward and one reverse) were synthesized:

10 forward PCR primer A: 5'-CGGTCTACCTGTATGGCAACC-3' (SEQ ID NO:29);
forward PCR primer B: 5'-GCAGGACAACCAGATAAACCAC-3' (SEQ ID NO:30);
reverse PCR primer 5'-ACGCAGATTTGAGAAGGCTGTC-3' (SEQ ID NO:31)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA33679 sequence which had the following nucleotide sequence

15 hybridization probe
 5'-TTCACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGCTGCAC-3' (SEQ ID NO:32)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO265 gene using the probe oligonucleotide and one of the PCR primers.

20 RNA for construction of the cDNA libraries was isolated from human a fetal brain library.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO265 [herein designated as UNQ232 (DNA36350-1158)] (SEQ ID NO:27) and the derived protein sequence for PRO265.

The entire nucleotide sequence of UNQ232 (DNA36350-1158) is shown in Figure 12 (SEQ ID NO:27). Clone UNQ232 (DNA36350-1158) contains a single open reading frame with an apparent translational initiation site
 25 at nucleotide positions 352-354 and ending at the stop codon at positions 2332-2334 (Figure 12). The predicted polypeptide precursor is 660 amino acids long (Figure 13). Clone UNQ232 (DNA36350-1158) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209378.

Analysis of the amino acid sequence of the full-length PRO265 polypeptide suggests that portions of it possess significant homology to the fibromodulin and the fibromodulin precursor, thereby indicating that PRO265
 30 may be a novel member of the leucine rich repeat family, particularly related to fibromodulin.

EXAMPLE 7: Isolation of cDNA Clones Encoding Human PRO219

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA28729. Based on the DNA28729 consensus
 35 sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO219.

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A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GTGACCCTGGTTGTGAATACTCC-3' (SEQ ID NO:35)

reverse PCR primer 5'-ACAGCCATGGTCTATAGCTTGG-3' (SEQ ID NO:36)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28729 sequence which had the following nucleotide sequence

5 hybridization probe

5'-GCCTGTCAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAAG-3' (SEQ ID NO:37)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO219 gene using the probe oligonucleotide and one of the PCR primers.

10 RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO219 [herein designated as UNQ193 (DNA32290-1164)] (SEQ ID NO:33) and the derived protein sequence for PRO219.

The entire nucleotide sequence of UNQ193 (DNA32290-1164) is shown in Figures 14A-B (SEQ ID NO:33). Clone UNQ193 (DNA32290-1164) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 204-206 and ending at the stop codon at nucleotide positions 2949-2951 (Figures 14A-B). The predicted polypeptide precursor is 915 amino acids long (Figure 15). Clone UNQ193 (DNA32290-1164) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209384.

Analysis of the amino acid sequence of the full-length PRO219 polypeptide suggests that portions of it possess significant homology to the mouse and human matrilin-2 precursor polypeptides.

20

EXAMPLE 8: Isolation of cDNA Clones Encoding Human PRO246

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA30955. Based on the DNA30955 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO246.

25

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AGGGTCTCCAGGAGAAAGACTC-3' (SEQ ID NO:40)

reverse PCR primer 5'-ATTGTGGGCCTTGCAGACATAGAC-3' (SEQ ID NO:41)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30955 sequence which had the following nucleotide sequence

30

hybridization probe

5'-GGCCACAGCATCAAAACCTTAGAACTCAATGTACTGGTTCCTCCAGCTCC-3' (SEQ ID NO:42)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO246 gene using the probe oligonucleotide and one of the PCR primers.

35

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO246 [herein designated as

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UNQ220 (DNA35639-1172)] (SEQ ID NO:38) and the derived protein sequence for PRO246.

The entire nucleotide sequence of UNQ220 (DNA35639-1172) is shown in Figure 16 (SEQ ID NO:38). Clone UNQ220 (DNA35639-1172) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 126-128 and ending at the stop codon at nucleotide positions 1296-1298 (Figure 16). The predicted polypeptide precursor is 390 amino acids long (Figure 17). Clone UNQ220 (DNA35639-1172) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209396.

Analysis of the amino acid sequence of the full-length PRO246 polypeptide suggests that it possess significant homology to the human cell surface protein HCAR, thereby indicating that PRO246 may be a novel cell surface virus receptor.

10 EXAMPLE 9: Isolation of cDNA Clones Encoding Human PRO228

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA28758. An EST proprietary to Genentech was employed in the consensus assembly. This EST is shown in Figure 20 (SEQ ID NO:50) and is herein designated as DNA21951.

15 Based on the DNA28758 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO228.

PCR primers (forward and reverse) were synthesized:

	<u>forward PCR primer</u>	5'-GGTAATGAGCTCCATTACAG-3' (SEQ ID NO:51)
20	<u>forward PCR primer</u>	5'-GGAGTAGAAAGCGCATGG-3' (SEQ ID NO:52)
	<u>forward PCR primer</u>	5'-CACCTGATACCATGAATGGCAG-3' (SEQ ID NO:53)
	<u>reverse PCR primer</u>	5'-CGAGCTCGAATTAATTCG-3' (SEQ ID NO:54)
	<u>reverse PCR primer</u>	5'-GGATCTCCTGAGCTCAGG-3' (SEQ ID NO:55)
	<u>reverse PCR primer</u>	5'-CCTAGTTGAGTGATCCTTGTAAG-3' (SEQ ID NO:56)

25 Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28758 sequence which had the following nucleotide sequence

hybridization probe

5'-ATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACATTTTGCAATT-3' (SEQ ID NO:57)

30 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO228 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO228 [herein designated as UNQ202 (DNA33092-1202)] (SEQ ID NO:48) and the derived protein sequence for PRO228.

35 The entire nucleotide sequence of UNQ202 (DNA33092-1202) is shown in Figure 18 (SEQ ID NO:48). Clone UNQ202 (DNA33092-1202) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 24-26 of SEQ ID NO:48 and ending at the stop codon after nucleotide position 2093 of SEQ

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ID NO:48. The predicted polypeptide precursor is 690 amino acids long (Figure 19). Clone UNQ202 (DNA33092-1202) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209420.

Analysis of the amino acid sequence of the full-length PRO228 polypeptide suggests that portions of it possess significant homology to the secretin-related proteins CD97 and EMR1 as well as the secretin member, latrophilin, thereby indicating that PRO228 may be a new member of the secretin related proteins.

5

EXAMPLE 10: Isolation of cDNA Clones Encoding Human PRO533

The EST sequence accession number AF007268, a murine fibroblast growth factor (FGF-15) was used to search various public EST databases (e.g., GenBank, Dayhoff, etc.). The search was performed using the computer program BLAST or BLAST2 [Altschul et al., *Methods in Enzymology*, 266:460-480 (1996);
10 <http://blast.wustl.edu/blast/README.html>] as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. The search resulted in a hit with GenBank EST AA220994, which has been identified as stratagene NT2 neuronal precursor 937230.

Based on the Genbank EST AA220994 sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length
15 coding sequence. Forward and reverse PCR primers may range from 20 to 30 nucleotides (typically about 24), and are designed to give a PCR product of 100-1000 bp in length. The probe sequences are typically 40-55 bp (typically about 50) in length. In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification, as per *Ausubel et al., Current Protocols in Molecular Biology*, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe
20 oligonucleotide and one of the PCR primers.

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified below. A positive library was then used to isolate clones encoding the PRO533 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal retina. The cDNA libraries used
25 to isolated the cDNA clones were constructed by standard methods using commercially available reagents (e.g., Invitrogen, San Diego, CA; Clontech, etc.) The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., *Science*, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

A cDNA clone was sequenced in its entirety. The full length nucleotide sequence of PRO533 is shown in
30 Figure 21 (SEQ ID NO:58). Clone DNA49435-1219 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 459-461 (Figure 21; SEQ ID NO:58). The predicted polypeptide precursor is 216 amino acids long. Clone DNA47412-1219 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209480.

35 Based on a BLAST-2 and FastA sequence alignment analysis of the full-length sequence, PRO533 shows amino acid sequence identity to fibroblast growth factor (53%).

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The oligonucleotide sequences used in the above procedure were the following:

FGF15.forward: 5'-ATCCGCCCAGATGGCTACAATGTGTA-3' (SEQ ID NO:60);

FGF15.probe: 5'-GCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGTGTA-3' (SEQ ID NO:61);

FGF15.reverse: 5'-CCAGTCCGGTGACAAGCCCAA-3' (SEQ ID NO:62).

5 EXAMPLE 11: Isolation of cDNA Clones Encoding Human PRO245

A consensus DNA sequence was assembled relative to the other identified EST sequences as described in Example 1 above, wherein the consensus sequence is designated herein as DNA30954.

Based on the DNA30954 consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding
10 sequence for PRO245.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-ATCGTTGTGAAGTTAGTGCCCC-3' (SEQ ID NO:65)

reverse PCR primer 5'-ACCTGCGATATCCAACAGAATTG-3' (SEQ ID NO:66)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30954
15 sequence which had the following nucleotide sequence

hybridization probe

5'-GGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTTCC-3' (SEQ ID NO:67)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones
20 encoding the PRO245 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO245 [herein designated as UNQ219 (DNA35638-1141)] and the derived protein sequence for PRO245.

The entire nucleotide sequence of UNQ219 (DNA35638-1141) is shown in Figure 23 (SEQ ID NO:63).
25 Clone UNQ219 (DNA35638-1141) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 89-91 and ending at the stop codon at nucleotide positions 1025-1027 (Fig. 23; SEQ ID NO:63). The predicted polypeptide precursor is 312 amino acids long (Fig. 24). Clone UNQ219 (DNA35638-1141) has been deposited with ATCC on September 16, 1997 and is assigned ATCC deposit no. ATCC 209265.

Analysis of the amino acid sequence of the full-length PRO245 suggests that a portion of it possesses 60%
30 amino acid identity with the human c-myb protein and, therefore, may be a new member of the transmembrane protein receptor tyrosine kinase family.

EXAMPLE 12: Isolation of cDNA Clones Encoding Human PRO220, PRO221 and PRO227

(a) PRO220

35 A consensus DNA sequence was assembled relative to the other identified EST sequences as described in Example 1 above, wherein the consensus sequence is designated herein as DNA28749. Based on the DNA28749 consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the

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sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO220.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TCACCTGGAGCCTTTATTGGCC-3' (SEQ ID NO:74)

reverse PCR primer 5'-ATACCAGCTATAACCAGGCTGCG-3' (SEQ ID NO:75)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28749

5 sequence which had the following nucleotide sequence:

hybridization probe

5'-CAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGATTCTGATGATTGGG-3' (SEQ ID NO:76).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO220 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO220 [herein designated as UNQ194 (DNA32298-1132) and the derived protein sequence for PRO220.

The entire nucleotide sequence of UNQ194 (DNA32298-1132) is shown in Figure 25 (SEQ ID NO:68). Clone UNQ194 (DNA32298-1132) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 480-482 and ending at the stop codon at nucleotide positions 2604-2606 (Figure 25). The predicted polypeptide precursor is 708 amino acids long (Figure 26). Clone UNQ194 (DNA32298-1132) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209257.

Analysis of the amino acid sequence of the full-length PRO220 shows it has homology to member of the leucine rich repeat protein superfamily, including the leucine rich repeat protein and the neuronal leucine-rich repeat protein 1.

(b) PRO221

A consensus DNA sequence was assembled relative to the other identified EST sequences as described in Example 1 above, wherein the consensus sequence is designated herein as DNA28756. Based on the DNA28756 consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO221.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCATGTGTCTCCTCCTACAAAG-3' (SEQ ID NO:77)

30 reverse PCR primer 5'-GGGAATAGATGTGATCTGATTGG-3' (SEQ ID NO:78)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28756 sequence which had the following nucleotide sequence:

hybridization probe

5'-CACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTG-3' (SEQ ID NO:79)

35 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO221 gene using the probe oligonucleotide and one of the PCR primers.

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RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO221 [herein designated as UNQ195 (DNA33089-1132) and the derived protein sequence for PRO221.

The entire nucleotide sequence of UNQ195 (DNA33089-1132) is shown in Figure 27 (SEQ ID NO:70). Clone UNQ195 (DNA33089-1132) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 179-181 and ending at the stop codon at nucleotide positions 956-958 (Figure 27). The predicted polypeptide precursor is 259 amino acids long (Figure 28). PRO221 is believed to have a transmembrane region at amino acids 206-225. Clone UNQ195 (DNA33089-1132) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209262.

Analysis of the amino acid sequence of the full-length PRO221 shows it has homology to member of the leucine rich repeat protein superfamily, including the SLIT protein.

(c) PRO227

A consensus DNA sequence was assembled relative to the other identified EST sequences as described in Example 1 above, wherein the consensus sequence is designated herein as DNA28740. Based on the DNA28740 consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO227.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AGCAACCGCCTGAAGCTCATCC-3' (SEQ ID NO:80)

reverse PCR primer 5'-AAGGCGCGGTGAAAGATGTAGACG-3' (SEQ ID NO:81)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28740 sequence which had the following nucleotide sequence:

hybridization probe

5'-GACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCGA-3' (SEQ ID NO:82).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO227 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO227 [herein designated as UNQ201 (DNA33786-1132) and the derived protein sequence for PRO227.

The entire nucleotide sequence of UNQ201 (DNA33786-1132) is shown in Figure 29 (SEQ ID NO:72). Clone UNQ201 (DNA33786-1132) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 117-119 and ending at the stop codon at nucleotide positions 1977-1979 (Figure 29). The predicted polypeptide precursor is 620 amino acids long (Figure 30). PRO227 is believed to have a transmembrane region. Clone UNQ201 (DNA33786-1132) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209253.

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Analysis of the amino acid sequence of the full-length PRO221 shows it has homology to member of the leucine rich repeat protein superfamily, including the platelet glycoprotein V precursor and the human glycoprotein V.

EXAMPLE 13: Isolation of cDNA Clones Encoding Human PRO258

5 A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA28746.

Based on the DNA28746 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO258.

10 PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GCTAGGAATTCCACAGAAGCCC-3' (SEQ ID NO:85)

reverse PCR primer 5'-AACCTGGAATGTCACCGAGCTG-3' (SEQ ID NO:86)

reverse PCR primer 5'-CCTAGCACAGTGACGAGGGGACTTGGC-3' (SEQ ID NO:87)

15 Additionally, synthetic oligonucleotide hybridization probes were constructed from the consensus DNA28740 sequence which had the following nucleotide sequence:

hybridization probe

5'-AAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAGCCTGCAGCC-3' (SEQ ID NO:88)

5'-GCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT-3' (SEQ ID NO:89)

20 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO258 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO258 [herein designated as UNQ225 (DNA35918-1174)] (SEQ ID NO:83) and the derived protein sequence for PRO258.

25 The entire nucleotide sequence of UNQ225 (DNA35918-1174) is shown in Figure 31 (SEQ ID NO:83). Clone UNQ225 (DNA35918-1174) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 147-149 of SEQ ID NO:83 and ending at the stop codon after nucleotide position 1340 of SEQ ID NO:83 (Figure 31). The predicted polypeptide precursor is 398 amino acids long (Figure 32). Clone UNQ225 (DNA35918-1174) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209402.

30 Analysis of the amino acid sequence of the full-length PRO258 polypeptide suggests that portions of it possess significant homology to the CRTAM and the poliovirus receptor and have an Ig domain, thereby indicating that PRO258 is a new member of the Ig superfamily.

EXAMPLE 14: Isolation of cDNA Clones Encoding Human PRO266

35 An expressed sequence tag database was searched for ESTs having homology to SLIT, resulting in the identification of a single EST sequence designated herein as T73996. Based on the T73996 EST sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and

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2) for use as probes to isolate a clone of the full-length coding sequence for PRO266.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GTTGGATCTGGGCAACAATAAC-3' (SEQ ID NO:92)

reverse PCR primer 5'-ATTGTTGTGCAGGCTGAGTTTAAG-3' (SEQ ID NO:93)

Additionally, a synthetic oligonucleotide hybridization probe was constructed which had the following nucleotide
5 sequence

hybridization probe

5'-GGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGG-3' (SEQ ID NO:94)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones
10 encoding the PRO266 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal brain tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO266 [herein designated as UNQ233 (DNA37150-1178)] (SEQ ID NO:90) and the derived protein sequence for PRO266.

The entire nucleotide sequence of UNQ233 (DNA37150-1178) is shown in Figure 33 (SEQ ID NO:90).
15 Clone UNQ233 (DNA37150-1178) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 167-169 and ending at the stop codon after nucleotide position 2254 of SEQ ID NO:90. The predicted polypeptide precursor is 696 amino acids long (Figure 34). Clone UNQ233 (DNA37150-1178) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209401.

Analysis of the amino acid sequence of the full-length PRO266 polypeptide suggests that portions of it
20 possess significant homology to the SLIT protein, thereby indicating that PRO266 may be a novel leucine rich repeat protein.

EXAMPLE 15: Isolation of cDNA Clones Encoding Human PRO269

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in
25 Example 1 above. This consensus sequence is herein designated DNA35705. Based on the DNA35705 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO269.

Forward and reverse PCR primers were synthesized:

forward PCR primer (.f1) 5'-TGGAAGGAGATGCGATGCCACCTG -3'
30 (SEQ ID NO:97)

forward PCR primer (.f2) 5'-TGACCAGTGGGGAAGGACAG-3' (SEQ ID NO:98)

forward PCR primer (.f3) 5'-ACAGAGCAGAGGGTGCCTTG-3' (SEQ ID NO:99)

reverse PCR primer (.r1) 5'-TCAGGGACAAGTGGTGTCTCTCCC-3'
(SEQ ID NO:100)

35 reverse PCR primer (.r2) 5'-TCAGGGAAGGAGTGTGCAGTTCTG-3'
(SEQ ID NO:101)

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Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35705 sequence which had the following nucleotide sequence:

hybridization probe

5'-ACAGCTCCCGATCTCAGTTACTTGCATCGCGGACGAAATCGGCGCTCGCT-3' (SEQ ID NO:102)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO269 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO269 [herein designated as UNQ236 (DNA38260-1180)] (SEQ ID NO:95) and the derived protein sequence for PRO269.

The entire nucleotide sequence of UNQ236 (DNA38260-1180) is shown in Figure 35 (SEQ ID NO:95). Clone UNQ236 (DNA38260-1180) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 314-316 and ending at the stop codon at nucleotide positions 1784-1786 (Fig. 35; SEQ ID NO:95). The predicted polypeptide precursor is 490 amino acids long (Fig. 36). Clone UNQ236 (DNA38260-1180) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209397.

Analysis of the amino acid sequence of the full-length PRO269 suggests that portions of it possess significant homology to the human thrombomodulin proteins, thereby indicating that PRO269 may possess one or more thrombomodulin-like domains.

EXAMPLE 16: Isolation of cDNA Clones Encoding Human PRO287

A consensus DNA sequence encoding PRO287 was assembled relative to the other identified EST sequences as described in Example 1 above, wherein the consensus sequence is designated herein as DNA28728. Based on the DNA28728 consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO287.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCGATTCATAGACCTCGAGAGT-3' (SEQ ID NO:105)

reverse PCR primer 5'-GTCAAGGAGTCCTCCACAATAC-3' (SEQ ID NO:106)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28728 sequence which had the following nucleotide sequence

hybridization probe

5'-GTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCGCTTCTGT-3'
(SEQ ID NO:107)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO287 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO287 [herein designated as UNQ250 (DNA39969-1185), SEQ ID NO:103] and the derived protein sequence for PRO287.

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The entire nucleotide sequence of UNQ250 (DNA39969-1185) is shown in Figure 37 (SEQ ID NO:103). Clone UNQ250 (DNA39969-1185) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 307-309 and ending at the stop codon at nucleotide positions 1552-1554 (Fig. 37; SEQ ID NO:103). The predicted polypeptide precursor is 415 amino acids long (Fig. 38). Clone UNQ250 (DNA39969-1185) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209400.

- 5 Analysis of the amino acid sequence of the full-length PRO287 suggests that it may possess one or more procollagen C-proteinase enhancer protein precursor or procollagen C-proteinase enhancer protein-like domains. Based on a BLAST and FastA sequence alignment analysis of the full-length sequence, PRO287 shows nucleic acid sequence identity to procollagen C-proteinase enhancer protein precursor and procollagen C-proteinase enhancer protein (47 and 54 %, respectively).

10

EXAMPLE 17: Isolation of cDNA Clones Encoding Human PRO214

- A consensus DNA sequence was assembled using phrap as described in Example 1 above. This consensus DNA sequence is designated herein as DNA28744. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes
15 to isolate a clone of the full-length coding sequence.

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified below. A positive library was then used to isolate clones encoding the PRO214 gene using the probe oligonucleotide and one of the PCR primers.

- RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. A cDNA clone
20 was sequenced in its entirety. The full length nucleotide sequence of DNA32286-1191 is shown in Figure 39 (SEQ ID NO:108). DNA32286-1191 contains a single open reading frame with an apparent translational initiation site at nucleotide position 103 (Fig. 39; SEQ ID NO:108). The predicted polypeptide precursor is 420 amino acids long (SEQ ID NO:109).

- Based on a BLAST and FastA sequence alignment analysis of the full-length sequence, PRO214 polypeptide
25 shows amino acid sequence identity to HT protein and/or Fibulin (49% and 38%, respectively).

The oligonucleotide sequences used in the above procedure were the following:

- 28744.p (OLI555)
5'-CCTGGCTATCAGCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGA-3' (SEQ ID NO:110)
28744.f (OLI556)
30 5'-ATTCTGCGTGAACACTGAGGGC-3' (SEQ ID NO:111)
28744.r (OLI557)
5'-ATCTGCTTGTAGCCCTCGGCAC-3' (SEQ ID NO:112)

EXAMPLE 18: Isolation of cDNA Clones Encoding Human PRO317

- 35 A consensus DNA sequence was assembled using phrap as described in Example 1 above, wherein the consensus sequence is herein designated as DNA28722. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes

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to isolate a clone of the full-length coding sequence. The forward and reverse PCR primers, respectively, synthesized for this purpose were:

5'-AGGACTGCCATAACTTGCCTG (OLI489) (SEQ ID NO:115) and

5'-ATAGGAGTTGAAGCAGCGCTGC (OLI490) (SEQ ID NO:116).

The probe synthesized for this purpose was:

5 5'-TGTGTGGACATAGACGAGTGCCGCTACCGCTACTGCCAGCACCGC (OLI488) (SEQ ID NO:117)

mRNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel *et al.*, *Current Protocols in Molecular Biology* (1989), with the PCR primer pair identified above. A positive library was then used to isolate clones containing the PRO317 gene using the probe
10 oligonucleotide identified above and one of the PCR primers.

A cDNA clone was sequenced in its entirety. The entire nucleotide sequence of DNA33461-1199 (encoding PRO317) is shown in Figure 41 (SEQ ID NO:113). Clone DNA33461-1199 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 68-70 (Fig. 41; SEQ ID NO:113). The predicted polypeptide precursor is 366 amino acids long. The predicted signal sequence is amino acids 1-18 of Figure 42 (SEQ
15 ID NO:114). There is one predicted N-linked glycosylation site at amino acid residue 160. Clone DNA33461-1199 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209367.

Based on BLASTTM and FastATM sequence alignment analysis (using the ALIGNTM computer program) of the full-length PRO317 sequence, PRO317 shows the most amino acid sequence identity to EBAF-1 (92%). The results also demonstrate a significant homology between human PRO317 and mouse LEFTY protein. The C-terminal
20 end of the PRO317 protein contains many conserved sequences consistent with the pattern expected of a member of the TGF- superfamily.

In situ expression analysis in human tissues performed as described below evidences that there is distinctly strong expression of the PRO317 polypeptide in pancreatic tissue.

25 EXAMPLE 19: Isolation of cDNA clones Encoding Human PRO301

A consensus DNA sequence designated herein as DNA35936 was assembled using phrap as described in Example 1 above. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence.

30 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified below. A positive library was then used to isolate clones encoding the PRO301 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney.

A cDNA clone was sequenced in its entirety. The full length nucleotide sequence of native sequence
35 PRO301 is shown in Figure 43 (SEQ ID NO:118). Clone DNA40628-1216 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 52-54 (Fig. 43; SEQ ID NO:118). The predicted polypeptide precursor is 299 amino acids long with a predicted molecular weight of 32,583 daltons and pI of 8.29.

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Clone DNA40628-1216 has been deposited with ATCC and is assigned ATCC deposit No. ATCC 209432.

Based on a BLAST and FastA sequence alignment analysis of the full-length sequence, PRO301 shows amino acid sequence identity to A33 antigen precursor (30%) and coxsackie and adenovirus receptor protein (29%).

The oligonucleotide sequences used in the above procedure were the following:

- 5 OLI2162 (35936.f1) 5'-TCGCGGAGCTGTGTTCTGTTTCCC-3' (SEQ ID NO:120)
 OLI2163 (35936.p1)
 5'-TGATCGCGATGGGGACAAAGGCGCAAGCTCGAGAGGAACTGTTGTGCCT-3' (SEQ ID NO:121)
 OLI2164 (35936.f2)
 5'-ACACCTGGTTCAAAGATGGG-3' (SEQ ID NO:122)
 10 OLI2165 (35936.r1)
 5'-TAGGAAGAGTTGCTGAAGGCACGG-3' (SEQ ID NO:123)
 OLI2166 (35936.f3)
 5'-TTGCCTTACTCAGGTGCTAC-3' (SEQ ID NO:124)
 OLI2167 (35936.r2)
 15 5'-ACTCAGCAGTGGTAGGAAAG-3' (SEQ ID NO:125)

EXAMPLE 20: Isolation of cDNA Clones Encoding Human PRO224

- A consensus DNA sequence assembled relative to the other identified EST sequences as described in Example 1, wherein the consensus sequence is designated herein as DNA30845. Based on the DNA30845 consensus
 20 sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO224.

A pair of PCR primers (forward and reverse) were synthesized:

- forward PCR primer 5'-AAGTTCCAGTGCCGCACCAAGTGGC-3' (SEQ ID NO:128)
reverse PCR primer 5'-TTGGTTCCACAGCCGAGCTCGTCG-3' (SEQ ID NO:129)
 25 Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30845 sequence which had the following nucleotide sequence
hybridization probe

5'-GAGGAGGAGTGCAGGATTGAGCCATGTACCCAGAAAGGGCAATGCCCACC-3' (SEQ ID NO:130)

- In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened
 30 by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO224 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO224 [herein designated as UNQ198 (DNA33221-1133)] and the derived protein sequence for PRO224.

- 35 The entire nucleotide sequence of UNQ198 (DNA33221-1133) is shown in Figure 45 (SEQ ID NO:126). Clone UNQ198 (DNA33221-1133) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 96-98 and ending at the stop codon at nucleotide positions 942-944 (Figure 45; SEQ ID NO:126). The start of a transmembrane region begins at nucleotide position 777. The predicted polypeptide precursor is 282 amino acids long (Figure 46). Clone UNQ198 (DNA33221-1133) has been deposited with ATCC
 40 and is assigned ATCC deposit no. ATCC 209263.

Analysis of the amino acid sequence of the full-length PRO224 suggests that it has homology to very low-

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density lipoprotein receptors, apolipoprotein E receptor and chicken oocyte receptors P95. Based on a BLAST and FastA sequence alignment analysis of the full-length sequence, PRO224 has amino acid identity to portions of these proteins in the range from 28% to 45%, and overall identity with these proteins in the range from 33% to 39%.

EXAMPLE 21: Isolation of cDNA Clones Encoding Human PRO222

5 A consensus DNA sequence was assembled relative to the other identified EST sequences as described in Example 1 above, wherein the consensus sequence is designated herein as DNA28771. Based on the DNA28771 consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO222.

A pair of PCR primers (forward and reverse) were synthesized:

10 forward PCR primer 5'-ATCTCCTATCGCTGCTTTCCCGG-3' (SEQ ID NO:133)

reverse PCR primer 5'-AGCCAGGATCGCAGTAAACTCC-3' (SEQ ID NO:134)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28771 sequence which had the following nucleotide sequence:

hybridization probe

15 5'-ATTTAAACTTGATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCT-3' (SEQ ID NO:135)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO222 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

20 DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO222 [herein designated as UNQ196 (DNA33107-1135)] and the derived protein sequence for PRO222.

The entire nucleotide sequence of UNQ196 (DNA33107-1135) is shown in Figure 47 (SEQ ID NO:131). Clone UNQ196 (DNA33107-1135) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 159-161 and ending at the stop codon at nucleotide positions 1629-1631 (Fig. 47; SEQ ID
25 NO:131). The predicted polypeptide precursor is 490 amino acids long (Fig. 48). Clone UNQ196 (DNA33107-1135) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209251.

Based on a BLAST and FastA sequence alignment analysis of the full-length sequence, PRO222 shows amino acid sequence identity to mouse complement factor h precursor (25-
26%), complement receptor (27-29%), mouse complement C3b receptor type 2 long form precursor (25-47%) and
30 human hypothetical protein k1aa0247 (40%).

EXAMPLE 22: Isolation of cDNA clones Encoding PRO234

A consensus DNA sequence was assembled (DNA30926) using phrap as described in Example 1 above. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that
35 contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence.

RNA for the construction of the cDNA libraries was isolated using standard isolation protocols, e.g., Ausubel *et al.*, *Current Protocols in Molecular Biology*, from tissue or cell line sources or it was purchased from

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commercial sources (e.g., Clontech). The cDNA libraries used to isolate the cDNA clones were constructed by standard methods (e.g., Ausubel *et al.*) using commercially available reagents (e.g., Invitrogen). This library was derived from 22 week old fetal brain tissue.

A cDNA clone was sequenced in its entirety. The entire nucleotide sequence of PRO234 is shown in Figure 49 (SEQ ID NO:136). The predicted polypeptide precursor is 382 amino acids long and has a calculated molecular weight of approximately 43.1 kDa.

The oligonucleotide sequences used in the above procedure were the following:

30926.p (OLI826) (SEQ ID NO:138): 5'-GTTCATTGAAAACCTCTTGCCATCT
GATGGTGACTTCTGGATTGGGCTCA-3'
30926.f (OLI827) (SEQ ID NO:139): 5'-AAGCCAAAGAAGCCTGCAGGAGGG-3'
10 30926.r (OLI828) (SEQ ID NO:140): 5'-CAGTCCAAGCATAAAGGTCCTGGC-3'

EXAMPLE 23: Isolation of cDNA Clones Encoding Human PRO231

A consensus DNA sequence was assembled relative to the other identified EST sequences as described in Example 1 above, wherein the consensus sequence was designated herein as DNA30933. Based on the DNA30933
15 consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO231.

Three PCR primers (two forward and one reverse) were synthesized:

forward PCR primer 1 5'-CCAACTACCAAAGCTGCTGGAGCC-3' (SEQ ID NO:143)
forward PCR primer 2 5'-GCAGCTCTATTACCACGGGAAGGA-3' (SEQ ID NO:144)
20 reverse PCR primer 5'-TCCTTCCCGTGGTAATAGAGCTGC-3' (SEQ ID NO:145)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30933 sequence which had the following nucleotide sequence

hybridization probe

5'-GGCAGAGAACCAGAGGCCGGAGGAGACTGCCTCTTTACAGCCAGG-3' (SEQ ID NO:146)
25

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO231 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO231 [herein designated as
30 UNQ205 (DNA34434-1139)] and the derived protein sequence for PRO231.

The entire nucleotide sequence of UNQ205 (DNA34434-1139) is shown in Figure 51 (SEQ ID NO:141). Clone UNQ205 (DNA34434-1139) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 173-175 and ending at the stop codon at nucleotide positions 1457-1459 (Fig. 51; SEQ ID NO:141). The predicted polypeptide precursor is 428 amino acids long (Fig. 52). Clone UNQ205 (DNA34434-1139)
35 has been deposited with ATCC on September 16, 1997 and is assigned ATCC deposit no. ATCC 209252.

Analysis of the amino acid sequence of the full-length PRO231 suggests that it possesses 30% and 31% amino acid identity with the human and rat prostatic acid phosphatase precursor proteins, respectively.

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EXAMPLE 24: Isolation of cDNA Clones Encoding Human PRO229

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA28762. Based on the DNA28762 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO229.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TTCAGCTCATCACCTTCACCTGCC-3' (SEQ ID NO:149)

reverse PCR primer 5'-GGCTCATACAAAATACCACTAGGG-3' (SEQ ID NO:150)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28762 sequence which had the following nucleotide sequence

hybridization probe

5'-GGGCCTCCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGT-3' (SEQ ID NO:151)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO229 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO229 [herein designated as UNQ203 (DNA33100-1159)] (SEQ ID NO:147) and the derived protein sequence for PRO229.

The entire nucleotide sequence of UNQ203 (DNA33100-1159) is shown in Figure 53 (SEQ ID NO:147). Clone UNQ203 (DNA33100-1159) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 98-100 and ending at the stop codon at nucleotide positions 1139-1141 (Figure 53). The predicted polypeptide precursor is 347 amino acids long (Figure 54). Clone UNQ203 (DNA33100-1159) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209377

Analysis of the amino acid sequence of the full-length PRO229 polypeptide suggests that portions of it possess significant homology to antigen wcl.1, M130 antigen and CD6.

EXAMPLE 25: Isolation of cDNA Clones Encoding Human PRO238

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described above in Example 1. This consensus sequence is herein designated DNA30908. Based on the DNA30908 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO238.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-GGTGCTAAACTGGTGCTCTGTGGC-3' (SEQ ID NO:154)

forward PCR primer 2 5'-CAGGGCAAGATGAGCATTCC-3' (SEQ ID NO:155)

reverse PCR primer 5'-TCATACTGTTCCATCTCGGCACGC-3' (SEQ ID NO:156)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30908 sequence which had the following nucleotide sequence

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hybridization probe

5'-AATGGTGGGGCCCTAGAAGAGCTCATCAGAGAACTCACCGCTTCTCATGC-3' (SEQ ID NO:157)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO238 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO238 and the derived protein sequence for PRO238.

The entire nucleotide sequence of DNA35600-1162 is shown in Figure 55 (SEQ ID NO:152). Clone DNA35600-1162 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 134-136 and ending prior to the stop codon at nucleotide positions 1064-1066 (Figure 55). The predicted polypeptide precursor is 310 amino acids long (Figure 56). Clone DNA35600-1162 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209370.

Analysis of the amino acid sequence of the full-length PRO238 polypeptide suggests that portions of it possess significant homology to reductase, particularly oxidoreductase, thereby indicating that PRO238 may be a novel reductase.

EXAMPLE 26: Isolation of cDNA Clones Encoding Human PRO233

The extracellular domain (ECD) sequences (including the secretion signal, if any) of from about 950 known secreted proteins from the Swiss-Prot public protein database were used to search expressed sequence tag (EST) databases. The EST databases included public EST databases (e.g., GenBank) and a proprietary EST DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequence. Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington; <http://bozeman.mbt.washington.edu/phrap.docs/phrap.html>).

An expressed sequence tag (EST) was identified by the EST database search and a consensus DNA sequence was assembled relative to other EST sequences using phrap. This consensus sequence is herein designated DNA30945. Based on the DNA30945 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO233.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-GGTGAAGGCAGAAATTGGAGATG-3' (SEQ ID NO:160)
reverse PCR primer 5'-ATCCCATGCATCAGCCTGTTTACC-3' (SEQ ID NO:161)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30945 sequence which had the following nucleotide sequence

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hybridization probe

5'-GCTGGTGTAGTCTATACATCAGATTTGTTTGCTACACAAGATCCTCAG-3'

(SEQ ID NO:162)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO233 gene using the probe oligonucleotide.

RNA for construction of the cDNA libraries was isolated from human fetal brain tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO233 [herein designated as UNQ207 (DNA34436-1238)] (SEQ ID NO:158) and the derived protein sequence for PRO233.

The entire nucleotide sequence of UNQ207 (DNA34436-1238) is shown in Figure 57 (SEQ ID NO:158). Clone UNQ207 (DNA34436-1238) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 101-103 and ending at the stop codon at nucleotide positions 1001-1003 (Figure 57). The predicted polypeptide precursor is 300 amino acids long (Figure 58). The full-length PRO233 protein shown in Figure 58 has an estimated molecular weight of about 32,964 daltons and a pI of about 9.52. Clone UNQ207 (DNA34436-1238) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209523.

Analysis of the amino acid sequence of the full-length PRO233 polypeptide suggests that portions of it possess significant homology to reductase proteins, thereby indicating that PRO233 may be a novel reductase.

EXAMPLE 27: Isolation of cDNA Clones Encoding Human PRO223

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA30836. Based on the DNA30836 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO223.

PCR primer pairs (one forward and two reverse) were synthesized:

forward PCR primer 5'-TTCCATGCCACCTAAGGGAGACTC-3' (SEQ ID NO:165)

reverse PCR primer 1 5'-TGGATGAGGTGTGCAATGGCTGGC-3' (SEQ ID NO:166)

reverse PCR primer 2 5'-AGCTCTCAGAGGCTGGTCATAGGG-3' (SEQ ID NO:167)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30836 sequence which had the following nucleotide sequence

30 hybridization probe

5'-GTCGGCCCTTTCCCAGGACTGAACATGAAGAGTTATGCCGGCTTCCTCAC-3' (SEQ ID NO:168)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO223 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO223 [herein designated as UNQ197 (DNA33206-1165)] (SEQ ID NO:163) and the derived protein sequence for PRO223.

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The entire nucleotide sequence of UNQ197 (DNA33206-1165) is shown in Figure 59 (SEQ ID NO:163). Clone UNQ197 (DNA33206-1165) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 97-99 and ending at the stop codon at nucleotide positions 1525-1527 (Figure 59). The predicted polypeptide precursor is 476 amino acids long (Figure 60). Clone UNQ197 (DNA33206-1165) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209372.

- 5 Analysis of the amino acid sequence of the full-length PRO223 polypeptide suggests that it possesses significant homology to various serine carboxypeptidase proteins, thereby indicating that PRO223 may be a novel serine carboxypeptidase.

EXAMPLE 28: Isolation of cDNA Clones Encoding Human PRO235

- 10 A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated "DNA30927". Based on the DNA30927 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO235.

A pair of PCR primers (forward and reverse) were synthesized:

- 15 forward PCR primer 5'-TGGAATACCGCCTCCTGCAG-3' (SEQ ID NO:171)
 reverse PCR primer 5'-CTTCTGCCCTTTGGAGAAGATGGC-3' (SEQ ID NO:172)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30927 sequence which had the following nucleotide sequence

hybridization probe

- 20 5'-GGACTCACTGGCCCAGGCCTTCAATATCACCAGCCAGGACGAT-3' (SEQ ID NO:173)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO235 gene using the probe oligonucleotide and one of the PCR primers.

- 25 RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO235 [herein designated as UNQ209 (DNA35558-1167)] (SEQ ID NO:169) and the derived protein sequence for PRO235.

- 30 The entire nucleotide sequence of UNQ209 (DNA35558-1167) is shown in Figure 61 (SEQ ID NO:169). Clone UNQ209 (DNA35558-1167) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 667-669 and ending at the stop codon at nucleotide positions 2323-2325 (Figure 61). The predicted polypeptide precursor is 552 amino acids long (Figure 62). Clone UNQ209 (DNA35558-1167) has been deposited with ATCC and is assigned ATCC deposit no. 209374.

Analysis of the amino acid sequence of the full-length PRO235 polypeptide suggests that portions of it possess significant homology to the human, mouse and *Xenopus* plexin protein, thereby indicating that PRO235 may be a novel plexin protein.

35

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EXAMPLE 29: Isolation of cDNA Clones Encoding Human PRO236 and Human PRO262

Consensus DNA sequences were assembled relative to other EST sequences using phrap as described in Example 1 above. These consensus sequences are herein designated DNA30901 and DNA30847. Based on the DNA30901 and DNA30847 consensus sequences, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO236 and PRO262, respectively.

Based upon the DNA30901 consensus sequence, a pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TGGCTACTCCAAGACCCTGGCATG-3' (SEQ ID NO:178)

reverse PCR primer 5'-TGGACAAATCCCCTTGCTCAGCCC-3' (SEQ ID NO:179)

10 Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30901 sequence which had the following nucleotide sequence

hybridization probe

5'-GGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACCTGATGTCCAGGG-3' (SEQ ID NO:180)

15 Based upon the DNA30847 consensus sequence, a pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCAGCTATGACTATGATGCACC-3' (SEQ ID NO:181)

reverse PCR primer 5'-TGGCACCCAGAATGGTGTGGCTC-3' (SEQ ID NO:182)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30847 sequence which had the following nucleotide sequence

20 hybridization probe

5'-CGAGATGTCATCAGCAAGTTCCAGGAAGTTCCTTTGGGACCTTTACCTCC-3' (SEQ ID NO:183)

In order to screen several libraries for a source of full-length clones, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. Positive libraries were then used to isolate clones encoding the PRO236 and PRO262 genes using the probe oligonucleotides and one of the PCR primers.

25 RNA for construction of the cDNA libraries was isolated from human fetal lung tissue for PRO236 and human fetal liver tissue for PRO262.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO236 [herein designated as UNQ210 (DNA35599-1168)] (SEQ ID NO:174), the derived protein sequence for PRO236, the full-length DNA sequence for PRO262 [herein designated as UNQ229 (DNA36992-1168)] (SEQ ID NO:176) and the derived protein sequence for PRO262.

35 The entire nucleotide sequence of UNQ210 (DNA35599-1168) is shown in Figure 63 (SEQ ID NO:174). Clone UNQ210 (DNA35599-1168) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 69-71 and ending at the stop codon at nucleotide positions 1977-1979 (Figure 63). The predicted polypeptide precursor is 636 amino acids long (Figure 64). Clone UNQ210 (DNA35599-1168) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209373.

The entire nucleotide sequence of UNQ229 (DNA36992-1168) is shown in Figure 65 (SEQ ID NO:176). Clone UNQ229 (DNA36992-1168) contains a single open reading frame with an apparent translational initiation site

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at nucleotide positions 240-242 and ending at the stop codon at nucleotide positions 2202-2204 (Figure 65). The predicted polypeptide precursor is 654 amino acids long (Figure 66). Clone UNQ229 (DNA36992-1168) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209382.

Analysis of the amino acid sequence of the full-length PRO236 and PRO262 polypeptides suggests that portions of those polypeptides possess significant homology to β -galactosidase proteins derived from various sources, thereby indicating that PRO236 and PRO262 may be novel β -galactosidase homologs.

EXAMPLE 30: Isolation of cDNA Clones Encoding Human PRO239

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA30909. Based on the DNA30909 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO239.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCTCCCTCTATTACCCATGTC-3' (SEQ ID NO:186)

reverse PCR primer 5'-GACCAACTTTCTCTGGGAGTGAGG-3' (SEQ ID NO:187)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30909 sequence which had the following nucleotide sequence

hybridization probe

5'-GTCACCTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAG-3'

(SEQ ID NO:188)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO239 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO239 [herein designated as UNQ213 (DNA34407-1169)] (SEQ ID NO:184) and the derived protein sequence for PRO239.

The entire nucleotide sequence of UNQ213 (DNA34407-1169) is shown in Figure 67 (SEQ ID NO:184). Clone UNQ213 (DNA34407-1169) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 72-74 and ending at the stop codon at nucleotide positions 1575-1577 (Figure 67). The predicted polypeptide precursor is 501 amino acids long (Figure 68). Clone UNQ213 (DNA34407-1169) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209383.

Analysis of the amino acid sequence of the full-length PRO239 polypeptide suggests that portions of it possess significant homology to the densin protein, thereby indicating that PRO239 may be a novel molecule in the densin family.

EXAMPLE 31: Isolation of cDNA Clones Encoding Human PRO257

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA28731. Based on the DNA28731 consensus

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sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO257.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-TCTCTATTCCAAACTGTGGCG-3' (SEQ ID NO:191)

reverse PCR primer 5'-TTTGATGACGATTCTGAAGGTGG-3' (SEQ ID NO:192)

- 5 Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28731 sequence which had the following nucleotide sequence

hybridization probe

5'-GGAAGGATCCTTCACCAGCCCCAATTACCCAAAGCCGCATCCTGAGC-3' (SEQ ID NO:193)

- 10 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO257 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO257 [herein designated as UNQ224 (DNA35841-1173) (SEQ ID NO:189) and the derived protein sequence for PRO257.

- 15 The entire nucleotide sequence of UNQ224 (DNA35841-1173) is shown in Figure 69 (SEQ ID NO:189). Clone UNQ224 (DNA35841-1173) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 964-966 and ending at the stop codon at nucleotide positions 2785-2787 (Figure 69). The predicted polypeptide precursor is 607 amino acids long (Figure 70). Clone UNQ224 (DNA35841-1173) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209403.

- 20 Analysis of the amino acid sequence of the full-length PRO257 polypeptide suggests that portions of it possess significant homology to the ebnerin protein, thereby indicating that PRO257 may be a novel protein member related to the ebnerin protein.

EXAMPLE 32: Isolation of cDNA Clones Encoding Human PRO260

- 25 A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA30834. Based on the DNA30834 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO260.

PCR primers (forward and two reverse) were synthesized:

- 30 forward PCR primer: 5'-TGGTTTGACCAGGCCAAGTTCGG-3' (SEQ ID NO:196);

reverse PCR primer A: 5'-GGATTCATCCTCAAGGAAGAGCGG-3' (SEQ ID NO:197); and

reverse PCR primer B: 5'-AACTTGCAGCATCAGCCACTCTGC-3' (SEQ ID NO:198)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30834 sequence which had the following nucleotide sequence:

- 35 hybridization probe:

5'-TTCCGTGCCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCA-3' (SEQ ID NO:199)

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In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO260 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO260
5 [herein designated as UNQ227 (DNA33470-1175)] (SEQ ID NO:194) and the derived protein sequence for PRO260.

The entire nucleotide sequence of UNQ227 (DNA33470-1175) is shown in Figure 71 (SEQ ID NO:194). Clone UNQ227 (DNA33470-1175) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 67-69 and ending at the stop codon 1468-1470 (see Figure 71). The predicted polypeptide precursor is 467 amino acids long (Figure 72). Clone UNQ227 (DNA33470-1175) has been deposited with ATCC
10 and is assigned ATCC deposit no. ATCC 209398.

Analysis of the amino acid sequence of the full-length PRO260 polypeptide suggests that portions of it possess significant homology to the alpha-1-fucosidase precursor, thereby indicating that PRO260 may be a novel fucosidase.

15 EXAMPLE 33: Isolation of cDNA Clones Encoding Human PRO263

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA30914. Based on the DNA30914 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO263.

20 PCR primers (two forward and one reverse) were synthesized:

forward PCR primer 1: 5'-GAGCTTTCCATCCAGGTGTCATGC-3' (SEQ ID NO:202);

forward PCR primer 2: 5'-GTCAGTGACAGTACCTACTCGG-3' (SEQ ID NO:203); reverse PCR primer:

5'-TGGAGCAGGAGGAGTAGTAGG-3' (SEQ ID NO:204)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30914
25 sequence which had the following nucleotide sequence:

hybridization probe:

5'-AGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTT-3' (SEQ ID NO:205)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones
30 encoding the PRO263 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO263 [herein designated as UNQ230 (DNA34431-1177)] (SEQ ID NO:200) and the derived protein sequence for PRO263.

The entire nucleotide sequence of UNQ230 (DNA34431-1177) is shown in Figure 73 (SEQ ID NO:200).
35 Clone UNQ230 (DNA34431-1177) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 160-162 of SEQ ID NO:200 and ending at the stop codon after the nucleotide at position 1126-1128 of SEQ ID NO:200 (Figure 73). The predicted polypeptide precursor is 322 amino acids long (Figure 74).

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Clone UNQ230 (DNA34431-1177) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209399.

Analysis of the amino acid sequence of the full-length PRO263 polypeptide suggests that portions of it possess significant homology to CD44 antigen, thereby indicating that PRO263 may be a novel cell surface adhesion molecule.

5 EXAMPLE 34: Isolation of cDNA Clones Encoding Human PRO270

A consensus DNA sequence was assembled relative to the other identified EST sequences as described in Example 1 above, wherein the consensus sequence was designated herein as DNA35712. Based on the DNA35712 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO270.

10 Forward and reverse PCR primers were synthesized:

forward PCR primer (.f1) 5'-GCTTGGATATTCGCATGGGCCTAC-3' (SEQ ID NO:208)

forward PCR primer (.f2) 5'-TGGAGACAATATCCCTGAGG-3' (SEQ ID NO:209)

reverse PCR primer (.r1) 5'-AACAGTTGGCCACAGCATGGCAGG-3' (SEQ ID NO:210)

15 Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35712 sequence which had the following nucleotide sequence

hybridization probe

5'-CCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAG-3'

(SEQ ID NO:211)

20 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO270 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO270 [herein designated as UNQ237, DNA39510-1181] (SEQ ID NO:206) and the derived protein sequence for PRO270.

25 The entire nucleotide sequence of UNQ237, DNA39510-1181 is shown in Figure 75 (SEQ ID NO:206). Clone UNQ237 (DNA39510-1181) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 3-5 and ending at the stop codon at nucleotide positions 891-893 (Fig. 75; SEQ ID NO:206). The predicted polypeptide precursor is 296 amino acids long (Fig. 76). Clone UNQ237 (DNA39510-1181) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209392.

30 Analysis of the amino acid sequence of the full-length PRO270 suggests that portions of it possess significant homology to the thioredoxin-protein, thereby indicating that the PRO270 protein may be a novel member of the thioredoxin family.

EXAMPLE 35: Isolation of cDNA Clones Encoding Human PRO271

35 A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35737. Based on the DNA35737 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of

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interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO271.

Forward and reverse PCR primers were synthesized:

- forward PCR primer 1 5'-TGCTTCGCTACTGCCCTC-3' (SEQ ID NO:214)
 forward PCR primer 2 5'-TTCCCTTGTGGGTTGGAG-3' (SEQ ID NO:215)
 forward PCR primer 3 5'-AGGGCTGGAAGCCAGTTC-3' (SEQ ID NO:216)
 5 reverse PCR primer 1 5'-AGCCAGTGAGGAAATGCG-3' (SEQ ID NO:217)
 reverse PCR primer 2 5'-TGTCCAAAGTACACACACCTGAGG-3' (SEQ ID NO:218)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35737 sequence which had the following nucleotide sequence

hybridization probe

- 10 5'-GATGCCACGATCGCCAAGGTGGGACAGCTCTTTGCCGCCTGGAAG-3' (SEQ ID NO:219)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO271 gene using the probe oligonucleotide and one of the PCR primers.

- RNA for construction of the cDNA libraries was isolated from human fetal brain tissue. DNA sequencing
 15 of the clones isolated as described above gave the full-length DNA sequence for PRO271 [herein designated as UNQ238 (DNA39423-1182)] (SEQ ID NO:212) and the derived protein sequence for PRO271.

- The entire nucleotide sequence of UNQ238 (DNA39423-1182) is shown in Figure 77 (SEQ ID NO:212). Clone UNQ238 (DNA39423-1182) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 101-103 and ending at the stop codon at nucleotide positions 1181-1183 (Figure 77). The
 20 predicted polypeptide precursor is 360 amino acids long (Figure 78). Clone UNQ238 (DNA39423-1182) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209387.

Analysis of the amino acid sequence of the full-length PRO271 polypeptide suggests that it possess significant homology to the proteoglycan link protein, thereby indicating that PRO271 may be a link protein homolog.

25 EXAMPLE 36: Isolation of cDNA Clones Encoding Human PRO272

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA36460. Based on the DNA36460 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO272.

- 30 Forward and reverse PCR primers were synthesized:

forward PCR primer (.f1) 5'-CGCAGGCCCTCATGGCCAGG-3' (SEQ ID NO:222)
 forward PCR primer (.f2) 5'-GAAATCCTGGGTAATTGG-3' (SEQ ID NO:223)
 reverse PCR primer 5'-GTGCGCGGTGCTCACAGCTCATC-3' (SEQ ID NO:224)

- 35 Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA36460 sequence which had the following nucleotide sequence

hybridization probe

5'-CCCCCTGAGCGACGCTCCCCCATGATGACGCCACGGGAAGTTC-3' (SEQ ID NO:225)

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In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO272 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO272 [herein designated as UNQ239 (DNA40620-1183)] (SEQ ID NO:220) and the derived protein sequence for PRO272.

The entire nucleotide sequence of UNQ239 (DNA40620-1183) is shown in Figure 79 (SEQ ID NO:220). Clone UNQ239 (DNA40620-1183) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 35-37 and ending at the stop codon at nucleotide positions 1019-1021 (Figure 79). The predicted polypeptide precursor is 328 amino acids long (Figure 80). Clone UNQ239 (DNA40620-1183) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209388.

Analysis of the amino acid sequence of the full-length PRO272 polypeptide suggests that portions of it possess significant homology to the human and mouse reticulocalbin proteins, respectively, thereby indicating that PRO272 may be a novel reticulocalbin protein.

15 EXAMPLE 37: Isolation of cDNA Clones Encoding Human PRO294

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35731. Based on the DNA35731 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO294.

20 Forward and reverse PCR primers were synthesized:

forward PCR primer (.f1) 5'-TGGTCTCGCACACCGATC-3' (SEQ ID NO:228)

forward PCR primer (.f2) 5'-CTGCTGTCCACAGGGGAG-3' (SEQ ID NO:229)

forward PCR primer (.f3) 5'-CCTTGAAGCATACTGCTC-3' (SEQ ID NO:230)

forward PCR primer (.f4) 5'-GAGATAGCAATTTCCGCC-3' (SEQ ID NO:231)

25 reverse PCR primer (.r1) 5'-TTCCTCAAGAGGGCAGCC-3' (SEQ ID NO:232)

reverse PCR primer (.r2) 5'-CTTGGCACCAATGTCCGAGATTTC-3'

(SEQ ID NO:233)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35731 sequence which had the following nucleotide sequence

30 hybridization probe

5'-GCTCTGAGGAAGGTGACGCGCGGGGCCTCCGAACCCTTGGCCTTG-3'

(SEQ ID NO:234)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO294 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal brain tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO294 [herein designated as

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UNQ257 (DNA40604-1187)] (SEQ ID NO:226) and the derived protein sequence for PRO294.

The entire nucleotide sequence of UNQ257 (DNA40604-1187) is shown in Figure 81 (SEQ ID NO:226). Clone UNQ257 (DNA40604-1187) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 396-398 and ending at the stop codon at nucleotide positions 2046-2048 (Figure 81). The predicted polypeptide precursor is 550 amino acids long (Figure 82). Clone UNQ257 (DNA40604-1187) has been deposited with ATCC and is assigned ATCC deposit no. 209394.

Analysis of the amino acid sequence of the full-length PRO294 polypeptide suggests that portions of it possess significant homology to portions of various collagen proteins, thereby indicating that PRO294 may be collagen-like molecule.

10 EXAMPLE 38: Isolation of cDNA Clones Encoding Human PRO295

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35814. Based on the DNA35814 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO295.

15 Forward and reverse PCR primers were synthesized:

forward PCR primer (.f1) 5'-GCAGAGCGGAGATGCAGCGGCTTG-3'

(SEQ ID NO:237)

forward PCR primer (.f2) 5'-CCCAGCATGTACTGCCAG-3' (SEQ ID NO:238)

forward PCR primer (.f3) 5'-TTGGCAGCTTCATGGAGG-3' (SEQ ID NO:239)

20 forward PCR primer (.f4) 5'-CCTGGGCAAAAATGCAAC-3' (SEQ ID NO:240)

reverse PCR primer (.r1) 5'-CTCCAGCTCCTGGCGCACCTCCTC-3' (SEQ ID NO:241)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35814 sequence which had the following nucleotide sequence

hybridization probe

25 5'-GGCTCTCAGCTACCGCGCAGGAGCGAGGCCACCCTCAATGAGATG-3'

(SEQ ID NO:242)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO295 gene using the probe oligonucleotide and one of the PCR primers.

30 RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO295 [herein designated as UNQ258 (DNA38268-1188)] (SEQ ID NO:235) and the derived protein sequence for PRO295.

The entire nucleotide sequence of UNQ258 (DNA38268-1188) is shown in Figure 83 (SEQ ID NO:235). Clone UNQ258 (DNA38268-1188) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 153-155 and ending at the stop codon at nucleotide positions 1202-1204 (Figure 83). The predicted polypeptide precursor is 350 amino acids long (Figure 84). Clone UNQ258 (DNA38268-1188) has been deposited with ATCC and is assigned ATCC deposit no. 209421.

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Analysis of the amino acid sequence of the full-length PRO295 polypeptide suggests that portions of it possess significant homology to the integrin proteins, thereby indicating that PRO295 may be a novel integrin.

EXAMPLE 39: Isolation of cDNA Clones Encoding Human PRO293

The extracellular domain (ECD) sequences (including the secretion signal, if any) of from about 950 known secreted proteins from the Swiss-Prot public protein database were used to search expressed sequence tag (EST) databases. The EST databases included public EST databases (e.g., GenBank) and a proprietary EST DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequence. Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington;

Based on an expression tag sequence designated herein as T08294 identified in the above analysis, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO293.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AACAAAGGTAAGATGCCATCCTG-3' (SEQ ID NO:246)

reverse PCR primer 5'-AAACTTGTCGATGGAGACCAGCTC-3' (SEQ ID NO:247)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the expression sequence tag which had the following nucleotide sequence

hybridization probe

5'-AGGGGCTGCAAAGCCTGGAGAGCCTCTCTCTATGACAACCAGC-3' (SEQ ID NO:248)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO293 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal brain tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO293 (herein designated as UNQ256 (DNA37151-1193)) (SEQ ID NO:244) and the derived protein sequence for PRO293.

The entire nucleotide sequence of UNQ256 (DNA37151-1193) is shown in Figures 85A-B (SEQ ID NO:244). Clone UNQ256 (DNA37151-1193) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 881-883 and ending at the stop codon after nucleotide position 3019 of SEQ ID NO:244, Figures 85A-B). The predicted polypeptide precursor is 713 amino acids long (Figure 86). Clone UNQ256 (DNA37151-1193) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209393.

Analysis of the amino acid sequence of the full-length PRO293 polypeptide suggests that portions of it possess significant homology to the NLRR proteins, thereby indicating that PRO293 may be a novel NLRR protein.

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EXAMPLE 40: Isolation of cDNA Clones Encoding Human PRO247

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA33480. Based on the DNA33480 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO247.

5 A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CAACAATGAGGGCACCAAGC-3' (SEQ ID NO:250)

reverse PCR primer 5'-GATGGCTAGGTTCTGGAGGTTCTG-3' (SEQ ID NO:251)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA33480 expression sequence tag which had the following nucleotide sequence

10 hybridization probe

5'-CAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCG-3' (SEQ ID NO:252)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO247 gene using the probe oligonucleotide and one of the PCR primers.

15 RNA for construction of the cDNA libraries was isolated from human fetal brain tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO247 [herein designated as UNQ221 (DNA35673-1201)] (SEQ ID NO:248) and the derived protein sequence for PRO247.

The entire nucleotide sequence of UNQ221 (DNA35673-1201) is shown in Figures 89A-B (SEQ ID NO:248). Clone UNQ221 (DNA35673-1201) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 80-82 of SEQ ID NO:248 and ending at the stop codon after nucleotide position 1717 of SEQ ID NO:248 (Figures 89A-B). The predicted polypeptide precursor is 546 amino acids long (Figure 88). Clone UNQ221 (DNA35673-1201) has been deposited with ATCC and is assigned ATCC deposit no. 209418.

25 Analysis of the amino acid sequence of the full-length PRO247 polypeptide suggests that portions of it possess significant homology to the densin molecule and KIAA0231, thereby indicating that PRO247 may be a novel leucine rich repeat protein.

EXAMPLE 41: Isolation of cDNA Clones Encoding Human PRO302, PRO303, PRO304, PRO307 and PRO343

Consensus DNA sequences were assembled relative to other EST sequences using phrap as described in Example 1 above. These consensus sequences are herein designated DNA35953, DNA35955, DNA35958, 30 DNA37160 and DNA30895. Based on the DNA35953 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO302.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-GTCCGCAAGGATGCCTACATGTTC-3' (SEQ ID NO:263)

35 forward PCR primer 2 5'-GCAGAGGTGTCTAAGGTTG-3' (SEQ ID NO:264)

reverse PCR primer 5'-AGCTCTAGACCAATGCCAGCTTCC-3' (SEQ ID NO:265)

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Also, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35953 sequence which had the following nucleotide sequence

hybridization probe

5'-GCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCATG-3' (SEQ ID NO:266)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO302 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB228).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO302 [herein designated as UNQ265 (DNA40370-1217)] (SEQ ID NO:253) and the derived protein sequence for PRO302.

The entire nucleotide sequence of UNQ265 (DNA40370-1217) is shown in Figure 89 (SEQ ID NO:253). Clone UNQ265 (DNA40370-1217) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 34-36 and ending at the stop codon at nucleotide positions 1390-1392 (Figure 89). The predicted polypeptide precursor is 452 amino acids long (Figure 90). Various unique aspects of the PRO302 protein are shown in Figure 90. Clone UNQ265 (DNA40370-1217) has been deposited with the ATCC on November 21, 1997 and is assigned ATCC deposit no. ATCC 209485.

Based on the DNA35955 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO303.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GGGGAATTCACCCTATGACATTGCC-3' (SEQ ID NO:267)

reverse PCR primer 5'-GAATGCCCTGCAAGCATCAACTGG-3' (SEQ ID NO:268)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35955 sequence which had the following nucleotide sequence:

hybridization probe

5'-GCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAGGCCTC-3' (SEQ ID NO:269)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO303 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB25).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO303 [herein designated as UNQ266 (DNA42551-1217)] (SEQ ID NO:255) and the derived protein sequence for PRO303.

The entire nucleotide sequence of UNQ266 (DNA42551-1217) is shown in Figure 91 (SEQ ID NO:255). Clone UNQ266 (DNA42551-1217) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 20-22 and ending at the stop codon at nucleotide positions 962-964 (Figure 91). The predicted polypeptide precursor is 314 amino acids long (Figure 92). Various unique aspects of the PRO303 protein are shown in Figure 92. Clone UNQ266 (DNA42551-1217) has been deposited on November 21, 1997 with the ATCC and is assigned ATCC deposit no. ATCC 209483.

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Based on the DNA35958 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO304.

Pairs of PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-GCGGAAGGGCAGAATGGGACTCCAAG-3' (SEQ ID NO:270)

5 forward PCR primer 2 5'-CAGCCCTGCCACATGTGC-3' (SEQ ID NO:271)

forward PCR primer 3 5'-TACTGGGTGGTCAGCAAC-3' (SEQ ID NO:272)

reverse PCR primer 5'-GGCGAAGAGCAGGGTGAGACCCCG-3' (SEQ ID NO:273)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35958 sequence which had the following nucleotide sequence

10 hybridization probe

5'-GCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCGAC-3' (SEQ ID NO:274)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO304 gene using the probe oligonucleotide and one of the PCR primers.

15 RNA for construction of the cDNA libraries was isolated from 22 week human fetal brain tissue (LIB153).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO304 [herein designated as UNQ267 (DNA39520-1217)] (SEQ ID NO:257) and the derived protein sequence for PRO304.

The entire nucleotide sequence of UNQ267 (DNA39520-1217) is shown in Figure 93 (SEQ ID NO:257). Clone UNQ267 (DNA39520-1217) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 34-36 and ending at the stop codon at nucleotide positions 1702-1704 (Figure 93). The predicted polypeptide precursor is 556 amino acids long (Figure 94). Various unique aspects of the PRO304 protein are shown in Figure 94. Clone UNQ267 (DNA39520-1217) has been deposited with ATCC on November 21, 1997 and is assigned ATCC deposit no. ATCC 209482.

25 Based on the DNA37160 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO307.

Pairs of PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-GGGCAGGGATTCCAGGGCTCC-3' (SEQ ID NO:275)

forward PCR primer 2 5'-GGCTATGACAGCAGGTTC-3' (SEQ ID NO:276)

30 forward PCR primer 3 5'-TGACAATGACCGACCAGG-3' (SEQ ID NO:277)

reverse PCR primer 5'-GCATCGCATTGCTGGTAGAGCAAG-3' (SEQ ID NO:278)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA37160 sequence which had the following nucleotide sequence

hybridization probe

35 5'-TTACAGTGCCCCCTGGAAACCCACTTGGCCTGCATACCGCCTCCC-3' (SEQ ID NO:279)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones

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encoding the PRO307 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO307 [herein designated as UNQ270 (DNA41225-1217)] (SEQ ID NO:259) and the derived protein sequence for PRO307.

The entire nucleotide sequence of UNQ270 (DNA41225-1217) is shown in Figure 95 (SEQ ID NO:259).

5 Clone UNQ270 (DNA41225-1217) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 92-94 and ending at the stop codon at nucleotide positions 1241-1243 (Figure 95). The predicted polypeptide precursor is 383 amino acids long (Figure 96). Various unique aspects of the PRO307 protein are shown in Figure 96. Clone UNQ270 (DNA41225-1217) has been deposited with ATCC on November 21, 1997 and is assigned ATCC deposit no. ATCC 209491.

10 Based on the DNA30895 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO343.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CGTCTCGAGCGCTCCATACAGTTCCCTTGCCCCA-3' (SEQ ID NO:280)

15 reverse PCR primer

5'-TGGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCC

CCCTCATGTGCCAGGTGGA-3' (SEQ ID NO:281)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30895 sequence which had the following nucleotide sequence

20 hybridization probe

5'-CCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGAC

TCGGAAGTCTGCAGCCATCTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGT
GTGCCGGCTACT-3' (SEQ ID NO:282)

25 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO343 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB26).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO343 [herein designated as UNQ302 (DNA43318-1217)] (SEQ ID NO:261) and the derived protein sequence for PRO343.

30 The entire nucleotide sequence of UNQ302 (DNA43318-1217) is shown in Figure 97 (SEQ ID NO:261). Clone UNQ302 (DNA43318-1217) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 53-55 and ending at the stop codon at nucleotide positions 1004-1006 (Figure 97). The predicted polypeptide precursor is 317 amino acids long (Figure 98). Various unique aspects of the PRO343 protein are shown in Figure 98. Clone UNQ302 (DNA43318-1217) has been deposited with ATCC on November 21, 1997
35 and is assigned ATCC deposit no. ATCC 209481.

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EXAMPLE 42: Isolation of cDNA Clones Encoding Human PRO328

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35615. Based on the DNA35615 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO328.

5 Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-TCCTGCAGTTTCCTGATGC-3' (SEQ ID NO:285)

reverse PCR primer 5'-CTCATATTGCACACCAGTAATTTCG-3' (SEQ ID NO:286)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35615 sequence which had the following nucleotide sequence

10 hybridization probe

5'-ATGAGGAGAAACGTTTGATGGTGGAGCTGCACAACCTCTACCGGG-3'

(SEQ ID NO:287)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO328 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO328 [herein designated as UNQ289 (DNA40587-1231)] (SEQ ID NO:283) and the derived protein sequence for PRO328.

The entire nucleotide sequence of UNQ289 (DNA40587-1231) is shown in Figure 99 (SEQ ID NO:283).

20 Clone UNQ289 (DNA40587-1231) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 15-17 and ending at the stop codon at nucleotide positions 1404-1406 (Figure 99). The predicted polypeptide precursor is 463 amino acids long (Figure 100). Clone UNQ289 (DNA40587-1231) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209438.

25 Analysis of the amino acid sequence of the full-length PRO328 polypeptide suggests that portions of it possess significant homology to the human glioblastoma protein and to the cysteine rich secretory protein thereby indicating that PRO328 may be a novel glioblastoma protein or cysteine rich secretory protein.

EXAMPLE 43: Isolation of cDNA Clones Encoding Human PRO335, PRO331 or PRO326

30 A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA36685. Based on the DNA36685 consensus sequence, and Incyte EST sequence no. 2228990, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO335, PRO331 or PRO326.

Forward and reverse PCR primers were synthesized for the determination of PRO335:

35 forward PCR primer 5'-GGAACCGAATCTCAGCTA-3' (SEQ ID NO:294)

forward PCR primer 5'-CCTAAACTGAACTGGACCA-3' (SEQ ID NO:295)

forward PCR primer 5'-GGCTGGAGACACTGAACCT-3' (SEQ ID NO:296)

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forward PCR primer 5'-ACAGCTGCACAGCTCAGAACAGTG-3' (SEQ ID NO:297)

reverse PCR primer 5'-CATTCCCAGTATAAAAATTTTC-3' (SEQ ID NO:298)

reverse PCR primer 5'-GGGTCTTGGTGAATGAGG-3' (SEQ ID NO:299)

reverse PCR primer 5'-GTGCCTCTCGGTTACCACCAATGG-3' (SEQ ID NO:300)

Additionally, a synthetic oligonucleotide hybridization probe was constructed for the determination of PRO335 which

5 had the following nucleotide sequence

hybridization probe

5'-GCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTAC-3'

(SEQ ID NO:301)

Forward and reverse PCR primers were synthesized for the determination of PRO331:

10 forward PCR primer 5'-GCCTTTGACAACCTTCAGTCACTAGTGG-3' (SEQ ID NO:302)

reverse PCR primer 5'-CCCCATGTGTCCATGACTGTTCCC-3' (SEQ ID NO:303)

Additionally, a synthetic oligonucleotide hybridization probe was constructed for the determination of PRO331 which

had the following nucleotide sequence

hybridization probe

15 5'-TACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTTAGAGCGG-3'

(SEQ ID NO:304)

Forward and reverse PCR primers were synthesized for the determination of PRO326:

forward PCR primer 5'-ACTCCAAGGAAATCGGATCCGTTC-3' (SEQ ID NO:305)

reverse PCR primer 5'-TTAGCAGCTGAGGATGGGCACAAC-3' (SEQ ID NO:306)

20 Additionally, a synthetic oligonucleotide hybridization probe was constructed for the determination of PRO331 which

had the following nucleotide sequence

hybridization probe

5'-GCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGACAACGC-3'

(SEQ ID NO:307)

25 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO335, PRO331 or PRO326 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (PRO335 and PRO326) and human fetal brain (PRO331).

30 DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO335, PRO331 or PRO326 [herein designated as SEQ ID NOS:288,290 and 292, respectively; see Figures 103A-B, 105 and 107, respectively], and the derived protein sequence for PRO335, PRO331 or PRO326 (see Figures 104, 106 and 108, respectively; SEQ ID NOS:289, 291 and 293, respectively).

35 The entire nucleotide sequences are shown in Figures 103A-B, 105 and 107, deposited with the ATCC on June 2, 1998, November 7, 1997 and November 21, 1997, respectively.

Analysis of the amino acid sequence of the full-length PRO335, PRO331 or PRO326 polypeptide suggests that portions of it possess significant homology to the LIG-1 protein, thereby indicating that PRO335, PRO331 and

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PRO326 may be a novel LIG-I-related protein.

EXAMPLE 44: Isolation of cDNA clones Encoding Human PRO332

Based upon an ECD homology search performed as described in Example 1 above, a consensus DNA sequence designated herein as DNA36688 was assembled. Based on the DNA36688 consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO332.

A pair of PCR primers (forward and reverse) were synthesized:

5'-GCATTGGCCGCGAGACTTTGCC-3' (SEQ ID NO:310)

5'-GCGGCCACGGTCCTTGGAATG-3' (SEQ ID NO:311)

A probe was also synthesized:

5'-TGGAGGAGCTCAACCTCAGCTACAACCGCATCACCAGCCCACAGG-3'
(SEQ ID NO:312)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO332 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from a human fetal liver library (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for DNA40982-1235 and the derived protein sequence for PRO332.

The entire nucleotide sequence of DNA40982-1235 is shown in Figures 109A-B (SEQ ID NO:308). Clone DNA40982-1235 contains a single open reading frame (with an apparent translational initiation site at nucleotide positions 342-344, as indicated in Figures 109A-B). The predicted polypeptide precursor is 642 amino acids long, and has a calculated molecular weight of 72,067 (pI: 6.60). Clone DNA40982-1235 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209433.

Based on a BLAST and FastA sequence alignment analysis of the full-length sequence, PRO332 shows about 30-40% amino acid sequence identity with a series of known proteoglycan sequences, including, for example, fibromodulin and fibromodulin precursor sequences of various species (FMOD_BOVIN, FMOD_CHICK, FMOD_RAT, FMOD_MOUSE, FMOD_HUMAN, P_R36773), osteomodulin sequences (AB000114_1, AB007848_1), decorin sequences (CFU83141_1, OCU03394_1, P_R42266, P_R42267, P_R42260, P_R89439), keratan sulfate proteoglycans (BTU48360_1, AF022890_1), corneal proteoglycan (AF022256_1), and bone/cartilage proteoglycans and proteoglycan precursors (PGS1_BOVIN, PGS2_MOUSE, PGS2_HUMAN).

EXAMPLE 45: Isolation of cDNA clones Encoding Human PRO334

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. Based on the consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO334.

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Forward and reverse PCR primers were synthesized for the determination of PRO334:

forward PCR primer 5'-GATGGTTCCTGCTCAAGTGCCCTG-3' (SEQ ID NO:315)

reverse PCR primer 5'-TTGCACTTGTAGGACCCACGTACG-3' (SEQ ID NO:316)

Additionally, a synthetic oligonucleotide hybridization probe was constructed for the determination of PRO334 which had the following nucleotide sequence

5 hybridization probe

5'-CTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCC-3'
(SEQ ID NO:317)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO334 gene using the probe oligonucleotide and one of the PCR primers.

Human fetal kidney cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO334 [herein designated as DNA41379-1236] (SEQ ID NO:313) and the derived protein sequence for PRO334.

15 The entire nucleotide sequence of DNA41379-1236 (also referred to as UNQ295) is shown in Figure 109 (SEQ ID NO:313). Clone DNA41379-1236 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 203-205 and ending at the stop codon at nucleotide positions 1730-1732 (Figure 109). The predicted polypeptide precursor is 509 amino acids long (Figure 110). Clone DNA41379-1236 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209488.

20 Analysis of the amino acid sequence of the full-length PRO334 polypeptide suggests that portions of it possess significant homology to the fibulin and fibrillin proteins, thereby indicating that PRO334 may be a novel member of the EGF protein family.

EXAMPLE 46: Isolation of cDNA Clones Encoding Human PRO346

25 A consensus DNA sequence was identified using phrap as described in Example 1 above. Specifically, this consensus sequence is herein designated DNA38240. Based on the DNA38240 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length PRO346 coding sequence.

30 RNA for construction of the cDNA libraries was isolated from human fetal liver. The cDNA libraries used to isolated the cDNA clones were constructed by standard methods using commercially available reagents (e.g., Invitrogen, San Diego, CA; Clontech, etc.) The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., *Science*, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

35 A cDNA clone was sequenced in entirety. The entire nucleotide sequence of DNA44167-1243 is shown in Figure 111 (SEQ ID NO:318). Clone DNA44167-1243 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 64-66 (Fig. 113; SEQ ID NO:318). The predicted polypeptide

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precursor is 450 amino acids long. Clone DNA44167-1243 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209434 (designation DNA44167-1243).

Based on a BLAST, BLAST-2 and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence, PRO346 shows amino acid sequence identity to carcinoembryonic antigen (28%).

The oligonucleotide sequences used in the above procedure were the following:

- 5 OLI2691 (38240.f1)
5'-GATCCTGTCACAAAGCCAGTGGTGC-3' (SEQ ID NO:320)
OLI2693 (38240.r1)
5'-CACTGACAGGGTTCCTCACCCAGG-3' (SEQ ID NO:321)
OLI2692 (38240.p1)
10 5'-CTCCCTCTGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATG-3' (SEQ ID NO:322)

EXAMPLE 47: Isolation of cDNA Clones Encoding Human PRO268

- A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35698. Based on the DNA35698 consensus
15 sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO268.

Forward and reverse PCR primers were synthesized:

- forward PCR primer 1 5'-TGAGGTGGGCAAGCGGCGAAATG-3' (SEQ ID NO:325)
forward PCR primer 2 5'-TATGTGGATCAGGACGTGCC-3' (SEQ ID NO:326)
20 forward PCR primer 3 5'-TGCAGGGTTCAGTCTAGATTG-3' (SEQ ID NO:327)
reverse PCR primer 5'-TTGAAGGACAAAGGCAATCTGCCAC-3' (SEQ ID NO:328)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35698 sequence which had the following nucleotide sequence

- hybridization probe
25 5'-GGAGTCTTGCAGTTCCTGGCAGTCCTGGTGCTGTGCTTTGGG-3' (SEQ ID NO:329)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO268 gene using the probe oligonucleotide and one of the PCR primers.

- RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNA sequencing
30 of the clones isolated as described above gave the full-length DNA sequence for PRO268 [herein designated as UNQ235 (DNA39427-1179)] (SEQ ID NO:323) and the derived protein sequence for PRO268.

- The entire nucleotide sequence of UNQ235 (DNA39427-1179) is shown in Figure 113 (SEQ ID NO:323). Clone UNQ235 (DNA39427-1179) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 13-15 and ending at the stop codon at nucleotide positions 853-855 (Figure 113). The
35 predicted polypeptide precursor is 280 amino acids long (Figure 114). Clone UNQ235 (DNA39427-1179) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209395.

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Analysis of the amino acid sequence of the full-length PRO268 polypeptide suggests that it possess significant homology to protein disulfide isomerase, thereby indicating that PRO268 may be a novel protein disulfide isomerase.

EXAMPLE 48: Isolation of cDNA Clones Encoding Human PRO330

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35730. Based on the DNA35730 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO330.

Forward and reverse PCR primers were synthesized:

forward PCR primer 1 5'-CCAGGCACAATTCCAGA-3' (SEQ ID NO:332)
 forward PCR primer 2 5'-GGACCCTTCTGTGTGCCAG-3' (SEQ ID NO:333)
 reverse PCR primer 1 5'-GGTCTCAAGAACTCCTGTC-3' (SEQ ID NO:334)
 reverse PCR primer 2 5'-ACACTCAGCATTGCCTGGTACTTG-3' (SEQ ID NO:335)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus sequence which had the following nucleotide sequence

hybridization probe

5'-GGGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAG-3' (SEQ ID NO:336)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO330 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO330 [herein designated as UNQ290 (DNA40603-1232)] (SEQ ID NO:330) and the derived protein sequence for PRO330.

The entire nucleotide sequence of UNQ290 (DNA40603-1232) is shown in Figure 115 (SEQ ID NO:330). Clone UNQ290 (DNA40603-1232) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 167-169 and ending at the stop codon at nucleotide positions 1766-1768 (Figure 115). The predicted polypeptide precursor is 533 amino acids long (Figure 116). Clone UNQ290 (DNA40603-1232) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209486 on November 21, 1997.

Analysis of the amino acid sequence of the full-length PRO330 polypeptide suggests that portions of it possess significant homology to the mouse prolyl 4-hydroxylase alpha subunit protein, thereby indicating that PRO330 may be a novel prolyl 4-hydroxylase alpha subunit polypeptide.

EXAMPLE 49: Isolation of cDNA Clones Encoding Human PRO310

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA40553. Based on the DNA40553 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO310.

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Forward and reverse PCR primers were synthesized:

forward PCR primer 1 5'-TCCCCAAGCCGTTCTAGACGCGG-3' (SEQ ID NO:341)

forward PCR primer 2 5'-CTGGTTCTTCCTTGCACG-3' (SEQ ID NO:342)

reverse PCR primer 5'-GCCCAAATGCCCTAAGGCGGTATACCCC-3' (SEQ ID NO:343)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus sequence which had the following nucleotide sequence

hybridization probe

5'-GGGTGTGATGCTTGAAGCATTTTCTGTGCTTTGATCACTATGCTAGGAC-3' (SEQ ID NO:344)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO310 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO310 [herein designated as DNA43046-1225 (SEQ ID NO:339)] and the derived protein sequence for PRO310 (SEQ ID NO:340).

The entire nucleotide sequence of DNA43046-1225 is shown in Figure 119 (SEQ ID NO:339). Clone DNA43046-1225 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 81-83 and ending at the stop codon at nucleotide positions 1035-1037 (Figure 119). The predicted polypeptide precursor is 318 amino acids long (Figure 120) and has a calculated molecular weight of approximately 36,382 daltons. Clone DNA43046-1225 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209484.

Analysis of the amino acid sequence of the full-length PRO310 polypeptide suggests that portions of it possess homology to *C. elegans* proteins and to fringe, thereby indicating that PRO310 may be involved in development.

EXAMPLE 50: Isolation of cDNA clones Encoding Human PRO339

An expressed sequence tag (EST) DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) was searched and ESTs were identified. An assembly of Incyte clones and a consensus sequence was formed using phrap as described in Example 1 above.

Forward and reverse PCR primers were synthesized based upon the assembly-created consensus sequence:

forward PCR primer 1 5'-GGGATGCAGGTGGTGTCTCATGGGG-3' (SEQ ID NO:345)

forward PCR primer 2 5'-CCCTCATGTACCGGCTCC-3' (SEQ ID NO:346)

forward PCR primer 3 5'-GTGTGACACAGCGTGGGC-3' (SEQ ID NO:43)

forward PCR primer 4 5'-GACCGGCAGGCTTCTGCG-3' (SEQ ID NO:44)

reverse PCR primer 1 5'-CAGCAGCTTCAGCCACCAGGAGTGG-3' (SEQ ID NO:45)

reverse PCR primer 2 5'-CTGAGCCGTGGGCTGCAGTCTCGC-3' (SEQ ID NO:46)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus sequence which had the following nucleotide sequence

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hybridization probe

5'-CCGACTACGACTGGTTCTTCATCATGCAGGATGACACATATGTGC-3' (SEQ ID NO:47)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO339 gene using the probe oligonucleotide and one of the PCR primers.

5 RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. A cDNA clone was sequenced in entirety. The entire nucleotide sequence of DNA43466-1225 is shown in Figure 117 (SEQ ID NO:337). Clone DNA43466-1225 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 333-335 and ending at the stop codon found at nucleotide positions 2649-2651 (Figure 117; SEQ ID NO:337). The predicted polypeptide precursor is 772 amino acids long and has a calculated molecular weight of approximately 86,226 daltons. Clone DNA43466-1225 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209490.

Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence, PRO339 has homology to *C. elegans* proteins and collagen-like polymer sequences as well as to fringe, thereby indicating that PRO339 may be involved in development or tissue growth.

EXAMPLE 51: Isolation of cDNA Clones Encoding Human PRO244

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. Based on this consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO244.

A pair of PCR primers (forward and reverse) were synthesized:

5'-TTCAGCTTCTGGGATGTAGGG-3' (30923.f1) (SEQ ID NO:377)

5'-TATTCCTACCATTTACAAATCCG-3' (30923.r1) (SEQ ID NO:378)

A probe was also synthesized:

25 5'-GGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGG-3' (30923.p1) (SEQ ID NO:379)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO244 gene using the probe oligonucleotide and one of the PCR primers.

30 RNA for construction of the cDNA libraries was isolated from a human fetal kidney library. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence and the derived protein sequence for PRO244.

35 The entire nucleotide sequence of PRO244 is shown in Figure 121 (SEQ ID NO:375). Clone DNA35668-1171 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 106-108 (Fig. 121). The predicted polypeptide precursor is 219 amino acids long. Clone DNA35668-1171 has been deposited with ATCC (designated as DNA35663-1171) and is assigned ATCC deposit no. ATCC209371. The protein has a cytoplasmic domain (aa 1-20), a transmembrane domain (aa 21-46), and an extracellular domain (aa 47-219), with

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a C-lectin domain at aa 55-206.

Based on a BLAST and FastA sequence alignment analysis of the full-length sequence, PRO244 shows notable amino acid sequence identity to hepatic lectin gallus gallus (43%), HIC hp120-binding C-type lectin (42%), macrophage lectin 2 (HUMHML2-1, 41%), and sequence PR32188 (44%).

5 EXAMPLE 52: Use of PRO Polypeptide-Encoding Nucleic Acid as Hybridization Probes

The following method describes use of a nucleotide sequence encoding a PRO polypeptide as a hybridization probe.

DNA comprising the coding sequence of of a PRO polypeptide of interest as disclosed herein may be employed as a probe or used as a basis from which to prepare probes to screen for homologous DNAs (such as those
10 encoding naturally-occurring variants of the PRO polypeptide) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO polypeptide-encoding nucleic acid-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM
15 sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO polypeptide can then be identified using standard techniques known in the art.

20 EXAMPLE 53: Expression of PRO Polypeptides in *E. coli*

This example illustrates preparation of an unglycosylated form of a desired PRO polypeptide by recombinant expression in *E. coli*.

The DNA sequence encoding the desired PRO polypeptide is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected
25 expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase
30 cleavage site), the specific PRO polypeptide coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with
35 antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

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After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO polypeptide can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO187, PRO317, PRO301, PRO224 and PRO238 were successfully expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO187, PRO317, PRO301, PRO224 or PRO238 was initially amplified using selected PCR primers. The primers contained restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences were then ligated into an expression vector, which was used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants were first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 was reached. Cultures were then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate-2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30°C with shaking. Samples were removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets were frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6-10 g pellets) was resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution was stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution was centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant was diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. Depending the clarified extract was loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column was washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein was eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein were pooled and stored at 4°C. Protein concentration was estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins were refolded by diluting sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes were chosen so that the final protein concentration was between 50 to 100 micrograms/ml. The refolding solution was stirred gently at 4°C for 12-36 hours. The refolding reaction was quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution was filtered through a 0.22 micron filter and acetonitrile was added to 2-10% final concentration. The refolded protein was chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance were analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein were pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the

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most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO187, PRO317, PRO301, PRO224 and PRO238 proteins, respectively, were pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution.

5 Proteins were formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

EXAMPLE 54: Expression of PRO Polypeptides in Mammalian Cells

This example illustrates preparation of a glycosylated form of a desired PRO polypeptide by recombinant
10 expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO polypeptide-encoding DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO polypeptide DNA using ligation methods such as described in Sambrook et al., *supra*. The resulting vector is called pRK5-PRO polypeptide.

15 In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μ g pRK5-PRO polypeptide DNA is mixed with about 1 μ g DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 μ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl_2 . To this mixture is added, dropwise, 500 μ l of 50 mM HEPES (pH 7.35),
20 280 mM NaCl, 1.5 mM NaPO_4 , and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture
25 medium (alone) or culture medium containing 200 μ Ci/ml ^{35}S -cysteine and 200 μ Ci/ml ^{35}S -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

30 In an alternative technique, PRO polypeptide may be introduced into 293 cells transiently using the dextran sulfate method described by Sompayrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-PRO polypeptide DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium,
35 and re-introduced into the spinner flask containing tissue culture medium, 5 μ g/ml bovine insulin and 0.1 μ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO polypeptide can then be concentrated and purified by any selected

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method, such as dialysis and/or column chromatography.

In another embodiment, PRO polypeptides can be expressed in CHO cells. The pRK5-PRO polypeptide can be transfected into CHO cells using known reagents such as CaPO_4 or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO polypeptide can then be concentrated and purified by any selected method.

Epitope-tagged PRO polypeptide may also be expressed in host CHO cells. The PRO polypeptide may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO polypeptide insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO polypeptide can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

PRO211, PRO217, PRO230, PRO219, PRO245, PRO221, PRO258, PRO301, PRO224, PRO222, PRO234, PRO229, PRO223, PRO328 and PRO332 were successfully expressed in CHO cells by both a transient and a stable expression procedure. In addition, PRO232, PRO265, PRO246, PRO228, PRO227, PRO220, PRO266, PRO269, PRO287, PRO214, PRO231, PRO233, PRO238, PRO244, PRO235, PRO236, PRO262, PRO239, PRO257, PRO260, PRO263, PRO270, PRO271, PRO272, PRO294, PRO295, PRO293, PRO247, PRO303 and PRO268 were successfully transiently expressed in CHO cells.

Stable expression in CHO cells was performed using the following procedure. The proteins were expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins were fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs were subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., *Current Protocols of Molecular Biology*, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., *Nucl. Acids Res.* 24: 9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA were introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect[®] (Quiagen), Dosper[®] or Fugene[®] (Boehringer Mannheim). The cells were grown and described in Lucas et al., supra. Approximately 3×10^7 cells are frozen in an ampule for further growth and production as described below.

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The ampules containing the plasmid DNA were thawed by placement into water bath and mixed by vortexing. The contents were pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant was aspirated and the cells were resuspended in 10 mL of selective media (0.2 μ m filtered PS20 with 5 % 0.2 μ m diafiltered fetal bovine serum). The cells were then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells were transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, a 250 mL, 500 mL and 2000 mL spinners were seeded with 3×10^5 cells/mL. The cell media was exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in US Patent No. 5,122,469, issued June 16, 1992 was actually used. 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH were determined. On day 1, the spinner was sampled and sparging with filtered air was commenced. On day 2, the spinner was sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion). Throughout the production, pH was adjusted as necessary to keep at around 7.2. After 10 days, or until viability dropped below 70%, the cell culture was harvested by centrifugation and filtering through a 0.22 μ m filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins were purified using a Ni-NTA column (Qiagen). Before purification, imidazole was added to the conditioned media to a concentration of 5 mM. The conditioned media was pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column was washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein was subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of were purified from the conditioned media as follows. The conditioned medium was pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column was washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein was immediately neutralized by collecting 1 ml fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein was subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity was assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

PRO211, PRO217, PRO230, PRO232, PRO187, PRO265, PRO219, PRO246, PRO228, PRO533, PRO245, PRO221, PRO227, PRO220, PRO258, PRO266, PRO269, PRO287, PRO214, PRO317, PRO301, PRO224, PRO222, PRO234, PRO231, PRO229, PRO233, PRO238, PRO223, PRO235, PRO236, PRO262, PRO239, PRO257, PRO260, PRO263, PRO270, PRO271, PRO272, PRO294, PRO295, PRO293, PRO247, PRO304, PRO302, PRO307, PRO303, PRO343, PRO328, PRO326, PRO331, PRO332, PRO334, PRO346, PRO268, PRO330, PRO310 and PRO339 were also successfully transiently expressed in COS cells.

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EXAMPLE 55: Expression of PRO Polypeptides in Yeast

The following method describes recombinant expression of a desired PRO polypeptide in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO polypeptides from the ADH2/GAPDH promoter. DNA encoding a desired PRO polypeptide, a selected signal peptide and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of the PRO polypeptide. For secretion, DNA encoding the PRO polypeptide can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, the yeast alpha-factor secretory signal/leader sequence, and linker sequences (if needed) for expression of the PRO polypeptide.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO polypeptide can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing the PRO polypeptide may further be purified using selected column chromatography resins.

EXAMPLE 56: Expression of PRO Polypeptides in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO polypeptides in Baculovirus-infected insect cells.

The desired PRO polypeptide is fused upstream of an epitope tag contained with a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the PRO polypeptide or the desired portion of the PRO polypeptide (such as the sequence encoding the extracellular domain of a transmembrane protein) is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4-5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression is performed as described by O'Reilley et al., Baculovirus expression vectors: A laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO polypeptide can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., *Nature*, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% Glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% Glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL

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of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A_{280} with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% Glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A_{280} baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or western blot with Ni^{2+} -NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO polypeptide are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO polypeptide can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

PRO211, PRO217, PRO230, PRO187, PRO265, PRO246, PRO228, PRO533, PRO245, PRO221, PRO220, PRO258, PRO266, PRO269, PRO287, PRO214, PRO301, PRO224, PRO222, PRO234, PRO231, PRO229, PRO235, PRO239, PRO257, PRO272, PRO294, PRO295, PRO328, PRO326, PRO331, PRO334, PRO346 and PRO310 were successfully expressed in baculovirus infected Sf9 or high5 insect cells. While the expression was actually performed in a 0.5-2 L scale, it can be readily scaled up for larger (e.g. 8 L) preparations. The proteins were expressed as an IgG construct (immunoadhesin), in which the protein extracellular region was fused to an IgG1 constant region sequence containing the hinge, CH2 and CH3 domains and/or in poly-His tagged forms.

Following PCR amplification, the respective coding sequences were subcloned into a baculovirus expression vector (pb.PH.IgG for IgG fusions and pb.PH.His.c for poly-His tagged proteins), and the vector and Baculogold[®] baculovirus DNA (Pharmingen) were co-transfected into 105 *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711), using Lipofectin^{*} (Gibco BRL). pb.PH.IgG and pb.PH.His are modifications of the commercially available baculovirus expression vector pVL1393 (Pharmingen), with modified polylinker regions to include the His or Fc tag sequences. The cells were grown in Hink's TNM-FH medium supplemented with 10% FBS (Hyclone). Cells were incubated for 5 days at 28°C. The supernatant was harvested and subsequently used for the first viral amplification by infecting Sf9 cells in Hink's TNM-FH medium supplemented with 10% FBS at an approximate multiplicity of infection (MOI) of 10. Cells were incubated for 3 days at 28°C. The supernatant was harvested and the expression of the constructs in the baculovirus expression vector was determined by batch binding of 1 ml of supernatant to 25 mL of Ni-NTA beads (QIAGEN) for histidine tagged proteins or Protein-A Sepharose CL-4B beads (Pharmacia) for IgG tagged proteins followed by SDS-PAGE analysis comparing to a known concentration of protein standard by Coomassie blue staining.

The first viral amplification supernatant was used to infect a spinner culture (500 ml) of Sf9 cells grown in ESF-921 medium (Expression Systems LLC) at an approximate MOI of 0.1. Cells were incubated for 3 days at 28°C. The supernatant was harvested and filtered. Batch binding and SDS-PAGE analysis was repeated, as necessary, until expression of the spinner culture was confirmed.

The conditioned medium from the transfected cells (0.5 to 3 L) was harvested by centrifugation to remove the cells and filtered through 0.22 micron filters. For the poly-His tagged constructs, the protein construct were purified using a Ni-NTA column (Qiagen). Before purification, imidazole was added to the conditioned media to a concentration of 5 mM. The conditioned media were pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After

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loading, the column was washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein was subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of proteins were purified from the conditioned media as follows.

- 5 The conditioned media were pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column was washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein was immediately neutralized by collecting 1 ml fractions into tubes containing 275 mL of 1 M Tris buffer, pH 9. The highly purified protein was subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity of the proteins was verified by
- 10 SDS polyacrylamide gel (PEG) electrophoresis and N-terminal amino acid sequencing by Edman degradation.

EXAMPLE 57: Preparation of Antibodies that Bind to PRO Polypeptides

This example illustrates preparation of monoclonal antibodies which can specifically bind to a PRO polypeptide.

- 15 Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified PRO polypeptide, fusion proteins containing the PRO polypeptide, and cells expressing recombinant PRO polypeptide on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

- Mice, such as Balb/c, are immunized with the PRO polypeptide immunogen emulsified in complete Freund's
- 20 adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for
- 25 testing in ELISA assays to detect anti-PRO polypeptide antibodies.

- After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO polypeptide. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can
- 30 then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against the PRO polypeptide. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against the PRO polypeptide is within the skill in the art.

- 35 The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO polypeptide monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished

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using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 58: Chimeric PRO Polypeptides

PRO polypeptides may be expressed as chimeric proteins with one or more additional polypeptide domains added to facilitate protein purification. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS™ extension/affinity purification system (Immunex Corp., Seattle Wash.). The inclusion of a cleavable linker sequence such as Factor XA or enterokinase (Invitrogen, San Diego Calif.) between the purification domain and the PRO polypeptide sequence may be useful to facilitate expression of DNA encoding the PRO polypeptide.

EXAMPLE 59: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (e.g., high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (e.g., a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 60: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in

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such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 61: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant

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structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

5 It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then
10 act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.
15

EXAMPLE 62: Diagnostic Test Using PRO317 Polypeptide-Specific Antibodies

Particular anti-PRO317 polypeptide antibodies are useful for the diagnosis of prepathologic conditions, and chronic or acute diseases such as gynecological diseases or ischemic diseases which are characterized by differences in the amount or distribution of PRO317. PRO317 has been found to be expressed in human kidney and is thus likely
20 to be associated with abnormalities or pathologies which affect this organ. Further, since it is so closely related to EBAF-1, it is likely to affect the endometrium and other genital tissues. Further, due to library sources of certain ESTs, it appears that PRO317 may be involved as well in forming blood vessels and hence to be a modulator of angiogenesis.

Diagnostic tests for PRO317 include methods utilizing the antibody and a label to detect PRO317 in human
25 body fluids, tissues, or extracts of such tissues. The polypeptide and antibodies of the present invention may be used with or without modification. Frequently, the polypeptide and antibodies will be labeled by joining them, either covalently or noncovalently, with a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are known and have been reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent agents, chemiluminescent
30 agents, magnetic particles, and the like. Patents teaching the use of such labels include U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241. Also, recombinant immunoglobulins may be produced as shown in U.S. Pat. No. 4,816,567.

A variety of protocols for measuring soluble or membrane-bound PRO317, using either polyclonal or monoclonal antibodies specific for that PRO317, are known in the art. Examples include enzyme-linked
35 immunosorbent assay (ELISA), radioimmunoassay (RIA), radioreceptor assay (RRA), and fluorescent activated cell sorting (FACS). A two-site monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on PRO317 is preferred, but a competitive binding assay may be employed. These assays

are described, among other places, in Maddox *et al.* J Exp. Med., 158:1211 (1983).

EXAMPLE 63: Identification of PRO317 Receptors

Purified PRO317 is useful for characterization and purification of specific cell surface receptors and other binding molecules. Cells which respond to PRO317 by metabolic changes or other specific responses are likely to express a receptor for PRO317. Such receptors include, but are not limited to, receptors associated with and activated by tyrosine and serine/threonine kinases. See Kolodziejczyk and Hall, *supra*, for a review on known receptors for the TGF- superfamily. Candidate receptors for this superfamily fall into two primary groups, termed type I and type II receptors. Both types are serine/threonine kinases. Upon activation by the appropriate ligand, type I and type II receptors physically interact to form hetero-oligomers and subsequently activate intracellular signaling cascades, ultimately regulating gene transcription and expression. In addition, TGF- binds to a third receptor class, type III, a membrane-anchored proteoglycan lacking the kinase activity typical of signal transducing molecules.

PRO317 receptors or other PRO317-binding molecules may be identified by interaction with radiolabeled PRO317. Radioactive labels may be incorporated into PRO317 by various methods known in the art. A preferred embodiment is the labeling of primary amino groups in PRO317 with ¹²⁵I Bolton-Hunter reagent (Bolton and Hunter, Biochem. J., 133:529 (1973)), which has been used to label other polypeptides without concomitant loss of biological activity (Hebert *et al.*, J. Biol. Chem., 266:18989 (1991); McColl *et al.*, J. Immunol., 150:4550-4555 (1993)). Receptor-bearing cells are incubated with labeled PRO317. The cells are then washed to removed unbound PRO317, and receptor-bound PRO317 is quantified. The data obtained using different concentrations of PRO317 are used to calculate values for the number and affinity of receptors.

Labeled PRO317 is useful as a reagent for purification of its specific receptor. In one embodiment of affinity purification, PRO317 is covalently coupled to a chromatography column. Receptor-bearing cells are extracted, and the extract is passed over the column. The receptor binds to the column by virtue of its biological affinity for PRO317. The receptor is recovered from the column and subjected to N-terminal protein sequencing. This amino acid sequence is then used to design degenerate oligonucleotide probes for cloning the receptor gene.

In an alternative method, mRNA is obtained from receptor-bearing cells and made into a cDNA library. The library is transfected into a population of cells, and those cells expressing the receptor are selected using fluorescently labeled PRO317. The receptor is identified by recovering and sequencing recombinant DNA from highly labeled cells.

In another alternative method, antibodies are raised against the surface of receptor bearing cells, specifically monoclonal antibodies. The monoclonal antibodies are screened to identify those which inhibit the binding of labeled PRO317. These monoclonal antibodies are then used in affinity purification or expression cloning of the receptor.

Soluble receptors or other soluble binding molecules are identified in a similar manner. Labeled PRO317 is incubated with extracts or other appropriate materials derived from the uterus. After incubation, PRO317 complexes larger than the size of purified PRO317 are identified by a sizing technique such as size-exclusion chromatography or density gradient centrifugation and are purified by methods known in the art. The soluble receptors or binding protein(s) are subjected to N-terminal sequencing to obtain information sufficient for database identification, if the soluble protein is known, or for cloning, if the soluble protein is unknown.

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EXAMPLE 64: Determination of PRO317-Induced Cellular Response

The biological activity of PRO317 is measured, for example, by binding of an PRO317 of the invention to an PRO317 receptor. A test compound is screened as an antagonist for its ability to block binding of PRO317 to the receptor. A test compound is screened as an agonist of the PRO317 for its ability to bind an PRO317 receptor and influence the same physiological events as PRO317 using, for example, the KIRA-ELISA assay described by Sadick
 5 *et al.*, Analytical Biochemistry, 235:207-214 (1996) in which activation of a receptor tyrosine kinase is monitored by immuno-capture of the activated receptor and quantitation of the level of ligand-induced phosphorylation. The assay may be adapted to monitor PRO317-induced receptor activation through the use of an PRO317 receptor-specific antibody to capture the activated receptor. These techniques are also applicable to other PRO polypeptides described herein.

10

EXAMPLE 65: Use of PRO224 for Screening Compounds

PRO224 is expressed in a cell stripped of membrane proteins and capable of expressing PRO224. Low density lipoproteins having a detectable label are added to the cells and incubated for a sufficient time for endocytosis. The cells are washed. The cells are then analysed for label bound to the membrane and within the cell after cell lysis.
 15 Detection of the low density lipoproteins within the cell determines that PRO224 is within the family of low density lipoprotein receptor proteins. Members found within this family are then used for screening compounds which affect these receptors, and particularly the uptake of cholesterol via these receptors.

**EXAMPLE 66: Ability of PRO Polypeptides to Inhibit Vascular Endothelial Growth Factor (VEGF) Stimulated
 20 Proliferation of Endothelial Cell Growth**

The ability of various PRO polypeptides to inhibit VEGF stimulated proliferation of endothelial cells was tested. Specifically, bovine adrenal cortical capillary endothelial (ACE) cells (from primary culture, maximum 12-14 passages) were plated on 96-well microtiter plates (Amersham Life Science) at a density of 500 cells/well per 100 μ L in low glucose DMEM, 10% calf serum, 2 mM glutamine, 1x pen/strept and fungizone, supplemented with 3
 25 ng/mL VEGF. Controls were plated the same way but some did not include VEGF. A test sample of the PRO polypeptide of interest was added in a 100 μ L volume for a 200 μ L final volume. Cells were incubated for 6-7 days at 37°C. The media was aspirated and the cells washed 1x with PBS. An acid phosphatase reaction mixture (100 μ L, 0.1M sodium acetate, pH 5.5, 0.1% Triton-100, 10 mM p-nitrophenyl phosphate) was added. After incubation for 2 hours at 37°C, the reaction was stopped by addition of 10 μ L 1N NaOH. OD was measured on microtiter plate
 30 reader at 405 nm. Controls were no cells, cells alone, cells + FGF (5 ng/mL), cells + VEGF (3 ng/mL), cells + VEGF (3 ng/mL) + TGF- β (1 ng/mL), and cells + VEGF (3ng/mL) + LIF (5 ng/mL). (TGF- β at a 1 ng/mL concentration is known to block 70-90% of VEGF stimulated cell proliferation.)

The results were assessed by calculating the percentage inhibition of VEGF (3 ng/mL) stimulated cells proliferation, determined by measuring acid phosphatase activity at OD405 nm, (1) relative to cells without
 35 stimulation, and (2) relative to the reference TGF- β inhibition of VEGF stimulated activity. The results, as shown in Table 2 below, are indicative of the utility of the PRO polypeptides in cancer therapy and specifically in inhibiting tumor angiogenesis. The numerical values (relative inhibition) shown in Table 2 are determined by calculating the

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percent inhibition of VEGF stimulated proliferation by the PRO polypeptide relative to cells without stimulation and then dividing that percentage into the percent inhibition obtained by TGF- β at 1 ng/ml which is known to block 70-90% of VEGF stimulated cell proliferation.

Table 2

5	<u>PRO Name</u>	<u>PRO Concentration</u>	<u>Relative Inhibition</u>
	PRO211	0.01 %	99.0
	PRO211	0.01 %	1.09
	PRO211	0.1 %	0.95
	PRO211	0.1 %	67.0
10	PRO211	1.0 %	0.27
	PRO211	1.0 %	20.0
	PRO217	0.01 %	1.06
	PRO217	0.1 %	0.84
	PRO217	1.0 %	0.39
15	PRO217	2.5 μ M	0.2
	PRO217	25 nM	0.88
	PRO217	250 nM	0.58
	PRO187	0.01 %	0.91
	PRO187	0.1 %	0.82
20	PRO187	1.0 %	0.44
	PRO219	5.7 μ M	0.61
	PRO219	57 nM	1.09
	PRO219	570 nM	0.97
	PRO246	0.01 %	1.04
25	PRO246	0.1 %	1.0
	PRO246	1.0 %	0.49
	PRO228	0.01 %	0.99
	PRO228	0.1 %	0.93
	PRO228	1.0 %	0.57
30	PRO228	0.01 %	0.95
	PRO228	0.01 %	0.98
	PRO228	0.1 %	0.77
	PRO228	0.1 %	0.88
	PRO228	1.0 %	0.16
35	PRO228	1.0 %	0.48
	PRO245	0.01 %	0.76
	PRO245	0.1 %	0.35
	PRO245	1.0 %	0.11
	PRO245	0.48 nM	1.03
40	PRO245	4.8 nM	0.95
	PRO245	48 nM	0.49
	PRO221	0.01 %	1.03
	PRO221	0.01 %	1.06
	PRO221	0.1 %	0.82
45	PRO221	0.1 %	0.93
	PRO221	1.0 %	0.31
	PRO221	1.0 %	0.43
	PRO258	0.01 %	0.98
	PRO258	0.01 %	1.06
50	PRO258	0.1 %	0.95
	PRO258	0.1 %	1.02
	PRO258	1.0 %	0.6
	PRO258	1.0 %	0.69

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Table 2 cont'

	<u>PRO Name</u>	<u>PRO Concentration</u>	<u>Relative Inhibition</u>
	PRO301	7.0 μ M	1.02
	PRO301	70 μ M	0.88
5	PRO301	700 μ M	0.44
	PRO301	0.01 %	0.92
	PRO301	0.1 %	0.85
	PRO301	1.0 %	0.68
	PRO224	0.01 %	101.0
10	PRO224	0.1 %	65.0
	PRO224	1.0 %	23.0
	PRO272	0.01 %	0.95
	PRO272	0.1 %	0.57
	PRO272	1.0 %	0.18
15	PRO328	0.01 %	0.98
	PRO328	0.1 %	0.96
	PRO328	1.0 %	0.6
	PRO331	0.01 %	0.88
	PRO331	0.1 %	0.82
20	PRO331	1.0 %	0.56

EXAMPLE 67: Retinal Neuron Survival

This example demonstrates that PRO220 polypeptides have efficacy in enhancing the survival of retinal neuron cells.

25 Sprague Dawley rat pups at postnatal day 7 (mixed population: glia and retinal neuronal types) are killed by decapitation following CO₂ anesthesia and the eyes are removed under sterile conditions. The neural retina is dissected away from the pigment epithelium and other ocular tissue and then dissociated into a single cell suspension using 0.25% trypsin in Ca²⁺, Mg²⁺-free PBS. The retinas are incubated at 37°C for 7-10 minutes after which the trypsin is inactivated by adding 1 ml soybean trypsin inhibitor. The cells are plated at 100,000 cells per well in 96

30 well plates in DMEM/F12 supplemented with N2 and with or without the specific test PRO polypeptide. Cells for all experiments are grown at 37°C in a water saturated atmosphere of 5% CO₂. After 2-3 days in culture, cells are stained with calcein AM then fixed using 4% paraformaldehyde and stained with DAPI for determination of total cell count. The total cells (fluorescent) are quantified at 20X objective magnification using CCD camera and NIH image software for MacIntosh. Fields in the well are chosen at random.

35 The effect of various concentration of PRO220 polypeptides are reported in Table 3 below where percent survival is calculated by dividing the total number of calcein AM positive cells at 2-3 days in culture by the total number of DAPI-labeled cells at 2-3 days in culture. Anything above 30% survival is considered positive.

Table 3

	<u>PRO Name</u>	<u>PRO Concentration</u>	<u>Percent Survival</u>
40	PRO220	0.01 %	2.4 %
	PRO220	0.01 %	4.1 %
	PRO220	0.1 %	3.0 %
	PRO220	0.1 %	3.1 %
45	PRO220	1.0 %	72.4 %
	PRO220	1.0 %	42.1 %

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EXAMPLE 68: Rod Photoreceptor Survival

This example demonstrates that PRO220 polypeptides have efficacy in enhancing the survival of rod photoreceptor cells.

Sprague Dawley rat pups at 7 day postnatal (mixed population: glia and retinal neuronal cell types) are killed by decapitation following CO₂ anesthesia and the eyes are removed under sterile conditions. The neural retina is dissected away from the pigment epithelium and other ocular tissue and then dissociated into a single cell suspension using 0.25% trypsin in Ca²⁺, Mg²⁺-free PBS. The retinas are incubated at 37°C for 7-10 minutes after which the trypsin is inactivated by adding 1 ml soybean trypsin inhibitor. The cells are plated at 100,000 cells per well in 96 well plates in DMEM/F12 supplemented with N2 and with or without the specific test PRO polypeptide. Cells for all experiments are grown at 37°C in a water saturated atmosphere of 5% CO₂. After 2-3 days in culture, cells are fixed using 4% paraformaldehyde, and then stained using CellTracker Green CMFDA. Rho 4D2 (ascites or IgG 1:100), a monoclonal antibody directed towards the visual pigment rhodopsin is used to detect rod photoreceptor cells by indirect immunofluorescence. The results are reported as % survival: total number of calcein/CellTracker - rhodopsin positive cells at 2-3 days in culture, divided by the total number of rhodopsin positive cells at time 2-3 days in culture. The total cells (fluorescent) are quantified at 20x objective magnification using a CCD camera and NIH image software for MacIntosh. Fields in the well are chosen at random.

The effect of various concentration of PRO220 polypeptides are reported in Table 4 below. Anything above 10% survival is considered positive..

Table 4

<u>PRO Name</u>	<u>PRO Concentration</u>	<u>Percent Survival</u>
PRO220	0.01%	0.0%
PRO220	0.1%	0.0%
PRO220	2.0%	0.0%
PRO220	10%	0.0%
PRO220	20%	66.9%
PRO220	1.0%	56.9%

EXAMPLE 69: Induction of Endothelial Cell Apoptosis

The ability of PRO228 polypeptides to induce apoptosis in endothelial cells was tested in human venous umbilical vein endothelial cells (HUVEC, Cell Systems), using a 96-well format, in 0% serum media supplemented with 100 ng/ml VEGF. (As HUVEC cells are easily dislodged from the plating surface, all pipetting in the wells must be done as gently as practicable.)

The media was aspirated and the cells washed once with PBS. 5 ml of 1 x trypsin was added to the cells in a T-175 flask, and the cells were allowed to stand until they were released from the plate (about 5-10 minutes). Trypsinization was stopped by adding 5 ml of growth media. The cells were spun at 1000 rpm for 5 minutes at 4°C. The media was aspirated and the cells were resuspended in 10 ml of 10% serum complemented medium (Cell Systems), 1 x penn/strep.

The cells were plated on 96-well microtiter plates (Amersham Life Science, cytostar-T scintillating microplate, RPNQ160, sterile, tissue-culture treated, individually wrapped), in 10% serum (CSG-medium, Cell

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Systems), at a density of 2×10^4 cells per well in a total volume of 100 μ l. The PRO228 polypeptide was added in triplicate at dilutions of 1%, 0.33% and 0.11%. Wells without cells were used as a blank and wells with cells only as a negative control. As a positive control 1:3 serial dilutions of 50 μ l of a 3x stock of staurosporine were used. The ability of the PRO228 polypeptide to induce apoptosis was determined using Annexin V, a member of the calcium and phospholipid binding proteins, to detect apoptosis.

- 5 0.2 ml Annexin V - Biotin stock solution (100 μ g/ml) were diluted in 4.6 ml $2 \times \text{Ca}^{2+}$ binding buffer and 2.5% BSA (1:25 dilution). 50 μ ls of the diluted Annexin V - Biotin solution were added to each well (except controls) to a final concentration of 1.0 μ g/ml. The samples were incubated for 10-15 minutes with Annexin-Biotin prior to direct addition of ^{35}S -Streptavidin. ^{35}S -Streptavidin was diluted in $2 \times \text{Ca}^{2+}$ binding buffer, 2.5% BSA and was added to all wells at a final concentration of 3×10^4 cpm/well. The plates were then sealed, centrifuged at 1000
- 10 rpm for 15 minutes and placed on orbital shaker for 2 hours. The analysis was performed on 1450 Microbeta Trilux (Wallac). The results are shown in Table 5 below where percent above background represents the percentage amount of counts per minute above the negative controls. Percents greater than or equal to 30% above background are considered positive.

15

Table 5

<u>PRO Name</u>	<u>PRO Concentration</u>	<u>Percent Above Background</u>
PRO228	0.11%	0.7%
PRO228	0.11%	47.6%
PRO228	0.33%	92.2%
20 PRO228	0.33%	123.7%
PRO228	1.0%	51.4%
PRO228	1.0%	95.3%

EXAMPLE 70: PDB12 Cell Inhibition

- 25 This example demonstrates that various PRO polypeptides have efficacy in inhibiting protein production by PDB12 pancreatic ductal cells.

- PDB12 pancreatic ductal cells are plated on fibronectin coated 96 well plates at 1.5×10^3 cells per well in 100 μ L/180 μ L of growth media. 100 μ L of growth media with the PRO polypeptide test sample or negative control lacking the PRO polypeptide is then added to well, for a final volume of 200 μ L. Controls contain growth medium
- 30 containing a protein shown to be inactive in this assay. Cells are incubated for 4 days at 37°C. 20 μ L of Alamar Blue Dye (AB) is then added to each well and the fluorescent reading is measured at 4 hours post addition of AB, on a microtiter plate reader at 530 nm excitation and 590 nm emission. The standard employed is cells without Bovine Pituitary Extract (BPE) and with various concentrations of BPE. Buffer or CM controls from unknowns are run 2 times on each 96 well plate.

- 35 The results from these assays are shown in Table 6 below wherein percent decrease in protein production is calculated by comparing the Alamar Blue Dye calculated protein concentration produced by the PRO polypeptide-treated cells with the Alamar Blue Dye calculated protein concentration produced by the negative control cells. A percent decrease in protein production of greater than or equal to 25% as compared to the negative control cells is considered positive.

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Table 6

	<u>PRO Name</u>	<u>PRO Concentration</u>	<u>Percent Decrease in Protein Production</u>
	PRO211	0.1%	0.0%
	PRO211	0.01%	0.6%
	PRO211	1.0%	59.7%
5	PRO287	2.0%	22.3%
	PRO287	10%	18.2%
	PRO287	50%	67.5%
	PRO287	2.0%	45.53%
	PRO287	10%	57.3%
10	PRO287	50%	52.24%
	PRO301	2.0%	0.0%
	PRO301	10%	59.8%
	PRO301	50%	65.6%
	PRO293	2.0%	0.0%
15	PRO293	10%	40.4%
	PRO293	50%	56.7%

EXAMPLE 71: Stimulation of Adult Heart Hypertrophy

20 This assay is designed to measure the ability of various PRO polypeptides to stimulate hypertrophy of adult heart.

Ventricular myocytes freshly isolated from adult (250g) Sprague Dawley rats are plated at 2000 cell/well in 180 μ l volume. Cells are isolated and plated on day 1, the PRO polypeptide-containing test samples or growth medium only (negative control) (20 μ l volume) is added on day 2 and the cells are then fixed and stained on day 5. After staining, cell size is visualized wherein cells showing no growth enhancement as compared to control cells are given a value of 0.0, cells showing small to moderate growth enhancement as compared to control cells are given a value of 1.0 and cells showing large growth enhancement as compared to control cells are given a value of 2.0. Any degree of growth enhancement as compared to the negative control cells is considered positive for the assay. The results are shown in Table 7 below.

30

Table 7

	<u>PRO Name</u>	<u>PRO Concentration</u>	<u>Growth Enhancement Score</u>
	PRO287	20%	1.0
	PRO287	20%	1.0
	PRO301	20%	1.0
35	PRO301	20%	1.0
	PRO293	20%	1.0
	PRO293	20%	1.0
	PRO303	20%	1.0
40	PRO303	20%	1.0

EXAMPLE 72: PDB12 Cell Proliferation

This example demonstrates that various PRO polypeptides have efficacy in inducing proliferation of PDB12 pancreatic ductal cells.

PDB12 pancreatic ductal cells are plated on fibronectin coated 96 well plates at 1.5×10^3 cells per well in 100 μ L/180 μ L of growth media. 100 μ L of growth media with the PRO polypeptide test sample or negative control

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lacking the PRO polypeptide is then added to well, for a final volume of 200 μ L. Controls contain growth medium containing a protein shown to be inactive in this assay. Cells are incubated for 4 days at 37°C. 20 μ L of Alamar Blue Dye (AB) is then added to each well and the fluorescent reading is measured at 4 hours post addition of AB, on a microtiter plate reader at 530 nm excitation and 590 nm emission. The standard employed is cells without Bovine Pituitary Extract (BPE) and with various concentrations of BPE. Buffer or growth medium only controls from unknowns are run 2 times on each 96 well plate.

The results from these assays are shown in Table 8 below wherein percent increase in protein production is calculated by comparing the Alamar Blue Dye calculated protein concentration produced by the PRO polypeptide-treated cells with the Alamar Blue Dye calculated protein concentration produced by the negative control cells. A percent increase in protein production of greater than or equal to 25% as compared to the negative control cells is considered positive.

Table 8

<u>PRO Name</u>	<u>PRO Concentration</u>	<u>Percent Increase in Protein Production</u>
PRO301	2.0%	44.0%
PRO301	10%	67.4%
PRO301	50%	185.8%
PRO303	2.0%	27.9%
PRO303	10%	174.9%
PRO303	50%	193.1%

EXAMPLE 73: Enhancement of Heart Neonatal Hypertrophy Induced by PRO224

This assay is designed to measure the ability of PRO224 polypeptides to stimulate hypertrophy of neonatal heart.

Cardiac myocytes from 1-day old Harlan Sprague Dawley rats were obtained. Cells (180 μ l at 7.5×10^4 /ml, serum <0.1%, freshly isolated) are added on day 1 to 96-well plates previously coated with DMEM/F12 + 4% FCS. Test samples containing the test PRO224 polypeptide or growth medium only (negative control) (20 μ l/well) are added directly to the wells on day 1. PGF (20 μ l/well) is then added on day 2 at final concentration of 10^{-6} M. The cells are then stained on day 4 and visually scored on day 5, wherein cells showing no increase in size as compared to negative controls are scored 0.0, cells showing a small to moderate increase in size as compared to negative controls are scored 1.0 and cells showing a large increase in size as compared to negative controls are scored 2.0. The results are shown in Table 9 below.

Table 9

<u>PRO Name</u>	<u>PRO Concentration</u>	<u>Growth Enhancement Score</u>
PRO224	0.01%	0.0
PRO224	0.1%	0.0
PRO224	1.0%	1.0

EXAMPLE 74: In situ Hybridization

In situ hybridization is a powerful and versatile technique for the detection and localization of nucleic acid sequences within cell or tissue preparations. It may be useful, for example, to identify sites of gene expression,

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analyze the tissue distribution of transcription, identify and localize viral infection, follow changes in specific mRNA synthesis and aid in chromosome mapping.

In situ hybridization was performed following an optimized version of the protocol by Lu and Gillett, Cell Vision 1:169-176 (1994), using PCR-generated ³³P-labeled riboprobes. Briefly, formalin-fixed, paraffin-embedded human tissues were sectioned, deparaffinized, deproteinized in proteinase K (20 g/ml) for 15 minutes at 37°C, and further processed for *in situ* hybridization as described by Lu and Gillett, *supra*. A [³³-P] UTP-labeled antisense riboprobe was generated from a PCR product and hybridized at 55°C overnight. The slides were dipped in Kodak NTB2 nuclear track emulsion and exposed for 4 weeks.

³³P-Riboprobe synthesis

6.0 µl (125 mCi) of ³³P-UTP (Amersham BF 1002, SA <2000 Ci/mmol) were speed vac dried. To each tube containing dried ³³P-UTP, the following ingredients were added:

- 2.0 µl 5x transcription buffer
- 1.0 µl DTT (100 mM)
- 2.0 µl NTP mix (2.5 mM : 10 µ; each of 10 mM GTP, CTP & ATP + 10 µl H₂O)
- 1.0 µl UTP (50 µM)
- 1.0 µl Rnasin
- 1.0 µl DNA template (1 µg)
- 1.0 µl H₂O
- 1.0 µl RNA polymerase (for PCR products T3 = AS, T7 = S, usually)

The tubes were incubated at 37°C for one hour. 1.0 µl RQ1 DNase were added, followed by incubation at 37°C for 15 minutes. 90 µl TE (10 mM Tris pH 7.6/1mM EDTA pH 8.0) were added, and the mixture was pipetted onto DE81 paper. The remaining solution was loaded in a Microcon-50 ultrafiltration unit, and spun using program 10 (6 minutes). The filtration unit was inverted over a second tube and spun using program 2 (3 minutes). After the final recovery spin, 100 µl TE were added. 1 µl of the final product was pipetted on DE81 paper and counted in 6 ml of Biofluor II.

The probe was run on a TBE/urea gel. 1-3 µl of the probe or 5 µl of RNA Mrk III were added to 3 µl of loading buffer. After heating on a 95°C heat block for three minutes, the gel was immediately placed on ice. The wells of gel were flushed, the sample loaded, and run at 180-250 volts for 45 minutes. The gel was wrapped in saran wrap and exposed to XAR film with an intensifying screen in -70°C freezer one hour to overnight.

³³P-Hybridization

A. Pretreatment of frozen sections

The slides were removed from the freezer, placed on aluminium trays and thawed at room temperature for 5 minutes. The trays were placed in 55°C incubator for five minutes to reduce condensation. The slides were fixed for 10 minutes in 4% paraformaldehyde on ice in the fume hood, and washed in 0.5 x SSC for 5 minutes, at room temperature (25 ml 20 x SSC + 975 ml SQ H₂O). After deproteinization in 0.5 µg/ml proteinase K for 10 minutes at 37°C (12.5 µl of 10 mg/ml stock in 250 ml prewarmed RNase-free RNase buffer), the sections were washed in 0.5 x SSC for 10 minutes at room temperature. The sections were dehydrated in 70%, 95%, 100% ethanol, 2 minutes each.

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B. Pretreatment of paraffin-embedded sections

The slides were deparaffinized, placed in SQ H₂O, and rinsed twice in 2 x SSC at room temperature, for 5 minutes each time. The sections were deproteinized in 20 µg/ml proteinase K (500 µl of 10 mg/ml in 250 ml RNase-free RNase buffer; 37°C, 15 minutes) - human embryo, or 8 x proteinase K (100 µl in 250 ml RNase buffer, 37°C, 30 minutes) - formalin tissues. Subsequent rinsing in 0.5 x SSC and dehydration were performed as described above.

C. Prehybridization

The slides were laid out in a plastic box lined with Box buffer (4 x SSC, 50% formamide) - saturated filter paper. The tissue was covered with 50 µl of hybridization buffer (3.75g Dextran Sulfate + 6 ml SQ H₂O), vortexed and heated in the microwave for 2 minutes with the cap loosened. After cooling on ice, 18.75 ml formamide, 3.75 ml 20 x SSC and 9 ml SQ H₂O were added, the tissue was vortexed well, and incubated at 42°C for 1-4 hours.

D. Hybridization

1.0 x 10⁶ cpm probe and 1.0 µl tRNA (50 mg/ml stock) per slide were heated at 95°C for 3 minutes. The slides were cooled on ice, and 48 µl hybridization buffer were added per slide. After vortexing, 50 µl ³²P mix were added to 50 µl prehybridization on slide. The slides were incubated overnight at 55°C.

E. Washes

Washing was done 2 x 10 minutes with 2xSSC, EDTA at room temperature (400 ml 20 x SSC + 16 ml 0.25M EDTA, V_f=4L), followed by RNaseA treatment at 37°C for 30 minutes (500 µl of 10 mg/ml in 250 ml RNase buffer = 20 µg/ml). The slides were washed 2 x 10 minutes with 2 x SSC, EDTA at room temperature. The stringency wash conditions were as follows: 2 hours at 55°C, 0.1 x SSC, EDTA (20 ml 20 x SSC + 16 ml EDTA, V_f=4L).

F. Oligonucleotides

In situ analysis was performed on a variety of DNA sequences disclosed herein. The oligonucleotides employed for these analyses are as follows.

(1) DNA33094-1131 (PRO217)

p1 5'-GGATTCTAATACGACTCACTATAGGGCTCAGAAAAGCGCAACAGAGAA-3' (SEQ ID NO:347)
p2 5'-CTATGAAATTAACCCTCACTAAAGGGATGTCTTCCATGCCAACCTTC-3' (SEQ ID NO:348)

(2) DNA33223-1136 (PRO230)

p1 5'-GGATTCTAATACGACTCACTATAGGGCGGCGATGTCCACTGGGGCTAC-3' (SEQ ID NO:349)
p2 5'-CTATGAAATTAACCCTCACTAAAGGGACGAGGAAGATGGGCGGATGGT-3' (SEQ ID NO:350)

(3) DNA34435-1140 (PRO232)

p1 5'-GGATTCTAATACGACTCACTATAGGGCACCCACGCGTCCGGCTGCTT-3' (SEQ ID NO:351)
p2 5'-CTATGAAATTAACCCTCACTAAAGGGACGGGGGACACCACGGACCAGA-3' (SEQ ID NO:352)

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(4) DNA35639-1172 (PRO246)

p1 5'-GGATTCTAATACGACTCACTATAGGGCTTGCTGCGGTTTTTGTTCCTG-3' (SEQ ID NO:353)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGAGCTGCCGATCCCACTGGTATT-3' (SEQ ID NO:354)

(5) DNA49435-1219 (PRO533)

5 p1 5'-GGATTCTAATACGACTCACTATAGGGCGGATCCTGGCCGGCCTCTG-3' (SEQ ID NO:355)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGAGCCCGGGCATGGTCTCAGTTA-3' (SEQ ID NO:356)

(6) DNA35638-1141 (PRO245)

p1 5'-GGATTCTAATACGACTCACTATAGGGCGGGAAGATGGCGAGGAGGAG-3' (SEQ ID NO:357)

10 p2 5'-CTATGAAATTAACCCTCACTAAAGGGACCAAGGCCACAAACGGAAATC-3' (SEQ ID NO:358)

(7) DNA33089-1132 (PRO221)

p1 5'-GGATTCTAATACGACTCACTATAGGGCTGTGCTTTCATTCTGCCAGTA-3' (SEQ ID NO:359)

15 p2 5'-CTATGAAATTAACCCTCACTAAAGGGAGGGTACAATTAAGGGGTGGAT-3' (SEQ ID NO:360)

(8) DNA35918-1174 (PRO258)

p1 5'-GGATTCTAATACGACTCACTATAGGGCCCGCCTCGCTCCTGCTCCTG-3' (SEQ ID NO:361)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGAGGATTGCCGCGACCCTCACAG-3' (SEQ ID NO:362)

20 (9) DNA32286-1191 (PRO214)

p1 5'-GGATTCTAATACGACTCACTATAGGGCCCCTCCTGCCTTCCCTGTCC-3' (SEQ ID NO:363)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGAGTGGTGGCCGCGATTATCTGC-3' (SEQ ID NO:364)

(10) DNA33221-1133 (PRO224)

25 p1 5'-GGATTCTAATACGACTCACTATAGGGCGCAGCGATGGCAGCGATGAGG-3' (SEQ ID NO:365)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGACAGACGGGGCAGAGGGAGTG-3' (SEQ ID NO:366)

(11) DNA35557-1137 (PRO234)

p1 5'-GGATTCTAATACGACTCACTATAGGGCCAGGAGGCGTGAGGAGAAAC-3' (SEQ ID NO:367)

30 p2 5'-CTATGAAATTAACCCTCACTAAAGGGAAAGACATGTCATCGGGAGTGG-3' (SEQ ID NO:368)

(12) DNA33100-1159 (PRO229)

p1 5'-GGATTCTAATACGACTCACTATAGGGCCGGGTGGAGGTGGAACAGAAA-3' (SEQ ID NO:369)

35 p2 5'-CTATGAAATTAACCCTCACTAAAGGGACACAGACAGAGCCCCATACGC-3' (SEQ ID NO:370)

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(13) DNA34431-1177 (PRO263)

p1 5'-GGATTCTAATACGACTCACTATAGGGCCAGGGAAATCCGGATGTCTC-3' (SEQ ID NO:371)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGAGTAAGGGGATGCCACCGAGTA-3' (SEQ ID NO:372)

(14) DNA38268-1188 (PRO295)

5 p1 5'-GGATTCTAATACGACTCACTATAGGGCCAGCTACCCGCAGGAGGAGG-3' (SEQ ID NO:373)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGATCCCAGGTGATGAGGTCCAGA-3' (SEQ ID NO:374)

G. Results

In situ analysis was performed on a variety of DNA sequences disclosed herein. The results from these analyses are as follows.

(1) DNA33094-1131 (PRO217)

Highly distinctive expression pattern, that does not indicate an obvious biological function. In the human embryo it was expressed in outer smooth muscle layer of the GI tract, respiratory cartilage, branching respiratory epithelium, osteoblasts, tendons, gonad, in the optic nerve head and developing dermis. In the adult expression was observed in the epidermal pegs of the chimp tongue, the basal epithelial/myoepithelial cells of the prostate and urinary bladder. Also expressed in the alveolar lining cells of the adult lung, mesenchymal cells juxtaposed to erectile tissue in the penis and the cerebral cortex (probably glial cells). In the kidney, expression was only seen in disease, in cells surrounding thyroidized renal tubules.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, myocardium, aorta, spleen, lymph node, gall bladder, pancreas, lung, skin, eye (inc. retina), prostate, bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

- 25 (a) Chimp Tissues: Salivary gland, stomach, thyroid, parathyroid, skin, thymus, ovary, lymph node.
 (b) Rhesus Monkey Tissues: Cerebral cortex, hippocampus, cerebellum, penis.

(2) DNA33223-1136 (PRO230)

Sections show an intense signal associated with arterial and venous vessels in the fetus. In arteries the signal appeared to be confined to smooth-muscle/pericytic cells. The signal is also seen in capillary vessels and in glomeruli. It is not clear whether or not endothelial cells are expressing this mRNA. Expression is also observed in epithelial cells in the fetal lens. Strong expression was also seen in cells within placental trophoblastic villi, these cells lie between the trophoblast and the fibroblast-like cells that express HGF - uncertain histogenesis. In the adult, there was no evidence of expression and the wall of the aorta and most vessels appear to be negative. However, expression was seen over vascular channels in the normal prostate and in the epithelium lining the gallbladder. Insurers expression was seen in the vessels of the soft-tissue sarcoma and a renal cell carcinoma. In summary, this is a molecule that shows relatively specific vascular expression in the fetus as well as in some adult organs. Expression was also

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observed in the fetal lens and the adult gallbladder.

In a secondary screen, vascular expression was observed, similar to that observed above, seen in fetal blocks. Expression is on vascular smooth muscle, rather than endothelium. Expression also seen in smooth muscle of the developing oesophagus, so as reported previously, this molecule is not vascular specific. Expression was examined in 4 lung and 4 breast carcinomas. Substantial expression was seen in vascular smooth-muscle of at least 3/4 lung cancers and 2/4 breast cancers. In addition, in one breast carcinoma, expression was observed in peritumoral stromal cells of uncertain histogenesis (possibly myofibroblasts). No endothelial cell expression was observed in this study.

(3) DNA34435-1140 (PRO232)

Strong expression in prostatic epithelium and bladder epithelium, lower level of expression in bronchial epithelium. High background / low level expression seen in a number of sites, including among others, bone, blood, chondrosarcoma, adult heart and fetal liver. It is felt that this level of signal represents background, partly because signal at this level was seen over the blood. All other tissues negative.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis, testis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, spleen, lymph node, pancreas, lung, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

Chimp Tissues: adrenal

Rhesus Monkey Tissues: Cerebral cortex, hippocampus

In a secondary screen, expression was observed in the epithelium of the prostate, the superficial layers of the urethelium of the urinary bladder, the urethelium lining the renal pelvis and the urethelium of the ureter (1 out of 2 experiments). The urethra of a rhesus monkey was negative; it is unclear whether this represents a true lack of expression by the urethra, or if it is the result of a failure of the probe to cross react with rhesus tissue. The findings in the prostate and bladder are similar to those previously described using an isotopic detection technique. Expression of the mRNA for this antigen is NOT prostate epithelial specific. The antigen may serve as a useful marker for urethelial derived tissues. Expression in the superficial, post-mitotic cells, of the urinary tract epithelium also suggest that it is unlikely to represent a specific stem cell marker, as this would be expected to be expressed specifically in basal epithelium.

(4) DNA35639-1172 (PRO246)

Strongly expressed in fetal vascular endothelium, including tissues of the CNS. Lower level of expression in adult vasculature, including the CNS. Not obviously expressed at higher levels in tumor vascular endothelium. Signal also seen over bone matrix and adult spleen, not obviously cell associated, probably related to non-specific background at these sites.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid,

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lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis, testis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, spleen, lymph node, pancreas, lung, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

5 Chimp Tissues: adrenal

Rhesus Monkey Tissues: Cerebral cortex, hippocampus

(5) DNA49435-1219 (PRO533)

10 Moderate expression over cortical neurones in the fetal brain. Expression over the inner aspect of the fetal retina, possible expression in the developing lens. Expression over fetal skin, cartilage, small intestine, placental villi and umbilical cord. In adult tissues there is an extremely high level of expression over the gallbladder epithelium. Moderate expression over the adult kidney, gastric and colonic epithelia. Low-level expression was observed over many cell types in many tissues, this may be related to stickiness of the probe, these data should therefore be interpreted with a degree of caution.

15 Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis, testis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, spleen, lymph node, pancreas, lung, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure).

20 Non-human primate tissues examined:

Chimp Tissues: adrenal

Rhesus Monkey Tissues: Cerebral cortex, hippocampus, cerebellum.

(6) DNA35638-1141 (PRO245)

25 Expression observed in the endothelium lining a subset of fetal and placental vessels. Endothelial expression was confined to these tissue blocks. Expression also observed over intermediate trophoblast cells of placenta. All other tissues negative.

30 Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult tissues examined: Liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma, thyroid (chimp), parathyroid (chimp) ovary (chimp) and chondrosarcoma. Acetaminophen induced liver injury and hepatic

35 cirrhosis

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(7) DNA33089-1132 (PRO221)

Specific expression over fetal cerebral white and grey matter, as well as over neurones in the spinal cord. Probe appears to cross react with rat. Low level of expression over cerebellar neurones in adult rhesus brain. All other tissues negative.

Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult tissues examined: Liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma and chondrosarcoma. Acetaminophen induced liver injury and hepatic cirrhosis

10

(8) DNA35918-1174 (PRO258)

Strong expression in the nervous system. In the rhesus monkey brain expression is observed in cortical, hippocampal and cerebellar neurones. Expression over spinal neurones in the fetal spinal cord, the developing brain and the inner aspects of the fetal retina. Expression over developing dorsal root and autonomic ganglia as well as enteric nerves. Expression observed over ganglion cells in the adult prostate. In the rat, there is strong expression over the developing hind brain and spinal cord. Strong expression over interstitial cells in the placental villi. All other tissues were negative.

Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult tissues examined: Liver, kidney, renal cell carcinoma, adrenal, aorta, spleen, lymph node, pancreas, lung, myocardium, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), bladder, prostate, stomach, gastric carcinoma, colon, colonic carcinoma, thyroid (chimp), parathyroid (chimp) ovary (chimp) and chondrosarcoma. Acetaminophen induced liver injury and hepatic cirrhosis.

25

(9) DNA32286-1191 (PRO214)

Fetal tissue: Low level throughout mesenchyme. Moderate expression in placental stromal cells in membranous tissues and in thyroid. Low level expression in cortical neurones. Adult tissue: all negative.

Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult tissues examined include: Liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung and skin.

35 (10) DNA33221-1133 (PRO224)

Expression limited to vascular endothelium in fetal spleen, adult spleen, fetal liver, adult thyroid and adult lymph node (chimp). Additional site of expression is the developing

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spinal ganglia. All other tissues negative.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

- Adult human tissues examined: Kidney (normal and end-stage), adrenal, myocardium, aorta, spleen, lymph node, 5 pancreas, lung, skin, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

Chimp Tissues: Salivary gland, stomach, thyroid, parathyroid, skin, thymus, ovary, lymph node.

Rhesus Monkey Tissues: Cerebral cortex, hippocampus, cerebellum, penis.

- 10 (11) DNA35557-1137 (PRO234)

Specific expression over developing motor neurones in ventral aspect of the fetal spinal cord (will develop into ventral horns of spinal cord). All other tissues negative. Possible role in growth, differentiation and/or development of spinal motor neurons.

- 15 Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult tissues examined: Liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma and chondrosarcoma. Acetaminophen induced liver injury and hepatic cirrhosis

20

- (12) DNA33100-1159 (PRO229)

Striking expression in mononuclear phagocytes (macrophages) of fetal and adult spleen, liver, lymph node and adult thymus (in tingible body macrophages). The highest expression is in the spleen. All other tissues negative. Localisation and homology are entirely consistent with a role as a scavenger receptor for cells of the 25 reticuloendothelial system. Expression also observed in placental mononuclear cells.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

- 30 Adult human tissues examined: Kidney (normal and end-stage), adrenal, myocardium, aorta, spleen, lymph node, gall bladder, pancreas, lung, skin, eye (inc. retina), prostate, bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

Chimp Tissues: Salivary gland, stomach, thyroid, parathyroid, skin, thymus, ovary, lymph node.

Rhesus Monkey Tissues: Cerebral cortex, hippocampus, cerebellum, penis.

- 35 (13) DNA34431-1177 (PRO263)

Widespread expression in human fetal tissues and placenta over mononuclear cells, probably macrophages +/- lymphocytes. The cellular distribution follows a perivascular pattern in many tissues. Strong expression also seen

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in epithelial cells of the fetal adrenal cortex. All adult tissues were negative.

Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

- Adult tissues examined: Liver, kidney, adrenal, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm),
5 hippocampus(rm), cerebellum(rm), bladder, stomach, colon and colonic carcinoma. Acetaminophen induced liver injury and hepatic cirrhosis.

A secondary screen evidenced expression over stromal mononuclear cells probably histiocytes.

(14) DNA38268-1188 (PRO295)

- 10 High expression over ganglion cells in human fetal spinal ganglia and over large neurones in the anterior horns of the developing spinal cord. In the adult there is expression in the chimp adrenal medulla (neural), neurones of the rhesus monkey brain (hippocampus [+ + +] and cerebral cortex) and neurones in ganglia in the normal adult human prostate (the only section that contains ganglion cells, ie expression in this cell type is presumed NOT to be confined to the prostate). All other tissues negative.

- 15 Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, great vessels, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis, testis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, spleen, lymph node, pancreas, lung, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure).

- 20 Non-human primate tissues examined:

Chimp Tissues: adrenal

Rhesus Monkey Tissues: Cerebral cortex, hippocampus, cerebellum.

Deposit of Material

- 25 The following materials have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA32292-1131	ATCC 209258	September 16, 1997
	DNA33094-1131	ATCC 209256	September 16, 1997
30	DNA33223-1136	ATCC 209264	September 16, 1997
	DNA34435-1140	ATCC 209250	September 16, 1997
	DNA27864-1155	ATCC 209375	October 16, 1997
	DNA36350-1158	ATCC 209378	October 16, 1997
	DNA32290-1164	ATCC 209384	October 16, 1997
35	DNA35639-1172	ATCC 209396	October 17, 1997
	DNA33092-1202	ATCC 209420	October 28, 1997
	DNA49435-1219	ATCC 209480	November 21, 1997
	DNA35638-1141	ATCC 209265	September 16, 1997
	DNA32298-1132	ATCC 209257	September 16, 1997
40	DNA33089-1132	ATCC 209262	September 16, 1997
	DNA33786-1132	ATCC 209253	September 16, 1997
	DNA35918-1174	ATCC 209402	October 17, 1997

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	DNA37150-1178	ATCC 209401	October 17, 1997
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5	DNA40628-1216	ATCC 209432	November 7, 1997
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	DNA43466-1225	ATCC 209490	November 21, 1997
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45	DNA35668-1171	ATCC 209371	October 16, 1997

These deposit were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined

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by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the
5 invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are
10 functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the
15 appended claims.

SEQUENCE LISTING

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 Asn Cys Ala Gly Ser Trp Ala Phe Ser Thr Ala Ala Val Ala Ser Asp
 225 230 235 240
 Arg Val Ser Ile His Ser Leu Gly His Met Thr Pro Val Leu Ser Pro
 245 250 255
 Gln Asn Leu Leu Ser Cys Asp Thr His Gln Gln Gln Gly Cys Arg Gly
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 Gly Arg Leu Asp Gly Ala Trp Trp Phe Leu Arg Arg Arg Gly Val Val
 275 280 285
 Ser Asp His Cys Tyr Pro Phe Ser Gly Arg Glu Arg Asp Glu Ala Gly
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 Pro Ala Pro Pro Cys Met Met His Ser Arg Ala Met Gly Arg Gly Lys
 305 310 315 320
 Arg Gln Ala Thr Ala His Cys Pro Asn Ser Tyr Val Asn Asn Asn Asp
 325 330 335
 Ile Tyr Gln Val Thr Pro Val Tyr Arg Leu Gly Ser Asn Asp Lys Glu
 340 345 350
 Ile Met Lys Glu Leu Met Glu Asn Gly Pro Val Gln Ala Leu Met Glu
 355 360 365

Val His Glu Asp Phe Phe Leu Tyr Lys Gly Gly Ile Tyr Ser His Thr
 370 375 380

Pro Val Ser Leu Gly Arg Pro Glu Arg Tyr Arg Arg His Gly Thr His
 385 390 395 400

Ser Val Lys Ile Thr Gly Trp Gly Glu Glu Thr Leu Pro Asp Gly Arg
 405 410 415

Thr Leu Lys Tyr Trp Thr Ala Ala Asn Ser Trp Gly Pro Ala Trp Gly
 420 425 430

Glu Arg Gly His Phe Arg Ile Val Arg Gly Val Asn Glu Cys Asp Ile
 435 440 445

Glu Ser Phe Val Leu Gly Val Trp Gly Arg Val Gly Met Glu Asp Met
 450 455 460

Gly His His
 465

<210> 13
 <211> 533
 <212> DNA
 <213> Homo sapiens

<400> 13
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 ccaccagcag cagggtgccc gcgntgggag tctcgatggt gcctgggtgg tcttgctgctg 180
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 gccagtgagc cttgggaggg cagagagata ccgccggcat gggacccact cag 533

<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 14
 ttcgaggcct ctgagaagtg gccc 24

<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 15
 ggcgggtatct ctctggcctc cc 22

<210> 16

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 16
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<210> 17
 <211> 960
 <212> DNA
 <213> Homo sapiens

<400> 17
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<210> 18
 <211> 114
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Leu Thr Val Ile Ser Lys Gly Cys Ser Leu Asn Cys Val Asp Asp
 50 55 60
 Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn Ile Thr Cys Cys Asp Thr
 65 70 75 80
 Asp Leu Cys Asn Ala Ser Gly Ala His Ala Leu Gln Pro Ala Ala Ala
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 Gln Leu

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 19
 tgctgtgcta ctcctgcaaa gccc 24

<210> 20
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 20
 tgcacaagtc ggtgtcacag cacg 24

<210> 21
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 21
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<210> 22
 <211> 1175
 <212> DNA
 <213> Homo sapiens

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23

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Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
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His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
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<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 24

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<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic

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<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic

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41

<210> 27

<211> 2479

<212> DNA

<213> Homo sapiens

<400> 27

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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
      20              25              30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
      35              40              45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
      50              55              60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
      65              70              75              80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
      85              90              95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
      100             105             110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
      115             120             125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
      130             135             140

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

Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
      165             170             175

Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
      180             185             190

Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
      195             200             205

Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
      210             215             220

Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
      225             230             235             240

Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
      245             250             255

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 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
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 405 410 415
 Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val
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 Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met
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 Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly
 450 455 460
 Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu
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 Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala
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 Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser
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 Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys
 565 570 575

Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly
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 Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln
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 Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu
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 Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His
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 His Cys His Thr
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<210> 29
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 29
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<210> 30
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 30
 gcaggacaac cagataaacc ac 22

<210> 31
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 31
 acgcagattt gagaaggctg tc 22

<210> 32
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Synthetic

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46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

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<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

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Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
      20              25              30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
      35              40              45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
      50              55              60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
      65              70              75              80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
      85              90              95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
      100              105              110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
      115              120              125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
      130              135              140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
      145              150              155              160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
      165              170              175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
      180              185              190

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

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
      210              215              220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His
      225              230              235              240

Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile
      245              250              255

Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser

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260							265							270						
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		275							280			285								
Asn	Cys	Glu	Gln	Leu	Cys	Val	Asn	Val	Pro	Gly	Ser	Phe	Val	Cys	Gln					
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Cys	Tyr	Ser	Gly	Tyr	Ala	Leu	Ala	Glu	Asp	Gly	Lys	Arg	Cys	Val	Ala					
305					310					315					320					
Val	Asp	Tyr	Cys	Ala	Ser	Glu	Asn	His	Gly	Cys	Glu	His	Glu	Cys	Val					
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Asn	Ala	Asp	Gly	Ser	Tyr	Leu	Cys	Gln	Cys	His	Glu	Gly	Phe	Ala	Leu					
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Asn	Pro	Asp	Glu	Lys	Thr	Cys	Thr	Arg	Ile	Asn	Tyr	Cys	Ala	Leu	Asn					
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Lys	Pro	Gly	Cys	Glu	His	Glu	Cys	Val	Asn	Met	Glu	Glu	Ser	Tyr	Tyr					
	370					375					380									
Cys	Arg	Cys	His	Arg	Gly	Tyr	Thr	Leu	Asp	Pro	Asn	Gly	Lys	Thr	Cys					
385					390					395					400					
Ser	Arg	Val	Asp	His	Cys	Ala	Gln	Gln	Asp	His	Gly	Cys	Glu	Gln	Leu					
				405					410					415						
Cys	Leu	Asn	Thr	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Ser	Glu	Gly	Phe					
			420					425					430							
Leu	Ile	Asn	Glu	Asp	Leu	Lys	Thr	Cys	Ser	Arg	Val	Asp	Tyr	Cys	Leu					
		435						440				445								
Leu	Ser	Asp	His	Gly	Cys	Glu	Tyr	Ser	Cys	Val	Asn	Met	Asp	Arg	Ser					
	450					455					460									
Phe	Ala	Cys	Gln	Cys	Pro	Glu	Gly	His	Val	Leu	Arg	Ser	Asp	Gly	Lys					
465					470					475					480					
Thr	Cys	Ala	Lys	Leu	Asp	Ser	Cys	Ala	Leu	Gly	Asp	His	Gly	Cys	Glu					
				485					490					495						
His	Ser	Cys	Val	Ser	Ser	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Phe	Glu					
			500					505					510							
Gly	Tyr	Ile	Leu	Arg	Glu	Asp	Gly	Lys	Thr	Cys	Arg	Arg	Lys	Asp	Val					
		515						520				525								
Cys	Gln	Ala	Ile	Asp	His	Gly	Cys	Glu	His	Ile	Cys	Val	Asn	Ser	Asp					
	530					535					540									
Asp	Ser	Tyr	Thr	Cys	Glu	Cys	Leu	Glu	Gly	Phe	Arg	Leu	Ala	Glu	Asp					
545					550					555					560					
Gly	Lys	Arg	Cys	Arg	Arg	Lys	Asp	Val	Cys	Lys	Ser	Thr	His	His	Gly					
				565					570					575						
Cys	Glu	His	Ile	Cys	Val	Asn	Asn	Gly	Asn	Ser	Tyr	Ile	Cys	Lys	Cys					
			580					585					590							

Ser	Glu	Gly	Phe	Val	Leu	Ala	Glu	Asp	Gly	Arg	Arg	Cys	Lys	Lys	Cys	595	600	605
Thr	Glu	Gly	Pro	Ile	Asp	Leu	Val	Phe	Val	Ile	Asp	Gly	Ser	Lys	Ser	610	615	620
Leu	Gly	Glu	Glu	Asn	Phe	Glu	Val	Val	Lys	Gln	Phe	Val	Thr	Gly	Ile	625	630	635
Ile	Asp	Ser	Leu	Thr	Ile	Ser	Pro	Lys	Ala	Ala	Arg	Val	Gly	Leu	Leu	645	650	655
Gln	Tyr	Ser	Thr	Gln	Val	His	Thr	Glu	Phe	Thr	Leu	Arg	Asn	Phe	Asn	660	665	670
Ser	Ala	Lys	Asp	Met	Lys	Lys	Ala	Val	Ala	His	Met	Lys	Tyr	Met	Gly	675	680	685
Lys	Gly	Ser	Met	Thr	Gly	Leu	Ala	Leu	Lys	His	Met	Phe	Glu	Arg	Ser	690	695	700
Phe	Thr	Gln	Gly	Glu	Gly	Ala	Arg	Pro	Leu	Ser	Thr	Arg	Val	Pro	Arg	705	710	715
Ala	Ala	Ile	Val	Phe	Thr	Asp	Gly	Arg	Ala	Gln	Asp	Asp	Val	Ser	Glu	725	730	735
Trp	Ala	Ser	Lys	Ala	Lys	Ala	Asn	Gly	Ile	Thr	Met	Tyr	Ala	Val	Gly	740	745	750
Val	Gly	Lys	Ala	Ile	Glu	Glu	Glu	Leu	Gln	Glu	Ile	Ala	Ser	Glu	Pro	755	760	765
Thr	Asn	Lys	His	Leu	Phe	Tyr	Ala	Glu	Asp	Phe	Ser	Thr	Met	Asp	Glu	770	775	780
Ile	Ser	Glu	Lys	Leu	Lys	Lys	Gly	Ile	Cys	Glu	Ala	Leu	Glu	Asp	Ser	785	790	795
Asp	Gly	Arg	Gln	Asp	Ser	Pro	Ala	Gly	Glu	Leu	Pro	Lys	Thr	Val	Gln	805	810	815
Gln	Pro	Thr	Glu	Ser	Glu	Pro	Val	Thr	Ile	Asn	Ile	Gln	Asp	Leu	Leu	820	825	830
Ser	Cys	Ser	Asn	Phe	Ala	Val	Gln	His	Arg	Tyr	Leu	Phe	Glu	Glu	Asp	835	840	845
Asn	Leu	Leu	Arg	Ser	Thr	Gln	Lys	Leu	Ser	His	Ser	Thr	Lys	Pro	Ser	850	855	860
Gly	Ser	Pro	Leu	Glu	Glu	Lys	His	Asp	Gln	Cys	Lys	Cys	Glu	Asn	Leu	865	870	875
Ile	Met	Phe	Gln	Asn	Leu	Ala	Asn	Glu	Glu	Val	Arg	Lys	Leu	Thr	Gln	885	890	895
Arg	Leu	Glu	Glu	Met	Thr	Gln	Arg	Met	Glu	Ala	Leu	Glu	Asn	Arg	Leu	900	905	910

Arg Tyr Arg
915

<210> 35
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 35
gtgaccctgg ttgtgaatac tcc 23

<210> 36
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 36
acagccatgg tctatagctt gg 22

<210> 37
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 37
gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag 45

<210> 38
<211> 1813
<212> DNA
<213> Homo sapiens

<400> 38
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gggccatgat ttccctcccg gggcccctgg tgaccaactt gctgcggttt ttgttcctgg 180
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<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

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Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu
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Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln
          20             25             30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
      35             40             45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
      50             55             60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
      65             70             75             80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro
          85             90             95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg
          100             105             110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val
          115             120             125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
          130             135             140

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

Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
          165             170             175

Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
          180             185             190

Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
          195             200             205

Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
          210             215             220

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Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
 225 230 235 240
 Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
 245 250 255
 Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
 260 265 270
 Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
 275 280 285
 Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300
 Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320
 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335
 Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350
 Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
 355 360 365
 Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
 370 375 380
 Gln Ala Gly Ser Leu Val
 385 390

<210> 40
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 40
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22

<210> 41
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 41
 attgtgggcc ttgcagacat agac

24

<210> 42
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 42
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<210> 43
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 43
 gtgtgacaca gcgtgggc 18

<210> 44
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 44
 gaccggcagg cttctgcg 18

<210> 45
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 45
 cagcagcttc agccaccagg agtgg 25

<210> 46
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 46
 ctgagccgtg ggctgcagtc tcgc 24

<210> 47
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 47
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48
 <211> 2799
 <212> DNA
 <213> Homo sapiens

<400> 48
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 aattgcacca agacaccttg tctcccaaat gcaaaatgtg aaatacgcaa tgggaattgaa 120
 gcctgctatt gcaacatggg attttcagga aatgggtgtca caatttgtga agatgataat 180
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 gctttgctac aagaagtcta tagaaattct gtgacagatc tttcaccaac agatataatt 480
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2799

<210> 49
 <211> 690
 <212> PRT
 <213> Homo sapiens

<400> 49

Met	Lys	Arg	Leu	Pro	Leu	Leu	Val	Val	Phe	Ser	Thr	Leu	Leu	Asn	Cys	1	5	10	15
Ser	Tyr	Thr	Gln	Asn	Cys	Thr	Lys	Thr	Pro	Cys	Leu	Pro	Asn	Ala	Lys	20	25	30	
Cys	Glu	Ile	Arg	Asn	Gly	Ile	Glu	Ala	Cys	Tyr	Cys	Asn	Met	Gly	Phe	35	40	45	
Ser	Gly	Asn	Gly	Val	Thr	Ile	Cys	Glu	Asp	Asp	Asn	Glu	Cys	Gly	Asn	50	55	60	
Leu	Thr	Gln	Ser	Cys	Gly	Glu	Asn	Ala	Asn	Cys	Thr	Asn	Thr	Glu	Gly	65	70	75	80
Ser	Tyr	Tyr	Cys	Met	Cys	Val	Pro	Gly	Phe	Arg	Ser	Ser	Ser	Asn	Gln	85	90	95	
Asp	Arg	Phe	Ile	Thr	Asn	Asp	Gly	Thr	Val	Cys	Ile	Glu	Asn	Val	Asn	100	105	110	
Ala	Asn	Cys	His	Leu	Asp	Asn	Val	Cys	Ile	Ala	Ala	Asn	Ile	Asn	Lys	115	120	125	
Thr	Leu	Thr	Lys	Ile	Arg	Ser	Ile	Lys	Glu	Pro	Val	Ala	Leu	Leu	Gln	130	135	140	
Glu	Val	Tyr	Arg	Asn	Ser	Val	Thr	Asp	Leu	Ser	Pro	Thr	Asp	Ile	Ile	145	150	155	160
Thr	Tyr	Ile	Glu	Ile	Leu	Ala	Glu	Ser	Ser	Ser	Leu	Leu	Gly	Tyr	Lys	165	170	175	
Asn	Asn	Thr	Ile	Ser	Ala	Lys	Asp	Thr	Leu	Ser	Asn	Ser	Thr	Leu	Thr	180	185	190	
Glu	Phe	Val	Lys	Thr	Val	Asn	Asn	Phe	Val	Gln	Arg	Asp	Thr	Phe	Val	195	200	205	
Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys	210	215	220	
Leu	Met	His	Thr	Val	Glu	Gln	Ala	Thr	Leu	Arg	Ile	Ser	Gln	Ser	Phe	225	230	235	240
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys	245	250	255	
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met	260	265	270	
Asn	Met	Asp	Gly	Asp	Tyr	Ile	Asn	Ile	Phe	Pro	Lys	Arg	Lys	Ala	Ala	275	280	285	
Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser	290	295	300	
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln	305	310	315	320
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile				

				325					330					335			
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys		
			340					345					350				
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser		
		355					360					365					
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp		
	370					375					380						
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser		
385					390					395					400		
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly		
				405					410					415			
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln		
			420					425					430				
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr		
		435					440					445					
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys		
	450					455					460						
Asn	Leu	Cys	Cys	Ser	Leu	Phe	Leu	Ala	Glu	Leu	Val	Phe	Leu	Val	Gly		
465					470					475					480		
Ile	Asn	Thr	Asn	Thr	Asn	Lys	Leu	Phe	Cys	Ser	Ile	Ile	Ala	Gly	Leu		
				485					490					495			
Leu	His	Tyr	Phe	Phe	Leu	Ala	Ala	Phe	Ala	Trp	Met	Cys	Ile	Glu	Gly		
			500					505					510				
Ile	His	Leu	Tyr	Leu	Ile	Val	Val	Gly	Val	Ile	Tyr	Asn	Lys	Gly	Phe		
		515					520					525					
Leu	His	Lys	Asn	Phe	Tyr	Ile	Phe	Gly	Tyr	Leu	Ser	Pro	Ala	Val	Val		
	530					535					540						
Val	Gly	Phe	Ser	Ala	Ala	Leu	Gly	Tyr	Arg	Tyr	Tyr	Gly	Thr	Thr	Lys		
545					550					555					560		
Val	Cys	Trp	Leu	Ser	Thr	Glu	Asn	Asn	Phe	Ile	Trp	Ser	Phe	Ile	Gly		
				565					570					575			
Pro	Ala	Cys	Leu	Ile	Ile	Leu	Val	Asn	Leu	Leu	Ala	Phe	Gly	Val	Ile		
			580					585					590				
Ile	Tyr	Lys	Val	Phe	Arg	His	Thr	Ala	Gly	Leu	Lys	Pro	Glu	Val	Ser		
		595					600					605					
Cys	Phe	Glu	Asn	Ile	Arg	Ser	Cys	Ala	Arg	Gly	Ala	Leu	Ala	Leu	Leu		
	610					615					620						
Phe	Leu	Leu	Gly	Thr	Thr	Trp	Ile	Phe	Gly	Val	Leu	His	Val	Val	His		
625					630					635					640		
Ala	Ser	Val	Val	Thr	Ala	Tyr	Leu	Phe	Thr	Val	Ser	Asn	Ala	Phe	Gln		
				645					650					655			

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
 675 680 685

Leu Arg
 690

<210> 50
 <211> 282
 <212> DNA
 <213> Homo sapiens

<400> 50
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 cagagggctg tgagctgaca tactcaaatg agaccacac ctcatgccgc tgtaatcacc 120
 tgacacattt tgcaattttg atgtcctctg gtccttccat tggattataa gattataata 180
 ttcttacaag gatcactcaa ctaggaataa ttatttcact gatttgtctt gccatatgca 240
 tttttacctt ctggttcttc agtgaaattc aaagcaccag ga 282

<210> 51
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 51
 ggtaatgagc tccattacag 20

<210> 52
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 52
 ggagtagaaa gcgcatgg 18

<210> 53
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 53
 cacctgatac catgaatggc ag 22

<210> 54
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 57

atgagacca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2133

<212> DNA

<213> Homo sapiens

<400> 58

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gctaagcgag gcctcctcct cccgcagatc cgaacggcct gggcggggtc acccgggctg 120
ggacaagaag ccgcccgcctg cctgccccggg cccggggagg gggctggggc tggggccgga 180
ggcgggggtgt gagtgggtgt gtgcgggggg cgagggttg atgcagtccc gataagaaat 240
gctcgggtgt cttgggcacc taccggtggg ggccgtaagg cgctactata taacgctgcc 300
ggccctgagc cgccgagccg tccgagcagg agcgctgcgt ccaggatcta gggcacgacc 360
atcccaacce ggcattcaca gccccgcagc gcatccggtc gccggccagc ttccgcaccc 420
catcgccgga gctgcgccga gagccccagg gaggtgccat gcggagcggg tgtgtggtgg 480
tccacgtatg gatcctggcc ggcctctggc tggcctggc cgggcgcccc ctgccttct 540
cggacgcggg gccccacgtg cactacggct ggggcgaccc catccgcctg cggcacctgt 600
acacctccgg cccccacggg ctctccagct gcttcctgcg catccgtgcc gacggcgtcg 660
tggactgcgc gcggggccag agcgcgcaca gtttgctgga gatcaaggca gtcgctctgc 720
ggaccgtggc catcaagggc gtgcacagcg tgcgtacct ctgcatgggc gccgacggca 780
agatgcaggg gctgcttcag tactcggagg aagactgtgc ttctgaggag gagatccgcc 840
cagatggcta caatgtgtac cgatccgaga agcaccgcct cccggtctcc ctgagcagtg 900
ccaaacagcg gcagctgtac aagaacagag gctttcttcc actctctcat ttccctgcca 960

```



```

tgctgccccat ggtcccagag gagcctgagg acctcagggg ccacttggaat tctgacatgt 1020
tctcttcgcc cctgggagacc gacagcatgg acccatttgg gcttgtcacc ggactggagg 1080
ccgtgaggag tcccagcttt gagaagtaac tgagaccatg cccgggcctc ttcactgctg 1140
ccaggggctg tggtagctgc agcgtggggg acgtgcttct acaagaacag tcctgagtc 1200
acgttctgtt tagctttagg aagaaacatc tagaagttgt acatattcag agttttccat 1260
tggcagtgcc agtttctagc caatagactt gtctgatcat aacattggaa gccttgtact 1320
tggcccagct gttgcctggg cccccattc tgctccctcg aggttgctgg acaagctgct 1380
gcactgtctc agttctgctt gaatacctcc atcgatgggg aactcacttc ctttggaata 1440
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agacaggcag tagttttaat ttcaggaaca ggtgatccac tctgtaaaac agcaggtaaa 1560
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ctcccagccc accagccctc tgcccacctc acatgcctcc ccatggattg gggcctccca 1860
ggccccccac cttatgtcaa cctgcacttc ttgttcaaaa atcaggaaaa gaaaagattt 1920
gaagacccca agtcttgtca ataacttgct gtgtggaagc agcgggggaa gacctagaac 1980
cctttcccca gcacttggtt ttccaacatg atatttatga gtaatttatt ttgatatgta 2040
catctcttat tttcttacat tatttatgcc ccaaattat atttatgtat gtaagtgagg 2100
tttgttttgt atattaaaat ggagtttgtt tgt 2133

```

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

```

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
  1              5              10              15

```

```

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
          20              25              30

```

```

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
      35              40              45

```

```

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
  50              55              60

```

```

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
  65              70              75              80

```

```

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
      85              90              95

```

```

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
      100              105              110

```

```

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
      115              120              125

```

```

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
      130              135              140

```

```

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
      145              150              155              160

```

```

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
      165              170              175

```

```

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu

```


	180		185		190
Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala					
	195		200		205
Val Arg Ser Pro Ser Phe Glu Lys					
	210		215		

<210> 60
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 60
 atccgcccag atggctacaa tgtgta 26

<210> 61
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 61
 gcctcccggg ctccctgagc agtgccaaac agcggcagtg ta 42

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 62
 ccagtcgggt gacaagccca aa 22

<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
 cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60
 cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120
 gctgctgctg cgctacctgg tggcgcgcct gggctatcat aaggcctatg ggttttctgc 180
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctatgt tagcctgcaa 240
 aaccccaaag aagactgttt cctccagatt agagtggaag aaactgggtc ggagtgtctc 300
 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360
 tttcaatatc cggatcaaaa atgtgacaag aagtgatgag gggaaatatc gttgtgaagt 420
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaagtatt 480
 agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggt 540
 agagctacga tgtcaagaca aagaaggga tccagctcct gaatacacat ggtttaagga 600
 tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660
 aatgaatata aaaactggaa ctctgcaatt taatactgtt tccaaactgg aactggaga 720
 atattcctgt gaagcccgca attctgttgg atatcgagg tgtcctggga aacgaatgca 780


```

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ttccgtttgt ggccttggtg tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900
ctccttccag aagagtaatt cttcatctaa agccacgaca atgagtgaaa atgtgcagtg 960
gctcacgcct gtaatcccag cactttggaa ggccgcggcg ggcggatcac gaggtcagga 1020
gttctagacc agtctggcca atatggtgaa accccatctc tactaaaata caaaaattag 1080
ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140
acccgggagg cggagggtgc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200
cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact ggtttttacc 1260
tgtagaattc ttacaataaa tatagcttga tattc 1295

```

<210> 64

<211> 312

<212> PRT

<213> Homo sapiens

<400> 64

```

Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Leu Arg Tyr
  1                      5                      10                      15

```

```

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
                20                      25                      30

```

```

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
                35                      40                      45

```

```

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
  50                      55                      60

```

```

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
  65                      70                      75                      80

```

```

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
                85                      90                      95

```

```

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
                100                      105                      110

```

```

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
                115                      120                      125

```

```

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
                130                      135                      140

```

```

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
  145                      150                      155                      160

```

```

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
                165                      170                      175

```

```

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
                180                      185                      190

```

```

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
                195                      200                      205

```

```

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
                210                      215                      220

```

```

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
  225                      230                      235                      240

```



```

tggcattcat catttgacaa atgcaagcat cttccttata aatcagctcc tattgaactt 420
actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480
tgaaggacat gccactcoga attcatgtgc tacttggcct agctatcact acactagtac 540
aagctgtaga taaaaaagtg gattgtccac gggttatgtac gtgtgaaatc aggccttggt 600
ttacacccag atccatttat atggaagcat ctacagtgga ttgtaatgat ttaggtcctt 660
taactttccc agccagattg ccagctaaca cacagattct tctcctacag actaacaata 720
ttgcaaaaat tgaatactcc acagactttc cagtaaacct tactggcctg gatttatctc 780
aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcctttctg 840
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gtaagtgggt tgatgctctt ccaaacttag agattctgat gattggggaa aatccaatta 1080
tcagaatcaa agacatgaac ttttaagcctc ttatcaatct tcgcagcctg gttatagctg 1140
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gtcaaaaact cttgcctaata accctgacag acaagttcta tgtccattct gagggaaacac 1920
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acaatggctc tttgaatatt aaaataagag atattcaggc caattcagtt ttggtgtcct 2100
ggaaagcaag ttctaaaatt ctcaaacta gtgttaaag gacagccttt gtcaagactg 2160
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taaattctctg ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580
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```

<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

```

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
  1                      5                      10                      15

```

```

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
          20                      25                      30

```

```

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
          35                      40                      45

```

```

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
          50                      55                      60

```

```

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn
          65                      70                      75                      80

```

```

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly

```


85					90					95					
Leu	Asp	Leu	Ser	Gln	Asn	Asn	Leu	Ser	Ser	Val	Thr	Asn	Ile	Asn	Val
			100					105					110		
Lys	Lys	Met	Pro	Gln	Leu	Leu	Ser	Val	Tyr	Leu	Glu	Glu	Asn	Lys	Leu
		115					120					125			
Thr	Glu	Leu	Pro	Glu	Lys	Cys	Leu	Ser	Glu	Leu	Ser	Asn	Leu	Gln	Glu
	130					135						140			
Leu	Tyr	Ile	Asn	His	Asn	Leu	Leu	Ser	Thr	Ile	Ser	Pro	Gly	Ala	Phe
145					150					155					160
Ile	Gly	Leu	His	Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Arg	Leu
				165					170					175	
Gln	Met	Ile	Asn	Ser	Lys	Trp	Phe	Asp	Ala	Leu	Pro	Asn	Leu	Glu	Ile
			180					185					190		
Leu	Met	Ile	Gly	Glu	Asn	Pro	Ile	Ile	Arg	Ile	Lys	Asp	Met	Asn	Phe
		195					200					205			
Lys	Pro	Leu	Ile	Asn	Leu	Arg	Ser	Leu	Val	Ile	Ala	Gly	Ile	Asn	Leu
	210					215					220				
Thr	Glu	Ile	Pro	Asp	Asn	Ala	Leu	Val	Gly	Leu	Glu	Asn	Leu	Glu	Ser
225					230					235					240
Ile	Ser	Phe	Tyr	Asp	Asn	Arg	Leu	Ile	Lys	Val	Pro	His	Val	Ala	Leu
				245					250					255	
Gln	Lys	Val	Val	Asn	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	Asn	Pro	Ile
			260					265					270		
Asn	Arg	Ile	Arg	Arg	Gly	Asp	Phe	Ser	Asn	Met	Leu	His	Leu	Lys	Glu
		275					280					285			
Leu	Gly	Ile	Asn	Asn	Met	Pro	Glu	Leu	Ile	Ser	Ile	Asp	Ser	Leu	Ala
	290					295					300				
Val	Asp	Asn	Leu	Pro	Asp	Leu	Arg	Lys	Ile	Glu	Ala	Thr	Asn	Asn	Pro
305					310					315					320
Arg	Leu	Ser	Tyr	Ile	His	Pro	Asn	Ala	Phe	Phe	Arg	Leu	Pro	Lys	Leu
				325					330					335	
Glu	Ser	Leu	Met	Leu	Asn	Ser	Asn	Ala	Leu	Ser	Ala	Leu	Tyr	His	Gly
			340					345					350		
Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn
		355					360					365			
Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr
						375					380				
Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro
385					390					395					400
Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met
				405					410					415	

Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu
 420 425 430
 Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala
 435 440 445
 Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu
 450 455 460
 Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr
 465 470 475 480
 Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys
 485 490 495
 Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys
 500 505 510
 Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys
 515 520 525
 Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser
 530 535 540
 Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr
 545 550 555 560
 Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys
 565 570 575
 Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys
 580 585 590
 Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn
 595 600 605
 Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn
 610 615 620
 Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
 625 630 635 640
 Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
 645 650 655
 Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
 660 665 670
 Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
 675 680 685
 Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
 690 695 700
 Thr Asn Met Ser
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<210> 70
 <211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

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ttaccacgct tggttgagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180
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aattgccaac aacccttggc actgcgactg tactctacag caagttctga ggagcatggc 660
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<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

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Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu
 1                      5                      10          15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
                20                      25          30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
      35                      40          45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
      50                      55          60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
      65                      70          75          80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
                85                      90          95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
                100                      105          110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
      115                      120          125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
      130                      135          140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met

```


145		150		155		160
Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val						
		165		170		175
Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala						
		180		185		190
Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val						
		195		200		205
Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr						
		210		215		220
Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys						
		225		230		235
Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser						
		245		250		255

Thr Val Val

<210> 72
 <211> 2290
 <212> DNA
 <213> Homo sapiens

<400> 72

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tgctgggctc	agtgtgtca	ggctcggcca	cgggctgccc	gccccgctgc	gagtgtctcc	180
cccaggaccg	cgctgtgctg	tgccaccgca	agtgtttgt	ggcagtcccc	gagggcatcc	240
ccaccgagac	gcgcctgctg	gacctaggca	agaaccgcat	caaaacgctc	aaccaggacg	300
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tggagcccgg	cgccttcaac	aacctcttca	acctccggac	gctgggtctc	cgcagcaacc	420
gcctgaagct	catcccgcta	ggcgtcttca	ctggcctcag	caacctgacc	aagcaggaca	480
tcagcgagaa	caagatcggt	atcctactgg	actacatgtt	tcaggacctg	tacaacctca	540
agtcactgga	ggttggcgac	aatgacctcg	tctacatctc	tcaccgcgcc	ttcagcggcc	600
tcaacagcct	ggagcagctg	acgctggaga	aatgcaacct	gacctccatc	cccaccgagg	660
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ccttccgcgg	cctcaactac	ctgcgcgtgc	tcaatgtctc	tggcaaccag	ctgaccacac	1080
tggaggaatc	agtcttccac	tcggtgggca	acctggagac	actcatcctg	gactccaacc	1140
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tcctgatgt	gctactgccc	aactacttca	cctgccgccg	cgcccgcatc	cgggaccgca	1320
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cccacctgca	tgtgcgcagc	tactcgcccc	actggcccca	tcagcccaac	aagaccttcg	1620
ctttcatctc	caaccagccg	ggcgagggag	aggccaacag	cacccgcgcc	actgtgcctt	1680
tccccttcga	catcaagacc	ctcatcatcg	ccaccaccat	gggcttcatc	tctttcctgg	1740
gcgtcgtcct	cttctgcctg	gtgctgctgt	ttctctggag	ccggggcaag	ggcaacacaa	1800
agcacaacat	cgagatcgag	tatgtgcccc	gaaagtcgga	cgcaggcatc	agctccgccc	1860


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acgcgccccg caagttcaac atgaagatga tatgaggccg gggcgggggg cagggacccc 1920
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cctcctccct acccttctac acacgttctc tttctccctc ccgcctccgt cccctgctgc 2040
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<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

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Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
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Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
      20              25              30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
      35              40              45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
      50              55              60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
      65              70              75              80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
      85              90              95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
      100             105             110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
      115             120             125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
      130             135             140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
      145             150             155             160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
      165             170             175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
      180             185             190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
      195             200             205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
      210             215             220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
      225             230             235             240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr

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					245						250						255	
Pro	Asn	Cys	Leu	Tyr	Gly	Leu	Asn	Leu	Thr	Ser	Leu	Ser	Ile	Thr	His			
			260					265					270					
Cys	Asn	Leu	Thr	Ala	Val	Pro	Tyr	Leu	Ala	Val	Arg	His	Leu	Val	Tyr			
		275					280					285						
Leu	Arg	Phe	Leu	Asn	Leu	Ser	Tyr	Asn	Pro	Ile	Ser	Thr	Ile	Glu	Gly			
	290					295					300							
Ser	Met	Leu	His	Glu	Leu	Leu	Arg	Leu	Gln	Glu	Ile	Gln	Leu	Val	Gly			
305					310					315					320			
Gly	Gln	Leu	Ala	Val	Val	Glu	Pro	Tyr	Ala	Phe	Arg	Gly	Leu	Asn	Tyr			
				325					330					335				
Leu	Arg	Val	Leu	Asn	Val	Ser	Gly	Asn	Gln	Leu	Thr	Thr	Leu	Glu	Glu			
			340					345					350					
Ser	Val	Phe	His	Ser	Val	Gly	Asn	Leu	Glu	Thr	Leu	Ile	Leu	Asp	Ser			
		355					360					365						
Asn	Pro	Leu	Ala	Cys	Asp	Cys	Arg	Leu	Leu	Trp	Val	Phe	Arg	Arg	Arg			
	370					375					380							
Trp	Arg	Leu	Asn	Phe	Asn	Arg	Gln	Gln	Pro	Thr	Cys	Ala	Thr	Pro	Glu			
385					390					395					400			
Phe	Val	Gln	Gly	Lys	Glu	Phe	Lys	Asp	Phe	Pro	Asp	Val	Leu	Leu	Pro			
				405					410					415				
Asn	Tyr	Phe	Thr	Cys	Arg	Arg	Ala	Arg	Ile	Arg	Asp	Arg	Lys	Ala	Gln			
			420					425					430					
Gln	Val	Phe	Val	Asp	Glu	Gly	His	Thr	Val	Gln	Phe	Val	Cys	Arg	Ala			
		435					440					445						
Asp	Gly	Asp	Pro	Pro	Pro	Ala	Ile	Leu	Trp	Leu	Ser	Pro	Arg	Lys	His			
	450					455					460							
Leu	Val	Ser	Ala	Lys	Ser	Asn	Gly	Arg	Leu	Thr	Val	Phe	Pro	Asp	Gly			
465					470					475					480			
Thr	Leu	Glu	Val	Arg	Tyr	Ala	Gln	Val	Gln	Asp	Asn	Gly	Thr	Tyr	Leu			
				485					490					495				
Cys	Ile	Ala	Ala	Asn	Ala	Gly	Gly	Asn	Asp	Ser	Met	Pro	Ala	His	Leu			
			500					505					510					
His	Val	Arg	Ser	Tyr	Ser	Pro	Asp	Trp	Pro	His	Gln	Pro	Asn	Lys	Thr			
			515				520					525						
Phe	Ala	Phe	Ile	Ser	Asn	Gln	Pro	Gly	Glu	Gly	Glu	Ala	Asn	Ser	Thr			
	530					535					540							
Arg	Ala	Thr	Val	Pro	Phe	Pro	Phe	Asp	Ile	Lys	Thr	Leu	Ile	Ile	Ala			
545					550					555					560			
Thr	Thr	Met	Gly	Phe	Ile	Ser	Phe	Leu	Gly	Val	Val	Leu	Phe	Cys	Leu			
				565					570					575				

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn
 580 585 590

Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser
 595 600 605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile
 610 615 620

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 74

tcacctggag cctttattgg cc

22

<210> 75

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 75

ataccagcta taaccaggct gcg

23

<210> 76

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 76

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52

<210> 77

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 77

ccatgtgtct cctcctacaa ag

22

<210> 78

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 78

gggaatagat gtgatctgat tgg

23

<210> 79

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 79

cacctgtagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg

50

<210> 80

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 80

agcaaccgcc tgaagctcat cc

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<210> 81

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic

<400> 81

aaggcgcggt gaaagatgta gacg

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<210> 82

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 82

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50

<210> 83

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 83

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 agccaggagg ccggccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180
 tcctgctgtt cgctgctgc tgggcgcccg gcggggccaa cctctcccag gacgacagcc 240
 agccctggac atctgatgaa acagtgggtg ctggtggcac cgtggtgctc aagtgccaaag 300
 tgaaagatca cgaggactca tccttgcaat ggtctaacc tgcctcagcag actctctact 360


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<210> 84

<211> 398

<212> PRT

<213> Homo sapiens

<400> 84

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      20              25              30

Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
      35              40              45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
      50              55              60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
      65              70              75              80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
      85              90              95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
      100              105              110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
      115              120              125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
      130              135              140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
      145              150              155              160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro

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				165						170					175				
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser				
			180					185					190						
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val				
		195					200					205							
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser				
		210				215					220								
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp				
					230					235					240				
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly				
				245					250					255					
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser				
			260					265					270						
Val	Pro	Pro	Leu	Lys	Met	Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe				
			275				280					285							
Leu	Asn	Lys	Ser	Asp	Ser	Gly	Thr	Tyr	Gly	Cys	Thr	Ala	Thr	Ser	Asn				
		290				295					300								
Met	Gly	Ser	Tyr	Lys	Ala	Tyr	Tyr	Thr	Leu	Asn	Val	Asn	Asp	Pro	Ser				
					310					315					320				
Pro	Val	Pro	Ser	Ser	Ser	Ser	Thr	Tyr	His	Ala	Ile	Ile	Gly	Gly	Ile				
				325					330					335					
Val	Ala	Phe	Ile	Val	Phe	Leu	Leu	Leu	Ile	Met	Leu	Ile	Phe	Leu	Gly				
			340					345					350						
His	Tyr	Leu	Ile	Arg	His	Lys	Gly	Thr	Tyr	Leu	Thr	His	Glu	Ala	Lys				
		355					360					365							
Gly	Ser	Asp	Asp	Ala	Pro	Asp	Ala	Asp	Thr	Ala	Ile	Ile	Asn	Ala	Glu				
		370				375					380								
Gly	Gly	Gln	Ser	Gly	Gly	Asp	Asp	Lys	Lys	Glu	Tyr	Phe	Ile						
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<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 87

cctagcacag tgacgagggga cttggc

26

<210> 88

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic

<400> 88

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<210> 89

<211> 51

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic

<400> 89

gccctggcag acgagggcgg agtacacctg ctcaatcttc actatgcctg t

51

<210> 90

<211> 2755

<212> DNA

<213> Homo sapiens

<400> 90

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```



```

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```

<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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```

```

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
                20                      25                      30

```

```

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
  35                      40                      45

```

```

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
  50                      55                      60

```

```

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
  65                      70                      75                      80

```

```

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
                85                      90                      95

```

```

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
  100                      105                      110

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```

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
  115                      120                      125

```


Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
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 305 310 315 320
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
 325 330 335
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 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380
 Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
 385 390 395 400
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 405 410 415
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 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro

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Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn					
465		470		475	480
Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu					
		485		490	495
Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala					
		500		505	510
Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly					
		515		520	525
Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala					
		530		535	540
Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr					
545		550		555	560
Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu					
		565		570	575
Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His					
		580		585	590
Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser					
		595		600	605
Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu					
		610		615	620
Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val					
625		630		635	640
Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser					
		645		650	655
Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr					
		660		665	670
Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp					
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Cys Gly Ser His Ser Leu Ser Asp					
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<210> 92

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 92

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22

<210> 93

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 93

attgttgtgc aggctgagtt taag

24

<210> 94

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 94

ggtaggctata catggatagc aattacctgg acacgctgtc ccggg

45

<210> 95

<211> 2226

<212> DNA

<213> Homo sapiens

<400> 95

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tggcgcgtgg gcccgcgggg ggattccttg cagttggggg gtccgtcggg agcgagggcg 180
gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
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 gttgat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

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		20						25					30			
Ala	Ser	Gly	Ala	Cys	Tyr	Ser	Leu	His	His	Ala	Thr	Met	Lys	Arg	Gln	
		35					40					45				
Ala	Ala	Glu	Glu	Ala	Cys	Ile	Leu	Arg	Gly	Gly	Ala	Leu	Ser	Thr	Val	
	50					55					60					
Arg	Ala	Gly	Ala	Glu	Leu	Arg	Ala	Val	Leu	Ala	Leu	Leu	Arg	Ala	Gly	
65					70					75					80	
Pro	Gly	Pro	Gly	Gly	Gly	Ser	Lys	Asp	Leu	Leu	Phe	Trp	Val	Ala	Leu	
			85						90					95		
Glu	Arg	Arg	Arg	Ser	His	Cys	Thr	Leu	Glu	Asn	Glu	Pro	Leu	Arg	Gly	
			100					105					110			
Phe	Ser	Trp	Leu	Ser	Ser	Asp	Pro	Gly	Gly	Leu	Glu	Ser	Asp	Thr	Leu	
		115					120					125				
Gln	Trp	Val	Glu	Glu	Pro	Gln	Arg	Ser	Cys	Thr	Ala	Arg	Arg	Cys	Ala	
	130					135					140					
Val	Leu	Gln	Ala	Thr	Gly	Gly	Val	Glu	Pro	Ala	Gly	Trp	Lys	Glu	Met	
145					150					155					160	
Arg	Cys	His	Leu	Arg	Ala	Asn	Gly	Tyr	Leu	Cys	Lys	Tyr	Gln	Phe	Glu	
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	210					215					220					
Thr	Cys	Ile	Ala	Asp	Glu	Ile	Gly	Ala	Arg	Trp	Asp	Lys	Leu	Ser	Gly	
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Asp	Val	Leu	Cys	Pro	Cys	Pro	Gly	Arg	Tyr	Leu	Arg	Ala	Gly	Lys	Cys	
				245					250					255		
Ala	Glu	Leu	Pro	Asn	Cys	Leu	Asp	Asp	Leu	Gly	Gly	Phe	Ala	Cys	Glu	
			260					265					270			

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
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 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
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 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
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 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
 325 330 335
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln
 340 345 350
 Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala
 355 360 365
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 370 375 380
 Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe
 385 390 395 400
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 405 410 415
 Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln
 420 425 430
 Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu
 435 440 445
 Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val
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<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 97

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24

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 98
tgaccagtgg ggaaggacag 20

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 99
acagagcaga gggcgccttg 20

<210> 100
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 100
tcagggacaa gtgggtgtctc tccc 24

<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 101
tcagggaagg agtgtgcagt tctg 24

<210> 102
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 102
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<210> 103
<211> 2026
<212> DNA
<213> Homo sapiens

<400> 103
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gtgttatattg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
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<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

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  1                      5                      10                      15

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Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20                      25                      30

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```

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35                      40                      45

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Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50                      55                      60

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```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
      65                      70                      75                      80

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```

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
      85                      90                      95

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```

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
     100                      105                      110

```

```

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
     115                      120                      125

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Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
     130                      135                      140

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Pro	Ser	Gly	Ser	Phe	Lys	Thr	Pro	Asn	Trp	Pro	Asp	Arg	Asp	Tyr	Pro	165	170	175	
Ala	Gly	Val	Thr	Cys	Val	Trp	His	Ile	Val	Ala	Pro	Lys	Asn	Gln	Leu	180	185	190	
Ile	Glu	Leu	Lys	Phe	Glu	Lys	Phe	Asp	Val	Glu	Arg	Asp	Asn	Tyr	Cys	195	200	205	
Arg	Tyr	Asp	Tyr	Val	Ala	Val	Phe	Asn	Gly	Gly	Glu	Val	Asn	Asp	Ala	210	215	220	
Arg	Arg	Ile	Gly	Lys	Tyr	Cys	Gly	Asp	Ser	Pro	Pro	Ala	Pro	Ile	Val	225	230	235	240
Ser	Glu	Arg	Asn	Glu	Leu	Leu	Ile	Gln	Phe	Leu	Ser	Asp	Leu	Ser	Leu	245	250	255	
Thr	Ala	Asp	Gly	Phe	Ile	Gly	His	Tyr	Ile	Phe	Arg	Pro	Lys	Lys	Leu	260	265	270	
Pro	Thr	Thr	Thr	Glu	Gln	Pro	Val	Thr	Thr	Thr	Phe	Pro	Val	Thr	Thr	275	280	285	
Gly	Leu	Lys	Pro	Thr	Val	Ala	Leu	Cys	Gln	Gln	Lys	Cys	Arg	Arg	Thr	290	295	300	
Gly	Thr	Leu	Glu	Gly	Asn	Tyr	Cys	Ser	Ser	Asp	Phe	Val	Leu	Ala	Gly	305	310	315	320
Thr	Val	Ile	Thr	Thr	Ile	Thr	Arg	Asp	Gly	Ser	Leu	His	Ala	Thr	Val	325	330	335	
Ser	Ile	Ile	Asn	Ile	Tyr	Lys	Glu	Gly	Asn	Leu	Ala	Ile	Gln	Gln	Ala	340	345	350	
Gly	Lys	Asn	Met	Ser	Ala	Arg	Leu	Thr	Val	Val	Cys	Lys	Gln	Cys	Pro	355	360	365	
Leu	Leu	Arg	Arg	Gly	Leu	Asn	Tyr	Ile	Ile	Met	Gly	Gln	Val	Gly	Glu	370	375	380	
Asp	Gly	Arg	Gly	Lys	Ile	Met	Pro	Asn	Ser	Phe	Ile	Met	Met	Phe	Lys	385	390	395	400
Thr	Lys	Asn	Gln	Lys	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Lys	Gln	Cys		405	410	415	

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 105

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<210> 106
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 106
 gtcaaggagt cctccacaat ac 22

<210> 107
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 107
 gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt 45

<210> 108
 <211> 1838
 <212> DNA
 <213> Homo sapiens

<400> 108
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<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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			20					25					30		
Pro	Pro	Pro	Gln	Ser	Ser	Pro	Pro	Pro	Gln	Pro	His	Pro	Cys	His	Thr
			35				40					45			
Cys	Arg	Gly	Leu	Val	Asp	Ser	Phe	Asn	Lys	Gly	Leu	Glu	Arg	Thr	Ile
	50					55					60				
Arg	Asp	Asn	Phe	Gly	Gly	Gly	Asn	Thr	Ala	Trp	Glu	Glu	Glu	Asn	Leu
65					70					75					80
Ser	Lys	Tyr	Lys	Asp	Ser	Glu	Thr	Arg	Leu	Val	Glu	Val	Leu	Glu	Gly
				85					90					95	
Val	Cys	Ser	Lys	Ser	Asp	Phe	Glu	Cys	His	Arg	Leu	Leu	Glu	Leu	Ser
			100					105					110		
Glu	Glu	Leu	Val	Glu	Ser	Trp	Trp	Phe	His	Lys	Gln	Gln	Glu	Ala	Pro
		115					120					125			
Asp	Leu	Phe	Gln	Trp	Leu	Cys	Ser	Asp	Ser	Leu	Lys	Leu	Cys	Cys	Pro
	130					135					140				
Ala	Gly	Thr	Phe	Gly	Pro	Ser	Cys	Leu	Pro	Cys	Pro	Gly	Gly	Thr	Glu
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Arg	Pro	Cys	Gly	Gly	Tyr	Gly	Gln	Cys	Glu	Gly	Glu	Gly	Thr	Arg	Gly
				165					170					175	
Gly	Ser	Gly	His	Cys	Asp	Cys	Gln	Ala	Gly	Tyr	Gly	Gly	Glu	Ala	Cys
			180					185					190		
Gly	Gln	Cys	Gly	Leu	Gly	Tyr	Phe	Glu	Ala	Glu	Arg	Asn	Ala	Ser	His
		195					200					205			
Leu	Val	Cys	Ser	Ala	Cys	Phe	Gly	Pro	Cys	Ala	Arg	Cys	Ser	Gly	Pro
	210					215					220				
Glu	Glu	Ser	Asn	Cys	Leu	Gln	Cys	Lys	Lys	Gly	Trp	Ala	Leu	His	His
225					230					235					240
Leu	Lys	Cys	Val	Asp	Ile	Asp	Glu	Cys	Gly	Thr	Glu	Gly	Ala	Asn	Cys
				245					250					255	
Gly	Ala	Asp	Gln	Phe	Cys	Val	Asn	Thr	Glu	Gly	Ser	Tyr	Glu	Cys	Arg
			260					265					270		
Asp	Cys	Ala	Lys	Ala	Cys	Leu	Gly	Cys	Met	Gly	Ala	Gly	Pro	Gly	Arg
		275					280					285			

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
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 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
 305 310 315 320
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
 325 330 335
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
 340 345 350
 Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365
 Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380
 Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
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 Ile Lys Gly Arg
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<210> 110
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 110
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<210> 111
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 111
 attctgcgtg aacactgagg gc 22

<210> 112
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 112
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<210> 113
 <211> 1616
 <212> DNA
 <213> Homo sapiens

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 aaagtcctcc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560
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<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

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 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45
 Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110


```

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
    115                      120                      125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
    130                      135                      140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
    145                      150                      155                      160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
    165                      170                      175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
    180                      185                      190

Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
    195                      200                      205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
    210                      215                      220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
    225                      230                      235                      240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
    245                      250                      255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
    260                      265                      270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
    275                      280                      285

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

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
    305                      310                      315                      320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
    325                      330                      335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
    340                      345                      350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
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<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 115

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21

<210> 116

<211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 116
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<210> 117
 <211> 45
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 117
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<210> 118
 <211> 1842
 <212> DNA
 <213> Homo sapiens

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<210> 119
 <211> 299

<210> 120
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 120
 tcgcggagct gtgttctggt tccc 24

 <210> 121
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 121
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 <210> 122
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 122
 acacctgggtt caaagatggg 20

 <210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 123
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 <210> 124
 <211> 20
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 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 124
 ttgccttact caggtgctac 20

 <210> 125
 <211> 20
 <212> DNA
 <213> Artificial Sequence

DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME 1 DE 2

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME 1 OF 2

NOTE: For additional volumes please contact the Canadian Patent Office.

JJ-10 792-3CA

THE EMBODIMENTS OF THE INVENTION IN WHICH AN EXCLUSIVE PROPERTY OR PRIVILEGE IS CLAIMED ARE DEFINED AS FOLLOWS:

1. An isolated nucleic acid comprising a nucleotide sequence encoding a polypeptide having the amino acid sequence shown in SEQ ID NO.: 119.
2. The isolated nucleic acid of claim 1 comprising the full-length coding sequence of the nucleotide sequence shown in SEQ ID NO.: 118.
3. A vector comprising the nucleic acid of claim 1 or claim 2.
4. The vector of claim 3 operably linked to control sequences recognized by a host cell transformed with the vector.
5. A host cell comprising the vector of claim 3.
6. The host cell of claim 5 wherein said cell is a CHO cell.
7. The host cell of claim 5 wherein said cell is an *E. coli*.
8. The host cell of claim 5 wherein said cell is a yeast cell.
9. A process for producing a polypeptide of SEQ ID NO: 119 comprising culturing the host cell of claim 5 under conditions suitable for expression of said polypeptide and recovering said polypeptide from the cell culture.
10. An isolated polypeptide comprising the amino acid sequence shown in SEQ ID NO: 119.
11. A chimeric molecule comprising the polypeptide of claim 10 fused to a heterologous amino acid sequences.
12. The chimeric molecule of claim 11 wherein said heterologous amino acid sequence is an epitope tag sequence.
13. The chimeric molecule of claim 11 wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

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14. An isolated polypeptide comprising an amino acid sequence having at least 95% sequence identity to the polypeptide comprising the amino acid sequence shown in SEQ ID NO: 119 that inhibits VEGF-stimulated proliferation of endothelial cells, for use in angiogenesis.

15. The isolated polypeptide of claim 14, wherein the level of sequence identity is at least 95-99%.

16. The isolated polypeptide of claim 14, for use in treating cancer.

17. The isolated polypeptide of claim 16, for use in inhibiting tumor angiogenesis.

18. Use of a polypeptide in the preparation of a medicament for the treatment of cancer, wherein the polypeptide comprises an amino acid sequence having at least 80% sequence identity to the polypeptide comprising the amino acid sequence shown in SEQ ID NO: 119 and inhibits VEGF-stimulated proliferation of endothelial cells.

19. The use according to claim 18 wherein the medicament is for the inhibition of tumor angiogenesis.

20. The use according to claim 18 or claim 19 wherein the level of sequence identity is at least 90%.

21. The use according to claim 18 or claim 19 wherein the level of sequence identity is at least 95%.

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FIGURE 1

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACCCG
CCATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCC
GCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTT
TAACCAGGGGATGGTGGACACCGCAAAGAAGAAGTTTGGCGGGCGGGAACACGGCTTGGGAGG
AAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCTGCTGGAGATCCTGGAGGGGCTG
TGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGC
CTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACAC
TGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCC
CAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTC
CTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCA
GCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGC
TCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGC
CTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGT
TCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGC
ACAGGGGAAGGCCCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACA
GTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAACCTGTGTGAGGAAAAACGAAACT
GCTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCCTGACGGCTTCGAAGAAACGGAAGAT
GCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCCTC
CCGCGAAGACCTGTAATGTGCCGACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGGA
AAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTC
TCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGA
CTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAA
AAAAAA

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FIGURE 2

Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu Leu
Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala
Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
Leu

FIGURE 3

CCAGGCCGGGAGGCGACGCGCCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGC
AGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGC
AGCGAGGAGGTCCTGAGCAGCATGGCCCCGAGGAGCGCCTTCCCTGCCGCCGCGCTCTGGCT
CTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGCCGGGCCGCCGAGGAGGAGA
GCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGAAGAAGATATC
CTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTTCAGAAAAGCGCAACAGAG
AATGCCAGCTATTCCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGG
CAGAATACTTCTATGAATTCCTGTCCTTGCGCTCCCTGGATAAAGGCATCATGGCAGATCCA
ACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCATCAGTTGTTCAAGTTGGTTT
CCCATGTCTTGGAACACAGGATGGGGTGGCAGCATTTGAAGTGGATGTGATTGTTATGAATT
CTGAAGGCAACACCATTCTCCAAACACCTCAAAATGCTATCTTCTTTAAACATGTCAACAA
GCTGAGTGCCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAATGAAAGACGCATCTGCGAGTG
TCCTGATGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATG
GTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCCACCTGGATTCTATGGAGTGAAGTGT
GACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACCTGTTTCTACCCTGGAAAATG
TATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAAATGCCACAACCCTGTC
GAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGGAGAC
CTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAA
CAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCC
TCATACATGCCCTGAGGCCAGCAGGCGCCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAG
GCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGGTGAACCTCCGACATCTGAAAC
GTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTTCATGTGTTGAATGTTCAAATAA
TGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGCT
GATATTTACTCTTCCTTTTAAAGTTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCT
TGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGATCAGGTAAAATTTTCAGTG
TGTAGTTGGCAGATATTTTCAAATTAACAATGCATTTATGGTGTCTGGGGGCAGGGGAACAT
CAGAAAGGTAAATTGGGCAAAAATGCGTAAGTCACAAGAATTTGGATGGTGCAGTTAATGT
TGAAGTTACAGCATTTTCAGATTTTATTGTCAGATATTTAGATGTTTGTTACATTTTAAAAA
TTGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATT
CAGTATTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
AACACAATGAAATAGGGAATATAATGTATGAACTTTTGCATTGGCTTGAAGCAATATAATA
TATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTATACTGTTTGTATGTATAAAAT
AAAGGTGCTGCTTTAGTTTTTTGGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA

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FIGURE 4

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser
Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly ProPro Gln
Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
CCCCAGCCCACACCTTCACCAGGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCTGTATCTA
TCCAGTCTTGGGAACGTACTGGGACAACGTAAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCAGTGTGACCAAGAACCATGCCTGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGC
AACTATGGCTGGCAGGCTGGGAACCACAGCGCCTTCTGGGGCATGACCCTGGATGAGGGCAT
TCGCTACCGCCTGGGCACCATCCGCCCATCTTCCTCGGTTCATGAACATGCATGAAATTTATA
CAGTGCTGAACCCAGGGGAGGTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAAC
CTGATTTCATGAGCCTCTTGACCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGC
TGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCC
AGAACCTGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGT
GCCTGGTGGTTCCTGCGTCGCCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCG
TGAACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTCCGG
GCAAGCGCCAGGCCACTGCCCACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTC
ACTCCTGTCTACCGCCTCGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGG
CCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACA
GCCACACGCCAGTGAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTC
AAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGC
GGCCAACCTCCTGGGGCCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC GCGGCGTCA
ATGAGTGCGACATCGAGAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATG
GGTCATCACTGAGGCTGCGGGCACCACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGG
CGGAAGAGGGCCCCAATGGGGCGGTGACCCCAGCCTCGCCCCGACAGAGCCCGGGGCGCAGGCG
GGCGCCAGGGCGCTAATCCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCTGGGAGCCGCG
GGCAGGCGAGACTGGCGGAGCCCCCAGACCTCCCAGTGGGGACGGGGCAGGGCCTGGCCTGG
GAAGAGCACAGCTGCAGATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGA
CACCTCAAGTCTCCAGCCCCAATAACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGAC
AGGGTCTTGCTCCGTTGCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCC
GACTCCTGGGTTCAGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCA
CCACCACACCTGGCTAATTTTTTGTATTTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAG
GCTGGTTTCGAACCTCCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGAT
TGCAGGCATGAGCCACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTCTTT
TCACTGTTTTTAAAATAAAACCAAAGTATTGATAAAAAAAA

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FIGURE 6

><ss.DNA33223

><subunit 1 of 1, 467 aa, 1 stop

><MW: 52387, pI: 6.95, NX(S/T): 2

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRAD
DCALPYLGAIICYCDLFCNRTVSDCCPDFWDFCLGVPPPPFPPIQGCMHGGRIYPVLGTYWD
NCNRCTCQENRQWQCDQEPCLVDPDMIKAINQGNYGWQAGNHSAFWGMTLDEGIRYRLGT
IRPSSSVMMNHEIYTVLNPGEVLPTAFEASEKWPNLIEPLDQGNCAGSWAFSTAAVASD
RVSIHSLGHMTPVLSPQNLLSCDTHQQQGCRRGLDGAWWFLRRRGVVSDHCYPFSGRER
DEAGPAPPCMMHSRAMGRGKRQATAHCPNSYVNNNDIYQVTPVYRLGSNDKEIMKELMEN
GPVQALMEVHEDFFLYKGGIYSHTPVSLGRPERYRRHGTHSVKITGWGEETLPDGRTLKY
WTAANSWGPWGERGHFRIVRGVNECDIESFVLGVWGRVGMEDMGHH

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FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATC
CAATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACAC
CCACCAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCG
CCGAGGGNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGG
CCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGGCAAGCGCCAGGCCAC
TGCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTA
CCGCCTCGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCA
AGCCCTCATGGAGGTGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACAC
GCCAGTGAGCCTTGGGAGGCCAGAGAGATAACGCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAGTGC GTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCACCCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCCTCCAACCCTCTCTGCTGCTGTTTCCAT
GGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTTCCC
TGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCAGGG
GACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGAGGA
CAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAAGGG
GCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTTAAT
AAACACCTGTTGGATAAGCCAAAAAAA

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FIGURE 9

MAGLALQPGTALLCYSCKAQVSNEDECLQVENCTQLGECWTARIRAVGLLTVISKGCSLNCV
DDSQDYVVGKKNITCCDLDLCNASGAHALQPAAAILALLPALGLLLWGPGQL

FIGURE 10

ATGGGAGCCGCCCCGCCTGCTGCCCCAACCTCACTCTGTGCTTACAGCTGCTGATTCTCTGCTG
TCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACCGACCAGCTGAGCAGGCGGCAGATCC
GCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCACGTGCAGGTCACCGGGCGTCGCATC
TCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGCTCATAGTGGAGACGGACACGTTTGG
CAGCCGGGTTCGCATCAAAGGGGGCTGAGAGTGAGAAGTACATCTGTATGAACAAGAGGGGCA
AGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTGCGTGTTACGGAGATCGTGCTGGAG
AACAACTATACGGCCTTCCAGAACGCCCCGGCACGAGGGCTGGTTCATGGCCTTCACGCGGCA
GGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAACCAGCGCGAGGCCCCTTCATCAAGC
GCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGCCGAGAAGCAGAAGCAGTTTCGAGTTT
GTGGGCTCCGCCCCCACC CGCCGGACCAAGCGCACACGGCGGGCCCCAGCCCCCTCACGTAGTC
TGGGAGGCAGGGGGGCAGCAGCCCCCTGGGCGCCTCCCCACCCCTTTCCCTTCTTAATCCAAG
GACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCCGAGGGAGGACCCTGAGGGCCGCGAA
GCATCCGAGCCCCCAGCTGGGAAGGGGGCAGGCCGGTGCCCCAGGGGGCGGCTGGCACAGTGCC
CCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACTGAGTGTCACCCTGATCTCAGGCCAC
CAGCCTTTGCCGGCCTCCCAGCCGGGCTCCTGAAGCCCGCTGAAAGGTCAGCGACTGAAGGC
CTTGACAGACAACCGTCTGGAGGTGGCTGTCCTCAAATCTGCTTCTCGGATCTCCCTCAGTC
TGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTAGGAAGGGACTTTTGTTTGTTTGTTT
GTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAATAGAGGGTTGTCCACTCCTCACATTCCA
CGACCCAGGCCTGCACCCCCACCCCCAACTCCCAGCCCCGGAATAAAACCATTTTCCTGC

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FIGURE 11

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln
Leu Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly
Ala Met Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln
Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg
Arg Ile Ser Ala Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu
Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Ile Lys Gly
Ala Glu Ser Glu Lys Tyr Ile Cys Met Asn Lys Arg Gly Lys Leu
Ile Gly Lys Pro Ser Gly Lys Ser Lys Asp Cys Val Phe Thr Glu
Ile Val Leu Glu Asn Asn Tyr Thr Ala Phe Gln Asn Ala Arg His
Glu Gly Trp Phe Met Ala Phe Thr Arg Gln Gly Arg Pro Arg Gln
Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu Ala His Phe Ile Lys
Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn His Ala Glu Lys
Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr Arg Arg Thr
Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr

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FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGATTTTGCTGTTTATTTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTTCCT
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC
TGGATTTCTGTCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAACAAT
ATTCAGACCATTTCACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGCTGCACCTGGA
TGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCCTCA
AATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGACTTG
CAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCATATCCGACATGGCCTTCCAGAATCT
CACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCGAGG
GCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCCCAC
CCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGATAAA
CCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACA
ACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTCACT
GCTCGGAATAACCCCTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAAATA
TATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTGAACAAGTCCGGGGGA
TGGCCGTCAGGGAATTAAATATGAATCTTTTGTCTGTCCCACCACGACCCCCGGCCTGCCT
CTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTATTCC
AAACCCTAGCAGAAGCTACACGCCTCCAACCTCTACCACATCGAAACTTCCCACGATTCTTG
ACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATCCAT
TTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCAACGTGATGGCATACAA
ACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTTCAGGAGCGCATAGTCA
GCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATTTGT
TTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTGTTCAGAGGCCAC
CACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGT
CCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTTGTG
CTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAGGGGCGCTACACCTCCCA
GAAGTGGAAATACAACCGGGGCGGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGAAGG
ACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGATCAA
CTCCTTAAAGGAGATTTTCAGACTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTACAC
AGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGCACT
GCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACAC
ACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCATTTG
TGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTGCTA
TCTTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACCTTTTGCTTTTTTAAATCTT

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FIGURE 13

><1158/ss.DNA36350

><subunit 1 of 1, 660 aa, 1 stop

><MW: 74049, pI: 8.09, NX(S/T): 7

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLG
IPEGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENN
IQTISRALAQLLKLEELHLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPV
DLQELRVDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRN
SLSHPPPDLPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLS
NLKQLTARNNPWFCDCSI KWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNLLSC
PTTTPGLPLFTPAPSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPP
ISERIQLSIHFVNDSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSL
VNLEPRSTYRICLVPLDAFN YRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSP
FLLAGLIGGAVIFVLVLLSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSIL
EMTETSFQIVSLNNDQLLKGD FRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

FIGURE 14A

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCTCG
 CCTCCCACGAGCGATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGG
 AAGACCCGGGTGGCTGCGCCCCTGCCTCGCTTCCCAGGCGCCGGCGGCTGCAGCCTTGCCCC
 TCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCTGCTTTCTGCTGATCCTCGGACAG
 ATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTACGTGGGAGGTCCATCTCTAGGGGCGAG
 ACACGCTCGGACCCACCCGCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAAAGCGGGCAG
 ACCTGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAG
 GAGTTCATCGTGGACATCTTGCAATTCTTGACATTGGTCCTGATGTCACCCGAGTGGGCCT
 GCTCCAATATGGCAGCACTGTCAAGAATGAGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCG
 AGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGGGCACCATGACTGGGCTGGCC
 ATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGAGGGAGAA
 TGTGCCACGGGTGATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGG
 CTGCTAAGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTC
 AACACCTTGAAGTCCATTGGGAGTGAGCCCCATGAGGACCATGTCTTCCTTGTGGCCAATTT
 CAGCCAGATTGAGACGCTGACCTCCGTGTTCCAGAAGAAGTTGTGCACGGGCCACATGTGCA
 GCACCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTGGCTCATACGTCTGCAGG
 TGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAAGAATCCAGGATCTGTGTGC
 CATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGT
 GCTACAGTGGCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCC
 TCAGAAAACACGGATGTGAACATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTG
 CCATGAAGGATTTGCTCTTAACCCAGATGAAAAAACGTGCACAAGGATCAACTACTGTGCAC
 TGAACAAACCGGGCTGTGAGCATGAGTGCGTCAACATGGAGGAGAGCTACTACTGCCGCTGC
 CACCGTGGCTACACTCTGGACCCCAATGGCAAACCTGCAGCCGAGTGGACCACTGTGCACA
 GCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCGTCTGCCAGTGCT
 CAGAAGGCTTCCTCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTG
 AGTGACCATGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCCTGTGAGTGTCC
 TGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTGCAAAATTGGACTCTTGTGCTCTGG
 GGGACCACGGTTGTGAACATTCGTGTGTAAAGCAGTGAAGATTCGTTTGTGTGCCAGTGCTTT
 GAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTAT
 AGACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACACGTGCGAGTGCTTGG
 AGGGATTCCGGCTCGCTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAATCAACC
 CACCATGGCTGCGAACACATTTGTGTGTTAATAATGGGAATTCCTACATCTGCAAATGCTCAGA
 GGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCCAATTGACC
 TGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCGTGAAGCAG
 TTTGTCACTGGAATTATAGATTCCTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCT
 CCAGTATTCCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACA
 TGAAAAAAGCCGTGGCCCAACATGAAATACATGGGAAGGGCTCTATGACTGGGCTGGCCCTG
 AAACACATGTTTGAGAGAAGTTTTACCCAAGGAGAAGGGGCCAGGCCCTTTCCACAAGGGT
 GCCCAGAGCAGCCATTGTGTTACCCGACGGACGGGCTCAGGATGACGTCTCCGAGTGGGCCA
 GTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTGAGGAG
 GAACTACAAGAGATTGCCTCTGAGCCCAACAACAAGCATCTCTTCTATGCCGAAGACTTCAG
 CACAATGGATGAGATAAGTGAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCG
 ATGGAAGACAGGACTCTCCAGCAGGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCT
 GAGCCAGTCACCATAAATATCCAAGACCTACTTTCCTGTTCTAATTTTGCAGTGCAACACAG
 ATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTTCCCATTCACAAAAC
 CTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGTTT
 CAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAG
 AATGGAAGCCCTGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGT
 AGTCATTGTATCACGGATTACAATGAACGCAGTGACAGAGCCCCAAAGCTCAGGCTATTGTTA
 AATCAATAATGTTGTGAAGTAAACAATCAGTACTGAGAAACCTGGTTTGGCCACAGAACAAA
 GACAAGAAGTATACACTAATTTGTATAAATTTATCTAGGAAAAAATCCTTCAGAATTCTAA
 GATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACA
 CAACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTT

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FIGURE 14B

GCACAGTCTTACTTCTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTT
ACCTTGATATATGTATATGGATGTATGCATAAAATCATAGGACATATGTACTTGTGGAACAA
GTTGGATTTTTTATAACAATATTAATAATTCACCACTTCAG

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FIGURE 15

><1164/ss.DNA32290

><subunit 1 of 1, 915 aa, 1 stop

><MW: 102233, pI: 6.02, NX(S/T): 1

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESSCENKRADLVF
IIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEV
ERAVKRMRLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEV
AAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAH
MCSTLEHNCAHFCINIPGSYVCRCCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGS
FVCQCYSGYALAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCT
RINYCALNKPGEHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNT
EDSFVCQCSEGFLINEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGK
TCAKLDSCALGDHGCEHSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHIC
VNSDDSYTCECLEGFRLAEDGKRCRRKDVCCKSTHHGCEHICVNNGNSYICKCSEGFVLAE
DGRRCKKCTEGPIDLVFVIDGSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLOYST
QVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPR
AAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIEEELQEIASPTNKHLFYAEDFS
TMDEISEKLKKGICEALEDS DGRQDSPAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQ
HRYLFEEFNLLRSTQKLSHSTKPSGSPLEEKHDQCKCENLIMFQNLANEEVRKLTQRLEE
MTQRMEALENRLRYR

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCCTCGCGGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCCTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAACTAACATGAAATATGTGTTGTTTTTCAATTTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

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FIGURE 17

><1172/ss.DNA35639

><subunit 1 of 1, 390 aa, 1 stop

><MW: 41176, pI: 9.61, NX(S/T): 5

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
SGPYSCSVNVQDKQKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSK
PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
SDTISKNGTLSSVTSARALRPPHGP RP RP GALTP T PSLSSQALPSPRLPTTDGAHPQPISP
IPGGVSSSGLSRMGAVPVMVPAQSQAQAGSLV

FIGURE 18

CGCCACCACTGCGGCCACCGCCA
 ><MET {trans=1-s, dir=f, res=1}>
 ATGAAACGCCTCCCGCTCCTAGTGGTTTTTTTCCACTTTGTTGAATTGTTCTTATACTCAA
 AATTGCACCAAGACACCTTGTCTCCCAAATGCAAAATGTGAAATACGCAATGGAATTGAA
 GCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTCACAATTTGTGAAGATGATAAT
 GAATGTGGAAATTTAACTCAGTCCTGTGGCGAAAATGCTAATTGCACTAACACAGAAGGA
 AGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCAAGACAGGTTTATC
 ACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACCTGCCATTTAGATAATGTC
 TGTATAGCTGCAAATATTAATAAACTTTAACA AAAAATCAGATCCATAAAAGAACCTGTG
 GCTTTGCTACAAGAAGTCTATAGAAATTTCTGTGACAGATCTTTCACCAACAGATATAATT
 ACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAACACTATC
 TCAGCCAAGGACACCCTTTCTAACTCAACTCTTACTGAATTTGTAAAAACCGTGAATAAT
 TTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAACA
 CATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTC
 CAAAAGACCACAGAGTTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTTCTTTTTT
 GATTCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAAT
 ATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTTTA
 TATTATAAGAGTATTGGTCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAA
 AATTATGATAATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATG
 AGCTCAAACCCACCCACATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGA
 AAGGTCACAGATAGGTATAGGAGTCTATGTGCATTTTGGAAATTACTCACCTGATACCATG
 AATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCA
 TGCCGCTGTAATCACCTGACACATTTTGAATTTTGATGTCCTCTGGTCTTCCATTGGT
 ATTAAGATTATAATATTCTTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATT
 TGTCTTGCCATATGCATTTTTTACCTTCTGGTCTTTCAGTGAAATTCAAAGCACCAGGACA
 ACAATTCACAAAATCTTTGCTGTAGCCTATTTCTTGCTGAACTTGTTTTTCTGTTGGG
 ATCAATACAAATACTAATAAGCTCTTCTGTTCAATCATTTGCCGGACTGCTACACTACTTC
 TTTTATAGCTGCTTTTGCATGGATGTGCATTGAAGGCATACATCTCTATCTCATTGTTGTG
 GGTGTCATCTACAACAAGGGATTTTTTGCACAAGAATTTTTATATCTTTGGCTATCTAAGC
 CCAGCCGTGGTAGTTGGATTTTTCGGCAGCACTAGGATACAGATATTATGGCACAACCAAA
 GTATGTTGGCTTAGCACCGAAAACAACCTTTATTTGGAGTTTTTATAGGACCAGCATGCCTA
 ATCATTCTTGTTAATCTCTTGGCTTTTGGAGTCATCATATACAAAGTTTTTTCGTCACACT
 GCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACATAAGGTCTTGTGCAAGAGGAGCC
 CTCGCTCTTCTGTTCTTCTCGGCACCACCTGGATCTTTGGGGTTCTCCATGTTGTGCAC
 GCATCAGTGGTTACAGCTTACCTCTTCACAGTCAGCAATGCTTTCCAGGGGATGTTCAAT
 TTTTATTCCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAATATTACAGATTGTTCAAA
 AATGTCCCCTGTTGTTTTTGATGTTTAAGGTAAACATAGAGAATGGTGGATAATTACAAC
 TGCACAAAATAAAAATTCCAAGCTGTGGATGACCAATGTATAAAAATGACTCATCAAAT
 TATCCAATTATTAATACTAGACAAAAAGTATTTTAAATCAGTTTTTCTGTTTATGCTAT
 AGGAACTGTAGATAATAAGGTAAAATTATGTATCATATAGATATACTATGTTTTTCTATG
 TGAAATAGTTCTGTCAAAAATAGTATTGCAGATATTTGGAAAGTAATTGGTTTCTCAGGA
 GTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTAACACGAGAAGTATATGAATGTCC
 TGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTTGCCCTTTGAAACTAGTCCCCT
 ACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGAA
 TATCAAACAGTGAAAAGGGAATGATAAGATGTATTTTGAATGAACTGTTTTTCTGTAGA
 CTAGCTGAGAAATTGTTGACATAAAATAAAGAATTGAAGAAACACATTTTACCATTTTGT
 GAATTGTTCTGAACTTAAATGTCCACTAAAACAACCTTAGACTTCTGTTTGCTAAATCTGT
 TTCTTTTTCTAATATTCTAAAAA AAAAAAAAAAAGGTTTACCTCCACAAATTGAAAAA AAAAA
 AA

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FIGURE 19

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33092

><subunit 1 of 1, 690 aa, 0 stop

><MW: 77825, pI: 7.96, NX(S/T): 11

MKRLPLLVFSTLLNCSYTQNCCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDN
ECGNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNV
CIAANINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSLLGYKNNTI
SAKDTLSNSTLTEFVKTVNNFVQRDTFVWWDKLSVNHRRTHLTKLMHTVEQATLRISQSF
QKTTEFDTNSTDIALKVFFFDSDYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAF
YYKSIGPLLSSSDNFFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHR
KVTDRYRSLCAFWNYSPTMNGSWSSEGCETYSNETHTSCRCNHLTHFAILMSSGPSIG
IKDYNILTRITQLGIIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVG
INTNTNKLFCSTIAGLLHYFFLAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLS
PAVVVGFSAAALGYRYYGTTKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHT
AGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFI
FLFLCVLSRKIQEEYYRLFKNVPCCFGCLR

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FIGURE 20

ATAGGAGTCTATGTGGCATT TTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCA
GAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGAC
ACATTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTA
CAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTTACC
TTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

CTCCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCGC
TAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTCACCCCGGCTGGGAC
AGAAGCCGCCGCCTGCCTGCCCCGGGCCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGGG
GTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAGTCCCGATAAGAAATGCTCGGGT
GTCTTGGGCACCTACCCGTGGGGGCGGTAAAGGCGCTACTATATAACGCTGCCGGCCCTGAGC
CGCCGAGCCGTCCGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCACGACCATCCCAACCCGG
CATTCACAGCCCCGCAGCGCATCCGGTCGCCGGCCAGCTTCCGCACCCCATCGCCGGAGCTG
CGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGGATCCT
GGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGGCCCCACG
TGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCCACGGG
CTCTCCAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGGCCAGAG
CGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGGCGTGC
ACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGTACTCG
GAGGAAGACTGTGCTTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGATCCGA
GAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAACAGAG
GCTTTCTTCCACTCTCTCATTTCTGCCCCATGCTGCCCATGGTCCCAGAGGAGCCTGAGGAC
CTCAGGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATGGACCC
ATTTGGGCTTGTCACCGGACTGGAGGCCGTGAGGAGTCCCAGCTTTGAGAAGTAACTGAGAC
CATGCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACGTGCTT
CTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAAGTTGT
ACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGATCATAA
CATTGGAAGCCTTGTAATTGGCCCAGCTGTTGCCTGGGCCCCCATCTGCTCCCTCGAGGT
TGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAACCTCA
CTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTCTCATCACTTCCCCA
GGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTTCAGGAACAGGTGATCCACTCTGTAAAC
AGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGGACCA
TTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAGGCTT
CAGAAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCCCTGA
GGCCAGTTCTGTGATGGATGCTGTCCTGAGAATAACTTGCTGTCCCGGTGTCACCTGCTTCC
ATCTCCCAGCCCACCAGCCCTCTGCCCCACCTCACATGCCTCCCCATGGATTGGGGCCTCCCA
GGCCCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGATTTGA
AGACCCCAAGTCTTGTCATAAATCTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAACCCTT
TCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACATCTC
TTATTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTTGT
GTATATTAAATGGAGTTTGT

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FIGURE 22

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly
Leu Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala
Gly Pro His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg
His Leu Tyr Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu
Arg Ile Arg Ala Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser
Ala His Ser Leu Leu Glu Ile Lys Ala Val Ala Leu Arg Thr Val
Ala Ile Lys Gly Val His Ser Val Arg Tyr Leu Cys Met Gly Ala
Asp Gly Lys Met Gln Gly Leu Leu Gln Tyr Ser Glu Glu Asp Cys
Ala Phe Glu Glu Glu Ile Arg Pro Asp Gly Tyr Asn Val Tyr Arg
Ser Glu Lys His Arg Leu Pro Val Ser Leu Ser Ser Ala Lys Gln
Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu Pro Leu Ser His Phe
Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro Glu Asp Leu Arg
Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu Glu Thr Asp
Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala Val Arg
Ser Pro Ser Phe Glu Lys

FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTCCGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATAACAATGAATACAAAAACTGGAAGT
CTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCAGCACTTTGGAAGG
CCGCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

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FIGURE 24

><ss.DNA35638

><subunit 1 of 1, 312 aa, 1 stop

><MW: 34554, pI: 9.39, NX(S/T): 4

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR
LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR
LGSQSTNSSYTMNTKTGTLOFNTVSKLDTGEYSCEARNVSGYRRCPGKRMQVDDLNISGI
IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFOKSNSSSKATTMSENVQWLTPVIPALW
KAAAGGSRGQEF

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCAT
CATGCTGCTATTCTTGCAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTTTGGACAATG
CAATTGTGGCACTGGCACTTATTTTCTGAGTGAAGAAAACTTTGTGGTTCTATGGCATTTCATCA
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
TGGAATCCTTAAGGGCCCATTAATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTTCTCCTACAGACTAACAATATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAAT
ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGA
ACTGCCTGAAAAATGTCTGTCCGAACTGAGCAACTTACAAGAACTCTATATTAATCACAAC
TGCTTTCTACAATTTTACCTGGAGCCTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT
TCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCA
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT
GGACTGGAAAACCTTAGAAAGCATCTCTTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTTGGATCTAAATAAAAATCCTATTAATAGAA
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAATAATATGCCT
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
TACTAACACCCTAGATTGTCTTACATTCACCCCAATGCATTTTTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTG
GATGAACATGAACAAAACCAACATTCGATTCATGGAGCCAGATTCAGTGTTTTGCCTGGACC
CACCTGAATTCCAAGGTCAGAAATGTTCCGGCAAGTGCATTTTCAAGGACATGATGGAAATTTGT
CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTCTTGCCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAAATGGCGTAACTCCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAATATTAAAATAAGAGATATTCAAGCCAATTCAAGTTTGGTGTCTTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAAATTTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
AGAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCCTAA
AAACCACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLG
LLTFPARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQL
LSVYLEENKLTTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLLRLHLNSNRLQ
MINSKWFDALPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLE
NLESISFYDNRLIKVPHVALQKVVNLFKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMP
ELISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTT
ESLPNLKEISIHSPNIRCD CVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGNVRQVHFR
DMMEICLPLIAPESFPSNLNVEAGSYVSFHCRAEAPQPEIYWITPSGQKLLPNTLTDK
FYVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRD
IQANSVLVSWKASSKILKSSVKWTAFVKTENSHAAQSARIPSDVKVYNLTHLNPSTEYK
ICIDIPTIYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTLMACLGLLGIIGVICLISCL
SPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKSTSLKV KATVIGLPTNMS

FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA
TGATACTGTGCTTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCAGTTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAAGCAAATAAAAGCTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

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FIGURE 28

><ss.DNA33089

><subunit 1 of 1, 259 aa, 1 stop

><MW: 29275, pI: 6.92, NX(S/T): 2

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPR
DLPPETVLLYLDSDNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDL
SDNRIQSVHKNAFNNLKHARARIANNPWCDCTLQQVLRSMASNHETAHNVICKTSVLDEH
AGRPFLNAANDADLCNLPKKTDDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLK
SLPSRQKKADEPDDISTVV

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTCAGGCTCGGCCACGGGCTGCCCGCCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTGCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCCGGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCT
CATCGTCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCTCAACCTCTCCTACAACCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCGCGGCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACCTGCCGCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT
GTGTGCCGGGGCCGATGGCGACCCGCCGCCGCCATCCTCTGGCTCTCACCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC
TCCATGCCCCGCCACCTGCATGTGCGCAGCTACTCGCCCCACTGGCCCCATCAGCCCAACAA
GACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCCTTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCGTCGTCCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCACAAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGCGGGGGGCAGGGACCCCCG
GGCGGCCGGGCAGGGGAAGGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCCTTCCCACCTC
CTCCCTACCCTTCTACACACGTTCTCTTTCTCCCTCCCGCCTCCGTCCCCTGCTGCCCCCG
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACCTTGGGTTTCAATAATTATGGATTTT
TATGAAAACCTTGAAATAATAAAAAAGAGAAAAAACTAAAAAAA

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FIGURE 30

><ss.DNA33786

><subunit 1 of 1, 620 aa, 1 stop

><MW: 69838, pI: 8.84, NX(S/T): 10

MQVSKRMLAGGVRSMPSPLLACWQPILLVLSVLSGSATGCPPRCECSAQDRAVLCHRK
CFVAVPEGIPTETRLDLGKNRIKTLNQDEFASFPHLEEELELNENIVSAVEPGAFNNLFN
LRTLGLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLV
YISHRAFSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYR
LKVLEISHWPYLDTMTPNCLYGLNLTSLSIHCNLTAVPYLAVRHLVYLRFLNLSYNPIS
TIEGSMHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTLEESVFHSGVN
LETILDSNPLACDCRLLWVFRRRWRLNFNRRQQPTCATPEFVQGKEFKDFPDVLLPNYFT
CRRARIRDRKAQQVFVDEGHTVQFVCRADGDPPAILWLSPRKHLVSAKSNGRLTVFPDG
TLEVRYAQVQDNGTYLCIAANAGGND SMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGE
ANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPR
KSDAGISSADAPRKFNMKMI

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FIGURE 32

MGAPAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVVKCQVKDHEDSS
LQWSNPAQQTLYFGEKRALRDNRIQLVTSTPHELSSISISNVALADEGEYTCSTFTMPVR
TAKSLVTVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPT
RIQEDPNGKTFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAM
IRPDPPHPREGQKLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSG
TYGCTATSNMGSYKAYYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHY
LIRHKGTYLTAEAKGSDDAPDADTAIINAEGGQSGGDDKKEYFI

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAACCCTTTTCTTCTCCTTTCCTGG
CTTCGGACATTGGAGCACTAAATGAACCTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGTCTCTTTGTTTTGCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA
TCTGTTCCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTACCATTATTTCTGCATGGCAATTC
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG
CTGCACATCAACAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCCAGGGTCCGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA
GCTTTTCTTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA
GAACGCTTGGGTTCGGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTGCGGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
GTTTGTACCTCCGCCTTACCGTGGTGGGCATGCTCGTGTTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG
ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTCGCACAACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCCAGCACGACCCTGCTGGAAG
AACTGACAGTGCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
TGTAATAAGTAACTTTGACTTCTGAC

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FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQ
FYHLFLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKI
KSF RKQTF LGLDDLEYLQADFNLLRDIDPGA FQDLNKLEVLILNDNLISTLPANVFQYV
PITHLDLRGNRLKTL PYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALI
GRVVCEAPTRLQ GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQ
EDHATPGSAPNGG TKIPGNWQIKIRPTAAIATGSSRNKPLANS LPCPGGCSCDHIPGSG
LKMNCNNRNVSSLADLKPKLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIAT
VENNTFKNLLDLRWLYMDSNYLDTLSREKFAGLQNL EYLNVEYN AIQLILPGTFNAMPK
LRILILNNNLLRSLPVDVFAGVSLSKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNW
ECSTIVPFKQWAERLGSEVLMSDLKCETPVNFFRKDFMLLSNDEICPQLYARISPTLT
SHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLLVFVTS AFTVVGMLVFILNRKR
KRRDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHSLSD

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCCCTGACCCCAGAATAACTCAGG
GCTGCACCGGGCCTGGCAGCGCTCCGCACACATTTCCCTGTGCGGGCCTAAGGGAAACTGT
TGGCCGCTGGGCCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTCGGGAGCGAGGGCG
GAGGGGAAGGGAGGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCT
CCAGACACAGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC
GGGGCCTCAGAGA
><MET {trans=1-s, dir=f, res=1}
ATGAGGCCGGCGTTGCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCGGGCGGC
GGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTG
CACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCG
CTCAGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGC
CCAGGGCCCCGGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGT
TCCCCTGACACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCC
GGCGGTCTCGAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCG
CGGAGATGCGCGGTACTCCAGGCCACCGGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATG
CGATGCCACCTGCGCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTCT
GCGCCGCGCCCCGGGGCCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGC
GCCGCTCTGGACTTCAGTCCACCTGGGACCGAGGTGAGTGCGCTCTGCCGGGGACAGCTC
CCGATCTCAGTTACTTGCATCGCGGACGAAATCGGCGCTCGCTGGGACAAACTCTCGGGC
GATGTGTTGTGTCCCTGCCCCGGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCT
AACTGCCTAGACGACTTGGGAGGCTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGG
AAGGACGGCCGCTCTTGTGTGACCAGTGGGGAAGGACAGCCGACCCTTGGGGGGACCGGG
GTGCCACACAGGCGCCCGCCGGCCACTGCAACCAGCCCCGTGCCGCAGAGAACATGGCCA
ATCAGGGTCGACGAGAAGCTGGGAGAGACACCACTTGTCCCTGAACAAGACAATTCAAGTA
ACATCTATTCTGAGATTCTCGATGGGGATCACAGAGCACGATGTCTACCCTTCAAATG
TCCCTTCAAGCCGAGTCAAAGGCCACTATCACCCCATCAGGGAGCGTGATTTCCAAGTTT
AATTCTACGACTTCCTCTGCCACTCCTCAGGCTTTGACTCCTCCTCTGCCGTGGTCTTC
ATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCTTGACCATGACAGTACTGGGGCTT
GTCAAGCTCTGCTTTCACGAAAGCCCCCTTCCCAGCCAAGGAAGGAGTCTATGGGCCCCG
CCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTCCAGTTCTGCACATTGCACA
AACAAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAGCAGAGGGTGCCTTGCTG
GCGGAGTCCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGACATGGGCACTCCTGT
GAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTACTTGTGTAAGTAC
AATTTCTGCAGAAATCCCCCTTCCCTCTAAATTCCCTTTACTCCACTGAGGAGCTAAATCA
GAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTTAGGATGGTGATAC
TGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTTCGGAGAATTTGGAG
AAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACATTAAA
AAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAGGCTAGGAGTATATT
GGTTCGAAATCCCAGGGAAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

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FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGA
LSTVRAGAE LR AVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDP
GGLESDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCF
APRPGAASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCTIADEIGARWDKLSG
DVLCPGPGRYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGOPTLGGTG
VPTRRPPATATSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQM
SLQAESKATITPSGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGL
VKLCFHESPSSQPRKESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALL
AESPLGSSDA

FIGURE 37

CGGACGCGTGGGATTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTA
AGCGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCG
TATCCCCCGGCTACCTGGGCGCGCCCGCGGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGC
AGCCGAGCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTG
GGTGCGGAGGGGCGTGTGTGCCGGCGCGCGCGCCGTGGGGTGCAAACCCCGAGCGTCTAC
GCTGCC

><MET {trans=1-s, dir=f, res=1}

ATGAGGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTC
TCGCGGCAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAG
TCTGGATTTATTGGCAGTGAAGGTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACT
TGGAATAACAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCATAGACCTC
GAGAGTGACAACCTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGC
CAGCGCATTGGCCGCTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAAC
AAGATGATGGTGCAGATGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATG
TTCTCCGCTGCTGAACCAAACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGA
CCTTCCGGCTCTTTTAAAACCCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACT
TGTGTGTGGCACATTGTAGCCCCAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTT
GATGTGGAGCGAGATAACTACTGCCGATATGATTATGTGGCTGTGTTTAATGGCGGGGAA
GTCAACGATGCTAGAAGAATTGGAAAGTATTGTGGTGATAGTCCACCTGCGCCAATTGTG
TCTGAGAGAAATGAACCTTCTTATTCAGTTTTTATCAGACTTAAGTTTAACTGCAGATGGG
TTTATTGGTCACTACATATTCAGGCCAAAAAACTGCCTACAACCTACAGAACAGCCTGTC
ACCACCACATTCCCTGTAACCACGGGTTTAAAACCCACCGTGGCCTTGTGTCAACAAAAG
TGTAGACGGACGGGGACTCTGGAGGGCAATTATTGTTCAAGTGACTTTGTATTAGCCGGC
ACTGTTATCACAACCATCACTCGCGATGGGAGTTTGCACGCCACAGTCTCGATCATCAAC
ATCTACAAAGAGGGGAAATTTGGCGATTCAAGCAGGCGGGCAAGAACATGAGTGCCAGGCTG
ACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTCTAAATTACATTATTATGGGC
CAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGCTTTATCATGATGTTCAAG
ACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATGTTAACAGTGAACGTG
TCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTCTCTCAGTAGAAAAA
AAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGGGACTGGTTGACT
CTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTTTGCCTGCTGT
CAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGAAGCTAAAA
GTGTCAAGCGTTGACAGCTTGAAGCGTTTATTTATACATCTCTGTAAAAGGATATTTTA
GAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTTAGAAGTGCAATATTTATAGTGTTA
TTTGTTTTACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTAAA
TCAATGCTTAATAAAATATTTTTTAAAGGAAAAA

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FIGURE 38

MRGANAWAPLCLLLAATQLSRQQSPERPVFCTCGGILTGESGFIGSEGFPGVYPPNSKCT
WKITVPEGKVVLNFRFIDLESDNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGN
KMMVQMISDANTAGNGFMAMFSAAEPNERGDQYCGLLDRPSGSFKTPNWPDRDYPAGVT
CVWHIVAPKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIV
SERNELLIQFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTGLKPTVALCQOK
CRRGTLEGNYCSSDFVLGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARL
TVVCKQCPLLRRGLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTTCGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGGCCCTCCTGC
CTTCCCTGTCCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTCCGGCTTGT
TTTGGCCCCCTGTGCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG
CTGGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTTGAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATAACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
TCTGTGTTCAACACATCCCCACACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCTTGGAAAGTTAAAAA

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FIGURE 40

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
 Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
 Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
 Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
 Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
 Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 Ile Lys Gly Arg

FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGG
CAGCACC
><MET {trans=1-s, dir=f, res=1}
ATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGGGCC
GCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGTG
CCCACCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAG
TACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTCAGCCAG
AGCTTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGCTGGTG
TTCGGCATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTC
TTCCAGGAGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGC
GCCCCGGGCCCCGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACC
TCCCTCATCGACTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTG
ACCGAGGCCGTGAACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAG
GTGTCCGTGCAGAGGGAGCATCTGGGCCCGCTGGCGTCCGGCGCCCAAGCTGGTCCGC
TTTGCCTCGCAGGGGGCGCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTG
GACCTTGGGGACTATGGAGCTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGC
ACCCGCTGCTGCCGCCAGGAGATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAAC
TGGGTGCTGGAGCCCCCGGGCTTCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCC
CCGGAGGCCCTGGCCTTCAAGTGGCCGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAG
ACTGACTCGCTGCCCATGATCGTCAGCATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTG
GTCAGCCTGCCCAACATGAGGGTGCAGAAGTGCAGCTGTGCCTCGGATGGTGCCTCGTG
CCAAGGAGGCTCCAGCCATAGGCGCCTAGTGTAGCCATCGAGGGACTTGACTTGTGTGTG
TTTCTGAAGTGTTTCGAGGGTACCAGGAGAGCTGGCGATGACTGAACTGCTGATGGACAAA
TGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTTCCTCTGACAAGTTACCTCACCTAAT
TTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGAGAGCCCTTGCTCAGTTTTTCTCTA
TTCTTATTATTCACTGCACTATATTCTAAGCACTTACATGTGGAGATACTGTAACCTGAG
GGCAGAAAGCCANTGTGTCATTGTTTACTTGTCTGTCACTGGATCTGGGCTAAAGTCC
TCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGTGTGCATCCCCAATCCA
GATAATAAAGACTTTGTAAAACATGAATAAAACACATTTTATTCTAAAA

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FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQ
YVALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRL
FQEPVPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV
TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTL
DLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQP
PEALAFKWPFLGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV
PRRLQP

FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTCATCGTGGCAGCCGTCTTGTAAACCCTGATTCTCCTGGGAAT
CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTTGGTGTGAGCCTGGTTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACCTTGTTTAAA
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTTCGGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCA

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FIGURE 44

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCGAGGCCCCAGCTCAG
GCTCGTGCCCACCCACCAAGTTCCAGTGCCGCACCAAGTGGCTTATGCGTGCCCCCTCACCTGG
CGCTGCGACAGGGACTTGGAAGTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCCTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

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FIGURE 46

><ss.DNA33221

><subunit 1 of 1, 282 aa, 1 stop

><MW: 28991, pI: 4.62, NX(S/T): 3

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQ
CRTSGLCVPLTWRCDRDLDCSDGSDEEEECRIEPC TQKGQCP PPPGLPCPCTGVSDCSGGT
DKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATT
MGPPVTLESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSA
SLVTATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCTGCGCACAGATGCGG
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCGAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCAGTCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAGCTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGTCT
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCCTCCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCACTGGGT
GTTGTTCCCTAAGAACTGATTGATTAAAAAATTTCCCAAAGTGTCCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCTTTCCTTCTCTTGGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAAGNAAAAA

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FIGURE 48

><ss.DNA33107

><subunit 1 of 1, 490 aa, 1 stop

><MW: 53920, pI: 5.41, NX(S/T): 4

MYHGMNPSNGDGFLEQQQQQQQQPQSPQRLLAVILWFQALALCFGPAQLTGGFDDLQVCADP
GIPENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQE
DCRIPQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGC
LRPLASSNGYVNISELQTSFPVGTVISYRCFPFGFKLDGSAYLECLQNLIWSSSPPRCLAL
EAQVCPLPPMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSY
QVYCIKSEQTWPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPR
SSSSDPDFVVVDGVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSG
D TDTGPGESETCDSVSGSSELLQSLYSPPRCQESTHPASDNPDI IASTAEVASTSPGIH
HAHWVLF LRN

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTCGCGCACGCCTCTGCCCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTCGGGGGGCGCACCCGAGTCGGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAATTTAGGAACTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA
CCGGTGCAACATGAAGAACAATTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATTCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACCTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTTTCTTGCTCTATACAG
CAGCACATATTATCATAACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCA
CAGGTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAA
AGAGCAGGAAAAAAA

FIGURE 50

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr

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FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
G TTCAGCATGCGCTTGTGGACCCCACTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCTGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAATC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAGGACCCATCATCAT
CCACACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTTGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTTATACAATG

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FIGURE 52

><ss.DNA34434

><subunit 1 of 1, 428 aa, 1 stop

><MW: 48886, pI: 6.39, NX(S/T): 0

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHG
ARSPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMF
AGQLTKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGL
FQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRTASLQPGISEDLLKKVKDRMG
IDSSDKVDFFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMA
VGPFLHILESNNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHWPPFAVDLT
MELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSPEKYHALCSQTQ
VMEVGNEE

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCC
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACCTACATCA
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAGATAGCAC
TATGTGTTCAA

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FIGURE 54

><ss.DNA33100

><subunit 1 of 1, 347 aa, 1 stop

><MW: 38130, pI: 5.40, NX(S/T): 0

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAV
LCRELGC GAASGTPSGILYEP PAEKEQKVLIQSVSCTGTEDTLAQCEQE EVYDCSHDEDA
GASCENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLG
CGRAVLTQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECED
PFDLRLVG GDNLCSGRLEVLHKG VWG SV CDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKC
YGP GVGRIWLDNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTTCGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTAC

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FIGURE 56

><ss.DNA35600

><subunit 1 of 1, 310 aa, 1 stop

><MW: 33524, pI: 9.55, NX(S/T): 1

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAA
GAKLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGY
VDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSE
QKMSIPFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSR
YGVMDTTTAQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRITLAPGLFFSLMASR
ARKERKSKNS

FIGURE 57

CCCACGCGTCCGCTGGTGTTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGG
><MET {trans=1-s, dir=f, res=1}>
ATGAAATTTCTTCTGGACATCCTCCTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTC
CTTCGTGAAGCTTTTTATTCTAAGAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTA
CAGGAGCTGGGCATGGAATTGGGAGACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAG
CTGGTTCTCTGGGATATAAATAAGCATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACT
GGGTGCCAAGGTTCATACCTTTGTGGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTG
CAAAGAAGGTGAAGGCAGAAATTGGAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTC
TATACATCAGATTTGTTTGCTACACAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGT
ACTTGCACATTTCTGGACTACAAAGGCATTTCTTCCTGCAATGACGAAGAATAACCATGGCC
ATATTGTCACTGTGGCTTCGGCAGCTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGT
TCAAGCAAGTTTGCTGCTGTTGGATTTCTATAAACTTTGACAGATGAACTGGCTGCCTTACA
AATAACTGGAGTCAAAACAACATGTCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAA
ATCCAAGTACAAGTTTGGGACCCACTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCAT
GGGATTCTGACTGAGCAGAAGATGATTTTTATTCCATCTTCTATAGCTTTTTTTAACAACATT
GGAAAGGATCCTTCCTGAGCGTTTCCTGGCAGTTTTTAAAACGAAAAATCAGTGTTAAGTTTG
ATGCAGTTATTGGATATAAAATGAAAGCGCAATAAGCACCTAGTTTTCTGAAAACCTGATTTA
CCAGGTTTAGGTTGATGTCATCTAATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTT
CTAATTATCCCCATTTCTTCAATATCATTTTTTGAGGCTTTGGCAGTCTTCATTTACTACCAC
TTGTTCTTTAGCCAAAAGCTGATTACATATGATATAAACAGAGAAATACCTTTAGAGGTGAC
TTTAAGGAAAATGAAGAAAAAGAACCAAAATGACTTTATTAAAATAATTTCCAAGATTATTT
GTGGCTCACCTGAAGGCTTTGCAAAATTTGTACCATAACCGTTTATTTAACATATATTTTTA
TTTTTGATTGCACTTAAATTTTGTATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAG
AACTTCAAGCTCTCTAAATAAAATGAAGGACTATATCTAGTGGTATTTCACAATGAATATC
ATGAACTCTCAATGGGTAGGTTTCATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCT
CACATTCCAATGCCAAACATTTCTGCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGT
ATAAAAGCATCACTGGGATTTAAGGAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAA
TAAATGGATCACACTTAAA
AAA

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FIGURE 58

> <subunit 1 of 1, 300 aa, 1 stop

> <MW: 32964, pI: 9.52

><signal peptide>

MKFLLDILLLLPLLIVCSL

><start mature protein>

ESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKLVLWDINKHGLEETAAK
CKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVVYTSDFATQDPQIEK
TFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLA

><putative oxidoreductase active site, by similarity to Y00P_MYCTU and BUDC_KLETE>

YCSSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVN
RLMHGILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCCCGCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA
CCTTGCGTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCACTAATTGAGTTTTTCCAGATATTTCTGAATATAAAAAATA
ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTTGGAGGCCCTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACCTATAGTTGAAAAGTACTTGCGAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACCTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTATGGAAAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAGAGAACAT
CAGAGGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAATTATCCTTGAAACAAGTGAGC
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGTCTTGAATAGGAAGTTTTAATTTCTTCTAAGAGTAAGTGAAAAGTGCAAGTTG
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA
TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA
AAAATATTATATATAAAAGTAAAAAAA

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FIGURE 60

><ss.DNA33206

><subunit 1 of 1, 476 aa, 1 stop

><MW: 54164, pI: 5.52, NX(S/T): 4

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGREL
SLVGPFPGGLNMKSYAGFLTVNKTYNNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGL
FVEHGPYVVTSNMTLRDRDFPWTTTSLMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY
SALIQQFFQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYS
DPESIIGGYAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLS
DPSYFQNVGTGCSNYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNTQTFNDGTIVEKYLR
EDTVQSVKPLTEIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEEKVWK
IFKSDSEVAGYIRQAGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT
TTTTCCCTTTCCTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCTGGGTC
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTCACCCCTACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCA
GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT
CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
CCCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
AGGCCTTCAATATCACCAAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG
CAGTATCACCAACCCGCCCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTTCTTGGGGAAACAAAGGTGAAATGGGGAGGTAAGAAGGGGTTAATTTTGTG
ACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCCAAACCTTTAAGAAAAAATTTAAGAAGGTACATCTGCAAAAGCAAA

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FIGURE 62

><ss.DNA35558

><subunit 1 of 1, 552 aa, 1 stop

><MW: 61674, pI: 6.95, NX(S/T): 4

MGTLGQASLFAPPGNYFWS DHSA LCF AESCEGQPGKVEQMSTHR S RLLTAAPLSMEQRQP
WPRALEVD SRSVLLSVVWVLLAPPAAGMPQFSTFHSEN RDWTFNH LTVHQGTGAVYVGA
INRVYKLTGNLTIQVAHKTGPEEDNKSRYPP LIVQPCSEVLTLTNNVNKLLIIDYSENRL
LACGS LYQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGT
AVDGKQDYFPTLSSRKLP RDP ESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYG
FASGGFVYFLTVQPETPEGVA IN SAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVE
YRLLQAAYLAKPGDSL AQA FNITSQDDVLFAIFSKGQKQYHHPDD SALCAFP IRAINLQ
IKERLQSCYQGEGNLELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYT
TSRDRMTSVASYVYNGYSVV FVGTKSGKLKKVRVYEFRC SNAIHLLSKESLLEGSYWWRF
NYRQLYFLGEQR

FIGURE 63

AGGCTCCCGCGCGCGGGCTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAA
 CACGCGATGACCACGTGGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGGACTCCTGCTGCT
 GGTCGTCTTGGGCTTCCTGGTGCTCCGCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGCGGC
 TCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGAACCTTCATGCTGGAGGATTCCACC
 TTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACTGGAGGGACCG
 CCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACCTGC
 ATGAGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCCTG
 ATGGCCGCGAGAGATCGGGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGAT
 GGACCTCGGGGGCTTGCCAGCTGGCTACTCCAAGACCCTGGCATGAGGCTGAGGACAACTT
 ACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACCTGATGTCCAGGGTGGTGCCA
 CTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATGGTTCCTA
 TAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACCTGGAGGACCGTGGCATTGTGG
 AACTGCTCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTG
 GCCACCATCAACTTGCAGTCAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGT
 CCAGGGGACTCAGCCCAAGATGGTGATGGAGTACTGGACGGGGTGGTTTGACTCGTGGGGGAG
 GCCCTCACAATATCTTGGATTCTTCTGAGGTTTTTGAAAACCGTGTCTGCCATTGTGGACGCC
 GGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATGGAGC
 CATGCACTTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAG
 AAGCCGGCGATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGC
 ATCCCTCTCCCTCCCCACCTGACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGT
 CTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACCTGGGGGAGCCAATCAAGTCTGAAAAGC
 CCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCTTCGGGTACATTCTC
 TATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGGT
 GTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCC
 TGATCCAGGGTTACACCGTGCTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGG
 GAGAAATATTGATGACCAGCGCAAAGGCTTAATTGGAAATCTCTATCTGAATGATTCACCCCT
 GAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGAGCTTCTTTCAGAGGTTTCGGCCTGG
 ACAAATGGNGTTCCCTCCCAGAAACACCCACATTACCTGCTTTCTTCTTGGGTAGCTTGTCC
 ATCAGCTCCACGCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTGTATT
 CATCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCCAGAAGACGCTTTACCTCC
 CAGGTCCCTGGTTGAGCAGCGGAATCAACCAGGTCACTGTTTTTGAGGAGACGATGGCGGGC
 CCTGCATTACAGTTCACGGAAACCCCCACCTGGGCAGGAACCAAGTACATTAAGTGAGCGGT
 GGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTCCTCTTGACCTGAAGCCTGGTG
 GCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGGACTGGGGG
 CTACAGTCTGCCCCGTGTCTCAGCTCAAAACCCTAAGCCTGCAGGGAAAGGTGGGATGGCTCT
 GGGCCTGGCTTTGTGATGATGGCTTTCCTACAGCCCTGCTCTTGTGCCGAGGCTGTGGGGC
 TGTCTCTAGGGTGGGAGCAGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGCTG
 AAACGTGCCCTTGCACCGGACGTACAGCCCTGCGAGCATCTGCTGGACTCAGGCGTGCTCT
 TTGCTGGTTCCTGGGAGGCTTGGCCACATCCCTCATGGCCCCATTTTATCCCCGAAATCCTG
 GGTGTGTCACCAAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTTCTTCC
 TTCACAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGAC
 TTCCCCTTTCCCTTCCCACCTCGCTGCTTCCCACAGGGTGACAGGCTGGGCTGGAGAAACAGA
 AATCCTCACCTGCGTCTTCCCAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATG
 TGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGGACAGAAGGCCAG
 CTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGGACAGA
 AGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGG
 AGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATC
 CAGGGAGGAGGACAGAAGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCACGCCCGAACA
 GCAGGGGCAGAGCAGCCCTCCTTCGAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTCTGGG
 GCCAGCCCAACACCTGGCTTGGGCTCACTGTCTGAGTTGCAGTAAAGCTATAACCTTGAA
 TCACAA

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FIGURE 64

MTTWSLRRRPPARTLGLLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDS
TFWIFGGSIHVFRVPREYWRDRLLKMKACGLNTLTTPVWNLHEPERGKFDFSGNLDLE
AFVLMAAEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDH
LMSRVVPLQYKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKDG
LSKGIVQGVLATINLQSTHELQLLTFFLFNVQGTQPKMVMYWTGWFDWGGPHNILDS
SEVLKTVSAIVDAGSSINLYMFHGGTNFGFMNGAMHFDYKSDVTSYDYDAVLTEAGDY
TAKYMKLRDFFGSISGIPLPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPI
NMENLPVNGGNGQSFGYILYETSITSSGILSGHVHVRGQVFNVTVSIGFLDYKTTKIAV
PLIQGYTVLRILVENRGRVNYGENIDDQRKGLIGNLYLNDSPKLNFRISLDMKKSFFQ
RFGLDKWXSLETPPTLPAFFLGSLSSSTPCDTFLKLEGWEKGVVFINGQNLGRYWNIG
PQKTLYLPGPWLSSGINQVIVFEETMAGPALQFTETPHLGRNQYIK

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA
GGCAGACACTCGGTTCGTTAGTAGTGGATAGGGGTTCATGACCGGTTTCTCCTAGACGGGGCCC
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC
CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACCTA
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTTCCTTGCCGCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTGAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGG
AGAAAAGATCTTGCTCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATAACCACTGTAGATTTTGGCCCAGCTGACAAACATGACCAAATCTTTACCCTGCTT
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTTGCTCTTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCCGAGCCCCAAGATGATGCTTGACCTGTG
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCAT
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
GAACCTATATGACCCATAACATTTTGGAGCCAACACCATTTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCTATGTGATGGTGGATGGGGTGTTCCAGGGTGTTGTGGAGCGAAATATGAG
AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTTCCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCTCTACGTGCCAAGATTCCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA
CATTGCTGGAACCTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC
CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCTTTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGGCGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAAAA

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FIGURE 66

MRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYICAEW
EMGGLPSWLLRKPEIHLRTSDPDLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENEY
GSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTK
IFTLLRKYE PHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNM MYMFH
GGTNFGYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLP
PPSPKMMLGPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHT
IFEPTPFWVPNNGVHDRA YVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLS
FGSNSSDFKGLLKPPILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFY
SKTFPILGSVGD TFLYLPGWTKGQVWINGFNLGRYWTKQGPQQTLYVPRFLLFPRGALN
KITLLELEDVPLQPQVQFLDKPILNSTSTLHRTHINSLSADTLSASEPMELSGH

FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
CTTGTGAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTTACGCAACGCCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT
GACTTGTTTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA
AAAACCTTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTTG
TGGAAGATCACCTTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTAAATTGTTTGTAACCTTGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAA

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FIGURE 68

><ss.DNA34407

><subunit 1 of 1, 501 aa, 1 stop

><MW: 57819, pI: 8.15, NX(S/T): 3

MAYMLKKLLISYISIIICVYGFICLYTLFWLFRIPLKEYSF EKVREESSFSDIPDVKNDF
FLLHMVDQYDQLYSKRFGVFLSEVSENKLREISLNHEWTFEKL RQHISRNAQDKQELHLF
MLSGVPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRD
HLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLREL RHLKILHVKS
NLTKVPSNITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAEELQNC ELERIPHAIFSL
SNLQELDLKSNNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNK
LESLPVAVFSLQKL RCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKL
RTLNLGQNCITSLPEKVGQLS QLTQLELKGNC LDR LPAQLGQCRMLKKSGLVVEDHLFDT
LPLEVKEALNQDINIPFANGI

FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCCTTTTCATTGACAAACTGAC
TTTTTTTATTTCTTTTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGA
CATTTGTGTTTTTACACACATAAGGATCTGTGTTTGGGGTTTCTTCTTCCCTCCCCTGACATTG
GCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCAGTGGGCTCAGTGCTTGCTTGCACTTAT
CTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTCATCGCTGGTG
GTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCTGTCTGTCTTTACTTCAAAATACAC
AACGCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAA
GGTGTGGTGGGCCAAGAACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCCTGCCCTGC
AGTGCTGTGAAGGATATAGAATGTGTGCCAGTTTTGATTCCCTGCCACCTTGCTGTTGCGAC
ATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAAAGCAGAGCCCTGAAGACTTCA
ATGATGTCAATGAGGCCACCTGTTTTGTGATGTGCAGGCACAGAAGAAAGGCACAGCTCCCCA
TCAGTTTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAG
AGCTTCCACTGGGGGCAACCCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGG
AATGCTGATAAACCAGTCACACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCT
GGAAGTACGTTTTCCCTGGAGGTGTCCAGAAAGCTGATGTAACACAGAGCCTATAAAAGCTG
TCGGTCCCTTAAGGCTGCCCAGCGCCTTGCCAAAATGGAGCTTGTAAGAAGGCTCATGCCATT
GACCCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAATGCAA
GCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAA
CTCAATCCCAGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAAGCATCAGAAT
TATCTTTTCCTATGTCCAGCTTGATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCT
TTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGGCAAGTCTGCAGTAAAAACGACTATGTT
CCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACTGACTCAGCAAGAAT
TCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCCTAACATCTCTATTCCAACTGTG
GCGGTTACCTGGATACCTTGGAAGGATCCTTACCAGCCCCAATTACCCAAAGCCGCATCCT
GAGCTGGCTTATTGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAACTT
CAAAGAGATTTTCCTAGAAATAGACAAACAGTGCAAATTTGATTTTCTTGCCATCTATGATG
GCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGTGGCCGTGTGACTCCCACCTTCGAA
TCGTCATCAAACCTCTCTGACTGTCTGTGTTGTCTACAGATTATGCCAATTCTTACCGGGGATT
TTCTGCTTCCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTT
CTGACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAAT
AACTTGCAACTAAAAGACCCAACTTGACAGACCAAATATCAAATGTTGTGGAATTTTCTGT
CCCTCTTAATGGATGTGGTACAATCAGAAAGGTAGAAGATCAGTCAATTACTTACACCAATA
TAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACCCGTGAGAAACAACTCCAGATT
ATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACAGAAGATGA
TGTAATACAAAGTCAAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTTGAATCCA
ATTCATTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTGTAACCAAACCTTTTTT
GTTCAAGTTAGTCTGCACACCTCAGATCCAAATTTGGTGGTGTCTTCTTGATACCTGTAGAGC
CTCTCCCACCTCTGACTTTGCATCTCCAACCTACGACCTAATCAAGAGTGGATGTAGTCGAG
ATGAAACTTGTAAGGTGTATCCCTTATTTGGACACTATGGGAGATTCCAGTTTAAATGCCTTT
AAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTTGATATGTGATAGCAG
TGACCACCAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCAT
ATAAATGGAAAACAGATTCCATCATAGGACCCATTCTGTCTGAAAAGGGATCGAAGTGCAAGT
GGCAATTCAGGATTTTCAGCATGAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAG
TGTGCATCTGTTTTCTTCATGGTTCTAGCTCTGAATGTGGTGAAGTGTAGCGACAATCACAG
TGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTGCAGAACTATTAATA
ACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGTGG
CTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAA

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FIGURE 70

><ss.DNA35841

><subunit 1 of 1, 607 aa, 1 stop

><MW: 68153, pI: 6.39, NX(S/T): 9

MELVRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTW
TIERPENKSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLQVCSKNDYVPVFESSS
STLTFQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYC
VWHIQVEKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSS
NSLTVVLSTDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNN
LQLKDPTCRPKLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQ
IIVKCEMGHNSTVEIIYITEDDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQ
TLFVQVSLHTSDPNLVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRF
QFNAFKFLRSMSSVYLQCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDISIIGPIRL
KRDRSASGNSGFQHETHAEETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYK
YQKLQNY

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGC
TGCTGCCGCGCGCCGCGTGGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC
CTGGACGCCCCGCCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTTTCCGTGCCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAAGTGGGCAGATATTTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTCGTGGAAGTGGAAATGCCATAGATGAGGGGGCCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTTGGACTGTACTATTCCCTTTTTGA
ATGGTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTTATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAAGTGCATGACAATAGACAAAGTGTCTGGGGCTATAGGAGGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTTCATGTG
GAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTCTGTAGTTTTTTGAG
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTTCATCAGATGC
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTTTCCCACTA
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACCTTTGCCATTAAAGTC
TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTTATAAAAAAAA
GTTTTTCTTTCTTCAATTATAAATTAACATAAGTGTACTGTAACCTTACAAACGTTTTTAATT
TTTAAACCTTTTTGGCTCTTTTGTAATAACACTTAGCTTAAACATAAACTCATTGTGCAA
ATGTAA

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FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFI
HWGVFSVPSFGSEFWWYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWA
DIFQASGAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAI RNRTDLRF
GLYYSLEFWFHPLFLEDESSSFHKRQFPVSKTLPELYELVN NYQPEVLWSDGDGGAPDQ
YWNSTGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCM
TIDKLSWGYRREAGISDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLR
QVGSWLKVNGEAIYETYTWRSQNDTVTPDVWYTSKPKEKLVYAI FLKWPTSGQLFLGHP
KAILGATEVKLLGHGQPLNWISLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGC
AGCTGAATTTTACAGAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA
TGGATTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCA
AACTGCAACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCCCTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTTGTGTACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA
AACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCCTGCCCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCCTAATAATATCCCCTGGGAGAAAGGAGTTTTGCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG
TGGGTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGAC
CCTTCTTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTA
AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTTCA
GTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTTTATTTTTTGCTGAGACTAATCTT
ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG
TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAACAAATGTATCACTA
GCCCTCCTTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA
AGCATTTAGAAAACCTT

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FIGURE 74

><ss.DNA34431

><subunit 1 of 1, 322 aa, 1 stop

><MW: 35213, pI: 8.71, NX(S/T): 3

MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA
CRLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPV
SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA
PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL
LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQOKEMIETKVVKEEKANDSNPNEESKKT
DKNPEESKSPSKTTVRCLEAEV

FIGURE 75

AG

><MET {trans=1-s, dir=f, res=1}>

ATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTCGGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGG
AAACTGCCGCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCCGTGTGAC
TTTGA CTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAAC
CGCAGATCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCC
AACACAATTCTTTTCTTCCGCTTGGATATTCGCATGGGCCTACTTTACATCACACTCTGC
ATAGTGTTCTGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTAC
TTCAATGATAAAACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTG
GAGTTCTTTGCCAATTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTC
TCCCTTAAATACA ACTGTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACT
GATGTTAGTACGCGGTACAAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTG
ATCCTGTTCCAAGGTGGCAAGGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGG
GCTGTCTCATGGACCTTCTCTGAGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTA
TACCAGCGGGCCAAGAACTATCAAAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTG
GCTTCAACCCCCACCACAGTGTGATGTTGAGGAAAACAAGAAGGATAAATAAGATCCTCAC
TTTGGCAGTGCTTCCTCTCCTGTCAATTCCAGGCTCTTTCCATAACCACAAGCCTGAGGC
TGCAGCCTTTNATTNATGTTTTCCCTTTGGCTGNGACTGGNTGGGGCAGCATGCAGCTTC
TGATTTTAAAGAGGCATCTAGGGAATTGTCAGGCACCCTACAGGAAGGCCTGCCATGCTG
TGGCCA ACTGTTTCACTGGAGCAAGAAAGAGATCTCATAGGACGGAGGGGGAAATGGTTT
CCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATCAGCTATTCAGACATCTCCATGGTT
TCTCCATGAACTCTGTGGTTTCATCATTCCTTCTTAGTTGACCTGCACAGCTTGGTTAG
ACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAACGCTAAGAATTTTCCCCCAA
GGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTCTTCATTAAAAGTATAAGC
CTAACTTTGTCGCTAGTCCTAAGGAGAAACCTTTAACCACAAAGTTTTTATCATTGAAGA
CAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAATAGAGGCTTGAGAC
TTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCACTAACCCCTCTGAC
ATACTCCCCACACCCAGTTGATGGCTTTCGTAATAAAAAGATTGGGATTTCTTTTG

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FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVKLPPLCHGLPTQREDGNPCD
FDWREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLC
IVFLMTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPYADL
SLKYNCTGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGR
AVSWTFSEENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

FIGURE 77

GGACAGCTCGCGGCCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG
GGGCCCCAGCCTGGCCCCGGGTCAACCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA
TTGCTCCTGCTGCCCCGGCTCCTACGGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCA
ACGGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG
GTGGCCTCCTTTGAGCAGCTCTTCCGGGCCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCCGGCAGCCCTGCGGTGGCC
CAGGCCTGGCACCTGGCGTGCGAAGCTACGGCCCCCGCCACCGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC
AGCTCTTTGCCGCTGGAAGTTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCCAGAGCCTGGGGT
CCGAAGCTTTGGCTTCCCCGACCCGCAGAGCCGCTTGTACGGTGTTTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCCTGCCGCATTCCCTCACTGGCTGTGTATTTATTGAGTGGTT
CGTTTTCCCTTGTGGGTGGAGCCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT
TTAAACATTTTTTTTACTATTTTTTTGTAAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTG
GATGCCCCACTCCAGGAATCATGCTTGCTCCCCTGGGCCATTTGCGGTTTTGTGGGCTTCTG
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCCAGAGTGGGC
GGTGGCCTGTCTAGAATGCCGCCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCT
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCCTCCGGAGCTGGGCTTTGGGCCTCTCCTGCC
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAAACTCCCCTCCCCGTCCCCT
TCCCCTCTCGGTTCCAAAGAATCTGTTTTGTGTGTCATTTGTTTCTCCTGTTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTGTACTTTGGACAATAAATGGTGCTATGACTGCCTTCCGCCAA
AA
AA

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FIGURE 78

><ss.DNA39423

><subunit 1 of 1, 360 aa, 1 stop

><MW: 40894, pI: 6.44, NX(S/T): 0

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFT
YQGASVILPCRYRYEPALVSPRRVRVKWWKLENGAPEKDVLVAIGLRHRSFGDYQGRVH
LRQDKEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFN
FHEGQQVCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAP
GVRSYGPRHRRLLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLF
AAWKFHGLDRCDAGWLADGSVRYPVVHHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG

><MET {trans=1-s, dir=f, res=1}

ATGATGTGGCGACCATCAGTTCTGCTGCTTCTGTTGCTACTGAGGCACGGGGCCCAGGGG
AAGCCATCCCCAGACGCAGGCCCTCATGGCCAGGGGAGGGTGCACCAGGCGGCCCCCCTG
AGCGACGCTCCCCATGATGACGCCACGGGAACCTCCAGTACGACCATGAGGCTTTCCTG
GGACGGGAAGTGGCCAAGGAATTCGACCAACTCACCCCAGAGGAAAGCCAGGCCCGTCTG
GGGCGGATCGTGGACCGCATGGACCGCGCGGGGGACGGCGACGGCTGGGTGTGCTGGCC
GAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCACATACGGGACTCGGTGAGCGCG
GCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGGGTGGGAGGAGCTGCGCAAC
GCCACCTATGGCCACTACGCGCCCCGGTGAAGAATTTTCATGACGTGGAGGATGCAGAGACC
TACAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGCCGACCAGGATGGGGAC
TCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGGAGTTCCTCACATG
CGGGACATCGTGATTGCTGAAACCTTGGAGGACCTGGACAGAAACAAAGATGGCTATGTC
CAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGAGGAGCCGGCG
TGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGGATGGGCAC
CTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCCAGGACCAGCCCCTGGTG
GAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAAAGCG
GAAATCCTGGGTAAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGGAC
CTGACCCGGCACCAACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGCAGG
AGGCAGATGCAGTCCCAGGCATCCTCCTGCCCCCTGGGCTCTCAGGGACCCCCTGGGTGCG
CTTCTGTCCCTGTCACACCCCCAACCCAGGGAGGGGCTGTCATAGTCCCAGAGGATAAG
CAATACCTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCTTGGCCCCAAGCTC
AGCTCTAAGAACCGCCCCAACCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTG
AAACTCCCCTGGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCC
AGGAGGCAATAAAAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 80

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40620

><subunit 1 of 1, 328 aa, 0 stop

><MW: 37493, pI: 4.77, NX(S/T): 1

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL
GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA
AWDTYDTDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGD
SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEPA
WVQTERQQFRDFRDLNKDGHLDGSEVGHWWLPPAQDQPLVEANHLLHESDTRDKDGRLSKA
EILGNWNMFVGSQATNYGEDLTRHHDEL

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FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCC
 GGGCGGCGGGCGCGGGGTGCGAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTC
 CCAGCCTGTCTGTCTGTCGTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTGACACACCG
 ATCCTGGGCTTCGCTCGATTTGCCGCCGAGGCGCCTCCCAGACCTAGAGGGGCGCTGGCC
 TGGAGCAGCGGGTCTGTCTGTCTCTCTCTCTGCGCCGCGCCCGGGGATCCGAAGGGT
 GCGGGGCTCTGAGGAGGTGACGCGCGGGGCCTCCCGCACCCTGGCCTTGCCCGCATTCTC
 CCTCTCTCCCAGGTGTGAGCAGCCTATCAGTCACC
 ><MET {trans=1-s, dir=f, res=1}
 ATGTCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTGTGTCTGCTGCTGCTGCCGGGG
 CCCGCGGGCAGCGAGGGAGCCGCTCCCATTTGCTATCACATGTTTTACCAGAGGCTTGGAC
 ATCAGGAAAGAGAAAGCAGATGTCCTCTGCCCAGGGGGCTGCCCTCTTGAGGAATTCTCT
 GTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGGGCTGCTGTCCACAGG
 GGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACCTGGTTCGAGAAAAC
 TATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGATGGTCTGCTTCT
 TTCACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCAGTGTCCACA
 GCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGGCAATAAA
 GATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGCGCCGA
 TTTAATTTACAGAAGAATTTTGTGGAAGAGTGGCTCTAATGTTGGGAATTGGAACAGAA
 GGACCACATGTGGGCCTTGTTCAAGCCAGTGAACATCCCAAATAGAATTTTACTTGAAA
 AACTTTACATCAGCCAAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGT
 AATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCT
 GGAGTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGAT
 GACATCGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCT
 GTGGCCAAGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTTGTTGACAAG
 GCTGTCTGTCTGGAATAATGGCTTCTTCTTACCACATGCCCAACTGGTTTGGCACCACA
 AAATACGTAAAGCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAG
 ACCTGTTATACTCAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTGAGAT
 AGCAATTTCCGCCTCATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCG
 GACATTGGTGCCAAGATAGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGT
 TTCACTGACTATAGCACCAAAGAGAATGTCCTAGCTGTCATCAGAAACATCCGCTATATG
 AGTGGTGGAACAGCTACTGGTGTATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCT
 ATAAGGGAGAGCCCCAACAAGAACTTCCTAGTAATTGTACAGATGGGCAGTCCTATGAT
 GATGTCCAAGGCCCTGCAGCTGCTGCACATGATGCAGGAATCACTATCTTCTCTGTTGGT
 GTGGCTTGGGCACCTCTGGATGACCTGAAAGATATGGCTTCTAAACCGAAGGAGTCTCAC
 GCTTTCTTCACAAGAGAGTTACACAGGATTAGAACCAATTGTTTCTGATGTCATCAGAGGC
 ATTTGTAGAGATTTCTTAGAATCCCAGCAATAATGGTAACATTTTGACAACCTGAAAGAAA
 AAGTACAAGGGGATCCAGTGTGTAAATTGTATTCTCATAATACTGAAATGCTTTAGCATA
 CTAGAATCAGATACAAAACCTATTAAGTATGTCAACAGCCATTTAGGCAAATAAGCACTCC
 TTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGTACTTTGTTAAAAACACTGCTGAG
 GCTTCATAATCATGGCTCTTAGAACTCAGGAAAGAGGAGATAATGTGGATTAAACCTT
 AAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAATTCCATAGCTCAATAAAAG
 AATCTGATACTTAGACCAAAAAAAAAA

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FIGURE 82

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40604

><subunit 1 of 1, 550 aa, 0 stop

><MW: 59483, pI: 8.34, NX(S/T): 2

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEF
VYGNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSAS
FTVTKGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRR
FNLQKNFVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGG
NSNTGKALKHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVS
VAKPIPEELGMVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSK
TCYNSVNIAFLIDGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFS
FTDYSTKENVLAVIRNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYD
DVQGPAAAAHDAGITIFSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRG
ICRDFLESQQ

FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGAGC
 CCGGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCA
 GTCGGGGCGGCGGCTGCGGGCGCAGAGCGGAG
 ><MET {trans=1-s, dir=f, res=1}
 ATGCAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGGCGGCGGTCCCCACGGCC
 CCGCGGCCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCCGGCTCTCAGCTAC
 CCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGATGGAGGAC
 ACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTAAA
 GCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTATCACAATGAGACCAACACA
 GACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTACAAAGATAACCAAC
 AACCAGACTGGACAAATGGTCTTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAA
 GGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCGAGCATGTACTGCCAG
 TTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGG
 GACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACC
 AGGGGCAGCAATGGGACCATCTGTGACAACAGAGGGACTGCCAGCCGGGGGCTGTGCTGT
 GCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGAGCTT
 TGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATGGA
 GCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
 GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTG
 CCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAG
 CTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCC
 GCCGCTGCACTGCTGGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGGTAGATGTG
 CAATAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCT
 TCTTCCTACATCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTG
 CATTTGTTTCAGCTCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTC
 AGGCAGGGTTAAACTGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGC
 CTCTACCAGTTGGCAGACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAG
 GAGATGGAAACAATGTGGAGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTG
 CCCTGCTTTGCAACATCAACCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCT
 TTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCC
 TGCATTACATGTGTTTATTCATCCAGCAGTGTGTGCTCAGCTCCTACCTCTGTGCCAGGGC
 AGCATTTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTG
 TTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCCCAAGTCA
 CACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCTCT
 CCACTACCCACACCAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGG
 GATTTTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAACCTAATTCTCACATCCCTCTA
 AAAGTAACTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCCTTCTAA
 TGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACTTTGAAAGGT
 ATATGACTGAGCGTAGCATAACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGG
 CGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAACTGAAGACAATTATCAACC
 ACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTTGTAATATGCGACTGCG
 AACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTCATGGACTGTTGCCAC
 CATGTATTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTATAAGCATGCTTT
 CTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGCATAAATCACT
 TCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMED
TQHKLRSAVEEMEAEEAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITN
NQTGQMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMCTR
DSECCGDQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGEL
CHDPASRLLDLITWELEPDGALDRCPGASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILL
PREVPDEYEVGSGFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGEEI

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FIGURE 85A

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGCT
 CAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAACACA
 CATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAAGACTCA
 CAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGACAGGCCTGG
 CCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGGCCAGGCACGG
 TGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAG
 GAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCCATCTCTACTAAAAATACAAAATT
 AGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATC
 GCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCGCTGCACTCCAGCCTGGGT
 GACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGAGGGGTAGATACTGCTTCTCT
 GCAACCTCCTTAACCTCTGCATCCTCTTCTTCCAGGGCTGCCCCCTGATGGGGCCTGGCAATGA
 CTGAGCAGGCCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
 CGCCCCGTGTAGAATGACTGCCCTGGGAGGGTGTTTCTTGGGCCCTGGCAGGGTTGCTGAC
 CCTTACCCTGCAAAACACAAAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCCTGCCC
 TGCAGCTCCACCATGAGGCTTCTCGTGGCCCCACTCTTGCTAGCTTGGGTGGCTGGTGCCAC
 TGCCACTGTGCCCCGTGGTACCCTGGCATGTTCCCTGCCCCCCTCAGTGTGCCTGCCAGATCC
 GGCCCTGGTATACGCCCCGCTCGTCTTACC CGAGGCTACCACTGTGGACTGCAATGACCTA
 TTCCTGACGGCAGTCCCCCGGCACTCCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAA
 CAGCATTGTCCGTGTGGACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACC
 TGTCCCAGAACAGCTTTTTCGGATGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTG
 AGCCTGCACCTAGAGGAGAACCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGC
 CAGCCTACAGGAACCTCTATCTCAACCACAACCAGCTCTACCGCATCGCCCCCAGGGCCTTTT
 CTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGC
 CGCTGGTTTGAAATGCTGCCCAACTTGAGATACTCATGATTGGCGGCAACAAGGTAGATGC
 CATCCTGGACATGAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGA
 ACCTGCGGGAGATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC
 TATGACAACCAGCTGGCCCCGGGTGCCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTT
 CCTAGACCTCAACAAGAACC CGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGC
 ACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTG
 GTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA
 CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCTCA
 GTGCCTTGACACCAGCAGACGGTGGAGTCCCTGCCCAACCTGCAGGAGGTAGGTCTCCACGGC
 AACCCCATCCGCTGTGACTGTGTCTATCCGCTGGGCCAATGCCACGGGCACCCGTGTCCGCTT
 CATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCCGGTCCGTG
 AGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGGCCCTCATCTCCCCACGAAGCTTCCCC
 CCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGCACTGGCCGAACC
 CGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACCTGCCCATGCAGGCA
 GGAGGTACCGGGTGTACCCCGAGGGGACCCTGGAGCTGCGGAGGGTGACAGCAGAAGAGGCA
 GGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGGGCTGACACTAAGACGGTTAGTGTGGT
 TGTGGGCGGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCGGGTGC
 AGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTCACCCCACCCAACACAGTGTCCACC
 AACCTCACCTGGTCCAGTGCTCCTCCCTCCGGGGCCAGGGGGCCACAGCTCTGGCCCCGCT
 GCCTCGGGGAACCCACAGCTACAACATTACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCT
 GCCTGCAAGTGGCCTTTGCTGATGCCACACCCAGTTGGCTTGTGTATGGGCCAGGACCAA
 GAGGCCACTTCTTGCCACAGAGCCTTAGGGGATCGTCTTGGGCTCATTGCCATCCTGGCTCT
 CGCTGTCTTCTCCTGGCAGCTGGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGAAGG
 GTGTGGGTGGGAGGCGGCCTCTCCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCCCTTCT
 GTCCGGGTGTGTCTGCTCCCCCTCGTCTTGGCCTGGAATCCAGGGAGGAAGCTGCCCAGATC
 CTCAGAAGGGGAGACACTGTTGCCACCATTTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTC
 AGCAGTAGAGAAATCACTAGGACTACTTTTTTACCAAAAGAGAAGCAGTCTGGGCCAGATGCC
 CTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGGCCAAGACAGATGG
 GGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTC
 ACCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCC

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FIGURE 85B

TGCCTCCCCATCTTCTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCTACCTGT
GTCCCCGGGCTGCACCCCTTCCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGT
GCCTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGT
GGGAGTGACCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAACGCCTCATC
TCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGG
AGAAATGTGTCACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAATAAAAA
TAAATAATAACAATAAAAAAA

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FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLF
LTAVPPALPAGTQTLLLOQNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQ
LLSLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLL
RAIDSRWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGL
QSLESLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNM
EELVSIDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPMETLMLNNNALSALHQQT
VESLPNLQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPF
REMTDHCLPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGR
RYRVYPEGTLELRRVTAEAEAGLYTCVAQNLVGADTKTVSVVVGRRALLOPGRDEGQGLEL
RVQETHPHYHILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQA
TEYWACLQVAFADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAH
LGTGQPRKGVGGRRPLPPAWAFWGWSAPSVRVVSAPLVLPWNPGRKLPRSSEGETLLPP
LSQNS

FIGURE 87A

GCAAGCCAAGGCGCTGTTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGA
CATTTGTGTACCGCCTCTAC
><MET {trans=1-s, dir=f, res=1}>
ATGCGGCAGACCATCATCAAGGTGATCAAGTTTCATCCTCATCATCTGCTACACCGTCTAC
TACGTGCACAACATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGC
TACCGCACCTACCGCTGTGCCACCCCTGGCCACACTCTTCAAGATCCTGGCGTCTCTC
TACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTACACACTGTGGTGGATGCTA
CGGCGCTCCCTCAAGAAGTACTCGTTTTGAGTCGATCCGTGAGGAGAGCAGCTACAGCGAC
ATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCG
CTCTACTCCAAGCGCTTCGCCGTCTTCCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAG
CTGAACCTCAACAACGAGTGGACGCTGGACAAGCTCCGGCAGCGGCTCACCAAGAACGCG
CAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCATCCCTGACACTGTGTTTGAC
CTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCGCCAGC
ATTGCCCAGCTCACGGGCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAA
GCGCCTGCGCTGGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGAC
ATCAAGGAGATCCCGCTGTGGATCTATAGCCTGAAGACACTGGAGGAGCTGCACCTGACG
GGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGACGGGCTGCGGGAGCTCAAA
CGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCACAGAT
GTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTC
AACAGCCTCAAGAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAG
CGCATCCCCCACTCCATCTTCAGCCTCCACAACCTGCAGGAGATTGACCTCAAGGACAAC
AACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCTGCACCGCCTCACCTGCCTT
AAGCTGTGGTACAACCACATCGCCTACATCCCATCCAGATCGGCAACCTCACCAACCTG
GAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGC
CGCAAGCTGCGCTACCTGGACCTCAGCCACAACAACCTGACCTTCCTCCCTGCCGACATC
GGCCTCCTGCAGAACCTCCAGAACCTAGCCATCACGGCCAACCGGATCGAGACGCTCCCT
CCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCTGGGCAACAACGTGCTGCAG
TCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGGCAAC
CGGCTGGAGTGCCTGCCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTG
GTGGTGGAGGAGGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGG
GCTGACAAGGAGCAGGCCTGAGCGAGGCCGGCCAGCACAGCAAGCAGCAGGACCGCTGC
CCAGTCTCAGGCCCCGAGGGGCAGGCCTAGCTTCTCCAGAACTCCCGGACAGCCAGGA
CAGCCTCGCGGCTGGGCAGGAGCCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGAGGAC
AGTATCTGTGGGGCTGGCCCCCTTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGC
TTGTGGAGGAGAGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGG
AGGCCAGCTCTGCCCCAGGGGCTGAGCTGCCACCAGAGGTCTGGGACCCTCACTTTAGT
TCTTGGTATTTATTTTTTCTCCATCTCCACCTCCTTCATCCAGATAACTTATACATTCCC
AAGAAAGTTTCAAGCCAGATGGAAGGTGTTTCAAGGAAAGGTGGGCTGCCTTTTCCCCTTGT
CCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCG
GGCGAACCAGCCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTC
CACGGGAGAGCAGGCCTCCAGCTGGAAAGGCCAGGCCTGGAGCTTGCCTCTTCAGTTTTT
GTGGCAGTTTTTAGTTTTTTTGTTTTTTTTTTTTAAATCAAAAAACAATTTTTTTTAAAAA
AAAGCTTTGAAAATGGATGGTTTGGGTATTAAGAAAGAAAAAAACTTAAAAA
GACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAG
CAGCCAGACGTTGAACTGTGTTTCCCTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGGA
TCTGGTGTGACCTTGGTCCAGGAGTCTATTTGTTCCCTGGGGAGGGAGGTTTTTTTGT
GTTTTTTGGGTTTTTTTGGTGTCTTGTTTTCTTCTCCTCCATGTGTCTTGGCAGGCACT
CATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAGACTC
GGGTTGGCTAATCCCCGGATGAACGGTGCTCCATTGCGACCTCCCTCCTCGTGCCTGCC
CTGCCTCTCCACGCACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTT
CCCCACCTCCTGCGGCATGGGTGTGTCCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCA
GCCCTGTGCGCCACCTGGTCTTTCATGAAGAGCAGACACTTAGAGGCTGGTCCGGGAATGGG
GAGGTGCCCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGCCTGG

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FIGURE 87B

AGTGCACACAGCCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGG
GTCCCCACCTTAGAAGGGTCCCCGCCTTAGATCAATCACGTGGACACTAAGGCACGTTTT
AGAGTCTCTTGTCTTAATGATTATGTCCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCG
TCGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAGCCTCTGACAACCATGAAGC
AAAAATCCGTTACATGTGGGTCTGAACTTGTAGACTCGGTCACAGTATCAAATAAAATCT
ATAACAGAAAAAAAAAAAAAAAAA

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FIGURE 88

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35673

><subunit 1 of 1, 546 aa, 0 stop

><MW: 63742, pI: 8.62, NX(S/T): 6

MRQTIIKVIKFILIICTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASF
YISLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDP
LYSKRFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFD
LVELEVLKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTD
IKEIPLWIYSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTD
VGVHLQKLSINNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDN
NLKTIEEIIISFQHLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYC
RKLRYLDLSHNNLTFLPADIGLLQNLQNLAITANRIETLPPELFFQCRKLRALHLGNNVLQ
SLPSRVGELTNLTQIELRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWR
ADKEQA

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTC

><MET {trans=1-s, dir=f, res=1}

ATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTG
CTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGG
GATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAAC
TCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGT
TCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGCCCCCTTGACAGTGATCTCAAACCA
CGGAAAACCACTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACT
GGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCA
GACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCA
TTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTT
TATAAGGCCATTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGAT
TCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCT
CTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCC
GTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATT
GAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTAAAAGCACTCCCACGTCT
ACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTTCAGCGCCAC
GTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAAG
CTCAAATATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAAC
ATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGG
ATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAG
GCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAG
GCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAAC
CTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATG
GCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGA
GCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCA
TTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGG
ATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAA
GATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

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FIGURE 90

><signal peptide>

MELALRRSPVPRWLLLLPLLLGLNA

><start mature protein>

GAVIDWPTEEGKEVW

><homology to peptidases 40-end>

DYVTVRKDAYMFWWLYYATNSCK

><potential N-glycosylation site>

NFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
GFSYV

><potential N-glycosylation site>

NGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELY
KAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVL
NAVNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCL
CQRHVRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGOATNVFVNMEEDFMKPVISIV
DELLEAGI

><potential N-glycosylation site>

NVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKS
YKNLAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

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FIGURE 91

GGCCGCGGGAGAGGAGGCC

><MET {trans=1-s, dir=f, res=1}

ATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTCGGGCTGGACTCAGGAAG
CCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGACGGGTTCATCACGTCTG
CGCATCGTGGGTGGAGAGGACGCCGAACCTCGGGCGTTGGCCGTGGCAGGGGAGCCTGCGC
CTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGGCACTCACGGCG
GCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATGGTCCAGTTT
GGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCGTTACTTC
GTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCTATGACATTGCCTTG
GTGAAGCTGTCTGCACCTGTCACCTAACTAAACACATCCAGCCCATCTGTCTCCAGGCC
TCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAAA
GAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCGCCATCATAAAC
AACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGAC
ATGGTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGA
CCCTTGGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTG
GGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGG
ATCCAGAAGCTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTC
TTTTTCCCTCTTCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCTACCTGAGCCCA
TGCAGCCTGGGGCCACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTTTGGTAATAA
ACACATTCCAGTTGATGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

A

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FIGURE 92

><signal peptide>

MGARGALLALLARAGL

><start mature protein>

RKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLWDSHVCGVSLLSHRWA

><Serine proteases, trypsin family, histidine active site 'LTAHC'>

LTAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNIYLSPRYLGNS

PYDIALVKLSAPVTYTKHIQPICLQASTFEFE

><potential N-glycosylation site>

NRTDCWVTGWGYIKEDEALPSPHTLQEVQVAII

><potential N-glycosylation site>

NNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNGLWYQIG

VVSWSGVGCGRPNRPGVYT

><potential N-glycosylation site>

NISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPLLGPV

FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGA

<MET {trans=1-s, dir=f, res=1}

ATGGGACTCCAAGCCTGCCTCCTAGGGCTCTTTGCCCTCATCCTCTCTGGCAAATGCAGT
TACAGCCCCGGAGCCCCGACCAGCGGAGGACGCTGCCCCCAGGCTGGGTGTCCCTGGGCCGT
GCGGACCCTGAGGAAGAGCTGAGTCTCACCTTTGCCCTGAGACAGCAGAATGTGGAAAGA
CTCTCGGAGCTGGTGCAGGCTGTGTGCGGATCCCAGCTCTCCTCAATACGGAAAATACCTG
ACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCCCACTGACCCTCCACACGGTGCAA
AAATGGCTCTTGGCAGCCGGAGCCCAGAAGTGCCATTCTGTGATCACACAGGACTTTCTG
ACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCCTGGGGCTGAGTTTCATCAC
TATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCACATCCCTACCAGCTTCCA
CAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGGACTGCACCGTTTTCCCCAACATCA
TCCCTGAGGCAACGTCCTGAGCCGCAGGTGACAGGGACTGTAGGCCTGCATCTGGGGGTA
ACCCCTCTGTGATCCGTAAGCGATACTTGACCTCACAAAGACGTGGGCTCTGGCACC
AGCAATAACAGCCAAGCCTGTGCCAGTTCTTGAGCAGTATTTCCATGACTCAGACCTG
GCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGCCCGTGTG
GTTGGACAACAGGGCCGGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGTACCTG
ATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAGGGA
CAGGAGCCCTTCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGTG
CATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTC
AACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCCTCAGGTGAC
AGTGGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCC
TCCAGCCCCTATGTCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCTCATCACA
AATGAAATTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCA
TACCAGGAGGAAGCTGTAACGAAGTTCTTGAGCTCTAGCCCCACCTGCCACCATCCAGT
TACTTCAATGCCAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGG
GTGGTCAGCAACAGAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTG
TTTGGGGGGATCCTATCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTT
GGCTTTCTCAACCCAAGGCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGT
GGCTGCCATGAGTCCTGTCTGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCCT
GGCTGGGATCCTGTAACAGGCTGGGGAACACCAACTTCCCAGCTTTGCTGAAGACTCTAC
TCAACCCCTGACCCTTTCCTATCAGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAG
TTCAGTCCCTTATTCTGCCCTGTTGGAAGCCCTGCTGAACCCTCAACTATTGACTGCTGC
AGACAGCTTATCTCCCTAACCTGAAATGCTGTGAGCTTGACTTGACTCCCAACCCTACC
ATGCTCCATCATACTCAGGTCTCCCTACTCCTGCCTTAGATTCCTCAATAAGATGCTGTA
ACTAGCATTTTTTTGAATGCCTCTCCCTCCGCATCTCATCTTTCTCTTTTCAATCAGGCTT
TTCCAAAGGGTTGTATACAGACTCTGTGCACTATTTCACTTGATATTCATTCCCCAATTC
ACTGCAAGGAGACCTCTACTGTCACCGTTTACTCTTTCTACCCTGACATCCAGAAACAA
TGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATGGCCTTTCCATCATAGTTGCCAC
TCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTTCTCTGACTACTCTTGTCTTCTCTCT
CATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGCTCCATTTGTAGATTTTGC
TCTTCTCAGTTTACTCATTGTCCCCTGGAACAAATCACTGACATCTACAACCATTACCAT
CTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAATGTAAAAA

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FIGURE 94

><signal peptide>

MGLQACLLGLFALILS

><start mature protein>

GKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLSELVQAVSDPSSP
QYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQQKCHSVITQDFLTCWLSIRQAEL
LLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRPEPQ
VTGTVGLHLGVTPSVIRKRY

><potential N-glycosylation site>

NLTSQDVGSGTS

><potential N-glycosylation site>

NNSQACAQFLEQYFHDSDLAQFMRLFGGNFAHQASVARVVGQQGRGRAGIEASLDV
QYLMSAGA

><potential N-glycosylation site>

NISTWVYSSPGRHEGQEPFLQWLMLLS

><potential N-glycosylation site>

NESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVS
GRHQFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKF
LSSSPHLPPSSYF

><potential N-glycosylation site>

NASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSGRPPL
GFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

FIGURE 95

GCCGCGCGCTCTCTCCCGGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGG
GCGGGCTGCTCGGCGCGGAACAGTGCTCGGC
><MET {trans=1-s, dir=f, res=1}>
ATGGCAGGGATTCCAGGGCTCCTCTTCCTTCTCTTCTTTCTGCTCTGTGCTGTTGGGCAA
GTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTGGCCTGCATACCGCCTCCCTGTCGTC
TTGCCCCAGTCTACCCTCAATTTAGCCAAGCCAGACTTTGGAGCCGAAGCCAAATTAGAA
GTATCTTCTTCATGTGGACCCAGTGTCATAAGGGAACCTCCACTGCCCACTTACGAAGAG
GCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGGCAGCCGCACAGAGACGCAG
GTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAACACCGAGACTCAGGGTCT
TCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGCAGGTTTCAGCATTTTT
GGGAAGGACTTCCTGCTCAACTACCCTTTCTCAACATCAGTGAAGTTATCCACGGGCTGC
ACCGGCACCCTGGTGGCAGAGAAGCATGTCCTCACAGCTGCCCACTGCATACACGATGGA
AAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCCAAGTTTAAA
GATGGTGGTTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCGAGCAGATGAAATTTTCAG
TGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCAATGAC
ATCGGCATGGATTATGATTATGCCCTCCTGGAACCTCAAAAAGCCCCACAAGAGAAAATTT
ATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACTTCTCT
GGTTATGACAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAG
ACCTATGACTTGCTCTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTC
TATGTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTT
TCAGGGCACCAGTGGGTGGACATGAATGGTTCCTCCACAGGATTTCAACGTGGCTGTCAGA
ATCACTCCTCTCAAATATGCCCAGATTTGCTATTGGATTAAAGGAAACTACCTGGATTGT
AGGGAGGGGTGACACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTT
TAGGAGAGGCCAAATTGTTTTTTGTCAATTGGCGTGACACCGTGTGTGTGTGTGTGTGTGT
GTGTGTAAGGTGTCTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTT
ACTATTTGAAAACCTGGTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATA
CTTTTGCATAGAAATAAAAAAAATACTGATTTGGGGCAATGAGGAATATTTGACAATTAA
GTTAATCTTCACGTTTTTTGCAAACCTTTGATTTTTTATTTTCATCTGAACTTGTTTCAAAGAT
TTATATTAAATATTTGGCATAACAAGAGATATGAAAAA

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FIGURE 96

><signal peptide>

MAGIPGLLFLFFLLCAVG

><start mature protein>

QVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSSCGPQCHKGTPLP
TYEEAKQYLSYETLYA

><potential N-glycosylation site>

NGSRTETQVGIYILSSSGDGAQHRDSGSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFS
TSVKLSTGCTGTLVAEKHV

><serine proteases, trypsin family, histidine active site 'LTAAHC'>

LTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGA

><potential N-glycosylation site>

NDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFM
KIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGS
GVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIK
GNYLDCREG

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FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCC
><MET {trans=1-s, dir=f, res=1}
ATGGTGGTTTCTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCC
CTGCTGCTGCTGGCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCC
TGTGGGAAGCCCCAGCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAG
TGGCCCTGGATCGTGAGCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTC
ACCAGCCGCTGGGTGATCACTGCTGCCCCACTGTTTCAAGGACAACCTGAACAAACCATAC
CTGTTCTCTGTGCTGCTGGGGGCCTGGCAGCTGGGGAACCCTGGCTCTCGGTCCCAGAAG
GTGGGTGTTGCCTGGGTGGAGCCCCACCCTGTGTATTCTGGAAGGAAGGTGCCTGTGCA
GACATTGCCCTGGTGCGTCTCGAGCGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATC
TGCCTACCTGATGCCTCTATCCACCTCCCTCCAAACACCCACTGCTGGATCTCAGGCTGG
GGGAGCATCCAAGATGGAGTTCCCTTGCCCCACCCTCAGACCCTGCAGAAGCTGAAGGTT
CCTATCATCGACTCGGAAGTCTGCAGCCATCTGTACTGGCGGGGAGCAGGACAGGGACCC
ATCACTGAGGACATGCTGTGTGCCGGCTACTTGGAGGGGGAGCGGGATGCTTGTCTGGGC
GACTCCGGGGGCCCCCTCATGTGCCAGGTGGACGGCGCCTGGCTGCTGGCCGGGCATCATC
AGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCCGGGGTCTACATCAGCCTCTCTGCG
CACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCAGCTCCGCGGGCGCGCTCAGGGG
GGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCGCGCGCGCTCCTAGGGCGCA
GCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACATCTGGATCTGGATCTGCG
GCGGCCTCGGGCGGTTTCCCCCGCCGTAAATAGGCTCATCTACCTCTACCTCTGGGGGCC
CGGACGGCTGCTGCGGAAAGGAAACCCCCTCCCCGACCCGCCCCGACGGCCTCAGGCCCCC
CTCCAAGGCATCAGGCCCCGCCCAACGGCCTCATGTCCCCGCCCCCAGACTTCCGGCCC
CGCCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTATAGGTATTTGT
AACCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATTCTCCAAAA
AAAAAA

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FIGURE 98

><signal peptide>

MVS GAPPALGGGCLGTFTSLLLLASTAILNA

><start mature peptide>

ARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQK

><potential N-glycosylation site>

NGTHHCAGSLLTSRWV

><Serine proteases active site ITAAHC>

ITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPVYSWKEGACA
DIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDGVPLPHPQTLQKLKV
PIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMCQVDGAWLL
AGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQGSGA
AARS

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FIGURE 99

GACGGCTGGCCACC

><MET {trans=1-s, dir=f, res=1}

ATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTACTGCTGGTGGCC
ACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGTGGAGCTGCAC
AACCTCTACCGGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGAGATGGGAC
GAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGGGTGTGGGGCCACAACAAG
GAGCGCGGGCGCCGCGGGCGAGAATCTGTTCCGCCATCACAGACGAGGGCATGGACGTGCCG
CTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGC
AGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTA
CTGGTGTGCAACTATGAGCCTCCGGGGAAACGTGAAGGGGAAACGGCCCTACCAGGAGGGG
ACTCCGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATC
GGAAGCCCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACCTGAGGCCCCATCCTTCCGG
GCGACTGAAGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATT
CCGGCTTTCTTGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTG
GAAACCCAGGCCCCAACTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCT
CCACCTTGCGTAACAACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTG
GATGAGGAGCCAGTTACCTTCCCCAAATCGACCCATGTTCCCTATCCCCAAATCAGCAGAC
AAAGTGACAGACAAAACAAAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAG
ATGTCCCTGACAGGGGCAAGGGAACTCCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAG
GCTGAGTTGCCTCCTTCCAGTGAGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCA
GGTGAGCTGCAGGCCACACTGGACCACACGGGGCACACCTCCTCCAAGTCCCTGCCCAAT
TTCCCCAATACTCTGCCACCGCTAATGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCG
TCCTTGCCAGGTGCAGAGGGCCCTGACAAGCCTAGCGTTGTGTCAGGGCTGAACTCGGGC
CCTGGTCATGTGTGGGGCCCTCTCCTGGGACTACTGCTCCTGCCTCCTCTGGTGTGGCT
GGAATCTTCTGAATGGGATACTCAAGGGTGAAGAGGTCAGCTGTCCTCCTGTCATC
TTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATACTTCTTGGTTAAGGCCCTCCGGAAGG
GAAAGGCTACGGGGCATGTGCCTCATCACACCATCCATCCTGGAGGCACAAGGCCTGGCT
GGCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACCGGGCCCACACCTCTCCTGCCCC
TCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCTCACTGCCTACCTGGCCTGGG
GCTGTCTGCCCACACAGCATGTGCGCTCTCCCTGAGTGCCTGTGTAGCTGGGGATGGGGA
TTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCTTTGAGTGGGGGAGGC
AGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCTGTCCAACCTGTGAA
A

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FIGURE 100

><signal peptide>

MHGSCSFLMLLLPLLLLVLVATT

><start of mature peptide, extracellular domain>

GPVGALTDEEKRLMVELHNLRYRAQVSPTASDMLHMRWDEELAAFAKAYARQCVW
GHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHY

><potential N-glycosylation site>

NLSAATCSPGQMC

><GHYTQVWVWAKT Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1 - CRISP
signature>

GHYTQVWVWAKTERIGCGSHFCEKLQGVEETNIEL

><LLVCNIEPPGNV Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2 -CRISP
signature>LVCNIEPPGNVKGKRPYQEGTPCSQCPSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFR
ATEASDSRKMGTSSLATGIPAFLVTEVSGSLATKALPAVETQAPTSLATKDPPSMATEA
PPCVTTEVPSILAAHSLPSLDEEPVTFPKSTHVPIPKSADKVTDKTKVPSRSPENSLDPK
MSLTGARELLPHAQEEAEAEAEELPPSSEVLASVFPAQDKPGELQATLDHTGHTSSKSLPN
FP

><potential N-glycosylation site>

NTSATA

><potential N-glycosylation site>

NATGGRALALQSSLPGAEGPDKPSVVSGLNS

><potential glycosylphosphatidylinositol attachment site>

GPGHVWGPLLGLLLLPLVLGIF

FIGURE 101A

GTAAGTGAAGTCAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCA
AGTT
><MET {trans=1-s, dir=f, res=1}
ATGGTGGACGTAAGTCTGTTGTTCTCCCTCTGCTTGCTTTTTTCACATTAGCAGACCGGAC
TTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCATGAGCCACCTTCAAAGCCTT
CGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCG
GCAAATATTACACTTCTCTCCTTGCTGGAAACAGGATTGTTGAAATACTCCCTGAACAT
CTGAAAGAGTTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTC
CAAAGTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACA
TCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCTGAAC
AGGAACCGAATCTCAGCTATCCACCCCAAGATGTTTAAACTGCCCCAACTGCAACATCTC
GAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCT
CTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTTTG
GGGCTGAGCAACATGGAAATTTTGACAGCTGGACCATAACAACCTAACAGAGATTACCAA
GGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTCATCTCAGCCAAAATGCCATCAAC
AGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAACTTTC
AATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTG
CACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGT
TTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAATGGT
GCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCGTTCT
ATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGACAAC
GCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATTGCAT
TTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCG
GAAAACAACCTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGA
AGAAGCATTTTTTGCTGTTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACCCAG
ATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCATCTGC
TCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAAGACAATGAACTA
CTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGGCCCAAGGTGGCGAGGTGATG
GAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAG
TGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACAGTAAAT
ATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCATGGCA
CGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGG
GGCACAGACTTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTG
TTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAAC
AGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTCTTAGAAACACCATCATTTTTG
CGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCATTGCT
GGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTTGGTGGTAACC
GAGAGGCACTTTTTTTCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGT
GATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTG
CGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCTCAGATGACAGCCCCATCGTTA
GACGATGACGGATGGGCCACTGTGGGTGTCTGATCATAGCCGTGGTGTGCTGTGTGGTG
GGCACGTCACTCGTGTGGGTGGTTCATCATATACCACACAAGGCGGAGGAATGAAGATTGC
AGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCATCT
CAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCAC
CAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGGGACC
TGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCCCTTTGT
CCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCT
TTTGAAACATATCATAAGGTTGCAGTCCTGACCCAAGAACAGTTTTTAATGGACCACTAT
GAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCC
TGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAACACT
AGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTCTTTA
GATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCCTCAGTAATTCTTTTCATGGGTACC
TTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCA

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FIGURE 101B

GATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTCTGGG
TCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTACCTTT
AAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACACATAG
ACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTAAAAG
AGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAATGCTTTA
TTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATGATGC
TCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTTATGCAAAAAAGTATCTT
ACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTTATAATGCCAGATTTCTT
TTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAA
ATAGAAGTTACTTCATTATATTTTGCACATTATTTAATAAAAATGTGTCAATTTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS
ANITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVT
SMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA
LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
RISPDWEFCQKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSS
LKTLDLKNNEISWTIEDMNGAFSGLDKLRRLLI LQGNRIRSITKKAFTGLDALEHLDLSDN
AIMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLLKG
RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNE
LHDAEMENYAH LRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN
MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDV
FFIVDVKIEDIGVYSCTAQNSAGSISANATLT VLETPSFLRPLLDRTVTKGETAVLQCIA
GGSPPPKLNWTKDDSPLVVTERHFFAAGNQLLIIVDS DVSDAGKYTCEMSNTLGTERGNV
RLSVIPTPTCDSPQMTAPSLDDD GWATVGVV IIAVVCCVVGTS LVWVVI IYHTRRRNEDC
SITNTDETNPADIPSYLSSQGT LADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGT
CHIDNSSEADVEAATDLFLCPFLGSTGPMY LKGNVYGSDPFETYHTGCSPDPRTVLMDHY
EPSYIKKKECYP CSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSL
DFSANPEPASVASSNSFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLD SG
SEEDGKERTDFQEENHICTFKQTL ENYRTPNFQSYDLDT

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTTGGTGGTGGTGGCTGTTGGG
 TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGAT
 AACTGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACCAGAGTTAGA
 CCCGCGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCCTCC
 CCACCCCCAAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCACAAAGAAAAAAGT
 ATGTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG
 TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTTCTTTTTTGAA
 TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTTAGAGAGAGAAAA
 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
 TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC
 TCCTTTTTTTTTAAATTTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTT
 AACCACCTGGATTTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTTGAAT
 TCCAGAAGGACCAACACCAGATAAATTATGA
 ><MET {trans=1-s, dir=f, res=1}
 ATGTTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAACAGG
 GCCCTATTTGACCCCCCTGCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 CTGGTGGCGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAACCAGTTCAGCAAGGTG
 ATTTGTGTTTCGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCTG
 CTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGG
 CACTTGGAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTC
 AATGGTCTGGCGAACCTCAACACTCTGGAACCTTTTGACAATCGTCTTACTACCATCCCG
 AATGGAGCTTTTGTATACTTGTCTAACTGAAGGAGCTCTGGTTGCGAAACAACCCCAT
 GAAAGCATCCCTTCTTATGCTTTTAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGGG
 GAATTGAAAAGACTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTTGAGG
 TATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAA
 CTAGATGAGCTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTTCCAG
 GGTTTGATGCACCTTCAAAAACCTGTGGATGATACAGTCCCAGATTCAAGTGATTGAACGG
 AATGCCTTTGACAACCTTCAGTCACTAGTGAGATCAACCTGGCACACAATAATCTAACA
 TTAAGTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCAC
 AACCTTGGAACCTGTAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCC
 CCTCGAACACAGCTTGTGTGCCCCGGTGTAAACACTCCTCCCAATCTAAAGGGGAGGTAC
 ATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCT
 GCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTCGGGCCTCCACATCC
 CTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAA
 GTGCGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTACAAATGTAACCTGTGCAAGAT
 ACAGGCATGTACACATGTATGGTGAGTAATTCGGTTGGGAATACTACTGCTTCAGCCACC
 CTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTACTTTTCAACCGTCACAGTAGAG
 ACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCCA
 GTGGTCTGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTG
 ACAGAGAAAACCTTCACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGAT
 GAGGTCATGAAGACTACCAAAATCATCATTGGGTGTTTTGTGGCCATCAACTCATGGCT
 GCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCAC
 GCCCCAACAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACCC
 ATGGAAAGCCACCTGCCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCA
 TACAAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATTCAATACACAGTTCA
 GTGCATGAACCGTTATTGATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAATC
 TAAAACATTTACAGAGTTACAAAAAACAACAATCAAAAAAAGACAGTTTATTAAAAA
 TGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACA
 AAAGAAAAGAAATTTATTTATTAATAAATTCTATTGTGATCTAAAGCAGACAAAAA

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FIGURE 104

><signal peptide>

MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRA

><start mature peptide, extracellular domain>

QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRL

><start leucine rich repeat domains>

LNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPN
GAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLR
LNLAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIER
NAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCDILWLSWWIK
DMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELK
CRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSN
SVGNTTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWE

><end leucine rich repeat domains>

TTNVTTSLTPQSTRSTEKFTTIPVTDINSGIPGIDE

><start transmembrane domain>

VMKTTKIIIGCFVAITLMAAVMLVI

><start intracellular domain>

FYKMRKQHHRQNHHPTRTVEIINVDDDEITGDTPMESHLPMPAIEHEHLNHYN
SYKSPFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

FIGURE 105A

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTG
CTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCG
CGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCTCGGCTGGAAGTTTGTGC
CGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGGACCGCGAT
GAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTGGGGCTGCTGCTGTGCGCGGTGCTGG
GGCGCGCTGGCCGGTCCGACAGCGGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGGTAGCC
GCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGCAGTCGTAA
GCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCCTGGGTGCTCGGCTGGACTTAAGTCACA
ACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAA
CTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCGGCAAATATTACACT
TCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAGTTTTCAGT
CCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTAGAGCTCCAAACTGCATTTCCAGCC
CTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTT
TGACAATTTGGCCAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCC
CACCCAAGATGTTTAAACTGCCCCAACTGCAACATCTCGAATTGAACCGAAACAAGATTAAA
AATGTAGATGGACTGACATTCGAAGGCTTGGTGCTCTGAAGTCTCTGAAAATGCAAAGAAA
TGGAGTAACGAACTTATGGATGGAGCTTTTTTGGGGGCTGAGCAACATGGAAATTTTGCAGC
TGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAG
GAACTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCA
GAAGCTCAGTGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCC
TTGGCCTAAGCTTACTAAATACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGAT
TGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCTTG
GACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCC
AAGGAAATCGGATCCGTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCAT
CTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTTCACAAATGAAGAA
ACTGCAACAATTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCC
CACAGTGGGTGGCGGAAAACAACCTTTAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAG
CTGCTAAAAGGAAGAAGCATTTTGTGCTGTAGCCAGATGGCTTTGTGTGTGATGATTTTCC
CAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTT
TCATCTGCTCAGCTGCCAGCAGCAGTGATTCCTCAATGACTTTTGTCTTGGAAAAAGACAAT
GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGT
GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATC
AGTGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACAGTAAAT
ATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCATGGCACG
CTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCA
CAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTT
ATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGG
AAGTATTTAGCAAATGCAACTCTGACTGTCTAGAAACACCATCATTTTTTGCGGCCACTGT
TGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCTACAGTGCATTGCTGGAGGAAGCCCT
CCCCCTAACTGAACTGGACCAAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCACTTTTT
TGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAAATACA
CATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGCTGCGCCTCAGTGTGATCCCC
ACTCCAACCTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCAC
TGTGGGTGTCGTGATCATAGCCGTGGTTTGTGCTGTGTGGTGGGCACGTCCTCGTGTGGGTGG
TCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACCAACACAGATGAGACC
AACTTGCCAGCAGATATTCCTAGTTATTTGTCTATCTCAGGGAACGTTAGCTGACAGGCAGGA
TGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGGAT
TTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGAT
GTGGAAGCTGCCACAGATCTGTTCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTT
GAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACATATCATAACAGGTTGCAGTCCTGACC
CAAGAACAGTTTTTAATGGACCACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCA
TGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACA
TGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGT
GTCTAAACAAGTCCTCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGT
AATTCCTTCATGGGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAG

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FIGURE 105B

CTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAG
ACTTGGACTCTGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCAC
ATTTGTACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTT
GGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTA
TTTAAAAGAGAGAGAGAATCTTATGTTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAT
GCTTTATTTATACAGATGAACCAAATTTACAAAAGTTATGAAAATTTTATACTGGGAATG
ATGCTCATATAAGAATACCTTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAGTATC
TTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGATTTCTT
TTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAAAT
AGAAGTTACTTCATTATATTTTGCACATTATTTAATAAAATGTGTCAATTTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 106

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA37140

><subunit 1 of 1, 1119 aa, 1 stop

><MW: 123434, pI: 6.09, NX(S/T): 12

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLLDC
SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS
ANITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVT
SMEPGYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA
LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
RISPD AWEFCQKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSS
LKTLDLKNNEISWTIEDMNGAFSGLDKLRRILILOGNRIRSITKKAFTGLDALEHLDLSDN
AIMSLQGN AFSQMKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKG
RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNE
LHDAEMENY AHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN
MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDV
FFIVDVKIEDIGVYSCTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIA
GGSPPPKLNWTKDDSPLVVTERHFFAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNV
RLSVIPTPTCDSPQMTAPSLDDD GWATVG VVIIAVVCCVVGTSLVWVVIIYHTRRRNEDC
SITNTDET NLPADIPSYLSSQGT LADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGT
CHIDNSSEADVEAATDLFLCPFLGSTGPMYLGKNVYGSDPFETYHTGCSPDPRTVLM DHY
EPSYIKKKECYP CSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSL
DFSANPEPASVASSNSFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLD SG
SEEDGKERTDFQEENHICTFKQTL ENYRTPNFQSYDLDT

FIGURE 107A

CAAAACTTGCGTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGA
GCGCAGCTGAGACTGGGGGAGCGCGTTCCGGCCTGTGGGGCGCCGCTCGGGCGCCGGGGCGCAG
CAGGGAAGGGGAAGCTGTGGTCTGCCCTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGA
GCCCCCTGGGTGGTCCCGTCCCCCTATCCCTCCTTTATATAGAAACCTTCCACACTGGGAAGGC
AGCGGCGAGGCGAGGAGGGCTCATGGTGAGCAAGGAGGCGCGGTGATCTGCAGGCGCACAGCA
TTCCGAGTTTACAGATTTTACAGATAACCAATGGAAGGCGAGGAGGCAGAACAGCCTGCCT
GGTTCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCC
CAGAGCCGGGTGCTGCTGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCT
TGCCGTGAGGGCCCCAGGATTTGGCCGAAGTGGCGGCCACAGCCTGAGCCCCGAAGAGAACG
AATTTGCGGAGGAGGAGCCGGTGCTGGTACTGAGCCCTGAGGAGCCCGGGCCTGGCCCAGCC
GCGGTGAGCTGCCCCCGAGACTGTGCCTGTTCCAGGAGGGCGTCTGTGGACTGTGGCGGTAT
TGACCTGCGTGAGTTCCCGGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACAA
ACCAGCTGGAAAAGATCTACCCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAAC
CTGCAAAACAACCGCCTGACTTCCCGAGGGCTCCCAGAGAAGGCGTTTGAGCATCTGACCAA
CCTCAATTACCTGTACTTGGCCAATAACAAGCTGACCTTGGCACCCCGCTTCCTGCCAAACG
CCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCTATGGGCTCACCTTTGGC
CAGAAGCCAAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGCTGCC
GGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCCTCATCCTGTCCAGCAACTTCCTGC
GCCACGTGCCCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTG
GAGAAGATCCCCCGGGGGCCTTCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAA
CAACTACCTGACTGACGAGGGCCTGGACAACGAGACCTTCTGGAAGCTCTCCAGCCTGGAGT
ACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGCCGCGCAGCCTGGTG
CTGCTGCACTTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCCG
CAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGG
CCTTCCAGGGCCTCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTG
CCCAGTGGCCTGCCTCGCCGCGTGGCGACCCCTCATGATCCTGCACAACCAGATCACAGGCAT
TGGCCGCGAAGACTTTGCCACCACCTACTTCCTGGAGGAGCTCAACCTCAGCTACAACCGCA
TCACCAGCCCACAGGTGCACCGCGACGCCTTCCGCAAGCTGCGCCTGCTGCGCTCGCTGGAC
CTGTCGGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAA
GGTCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGC
GTGAGCTGTACCTCACAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTG
GACCTCGCCCATCTGCAGCTGCTGGACATCGCCGGGAATCAGCTCACAGAGATCCCCGAGGG
GCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAAACAAGATTAGTGCGGTGCCCGCCA
ATGCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAACAAGCTGGCTGTG
GGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGG
CAACTTAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGG
AGGAAGAGGAGGAGGAGGAGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACC
TAGGATGATGGACCGCCGGACTCTTTTCTGCAGCACACGCCTGTGTGCTGTGAGCCCCCAC
TCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCATCCACATGACACGGGCT
GACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCACGGCCAGACACATGCACACA
CATCACACCCTCAAACACCCAGCTCAGCCACACACAACCTACCCTCAAACCACCACAGTCTC
TGTCACACCCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCTGC
CCTGGCACACACAGGCACCCATTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACA
CCACACACACACATGCACAAGTCATGTGCGAACAGCCCTCAAAGCCTATGCCACAGACA
GCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCTGTCCATCTGTCCGTC
CGTTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCTCTGG
AACTCACAAAAGCTGGCTTTTATTCTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTG
CTGGCCTGGCCTGGCCCACCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCC
TCCCTGCCACGCCCTGGCAGGACACAGGCACTTTTCCAATGGGCAAGCCCAGTGGAGGCAGG
ATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGGCAGGAGTGAAGCAGAGGTGATGGGG

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FIGURE 107B

CTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTTGTTCTTCAGGCC
TGTGGGGGAAGTTCCGGGTGCCTTTATTTTTTATTCTTTTCTAAGGAAAAAATGATAAAA
TCTCAAAGCTGATTTTCTTGTTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGC
AAAAAAAAAA

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FIGURE 108

Met	Glu	Gly	Glu	Glu	Ala	Glu	Gln	Pro	Ala	Trp	Phe	His	Gln	Pro	Trp
Arg	Pro	Gly	Ala	Ser	Asp	Ser	Ala	Pro	Pro	Ala	Gly	Thr	Met	Ala	Gln
Ser	Arg	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Pro	Gln	Leu	His	Leu
Gly	Pro	Val	Leu	Ala	Val	Arg	Ala	Pro	Gly	Phe	Gly	Arg	Ser	Gly	Gly
His	Ser	Leu	Ser	Pro	Glu	Glu	Asn	Glu	Phe	Ala	Glu	Glu	Glu	Pro	Val
Leu	Val	Leu	Ser	Pro	Glu	Glu	Pro	Gly	Pro	Gly	Pro	Ala	Ala	Val	Ser
Cys	Pro	Arg	Asp	Cys	Ala	Cys	Ser	Gln	Glu	Gly	Val	Val	Asp	Cys	Gly
Gly	Ile	Asp	Leu	Arg	Glu	Phe	Pro	Gly	Asp	Leu	Pro	Glu	His	Thr	Asn
His	Leu	Ser	Leu	Gln	Asn	Asn	Gln	Leu	Glu	Lys	Ile	Tyr	Pro	Glu	Glu
Leu	Ser	Arg	Leu	His	Arg	Leu	Glu	Thr	Leu	Asn	Leu	Gln	Asn	Asn	Arg
Leu	Thr	Ser	Arg	Gly	Leu	Pro	Glu	Lys	Ala	Phe	Glu	His	Leu	Thr	Asn
Leu	Asn	Tyr	Leu	Tyr	Leu	Ala	Asn	Asn	Lys	Leu	Thr	Leu	Ala	Pro	Arg
Phe	Leu	Pro	Asn	Ala	Leu	Ile	Ser	Val	Asp	Phe	Ala	Ala	Asn	Tyr	Leu
Thr	Lys	Ile	Tyr	Gly	Leu	Thr	Phe	Gly	Gln	Lys	Pro	Asn	Leu	Arg	Ser
Val	Tyr	Leu	His	Asn	Asn	Lys	Leu	Ala	Asp	Ala	Gly	Leu	Pro	Asp	Asn
Met	Phe	Asn	Gly	Ser	Ser	Asn	Val	Glu	Val	Leu	Ile	Leu	Ser	Ser	Asn
Phe	Leu	Arg	His	Val	Pro	Lys	His	Leu	Pro	Pro	Ala	Leu	Tyr	Lys	Leu
His	Leu	Lys	Asn	Asn	Lys	Leu	Glu	Lys	Ile	Pro	Pro	Gly	Ala	Phe	Ser
Glu	Leu	Ser	Ser	Leu	Arg	Glu	Leu	Tyr	Leu	Gln	Asn	Asn	Tyr	Leu	Thr
Asp	Glu	Gly	Leu	Asp	Asn	Glu	Thr	Phe	Trp	Lys	Leu	Ser	Ser	Leu	Glu
Tyr	Leu	Asp	Leu	Ser	Ser	Asn	Asn	Leu	Ser	Arg	Val	Pro	Ala	Gly	Leu
Pro	Arg	Ser	Leu	Val	Leu	Leu	His	Leu	Glu	Lys	Asn	Ala	Ile	Arg	Ser
Val	Asp	Ala	Asn	Val	Leu	Thr	Pro	Ile	Arg	Ser	Leu	Glu	Tyr	Leu	Leu
Leu	His	Ser	Asn	Gln	Leu	Arg	Glu	Gln	Gly	Ile	His	Pro	Leu	Ala	Phe
Gln	Gly	Leu	Lys	Arg	Leu	His	Thr	Val	His	Leu	Tyr	Asn	Asn	Ala	Leu
Glu	Arg	Val	Pro	Ser	Gly	Leu	Pro	Arg	Arg	Val	Arg	Thr	Leu	Met	Ile
Leu	His	Asn	Gln	Ile	Thr	Gly	Ile	Gly	Arg	Glu	Asp	Phe	Ala	Thr	Thr
Tyr	Phe	Leu	Glu	Glu	Leu	Asn	Leu	Ser	Tyr	Asn	Arg	Ile	Thr	Ser	Pro
Gln	Val	His	Arg	Asp	Ala	Phe	Arg	Lys	Leu	Arg	Leu	Leu	Arg	Ser	Leu
Asp	Leu	Ser	Gly	Asn	Arg	Leu	His	Thr	Leu	Pro	Pro	Gly	Leu	Pro	Arg
Asn	Val	His	Val	Leu	Lys	Val	Lys	Arg	Asn	Glu	Leu	Ala	Ala	Leu	Ala
Arg	Gly	Ala	Leu	Ala	Gly	Met	Ala	Gln	Leu	Arg	Glu	Leu	Tyr	Leu	Thr
Ser	Asn	Arg	Leu	Arg	Ser	Arg	Ala	Leu	Gly	Pro	Arg	Ala	Trp	Val	Asp
Leu	Ala	His	Leu	Gln	Leu	Leu	Asp	Ile	Ala	Gly	Asn	Gln	Leu	Thr	Glu
Ile	Pro	Glu	Gly	Leu	Pro	Glu	Ser	Leu	Glu	Tyr	Leu	Tyr	Leu	Gln	Asn
Asn	Lys	Ile	Ser	Ala	Val	Pro	Ala	Asn	Ala	Phe	Asp	Ser	Thr	Pro	Asn
Leu	Lys	Gly	Ile	Phe	Leu	Arg	Phe	Asn	Lys	Leu	Ala	Val	Gly	Ser	Val
Val	Asp	Ser	Ala	Phe	Arg	Arg	Leu	Lys	His	Leu	Gln	Val	Leu	Asp	Ile
Glu	Gly	Asn	Leu	Glu	Phe	Gly	Asp	Ile	Ser	Lys	Asp	Arg	Gly	Arg	Leu
Gly	Lys	Glu	Lys	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu
Thr	Arg														

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTC
 CTCCGGGAGCGGCAGCAGTAGCCCGGGCGGCGAGGGCTGGGGGTTCTCGAGACTCTCAG
 AGGGGCGCCTCCCATCGGCGGCCACCAACCTGTTCTCGCGCGCCACTGCGCTGC
 GCCCCAGGACCCGCTGCCCAACATGGATTTTCTCCTGGCGCTGGTGCTGGTATCCTCGCT
 CTACCTGCAGGCGGCGCGGAGTTCGACGGGAGGTGGCCCAGGCAAATAGTGTCATCGAT
 TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTG
 GGGACAGTGTCAGCCTGTGTGCCAACCACGATGCAAACATGGTGAATGTATCGGGCCAAA
 CAAGTGCAAGTGTCATCCTGGTTATGCTGGAAAAACCTGTAATCAAGATCTAAATGAGTG
 TGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTACGGCAGCTACAAGTG
 CTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCCTGCTCAAGTGCCCTGACCTG
 CTCCATGGCAAACCTGTCAGTATGGCTGTGATGTTGTAAAGGACAAATACGGTGCCAGTG
 CCCATCCCCCTGGCCTGCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATG
 TGCTACAGGAAGAGCCTCCTGCCCTAGATTTAGGCAATGTGTCAACACTTTTGGGAGCTA
 CATCTGCAAGTGTCATAAAGGCTTCGATCTCATGTATATTGGAGGCAAATATCAATGTCA
 TGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAA
 CGTACGTGGGTCCTACAAGTGCAAATGTAAAGAAGGATACCAGGGTGATGGACTGACTTG
 TGTGTATATCCCAAAGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGGAAA
 TGGTACCATTTTAAAGGGTGACACAGGAAATAATAATTGGATTCTTGATGTTGGAAGTAC
 TTGGTGGCCTCCGAAGACACCATATATTCCTCCTATCATTACCAACAGGCCTACTTCTAA
 GCCAACAAACAGACCTACACCAAAGCCAACACCAATTCCTACTCCACCACCACCACC
 CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACACCGG
 ACTGACAACTATAGCACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAG
 GGTACAGACAGACCCCTCAGAAACCCAGAGGAGATGTGTTTCAGTGTTCCTGGTACACAGTTG
 TAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAATGACTTGCACTGGGA
 ACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTCCGCAGCCAAAGCCCCAGG
 GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCATTCAGGGGACCTGTG
 CCTGTCAATTCAGGCACAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAG
 AAAACACGGTGCCACGGAGCAGCCCTGTGGGGAAGAAATGGTGGCCATGGCTGGAGGCA
 AACACAGATCACCTTGCGAGGGGCTGACATCAAGAGCGAATCACAAAGATGATTAAAGGG
 TTGGAAAAAAGATCTATGATGGAAAATTAAAGGAACTGGGATTATTGAGCCTGGAGAAG
 AGAAGACTGAGGGGCAAACCATTTGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAG
 GGTGGCGACCAGCTGTTCTCCATATGCACTAAGAATAGAACAAGAGGAAACTGGCTTAGA
 CTAGAGTATAAGGGAGCATTTCTTGGCAGGGGCCATTGTTAGAATACTTCATAAAAAAAG
 AAGTGTGAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGATAAAAAATTTGTCTAT
 TTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTTCCCAA
 AGATGTTTTGATCCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGAC
 AAGGCTTAATTTAGGCATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAG
 AGCCCAACCAATGCTGAGCTCACTGAAATATCTCTCCCTTATGGCAATCCTAGCAGTATT
 AAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGACAGATATTTTAGTATC
 TCAGTAATGTCCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC
 TTTCAATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAGAGATCCTTCAAGGA
 ACACAGTTCAGAGAGATTTTCATCGGGTGCAATTCCTCTGCTTCGTGTGTGACAAGTTAT
 CTTGGCTGCTGAGAAAGAGTGCCCTGCCCCACACCGGCAGACCTTTCCTTCACCTCATCA
 GTATGATTCAGTTTCTCTTATCAATTGGACTCTCCAGGTTCCACAGAACAGTAATATTT
 TTTGAACAATAGGTACAATAGAAGGTCTTCTGTCAATTAACCTGGTAAAGGCAGGGCTGG
 AGGGGGAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCAT
 TTTTAATGGTTCATTTCTTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAA
 ATAAATGAAAATTTTACTTTTCGATGCCAATGATACATTGCACTAAACTGATGGAAGAAG
 TTATCCAAAGTACTGTATAACATCTTGTTTATTATTTAATGTTTTCTAAAATAAAAAATG
 TTAGTGGTTTTCCAAATGGCCTAATAAAAAACAATTATTTGTAAATAAAAACACTGTTAGT
 AAT

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FIGURE 110

><signal peptide>

MDFLLALVLVSSLYLQA

><start mature protein>

AAEFDGRWPRQIVSSIGLCRYGGRIDCCGWARQSWGQCQPV

><EGF-like repeats, 60-253>

CQPRCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYML
MPDGSCSSALTCSMANCQYGCDVVKQIIRCQCPSGLHLAPDGRTCVDVDECATGRASCPRF
RQCVNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEG
YQGDGLTCVYIPKVMIEPSGPIHVPKG

><potential N-glycosylation site>

NGTILKGD TGNNWIPDVGSTWWPPKTPYIPPIITNRPTSKPTTRPTPKPTPIPTPPPPPL
PTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDNRVQTDPOKPRGDVFSVLVHSCNFD
HGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVLPGLRLMHSGDLCLSFRH
KVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIKSESQR

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCCTTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACCTTTCCTTTCCCTTTGCAACAGGTGCTTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCCTGACTTGGAATACC
AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTTCATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATT
ATATCCATGTGTCTTCTCTTCCCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
GTATGAAGTTATTCAGCACATCCCTGCCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG
GCTAAACAGTACATTCGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAGT
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA
TGCAGAATAGAGGCATTTTATGCAAATTGAACTGCAGGTTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTCCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTTCCTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAACTTTACATTGTTTCGATTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA
CAAAGTAATAAGGATGGTTGTCACAAAAACAAAACCTATGCCTTCTCTTTTTTTTCAATCACC
AGTAGTATTTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTA
TTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGCTTTTAAAAA

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FIGURE 112

Met Trp Leu Lys Val Phe Thr Thr Phe Leu Ser Phe Ala Thr Gly Ala
Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His Gly Val
Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe His Thr Pro
Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg Pro His Thr Met
Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser Val Val Pro Asp Leu
Glu Tyr Gln His Lys Phe Thr Met Met Pro Pro Asn Ala Ser Leu Leu
Ile Asn Pro Leu Gln Phe Pro Asp Glu Gly Asn Tyr Ile Val Lys Val
Asn Ile Gln Gly Asn Gly Thr Leu Ser Ala Ser Gln Lys Ile Gln Val
Thr Val Asp Asp Pro Val Thr Lys Pro Val Val Gln Ile His Pro Pro
Ser Gly Ala Val Glu Tyr Val Gly Asn Met Thr Leu Thr Cys His Val
Glu Gly Gly Thr Arg Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro
Val His Thr Ser Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu
His Ile Ala Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu
Val Arg Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile
Ile Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu Phe
Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp Ile Arg
Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro Arg Leu Glu
Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp Tyr Val Cys Cys
Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu Thr His Phe Thr Val
Ile Ile Thr Ser Val Gly Leu Glu Lys Leu Ala Gln Lys Gly Lys Ser
Leu Ser Pro Leu Ala Ser Ile Thr Gly Ile Ser Leu Phe Leu Ile Ile
Ser Met Cys Leu Leu Phe Leu Trp Lys Lys Tyr Gln Pro Tyr Lys Val
Ile Lys Gln Lys Leu Glu Gly Arg Pro Glu Thr Glu Tyr Arg Lys Ala
Gln Thr Phe Ser Gly His Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr
Glu Phe Val Ala Phe Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser
Arg Ser Val Pro Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser
Thr Val Tyr Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His
Pro Glu

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FIGURE 113

GCAAGCGGCGAA

><MET {trans=1-s, dir=f, res=1}

ATGGCGCCCTCCGGGAGTCTTGCAGTTCCCCTGGCAGTCCTGGTGCTGTTGCTTTGGGGT
GCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGAACTGGAGA
GAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCTTGTCAA
AATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGAGAAAGATCTTGAGGTTAATATT
GCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTCTT
CCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTCATCA
TGGTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATG
TGGATCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCA
TATACTGTTTTTGGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATA
TTTGTGGCAGATTGCCTTTGTCCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCT
TCAAAAAAATTATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAG
GCGGATGAAGAAGATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGAC
TTTCCACAGAATGCCATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCC
TAGTTAAATTTTATAGTTATCTTAATATTATGATTTTGATAAAACAGAAGATTGATCAT
TTTGTTTGGTTTGAAGTGAAGTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTG
TCATTAAATTGAAGAGTCTACATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAAAT
ATGATTTAAGCACAGTATGATGGTTTAAATAGTTCTCTAATTTTTTGAAAAATCGTGCCAA
GCAATAAGATTTATGTATATTTGTTTAAATAAACCTATTTCAAGTCTGAGTTTTGAAAA
TTTACATTTCCCAAGTATTGCATTATTGAGGTATTTAAGAAGATTATTTTAGAGAAAAAT
ATTTCTCATTTGATATAATTTTCTCTGTTTCACTGTGTGAAAAAAGAAGATATTTCCC
ATAAATGGGAAGTTTGCCCATTTGTCTCAAGAAATGTGTATTTTCAGTGACAATTTCTGTGGT
CTTTTTAGAGGTATATTCCAAAATTTCTTGTATTTTTTAGGTTATGCACTAATAAAAAC
TACCTTACATTAATTAATTACAGTTTTCTACACATGGTAATACAGGATATGCTACTGATT
TAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTCCAACAAAGTTTGATTTTCTCTTGT
ATTTTTCTTACTTACTATGGGTACATTTTTTTATTTTTCAAATTGGATGATAATTTCTTG
GAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTTGTGTTTCAAAGTGAAGTTTACT
GAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAATTTTGGCCACTTTTTTTCAGA
TTTTACATCATTCTTGCTGAACTTCAACTTGAAATTGTTTTTTTTTTCCTTTTGGATGTG
AAGGTGAACATTCCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTATTTTACATTTTGAA
AATTCAAAGAAGCTTAATATAAAAGTTTGCATTCTACTCAGGAAAAAGCATCTTCTTGTA
TATGTCTTAAATGTATTTTTGTCTCATATACAGAAAGTTCTTAATTGATTTTACAGTCT
GTAATGCTTGATGTTTTAAATAAATAACATTTTTTATATTTTTTAAAGACAAACTTCATA
TTATCCTGTGTTCTTTCCTGACTGGTAATATTGTGTGGGATTTACAGGTAAAAGTCAGT
AGGATGGAACATTTTAGTGTATTTTTTACTCCTTAAAGAGCTAGAATACATAGTTTTTCACC
TTAAAAGAAGGGGGGAAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGACAA
TTTCTGTAATGTCCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCA
TTAAAGAGTTTGGATGTGTAAGTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAA
ACCTTTCTAACCCTTCATTAAAGCTGAAAAAATAAAAAAAAAA

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FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQ
NLQPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTK
KDFINFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGS
YTVFALATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPYPSKKLLSESAQPLKKVEEEQE
ADEEDVSEEEAESKEGTNKDFPQNARQPSLGPSLATDKS

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCC
TTCTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAG
CGGGAAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACC
><MET {trans=1-s, dir=f, res=1}
ATGAAACTCTGGGTGTCTGCATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAG
GCCGAATTCTTCACCTCTATTGGGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTG
GTGCAGTCTCTGAAAGAGTACATCCTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAGAGC
TGGGCCAACAAAATGGAAGCCTTGACTAGCAAGTCAGCTGCTGATGCTGAGGGGCTACCTG
GCTCACCTGTGAATGCCTACAACTGGTGAAGCGGCTAAACACAGACTGGCCTGCGCTG
GAGGACCTTGTCTGCAAGACTCAGCTGCAGGTTTTATCGCCAACCTCTCTGTGCAGCGG
CAGTTCTTCCCCACTGATGAGGACGAGATAGGAGCTGCCAAAGCCCTGATGAGACTTCAG
GACACATACAGGCTGGACCCAGGCACAATTTCCAGAGGGGAAGCTTCCAGGAACCAAGTAC
CAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATGGGCCGCTCGGCCTACAATGAAGGG
GACTATTATCATACGGTGTGTGGATGGAGCAGGTGCTAAAGCAGCTTGATGCCGGGGAG
GAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCAGCTATGCTGTCTTCCAGTTG
GGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTCTCCCTTGACCCAAGCCAC
GAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGAGGAAGAGAGAGAAAA
ACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAAGGCATCTATGAGAGGCCT
GTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGGGAGGGTGTCAA
CTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAACAGGGCCCCA
CAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACATCGTCAGG
TACTACGATGTCTGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAACCTAAA
CTTGACAGGCCACCGTTCGTGATCCCAAGACAGGAGTCTCACTGTCCGACGCTACCGG
GTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATCGT
CGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGC
GGCCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAA
GCTGGTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACA
GCTGTGTTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAGACATGCT
GCCTGCCCTGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGA
CAGGAGTTCTTGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCCTTC
CCCTTCCTGGTCCTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCCCTTTGTAT
GTTCCCTATCAGGCTGATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATA
CTAGGGCGACTCCTGTGTGACTGAAGTCCCAGCCCTTCCATTACGCCTGTGCCATCCCTG
GCCCCAAGGCTAGGATCAAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGT
GCCTTTGTACCTCAGGTGTTTTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACC
TTGTTTACATGTTTGTGTTTTATGGCATTCTATCTATTGTGGCTTTACCAAAAAATAAAA
TGTCCTTACCAGAAAAA

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FIGURE 116

><signal peptide>

MKLWVSALLMAWFGVLS

><start mature protein>

CVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWANKMEALTSKSAADAE

GYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIA

><N-glycosylation site.>

NLSVQRQFFPTDEDEIGAALKMRLQDTYRLDPGTISRGEPLPGTKYQAMLSVDDCF

GMGRSAYNEGDYYHTVLWMEQVLKQLDAGEEATTTKSQVLDY

><potential Leucine zipper 213-234>

LSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLRYFEQLLEEEREKTLT

><N-glycosylation site.>

NQTEAELATPEGIYERPVDYLPERDVYESLCRGEGVKLTPRRQKRLFCRYHHGNRAP

QLLIAPFKEEDEWDSPHIVRYDVMSEEEIERIKEIAKPKLARATVRDPKTGVLTVAS

YRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS

RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRS

GEGDYRTRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTVD

FIGURE 117

GCAGTATTGAGTTTTACTTCCTCCTCTTTTTAGTGGAAGACAGACCATAATCCCAGTGTGAG
TGAAATTGATTGTTTCATTTATTACCGTTTTGGCTGGGGGTTAGTTCCGACACCTTCACAGT
TGAAGAGCAGGCAGAAGGAGTTGTGAAGACAGGACAATCTTCTTGGGGATGCTGGTCCTGGA
AGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTGACCCCAGGTTCTCTGGTTAAACTGAA
AGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCCCCCTGGGGCAC
CCACCTGGCAGGGCCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGC
TCCCCCTCATCTTAGGGCTGTCTCTGGGGTGACGCTGAGCCTCCTGCGGGTTTCTTGATC
CAGGGGGAGGGAGAAGATCCCTGTGTGCGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCC
AGATTCGAGAGCTCGGCTAGACCAAAGTGATGAAGACTTCAAACCCCGGATTGTCCCCTACT
ACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTCGGTACATCCAGACAGAGCTG
GGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTGACCTCCCGAGCTACACTGTCCACTTTGGC
CGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCACTGGGCAGC
GGGGGGCCCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGCCCGCCTGG
CTCATGTCAGAGACCCTGCGCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTT
CATCATGCAGGATGACACATATGTGCAGGCCCCCGCCTGGCAGCCCTTGCTGGCCACCTCA
GCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTATTGGCGCAGGCGAGCAGGCC
CGGTACTGTCTATGGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGTCTGCGGCC
ACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCCGTCCCTGACGAGTGGCTTGACGCT
GCCTCATTGACTCTCTGGGCGTCCGCTGTGTCTCACAGCACCAGGGGCAGCAGTATCGCTCA
TTTGAAGTGGCCAAAAATAGGGACCCTGAGAAGGAAGGGAGCTCGGCTTTCTCTGAGTGCCTT
CGCCGTGCACCCTGTCTCCGAAGGTACCCTCATGTACCGGCTCCACAAACGCTTCAGCGCTC
TGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAAGTGCAGGCTCAGATCCGGAACCTGACC
GTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTTAC
ACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCT
GTGCAGATGGGGCTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCG
TTGGAGACTGCCCTGGAGCAGCTCAATCGGCGCTATCAGCCCCGCTGCGCTTCCAGAAGCA
GCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCACGGGGCATGGAGTACACCCTGGACC
TGCTGTTGGAATGTGTGACACAGCGTGGGCACCGGCGGGCCCTGGCTCGCAGGGTCAGCCTG
CTGCGGCCACTGAGCCGGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGT
GCAGCTGGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTTCTCTGAGGCGT
TTGCAGCCAATGTCCTGGAGCCACGAGAACATGCATTGCTCACCTGTTGCTGGTCTACGGG
CCACGAGAAGGTGGCCGTGGAGCTCCAGACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGA
GTTAGAGCGACGGTACCCTGGGACGAGGCTGGCCTGGCTCGCTGTGCGAGCAGAGGCCCTT
CCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCCCTGTGGACACTCTCTTCTTCTT
ACCACCGTGTGGACAAGGCCTGGGCCCCGAAGTCCCTCAACCGCTGTGCGATGAATGCCATCTC
TGGCTGGCAGGCCTTCTTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTCACCACAGA
GATCACCCCCAGGGCCCCCGGGGGCTGGCCCTGACCCCCCTCCCTCCTGGTGCTGACCCC
TCCCGGGGGGCTCCTATAGGGGGGAGATTTGACCGGCAGGCTTCTGCGGAGGGCTGCTTCTA
CAACGCTGACTACCTGGCGGCCCGAGCCCGGCTGGCAGGTGAACTGGCAGGCCAGGAAGAGG
AGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTTCTCTCCGGTTCTCAGGGCTCCACCTC
TTTCGGGCGGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCACGGCT
CAGTGAAGAACTCTACCACCGCTGCCGCCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCC
AGCTGGCTATGGCTCTCTTTGAGCAGGAGCAGGCCAATAGCACTTAGCCCGCCTGGGGGCC
TAACCTCATTAACCTTTCTTTGTCTGCCTCAGCCCCAGGAAGGGCAAGGCAAGATGGTGGAC
AGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAAATGTTATTAAACATGTCTTCTGCC

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FIGURE 118

><signal peptide>

MRLSSLLALLRPALP

><start mature protein>

LILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLDQSDDEDFKPRIVPY
YRDPNKPYPKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAV

><potential N-glycosylation site>

NRTVAHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYD

><homology to radical fringe -177-241>

WFFIMQDDTYVQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLR
LRPHLDGCRGDILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFL
SAFAVHPVSEGTLMYRLHKRFSALELERAYSEIEQLQAQIR

><potential N-glycosylation site>

NLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLGWDYFTEQHTFSCADGAPKCPLOGASRADV
GDALETALEQLNRRYQPRLRFQKQRLNNGYRRFDPARGMEYTLDLLLECVTQRGHRRALARR
VSLLRPLSRVEILPMPYVTEATRVQLVPLLVAAEAAAAPAFLEAFAANVLEPREHALLTLLL
VYGPREGGRGAPDPFLGVKAAAELERRYPGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTL
FFLTTVWTRPGPEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPGPPGAGPDPPSPPG
ADPSRGAPIGGRFDRQASAEGCFYNADYLAARARLAVNWQARKRRKPLEGLEVMDFLRFSG
LHLFRAVEPGLVQKFSLRDCSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQANST

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FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTTTTGAAGGGTGTGATGCTTGG
AAGCATTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCCTTCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTG
GTTCTTCCTTGACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTTCAAGATATGGCTGTTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGTTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACACTACATATCCAA
TACAGCTGTATGTTTCTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATG
TGTTGGAAAGAAGTGTTTAAAGAATAATAATTTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTGCTGATTGGTT
AAAAAATTTTAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAATGTACAATAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

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FIGURE 120

><signal peptide>

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHG

><start mature protein>

NRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCILVKPKDVSLWAAVKETW
TKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDKYRDQYNWFFLARP
TTFAIHENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSLLNIP
EKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNKTSVGLSIKEAMT
YHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFLPP

><potential N-glycosylation site>

NGSDND

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FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAGAAACAAAAAACCAAGAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA
AACCTAAAATGAGAGAGTTTTTTTATTGGACTGTCAGACCAGGTTGTGCGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTGTGAAATGGTAGGAATAAATCCTTTG
AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATACAAATAAAAATAAGTAGTTTTAAATGTTAAAAA
AA
AAAAA

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FIGURE 122

><subunit 1 of 1, 219 aa, 0 stop

><MW: 25072, pI: 5.16, NX(S/T): 3

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFSLACFITRCVVTFRI FQTCDEKKFQLPEN
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLED CATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGGCTGCGTCTTCCCGCAGCGCTACCCG
CCATGCGCCTGCCGCGCCGGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCC
GCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGGCTGGTGGACAAGTT
TAACCAGGGGATGGTGGACACCGCAAAGAAGAAGTTTGGCGGGCGGGGAACACGGCTTGGGAGG
AAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCTGCTGGAGATCCTGGAGGGGGCTG
TGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGC
CTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACAC
TGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGGATCC
CAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGGTC
CTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCA
GCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGC
TCGGGGCCTGACCAACAGAGACTGCGGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGC
CTGTGTGGATGTGGACGAGTGTGCGGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGT
TCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGGCTGC
ACAGGGGAAGGCCCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGGAGCACGGACA
GTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAACT
GCTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCCTGACGGCTTCGAAGAAACGGAAGAT
GCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCCTC
CCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGGA
AAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGCGGGGAGAGGCTGCCTGCTC
TCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGA
CTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAA
AAAAAA