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(54) Title: SECRETED PROTEINS

(57) **Abrégé/Abstract:**

The invention provides human secreted proteins (SECP) and polynucleotides which identify and encode SECP. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of SECP.



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(54) Title: SECRETED PROTEINS

(57) Abstract: The invention provides human secreted proteins (SECP) and polynucleotides which identify and encode SECP. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of SECP.



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SECRETED PROTEINS

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of secreted proteins and to the use of these sequences in the diagnosis, treatment, and prevention of cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, and developmental disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of secreted proteins.

BACKGROUND OF THE INVENTION

Protein transport and secretion are essential for cellular function. Protein transport is mediated by a signal peptide located at the amino terminus of the protein to be transported or secreted. The signal peptide is comprised of about ten to twenty hydrophobic amino acids which target the nascent protein from the ribosome to a particular membrane bound compartment such as the endoplasmic reticulum (ER). Proteins targeted to the ER may either proceed through the secretory pathway or remain in any of the secretory organelles such as the ER, Golgi apparatus, or lysosomes. Proteins that transit through the secretory pathway are either secreted into the extracellular space or retained in the plasma membrane. Proteins that are retained in the plasma membrane contain one or more transmembrane domains, each comprised of about 20 hydrophobic amino acid residues.

Secreted proteins are generally synthesized as inactive precursors that are activated by post-translational processing events during transit through the secretory pathway. Such events include glycosylation, proteolysis, and removal of the signal peptide by a signal peptidase. Other events that may occur during protein transport include chaperone-dependent unfolding and folding of the nascent protein and interaction of the protein with a receptor or pore complex. Examples of secreted proteins with amino terminal signal peptides are discussed below and include proteins with important roles in cell-to-cell signaling. Such proteins include transmembrane receptors and cell surface markers, extracellular matrix molecules, cytokines, hormones, growth and differentiation factors, enzymes, neuropeptides, vasomediators, cell surface markers, and antigen recognition molecules. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, New York, NY, pp. 557-560, 582-592.)

Cell surface markers include cell surface antigens identified on leukocytic cells of the immune system. These antigens have been identified using systematic, monoclonal antibody (mAb)-based "shot gun" techniques. These techniques have resulted in the production of hundreds of mAbs directed against unknown cell surface leukocytic antigens. These antigens have been grouped into "clusters of differentiation" based on common immunocytochemical localization patterns in various

differentiated and undifferentiated leukocytic cell types. Antigens in a given cluster are presumed to identify a single cell surface protein and are assigned a "cluster of differentiation" or "CD" designation. Some of the genes encoding proteins identified by CD antigens have been cloned and verified by standard molecular biology techniques. CD antigens have been characterized as both

5 transmembrane proteins and cell surface proteins anchored to the plasma membrane via covalent attachment to fatty acid-containing glycolipids such as glycosylphosphatidylinositol (GPI). (Reviewed in Barclay, A. N. et al. (1995) The Leucocyte Antigen Facts Book, Academic Press, San Diego, CA, pp. 17-20.)

Matrix proteins (MPs) are transmembrane and extracellular proteins which function in

10 formation, growth, remodeling, and maintenance of tissues and as important mediators and regulators of the inflammatory response. The expression and balance of MPs may be perturbed by biochemical changes that result from congenital, epigenetic, or infectious diseases. In addition, MPs affect leukocyte migration, proliferation, differentiation, and activation in the immune response. MPs are frequently characterized by the presence of one or more domains which may include collagen-like

15 domains, EGF-like domains, immunoglobulin-like domains, and fibronectin-like domains. In addition, MPs may be heavily glycosylated and may contain an Arginine-Glycine-Aspartate (RGD) tripeptide motif which may play a role in adhesive interactions. MPs include extracellular proteins such as fibronectin, collagen, galectin, vitronectin and its proteolytic derivative somatomedin B; and cell adhesion receptors such as cell adhesion molecules (CAMs), cadherins, and integrins. (Reviewed

20 in Ayad, S. et al. (1994) The Extracellular Matrix Facts Book, Academic Press, San Diego, CA, pp. 2-16; Ruoslahti, E. (1997) *Kidney Int.* 51:1413-1417; Sjaastad, M.D. and Nelson, W.J. (1997) *BioEssays* 19:47-55.)

Mucins are highly glycosylated glycoproteins that are the major structural component of the mucus gel. The physiological functions of mucins are cytoprotection, mechanical protection,

25 maintenance of viscosity in secretions, and cellular recognition. MUC6 is a human gastric mucin that is also found in gall bladder, pancreas, seminal vesicles, and female reproductive tract (Toribara, N.W. et al. (1997) *J. Biol. Chem.* 272:16398-16403). The MUC6 gene has been mapped to human chromosome 11 (Toribara, N.W. et al. (1993) *J. Biol. Chem.* 268:5879-5885). Hemomucin is a novel Drosophila surface mucin that may be involved in the induction of antibacterial effector molecules

30 (Theopold, U. et al. (1996) *J. Biol. Chem.* 271:12708-12715).

Tuftelins are one of four different enamel matrix proteins that have been identified so far. The other three known enamel matrix proteins are the amelogenins, enamelin and ameloblastin. Assembly of the enamel extracellular matrix from these component proteins is believed to be critical in producing a matrix competent to undergo mineral replacement. (Paine C.T. et al. (1998) *Connect*

35 *Tissue Res.*38:257-267). Tuftelin mRNA has been found to be expressed in human ameloblastoma

tumor, a non-mineralized odontogenic tumor (Deutsch D. et al. (1998) Connect Tissue Res. 39:177-184).

Olfactomedin-related proteins are extracellular matrix, secreted glycoproteins with conserved C-terminal motifs. They are expressed in a wide variety of tissues and in broad range of species, from *Caenorhabditis elegans* to *Homo sapiens*. Olfactomedin-related proteins comprise a gene family with at least 5 family members in humans. One of the five, TIGR/myocilin protein, is expressed in the eye and is associated with the pathogenesis of glaucoma (Kulkarni, N.H. et al., (2000) Genet. Res. 76:41-50). Research by Yokoyama et al. (1996) found a 135-amino acid protein, termed AMY, having 96% sequence identity with rat neuronal olfactomedin-related ER localized protein in a neuroblastoma cell line cDNA library, suggesting an essential role for AMY in nerve tissue (Yokoyama, M. et al., (1996) DNA Res. 3:311-320). Neuron-specific olfactomedin-related glycoproteins isolated from rat brain cDNA libraries show strong sequence similarity with olfactomedin. This similarity is suggestive of a matrix-related function of these glycoproteins in neurons and neurosecretory cells (Danielson, P.E. et al., (1994) J. Neurosci. Res. 38:468-478).

Mac-2 binding protein is a 90-kD serum protein (90K) and another secreted glycoprotein, isolated from both the human breast carcinoma cell line SK-BR-3, and human breast milk. It specifically binds to a human macrophage-associated lectin, Mac-2. Structurally, the mature protein is 567 amino acids in length and is preceded by an 18-amino acid leader. There are 16 cysteines and seven potential N-linked glycosylation sites. The first 106 amino acids represent a domain very similar to an ancient protein superfamily defined by a macrophage scavenger receptor cysteine-rich domain (Koths, K. et al., (1993) J. Biol. Chem. 268:14245-14249). 90K is elevated in the serum of subpopulations of AIDS patients and is expressed at varying levels in primary tumor samples and tumor cell lines. Ullrich et al. (1994) have demonstrated that 90K stimulates host defense systems and can induce interleukin-2 secretion. This immune stimulation is proposed to be a result of oncogenic transformation, viral infection or pathogenic invasion (Ullrich, A., et al. (1994) J. Biol. Chem. 269:18401-18407).

Semaphorins are a large group of axonal guidance molecules consisting of at least 30 different members and are found in vertebrates, invertebrates, and even certain viruses. All semaphorins contain the sema domain which is approximately 500 amino acids in length. Neuropilin, a semaphorin receptor has been shown to promote neurite outgrowth in vitro. The extracellular region of neuropilins consists of three different domains: CUB, discoidin, and MAM domains. The CUB and the MAM motifs of neuropilin have been suggested as having roles in protein-protein interactions and are suggested to be involved in the binding of semaphorins through the sema and the C-terminal domains (reviewed in Raper, J.A. (2000) Curr. Opin. Neurobiol. 10:88-94). Plexins are neuronal cell surface molecules that mediate cell adhesion via a homophilic binding mechanism in the

presence of calcium ions. Plexins have been shown to be expressed in the receptors and neurons of particular sensory systems (Ohta, K. et al. (1995) Cell 14:1189-1199). There is evidence that suggests that some plexins function to control motor and CNS axon guidance in the developing nervous system. Plexins, which themselves contain complete semaphorin domains, may be both the
 5 ancestors of classical semaphorins and binding partners for semaphorins (Winberg, M.L. et al (1998) Cell 95:903-916).

Human pregnancy-specific beta 1-glycoprotein (PSG) is a family of closely related glycoproteins of molecular weights of 72 KDa, 64KDa, 62KDa, and 54KDa. Together with the carcinoembryonic antigen, they comprise a subfamily within the immunoglobulin superfamily
 10 (Plouzek C.A. and Chou J.Y., Endocrinology 129:950-958) Different subpopulations of PSG have been found to be produced by the trophoblasts of the human placenta, and the amnionic, and chorionic membranes (Plouzek C.A. et al. (1993) Placenta 14:277-285).

Autocrine motility factor (AMF) is one of the motility cytokines regulating tumor cell migration, therefore identification of the signaling pathway coupled with it has critical importance.
 15 Autocrine motility factor receptor (AMFR) expression has been found to be associated with tumor progression in thymoma (Ohta Y. et al. (2000) Int. J. Oncol. 17:259-264). AMFR is a cell surface glycoprotein of molecular weight 78KDa.

Hormones are secreted molecules that travel through the circulation and bind to specific receptors on the surface of, or within, target cells. Although they have diverse biochemical
 20 compositions and mechanisms of action, hormones can be grouped into two categories. One category includes small lipophilic hormones that diffuse through the plasma membrane of target cells, bind to cytosolic or nuclear receptors, and form a complex that alters gene expression. Examples of these molecules include retinoic acid, thyroxine, and the cholesterol-derived steroid hormones such as progesterone, estrogen, testosterone, cortisol, and aldosterone. The second category includes
 25 hydrophilic hormones that function by binding to cell surface receptors that transduce signals across the plasma membrane. Examples of such hormones include amino acid derivatives such as catecholamines (epinephrine, norepinephrine) and histamine, and peptide hormones such as glucagon, insulin, gastrin, secretin, cholecystokinin, adrenocorticotrophic hormone, follicle stimulating hormone, luteinizing hormone, thyroid stimulating hormone, and vasopressin. (See, for example, Lodish et al.
 30 (1995) Molecular Cell Biology, Scientific American Books Inc., New York, NY, pp. 856-864.)

Pro-opiomelanocortin (POMC) is the precursor polypeptide of corticotropin (ACTH) a hormone synthesized by the anterior pituitary gland, which functions in the stimulation of the adrenal cortex. POMC is also the precursor polypeptide of the hormone, beta-lipotropin (beta-LPH),. Each hormone includes smaller peptides with distinct biological activities: alpha-melanotropin (alpha-
 35 MSH) and corticotropin-like intermediate lobe peptide (CLIP) are formed from ACTH; gamma-

lipotropin (gamma-LPH) and beta-endorphin are peptide components of beta-LPH, while beta-MSH is contained within gamma-LPH. Adrenal insufficiency due to ACTH deficiency, resulting from a genetic mutation in exons 2 and 3 of POMC results in an endocrine disorder characterized by early-onset obesity, adrenal insufficiency, and red hair pigmentation (Chretien, M. et al., (1979) *Canad. J. Biochem.* 57:1111-1121, Krude, H. et al., (1998) *Nature Genet.* 19:155-157, Online Mendelian Inheritance in Man, OMIM. Johns Hopkins University, Baltimore, MD. OMIM Number: 176830: August 1, 2000. World Wide Web URL: www.ncbi.nlm.nih.gov/omim/).

Growth and differentiation factors are secreted proteins which function in intercellular communication. Some factors require oligomerization or association with membrane proteins for activity. Complex interactions among these factors and their receptors trigger intracellular signal transduction pathways that stimulate or inhibit cell division, cell differentiation, cell signaling, and cell motility. Most growth and differentiation factors act on cells in their local environment (paracrine signaling). There are three broad classes of growth and differentiation factors. The first class includes the large polypeptide growth factors such as epidermal growth factor, fibroblast growth factor, transforming growth factor, insulin-like growth factor, and platelet-derived growth factor. The second class includes the hematopoietic growth factors such as the colony stimulating factors (CSFs). Hematopoietic growth factors stimulate the proliferation and differentiation of blood cells such as B-lymphocytes, T-lymphocytes, erythrocytes, platelets, eosinophils, basophils, neutrophils, macrophages, and their stem cell precursors. The third class includes small peptide factors such as bombesin, vasopressin, oxytocin, endothelin, transferrin, angiotensin II, vasoactive intestinal peptide, and bradykinin which function as hormones to regulate cellular functions other than proliferation.

Growth and differentiation factors play critical roles in neoplastic transformation of cells in vitro and in tumor progression in vivo. Inappropriate expression of growth factors by tumor cells may contribute to vascularization and metastasis of tumors. During hematopoiesis, growth factor misregulation can result in anemias, leukemias, and lymphomas. Certain growth factors such as interferon are cytotoxic to tumor cells both in vivo and in vitro. Moreover, some growth factors and growth factor receptors are related both structurally and functionally to oncoproteins. In addition, growth factors affect transcriptional regulation of both proto-oncogenes and oncosuppressor genes. (Reviewed in Pimentel, E. (1994) Handbook of Growth Factors, CRC Press, Ann Arbor, MI, pp. 1-9.)

The Slit protein, first identified in *Drosophila*, is critical in central nervous system midline formation and potentially in nervous tissue histogenesis and axonal pathfinding. Itoh et al. have identified mammalian homologues of the slit gene (human Slit-1, Slit-2, Slit-3 and rat Slit-1). The encoded proteins are putative secreted proteins containing EFG-like motifs and leucine-rich repeats, both are conserved protein-protein interaction domains. Slit-1, -2, and -3 mRNAs are expressed in the brain, spinal cord, and thyroid, respectively (Itoh, A. et al., (1998) *Brain Res. Mol. Brain Res.*

62:175-186). The Slit family of proteins are indicated to be functional ligands of glypican-1 in nervous tissue and suggests that their interactions may be critical in certain stages during central nervous system histogenesis (Liang, Y. et al., (1999) J. Biol. Chem. 274:17885-17892).

Neuropeptides and vasomediators (NP/VM) comprise a large family of endogenous signaling molecules. Included in this family are neuropeptides and neuropeptide hormones such as bombesin, neuropeptide Y, neurotensin, neuromedin N, melanocortins, opioids, galanin, somatostatin, tachykinins, urotensin II and related peptides involved in smooth muscle stimulation, vasopressin, vasoactive intestinal peptide, and circulatory system-borne signaling molecules such as angiotensin, complement, calcitonin, endothelins, formyl-methionyl peptides, glucagon, cholecystokinin and gastrin. NP/VMs can transduce signals directly, modulate the activity or release of other neurotransmitters and hormones, and act as catalytic enzymes in cascades. The effects of NP/VMs range from extremely brief to long-lasting. (Reviewed in Martin, C.R. et al. (1985) Endocrine Physiology, Oxford University Press, New York, NY, pp. 57-62.)

NP/VMs are involved in numerous neurological and cardiovascular disorders. For example, neuropeptide Y is involved in hypertension, congestive heart failure, affective disorders, and appetite regulation. Somatostatin inhibits secretion of growth hormone and prolactin in the anterior pituitary, as well as inhibiting secretion in intestine, pancreatic acinar cells, and pancreatic beta-cells. A reduction in somatostatin levels has been reported in Alzheimer's disease and Parkinson's disease. Vasopressin acts in the kidney to increase water and sodium absorption, and in higher concentrations stimulates contraction of vascular smooth muscle, platelet activation, and glycogen breakdown in the liver. Vasopressin and its analogues are used clinically to treat diabetes insipidus. Endothelin and angiotensin are involved in hypertension, and drugs, such as captopril, which reduce plasma levels of angiotensin, are used to reduce blood pressure (Watson, S. and S. Arkininstall (1994) The G-protein Linked Receptor Facts Book, Academic Press, San Diego CA, pp. 194; 252; 284; 55; 111).

Neuropeptides have also been shown to have roles in nociception (pain). Vasoactive intestinal peptide appears to play an important role in chronic neuropathic pain. Nociceptin, an endogenous ligand for the opioid receptor-like 1 receptor, is thought to have a predominantly anti-nociceptive effect, and has been shown to have analgesic properties in different animal models of tonic or chronic pain (Dickinson, T. and Fleetwood-Walker, S.M. (1998) Trends Pharmacol. Sci. 19:346-348).

Other proteins that contain signal peptides include secreted proteins with enzymatic activity. Such activity includes, for example, oxidoreductase/dehydrogenase activity, transferase activity, hydrolase activity, lyase activity, isomerase activity, or ligase activity. For example, matrix metalloproteinases are secreted hydrolytic enzymes that degrade the extracellular matrix and thus play an important role in tumor metastasis, tissue morphogenesis, and arthritis (Reponen, P. et al.

(1995) Dev. Dyn. 202:388-396; Firestein, G.S. (1992) Curr. Opin. Rheumatol. 4:348-354; Ray, J.M. and Stetler-Stevenson, W.G. (1994) Eur. Respir. J. 7:2062-2072; and Mignatti, P. and Rifkin, D.B. (1993) Physiol. Rev. 73:161-195). Additional examples are the acetyl-CoA synthetases which activate acetate for use in lipid synthesis or energy generation (Luong, A. et al. (2000) J. Biol. Chem. 275:26458-26466). The result of acetyl-CoA synthetase activity is the formation of acetyl-CoA from acetate and CoA. Acetyl-CoA synthetases share a region of sequence similarity identified as the AMP-binding domain signature. Acetyl-CoA synthetase has been shown to be associated with hypertension (H. Toh (1991) Protein Seq. Data Anal. 4:111-117 and Iwai, N. et al., (1994) Hypertension 23:375-380).

Other proteins that contain signal peptides include enzymes involved in the glycosylation of proteins in transit through the secretory pathway. Mucin-type O-linked glycosylation is a dominant form of protein glycosylation. Initiation of mucin-type glycosylation occurs by the addition of the monosaccharide N-acetylgalactosamine to the hydroxyl group of serine and threonine amino acids (GalNAc α 1-O-Ser/Thr). GalNAc O-glycosylation is more prominent on high molecular weight secretory glycoproteins such as mucins, but is also found on a variety of glycoproteins (White, T. et al., J. Biol. Chem. (1995) 270:24156-24165). Additionally, serine/threonine-rich tandem repeats are a characteristic of human mucin core proteins. The tandem repeat region also contains numerous antigenic determinants as recognized by the monoclonal antibodies HMFG-1, HMFG-1, and SM-3. Glycosylation sites within the tandem repeat region were found to be differentially glycosylated depending on the organ from which Muc1 was isolated. The finding of variable glycosylation activity may be critical to further understanding of the molecular basis of cancer-associated epitopes which map to the Muc1 tandem repeat (Gendler, S.J. et al. (1990) J. Biol. Chem. 265:15286-15293):

Antigen recognition molecules are key players in the sophisticated and complex immune systems which all vertebrates have developed to provide protection from viral, bacterial, fungal, and parasitic infections. A key feature of the immune system is its ability to distinguish foreign molecules, or antigens, from "self" molecules. This ability is mediated primarily by secreted and transmembrane proteins expressed by leukocytes (white blood cells) such as lymphocytes, granulocytes, and monocytes. Most of these proteins belong to the immunoglobulin (Ig) superfamily, members of which contain one or more repeats of a conserved structural domain. This Ig domain is comprised of antiparallel β sheets joined by a disulfide bond in an arrangement called the Ig fold. Members of the Ig superfamily include T-cell receptors, major histocompatibility (MHC) proteins, antibodies, and immune cell-specific surface markers such as the "cluster of differentiation" or CD antigens. These antigens have been identified using systematic, monoclonal antibody (mAb)-based "shot gun" techniques. These techniques have resulted in the production of hundreds of mAbs directed against unknown cell surface leukocytic antigens. These antigens have been grouped into

“clusters of differentiation” based on common immunocytochemical localization patterns in various differentiated and undifferentiated leukocytic cell types. Antigens in a given cluster are presumed to identify a single cell surface protein and are assigned a “cluster of differentiation” or “CD” designation. Some of the genes encoding proteins identified by CD antigens have been cloned and verified by standard molecular biology techniques. CD antigens have been characterized as both transmembrane proteins and cell surface proteins anchored to the plasma membrane via covalent attachment to fatty acid-containing glycolipids such as glycosylphosphatidylinositol (GPI). (Reviewed in Barclay, A. N. et al. (1995) The Leucocyte Antigen Facts Book, Academic Press, San Diego, CA, pp. 17-20.)

MHC proteins are cell surface markers that bind to and present foreign antigens to T cells. MHC molecules are classified as either class I or class II. Class I MHC molecules (MHC I) are expressed on the surface of almost all cells and are involved in the presentation of antigen to cytotoxic T cells. For example, a cell infected with virus will degrade intracellular viral proteins and express the protein fragments bound to MHC I molecules on the cell surface. The MHC I/antigen complex is recognized by cytotoxic T-cells which destroy the infected cell and the virus within. Class II MHC molecules are expressed primarily on specialized antigen-presenting cells of the immune system, such as B-cells and macrophages. These cells ingest foreign proteins from the extracellular fluid and express MHC II/antigen complex on the cell surface. This complex activates helper T-cells, which then secrete cytokines and other factors that stimulate the immune response. MHC molecules also play an important role in organ rejection following transplantation. Rejection occurs when the recipient’s T-cells respond to foreign MHC molecules on the transplanted organ in the same way as to self MHC molecules bound to foreign antigen. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of the Cell, Garland Publishing, New York, NY, pp. 1229-1246.)

Antibodies, or immunoglobulins, are either expressed on the surface of B-cells or secreted by B-cells into the circulation. Antibodies bind and neutralize foreign antigens in the blood and other extracellular fluids. The prototypical antibody is a tetramer consisting of two identical heavy polypeptide chains (H-chains) and two identical light polypeptide chains (L-chains) interlinked by disulfide bonds. This arrangement confers the characteristic Y-shape to antibody molecules. Antibodies are classified based on their H-chain composition. The five antibody classes, IgA, IgD, IgE, IgG and IgM, are defined by the α , δ , ϵ , γ , and μ H-chain types. There are two types of L-chains, κ and λ , either of which may associate as a pair with any H-chain pair. IgG, the most common class of antibody found in the circulation, is tetrameric, while the other classes of antibodies are generally variants or multimers of this basic structure.

H-chains and L-chains each contain an N-terminal variable region and a C-terminal constant region. The constant region consists of about 110 amino acids in L-chains and about 330 or 440

amino acids in H-chains. The amino acid sequence of the constant region is nearly identical among H- or L-chains of a particular class. The variable region consists of about 110 amino acids in both H- and L-chains. However, the amino acid sequence of the variable region differs among H- or L-chains of a particular class. Within each H- or L-chain variable region are three hypervariable regions of extensive sequence diversity, each consisting of about 5 to 10 amino acids. In the antibody molecule, the H- and L-chain hypervariable regions come together to form the antigen recognition site.

(Reviewed in Alberts, *supra*, pp. 1206-1213 and 1216-1217.)

Both H-chains and L-chains contain repeated Ig domains. For example, a typical H-chain contains four Ig domains, three of which occur within the constant region and one of which occurs within the variable region and contributes to the formation of the antigen recognition site. Likewise, a typical L-chain contains two Ig domains, one of which occurs within the constant region and one of which occurs within the variable region.

The immune system is capable of recognizing and responding to any foreign molecule that enters the body. Therefore, the immune system must be armed with a full repertoire of antibodies against all potential antigens. Such antibody diversity is generated by somatic rearrangement of gene segments encoding variable and constant regions. These gene segments are joined together by site-specific recombination which occurs between highly conserved DNA sequences that flank each gene segment. Because there are hundreds of different gene segments, millions of unique genes can be generated combinatorially. In addition, imprecise joining of these segments and an unusually high rate of somatic mutation within these segments further contribute to the generation of a diverse antibody population.

A number of isomerases catalyze steps in protein folding, phototransduction, and various anabolic and catabolic pathways. One class of isomerases is known as peptidyl-prolyl *cis-trans* isomerases (PPIases). PPIases catalyze the *cis* to *trans* isomerization of certain proline imidic bonds in proteins. Two families of PPIases are the FK506 binding proteins (FKBPs), and cyclophilins (CyPs). FKBPs bind the potent immunosuppressants FK506 and rapamycin, thereby inhibiting signaling pathways in T-cells. Specifically, the PPIase activity of FKBPs is inhibited by binding of FK506 or rapamycin. There are five members of the FKBP family which are named according to their calculated molecular masses (FKBP12, FKBP13, FKBP25, FKBP52, and FKBP65), and localized to different regions of the cell where they associate with different protein complexes (Coss, M. et al. (1995) J. Biol. Chem. 270:29336 - 29341; Schreiber, S.L. (1991) Science 251:283 - 287).

The peptidyl-prolyl isomerase activity of CyP may be part of the signaling pathway that leads to T-cell activation. CyP isomerase activity is associated with protein folding and protein trafficking, and may also be involved in assembly/disassembly of protein complexes and regulation of protein activity. For example, in *Drosophila*, the CyP NinaA is required for correct localization of

rhodopsins, while a mammalian CyP (Cyp40) is part of the Hsp90/Hsc70 complex that binds steroid receptors. The mammalian CypA has been shown to bind the *gag* protein from human immunodeficiency virus 1 (HIV-1), an interaction that can be inhibited by cyclosporin. Since cyclosporin has potent anti-HIV-1 activity, CypA may play an essential function in HIV-1 replication.

5 Finally, Cyp40 has been shown to bind and inactivate the transcription factor c-Myb, an effect that is reversed by cyclosporin. This effect implicates CyPs in the regulation of transcription, transformation, and differentiation (Bergsma, D.J. et al (1991) J. Biol. Chem. 266:23204 - 23214; Hunter, T. (1998) Cell 92: 141-143; and Levenson, J.D. and Ness, S.A. (1998) Mol. Cell. 1:203-211).

Gamma-carboxyglutamic acid (Gla) proteins rich in proline (PRGPs) are members of a family

10 of vitamin K-dependent single-pass integral membrane proteins. These proteins are characterized by an extracellular amino terminal domain of approximately 45 amino acids rich in Gla. The intracellular carboxyl terminal region contains one or two copies of the sequence PPXY, a motif present in a variety of proteins involved in such diverse cellular functions as signal transduction, cell cycle progression, and protein turnover (Kulman, J.D. et al., (2001) Proc. Natl. Acad. Sci. U.S.A.

15 98:1370-1375). The process of post-translational modification of glutamic residues to form Gla is Vitamin K-dependent carboxylation. Proteins which contain Gla include plasma proteins involved in blood coagulation. These proteins are prothrombin, proteins C, S, and Z, and coagulation factors VII, IX, and X. Osteocalcin (bone-Gla protein, BGP) and matrix Gla-protein (MGP) also contain Gla (Friedman, P.A., and C.T. Przysiecki (1987) Int. J. Biochem. 19:1-7; C. Vermeer (1990) Biochem. J.

20 266:625-636).

The *Drosophila* sp. gene *crossveinless 2* is characterized as having a putative signal or transmembrane sequence, and a partial Von Willebrand Factor D domain similar to those domains known to regulate the formation of intramolecular and intermolecular bonds and five cysteine-rich domains, known to bind BMP-like (bone morphogenetic proteins) ligands. These features suggest

25 that *crossveinless 2* may act extracellularly or in the secretory pathway to directly potentiate ligand signaling and hence, involvement in the BMP-like signaling pathway known to play a role in vein specification (Conley, C.A. et al., (2000) Development 127:3947-3959). The dorsal-ventral patterning in both vertebrate and *Drosophila* embryos requires a conserved system of extracellular proteins to generate a positional informational gradient.

30 Another protein that contains a signal peptide is encoded by the seizure-related gene, SEZ-6, a brain specific cDNA whose expression is increased by the convulsant drug pentylentetrazole. The SEZ-6 protein is expressed in the cerebrum and cerebellum. SEZ-6 contains five short consensus repeats (SCR, or sushi domains) and two CUB (complement C1r/s-like repeat) domains in addition to a signal peptide and a single transmembrane domain (Shimizu-Nishikawa, K. et al. (1995) Biochem.

35 Biophys. Res. Commun. 216:382-389).

The discovery of new secreted proteins and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, and developmental disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of secreted proteins.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, secreted proteins, referred to collectively as "SECP" and individually as "SECP-1," "SECP-2," "SECP-3," "SECP-4," "SECP-5," "SECP-6," "SECP-7," "SECP-8," "SECP-9," "SECP-10," "SECP-11," "SECP-12," "SECP-13," "SECP-14," "SECP-15," "SECP-16," "SECP-17," "SECP-18," "SECP-19," "SECP-20," "SECP-21," "SECP-22," "SECP-23," "SECP-24," "SECP-25," "SECP-26," "SECP-27," "SECP-28," "SECP-29," "SECP-30," "SECP-31," "SECP-32," "SECP-33," "SECP-34," "SECP-35," "SECP-36," "SECP-37," "SECP-38," "SECP-39," "SECP-40," "SECP-41," "SECP-42," "SECP-43," and "SECP-44." In one aspect, the invention provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-44.

The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44. In one alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-44. In another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:45-88.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting

of SEQ ID NO:1-44, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44.

The invention further provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:45-88, b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:45-88, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous nucleotides.

Additionally, the invention provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group

consisting of SEQ ID NO:45-88, b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:45-88, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:45-88, b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:45-88, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention further provides a composition comprising an effective amount of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-44. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional SECP, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino

acid sequence selected from the group consisting of SEQ ID NO:1-44, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional SECP, comprising administering to a patient in need of such treatment the composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional SECP, comprising administering to a patient in need of such treatment the composition.

The invention further provides a method of screening for a compound that specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

The invention further provides a method of screening for a compound that modulates the

activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO:45-88, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:45-88, ii) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:45-88, iii) a polynucleotide having a sequence complementary to i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:45-88, ii) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:45-88, iii) a polynucleotide complementary to the polynucleotide of i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting

of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

5

BRIEF DESCRIPTION OF THE TABLES

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the present invention.

Table 2 shows the GenBank identification number and annotation of the nearest GenBank homolog for polypeptides of the invention. The probability score for the match between each polypeptide and its GenBank homolog is also shown.

Table 3 shows structural features of polypeptide sequences of the invention, including predicted motifs and domains, along with the methods, algorithms, and searchable databases used for analysis of the polypeptides.

Table 4 lists the cDNA and/or genomic DNA fragments which were used to assemble polynucleotide sequences of the invention, along with selected fragments of the polynucleotide sequences.

Table 5 shows the representative cDNA library for polynucleotides of the invention.

Table 6 provides an appendix which describes the tissues and vectors used for construction of the cDNA libraries shown in Table 5.

Table 7 shows the tools, programs, and algorithms used to analyze the polynucleotides and polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

25

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

35

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now
5 described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

10 “SECP” refers to the amino acid sequences of substantially purified SECP obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term “agonist” refers to a molecule which intensifies or mimics the biological activity of SECP. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other
15 compound or composition which modulates the activity of SECP either by directly interacting with SECP or by acting on components of the biological pathway in which SECP participates.

An “allelic variant” is an alternative form of the gene encoding SECP. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or
20 many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

“Altered” nucleic acid sequences encoding SECP include those sequences with deletions,
25 insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as SECP or a polypeptide with at least one functional characteristic of SECP. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding SECP, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding
30 SECP. The encoded protein may also be “altered,” and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent SECP. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of SECP is retained. For example,
35 negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged

amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

5 The terms “amino acid” and “amino acid sequence” refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. Where “amino acid sequence” is recited to refer to a sequence of a naturally occurring protein molecule, “amino acid sequence” and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

10 “Amplification” relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

 The term “antagonist” refers to a molecule which inhibits or attenuates the biological activity of SECP. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small
15 molecules, or any other compound or composition which modulates the activity of SECP either by directly interacting with SECP or by acting on components of the biological pathway in which SECP participates.

 The term “antibody” refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant.
20 Antibodies that bind SECP polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin,
25 and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

 The term “antigenic determinant” refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures
30 on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

 The term “antisense” refers to any composition capable of base-pairing with the “sense” (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as
35 phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified

sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring
5 nucleic acid sequence produced by the cell to form duplexes which block either transcription or translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic"
10 refers to the capability of the natural, recombinant, or synthetic SECP, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement,
15 3'-TCA-5'.

A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding SECP or fragments of SECP may be
20 employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been subjected to repeated
25 DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (Applied Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and
30 assembled to produce the consensus sequence.

"Conservative amino acid substitutions" are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded
35 as conservative amino acid substitutions.

	Original Residue	Conservative Substitution
	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
5	Asp	Asn, Glu
	Cys	Ala, Ser
	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
10	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
15	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
	Thr	Ser, Val
	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
20	Val	Ile, Leu, Thr

Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

"Differential expression" refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

A "fragment" is a unique portion of SECP or the polynucleotide encoding SECP which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up

to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present
10 embodiments.

A fragment of SEQ ID NO:45-88 comprises a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:45-88, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:45-88 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish
15 SEQ ID NO:45-88 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:45-88 and the region of SEQ ID NO:45-88 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-44 is encoded by a fragment of SEQ ID NO:45-88. A fragment of SEQ ID NO:1-44 comprises a region of unique amino acid sequence that specifically identifies
20 SEQ ID NO:1-44. For example, a fragment of SEQ ID NO:1-44 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-44. The precise length of a fragment of SEQ ID NO:1-44 and the region of SEQ ID NO:1-44 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

25 A "full length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full length" polynucleotide sequence encodes a "full length" polypeptide sequence.

"Homology" refers to sequence similarity or, interchangeably, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

30 The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

35 Percent identity between polynucleotide sequences may be determined using the default

parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to

describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases “percent identity” and “% identity,” as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of substitution, thus preserving the structure (and therefore function) of the polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and “diagonals saved”=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the “percent similarity” between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the “BLAST 2 Sequences” tool Version 2.0.12 (April-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

“Human artificial chromosomes” (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term “humanized antibody” refers to an antibody molecule in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

“Hybridization” refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the “washing” step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high

stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C₀t or R₀t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of SECP which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of SECP which is useful in any of the antibody production methods disclosed herein or known in the art.

The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, or other chemical compounds on a substrate.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of SECP. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of SECP.

The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

“Peptide nucleic acid” (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript
5 elongation, and may be pegylated to extend their lifespan in the cell.

“Post-translational modification” of an SECP may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu of SECP.

10 “Probe” refers to nucleic acid sequences encoding SECP, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. “Primers” are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target
15 polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also
20 be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for
25 example Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel, F.M. et al. (1987) Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al. (1990) PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that
30 purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to
35 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer

selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a “mispriming library,” in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user’s specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A “recombinant nucleic acid” is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, *supra*. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

A “regulatory element” refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription, translation, or RNA stability.

“Reporter molecules” are chemical or biochemical moieties used for labeling a nucleic acid,

amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An “RNA equivalent,” in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The term “sample” is used in its broadest sense. A sample suspected of containing SECP, nucleic acids encoding SECP, or fragments thereof may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms “specific binding” and “specifically binding” refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope “A,” the presence of a polypeptide comprising the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The term “substantially purified” refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated.

A “substitution” refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

“Substrate” refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A “transcript image” refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

“Transformation” describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or

viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed cells" includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

5 A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with
10 a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection,
15 transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of
20 the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. A variant may be described as, for example, an
25 "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternative splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to
30 another. The resulting polypeptides will generally have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a
35 propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length of one of the polypeptides.

THE INVENTION

The invention is based on the discovery of new human secreted proteins (SECP), the polynucleotides encoding SECP, and the use of these compositions for the diagnosis, treatment, or prevention of cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, and developmental disorders.

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the invention. Each polynucleotide and its corresponding polypeptide are correlated to a single Incyte project identification number (Incyte Project ID). Each polypeptide sequence is denoted by both a polypeptide sequence identification number (Polypeptide SEQ ID NO:) and an Incyte polypeptide sequence number (Incyte Polypeptide ID) as shown. Each polynucleotide sequence is denoted by both a polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and an Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) as shown.

Table 2 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (genpept) database. Columns 1 and 2 show the polypeptide sequence identification number (Polypeptide SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for polypeptides of the invention. Column 3 shows the GenBank identification number (Genbank ID NO:) of the nearest GenBank homolog. Column 4 shows the probability score for the match between each polypeptide and its GenBank homolog. Column 5 shows the annotation of the GenBank homolog along with relevant citations where applicable, all of which are expressly incorporated by reference herein.

Table 3 shows various structural features of the polypeptides of the invention. Columns 1 and 2 show the polypeptide sequence identification number (SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for each polypeptide of the invention. Column 3 shows the number of amino acid residues in each polypeptide. Column 4 shows potential phosphorylation sites, and column 5 shows potential glycosylation sites, as determined by the MOTIFS program of the GCG sequence analysis software package (Genetics Computer Group, Madison WI). Column 6 shows amino acid residues comprising signature sequences, domains, and

motifs. In particular, the locations of signal peptides (as indicated by “Signal_peptide” or “Signal_cleavage”) are shown. Column 7 shows analytical methods for protein structure/function analysis and in some cases, searchable databases to which the analytical methods were applied.

Together, tables 2 and 3 summarize the properties of each polypeptide of the invention, and these properties establish that the claimed polypeptides are secreted proteins. For example, SEQ ID NO:1 is 51% identical to human UDP-Ga1NAc:polypeptide N-acetylgalactosaminyltransferase (GenBank ID g971461) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $1.5e-141$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:1 also contains a signal peptide and a transmembrane domain as determined by hidden Markov model (HMM)-based methods. (See Table 3.) Likewise, SPScan analysis also indicates the presence of an N-terminal signal peptide in SEQ ID NO:1. Taken together, the evidence shows that SEQ ID NO:1 is present in the secretory pathway as an N-acetylgalactosaminyl transferase.

For example, SEQ ID NO:2 is 90% identical to mouse seizure-related gene product 6 type 2 precursor (GenBank ID g1139548) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 0.0, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:2 also contains five sushi domains and two CUB domains as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) In addition, SEQ ID NO:2 contains a signal peptide and a single transmembrane domain, as identified by HMMER analysis.

For example, SEQ ID NO:3 is 43% identical to Gallus gallus lysozyme (GenBank ID g4467410) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $5.2e-40$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:3 also contains a G-lysozyme signature domain as determined by searching for statistically significant matches in the BLIMPS analysis of the PRINTS database of conserved protein motifs. (See Table 3.) Data from the PFAM, PRODOM and DOMO databases provide further corroborative evidence that SEQ ID NO:3 is a lysozyme.

For example, SEQ ID NO:17 has a signal peptide, as determined by SPScan and hidden Markov model (HMM) based analyses. SEQ ID NO:17 is 86% identical to human immunoglobulin lambda light chain (GenBank ID g33702) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $2.2e-106$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:17 also contains an immunoglobulin domain as determined by searching for statistically significant matches in the HMM-based PFAM database of conserved protein family domains. (See Table 3.) Data from

BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:17 is a secreted immunoglobulin. The available evidence shows that SEQ ID NO:19 is also a secreted immunoglobulin.

For example, SEQ ID NO:38 shows 95% identity to human immunoglobulin lambda light chain (GenBank ID g33718) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $5.2e-114$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:38 also contains an immunoglobulin domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.)

Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:38 is a secreted protein, and more specifically an immunoglobulin. SEQ ID NO:4-16, SEQ ID NO:18-37, and SEQ ID NO:39-44 were analyzed and annotated in a similar manner. The algorithms and parameters for the analysis of SEQ ID NO:1-44 are described in Table 7.

As shown in Table 4, the full length polynucleotide sequences of the present invention were assembled using cDNA sequences or coding (exon) sequences derived from genomic DNA, or any combination of these two types of sequences. Columns 1 and 2 list the polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and the corresponding Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) for each polynucleotide of the invention. Column 3 shows the length of each polynucleotide sequence in basepairs. Column 4 lists fragments of the polynucleotide sequences which are useful, for example, in hybridization or amplification technologies that identify SEQ ID NO:45-88 or that distinguish between SEQ ID NO:45-88 and related polynucleotide sequences. Column 5 shows identification numbers corresponding to cDNA sequences, coding sequences (exons) predicted from genomic DNA, and/or sequence assemblages comprised of both cDNA and genomic DNA. These sequences were used to assemble the full length polynucleotide sequences of the invention. Columns 6 and 7 of Table 4 show the nucleotide start (5') and stop (3') positions of the cDNA and/or genomic sequences in column 5 relative to their respective full length sequences.

The identification numbers in Column 5 of Table 4 may refer specifically, for example, to Incyte cDNAs along with their corresponding cDNA libraries. For example, 6735891H1 is the identification number of an Incyte cDNA sequence, and LIVRTUT13 is the cDNA library from which it is derived. Incyte cDNAs for which cDNA libraries are not indicated were derived from pooled cDNA libraries (e.g., 71013085V1). Alternatively, the identification numbers in column 5 may refer to GenBank cDNAs or ESTs (e.g., g1496797) which contributed to the assembly of the full length polynucleotide sequences. Alternatively, the identification numbers in column 5 may refer to coding regions predicted by Genscan analysis of genomic DNA. The Genscan-predicted coding sequences

may have been edited prior to assembly. (See Example IV.) Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon stitching" algorithm. (See Example V.) Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon-stretching" algorithm. (See Example V.) In some cases, Incyte cDNA coverage redundant with the sequence coverage shown in column 5 was obtained to confirm the final consensus polynucleotide sequence, but the relevant Incyte cDNA identification numbers are not shown.

Table 5 shows the representative cDNA libraries for those full length polynucleotide sequences which were assembled using Incyte cDNA sequences. The representative cDNA library is the Incyte cDNA library which is most frequently represented by the Incyte cDNA sequences which were used to assemble and confirm the above polynucleotide sequences. The tissues and vectors which were used to construct the cDNA libraries shown in Table 5 are described in Table 6.

The invention also encompasses SECP variants. A preferred SECP variant is one which has at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid sequence identity to the SECP amino acid sequence, and which contains at least one functional or structural characteristic of SECP.

The invention also encompasses polynucleotides which encode SECP. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:45-88, which encodes SECP. The polynucleotide sequences of SEQ ID NO:45-88, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses a variant of a polynucleotide sequence encoding SECP. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding SECP. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:45-88 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:45-88. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of SECP.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding SECP, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide

sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring SECP, and all such variations are to be considered as being specifically disclosed.

5 Although nucleotide sequences which encode SECP and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring SECP under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding SECP or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide
10 occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding SECP and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

15 The invention also encompasses production of DNA sequences which encode SECP and SECP derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding SECP or any fragment thereof.

20 Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:45-88 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in
25 “Definitions.”

 Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied Biosystems), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or
30 combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA
35 sequencing system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system

(Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

5 The nucleic acid sequences encoding SECP may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) *PCR Methods Applic.* 2:318-322.)

10 Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) *Nucleic Acids Res.* 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom,

15 M. et al. (1991) *PCR Methods Applic.* 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) *Nucleic Acids Res.* 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries

20 (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of

25 about 68°C to 72°C.

 When screening for full length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence

30 into 5' non-transcribed regulatory regions.

 Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the

35 emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate

software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Applied Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

5 In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode SECP may be cloned in recombinant DNA molecules that direct expression of SECP, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express SECP.

10 The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter SECP-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-
15 mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat.
20 Biotechnol. 17:259-264; and Cramer, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of SECP, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired
25 properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of
30 homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding SECP may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucleic Acids
35 Symp. Ser. 7:215-223; and Horn, T. et al. (1980) Nucleic Acids Symp. Ser. 7:225-232.)

Alternatively, SECP itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) *Science* 269:202-204.) Automated synthesis
5 may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems). Additionally, the amino acid sequence of SECP, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid
10 chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) *Methods Enzymol.* 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, supra, pp. 28-53.)

In order to express a biologically active SECP, the nucleotide sequences encoding SECP or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains
15 the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding SECP. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding SECP. Such signals
20 include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding SECP and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be
25 provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression
30 vectors containing sequences encoding SECP and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

35 A variety of expression vector/host systems may be utilized to contain and express sequences

encoding SECP. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al. (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding SECP. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding SECP can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPT1 plasmid (Life Technologies). Ligation of sequences encoding SECP into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of SECP are needed, e.g. for the production of antibodies, vectors which direct high level expression of SECP may be used. For example, vectors containing the strong, inducible SP6 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of SECP. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; and Scorer, C.A. et al. (1994)

Bio/Technology 12:181-184.)

Plant systems may also be used for expression of SECP. Transcription of sequences encoding SECP may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105.)

These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding SECP may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses SECP in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of SECP in cell lines is preferred. For example, sequences encoding SECP can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk*⁻ and *apr*⁻ cells, respectively. (See, e.g., Wigler, M. et

al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g.,

5 Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate

10 luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the

15 sequence encoding SECP is inserted within a marker gene sequence, transformed cells containing sequences encoding SECP can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding SECP under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

20 In general, host cells that contain the nucleic acid sequence encoding SECP and that express SECP may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

25 Immunological methods for detecting and measuring the expression of SECP using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on SECP is preferred, but a

30 competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

35 A wide variety of labels and conjugation techniques are known by those skilled in the art and

may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding SECP include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding SECP, or any fragments thereof, may be cloned into a vector
5 for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for
10 ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding SECP may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence
15 and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode SECP may be designed to contain signal sequences which direct secretion of SECP through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of
20 the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the
25 American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding SECP may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric SECP protein
30 containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of SECP activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG,
35 *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their

cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the SECP encoding sequence and the heterologous protein sequence, so that SECP may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled SECP may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

SECP of the present invention or fragments thereof may be used to screen for compounds that specifically bind to SECP. At least one and up to a plurality of test compounds may be screened for specific binding to SECP. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

In one embodiment, the compound thus identified is closely related to the natural ligand of SECP, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner. (See, e.g., Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which SECP binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the compound can be rationally designed using known techniques. In one embodiment, screening for these compounds involves producing appropriate cells which express SECP, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing SECP or cell membrane fractions which contain SECP are then contacted with a test compound and binding, stimulation, or inhibition of activity of either SECP or the compound is analyzed.

An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with SECP, either in solution or affixed to a solid support, and detecting the binding of SECP to the compound. Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical

libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a solid support.

SECP of the present invention or fragments thereof may be used to screen for compounds that modulate the activity of SECP. Such compounds may include agonists, antagonists, or partial or
5 inverse agonists. In one embodiment, an assay is performed under conditions permissive for SECP activity, wherein SECP is combined with at least one test compound, and the activity of SECP in the presence of a test compound is compared with the activity of SECP in the absence of the test compound. A change in the activity of SECP in the presence of the test compound is indicative of a compound that modulates the activity of SECP. Alternatively, a test compound is combined with an
10 in vitro or cell-free system comprising SECP under conditions suitable for SECP activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of SECP may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

In another embodiment, polynucleotides encoding SECP or their mammalian homologs may
15 be “knocked out” in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the
20 gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic
25 Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

30 Polynucleotides encoding SECP may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

35 Polynucleotides encoding SECP can also be used to create “knockin” humanized animals

(pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding SECP is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and
 5 treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress SECP, e.g., by secreting SECP in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) *Biotechnol. Annu. Rev.* 4:55-74).

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists
 10 between regions of SECP and secreted proteins. In addition, the expression of SECP is closely associated with reproductive, endocrine, immune system, gastrointestinal, fibroblastic, lung, brain and neurological tissue. Therefore, SECP appears to play a role in cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, and developmental disorders. In the treatment of disorders associated with increased SECP expression or activity, it is desirable to
 15 decrease the expression or activity of SECP. In the treatment of disorders associated with decreased SECP expression or activity, it is desirable to increase the expression or activity of SECP.

Therefore, in one embodiment, SECP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of SECP. Examples of such disorders include, but are not limited to, a cell proliferative
 20 disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia,
 25 gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-
 30 candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or
 35 pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's

syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic
 lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner
 syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial,
 fungal, parasitic, protozoal, and helminthic infections, and trauma; a cardiovascular disorder such as
 5 congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive
 heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid
 aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart
 disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus
 erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart
 10 disease, congenital heart disease, complications of cardiac transplantation, arteriovenous fistula,
 atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose
 veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis,
 balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery; congenital lung
 anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary
 15 hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive
 pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease,
 emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and
 mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases,
 pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis,
 20 hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia,
 diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary
 hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar
 proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax,
 pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung
 25 transplantation; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke,
 cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's
 disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron
 disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple
 sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural
 30 empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral
 central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and
 Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases
 of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis,
 encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central
 35 nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic

nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD),
5 akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia and seizures; and a developmental disorder such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia,
10 genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss.

15 In another embodiment, a vector capable of expressing SECP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of SECP including, but not limited to, those described above.

In a further embodiment, a composition comprising a substantially purified SECP in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent
20 a disorder associated with decreased expression or activity of SECP including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of SECP may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of SECP including, but not limited to, those listed above.

25 In a further embodiment, an antagonist of SECP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of SECP. Examples of such disorders include, but are not limited to, those cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, and developmental disorders described above. In one aspect, an antibody which specifically binds SECP may be used directly as an antagonist or indirectly as a
30 targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express SECP.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding SECP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of SECP including, but not limited to, those described above.

35 In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary

sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of SECP may be produced using methods which are generally known in the art. In particular, purified SECP may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind SECP. Antibodies to SECP may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with SECP or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to SECP have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches of SECP amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to SECP may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. USA 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc.

Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce SECP-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton, D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. USA 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for SECP may also be generated. For example, such fragments include, but are not limited to, $F(ab')_2$ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the $F(ab')_2$ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between SECP and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering SECP epitopes is generally used, but a competitive binding assay may also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for SECP. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of SECP-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple SECP epitopes, represents the average affinity, or avidity, of the antibodies for SECP. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular SECP epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the SECP-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of SECP, preferably in active form, from the

antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to
5 determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of SECP-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g.,
10 Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding SECP, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding
15 SECP. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding SECP. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered
20 intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) J. Allergy Clin. Immunol. 102(3):469-475; and Scanlon, K.J. et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) Blood
25 76:271; Ausubel, supra; Uckert, W. and W. Walther (1994) Pharmacol. Ther. 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) Br. Med. Bull. 51(1):217-225; Boado, R.J. et al. (1998) J. Pharm. Sci. 87(11):1308-1315; and Morris, M.C. et al. (1997) Nucleic Acids Res. 25(14):2730-2736.)

30 In another embodiment of the invention, polynucleotides encoding SECP may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) Science 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency
35 (Blaese, R.M. et al. (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475),

cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassamias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) *Science* 270:404-410; Verma, I.M. and N. Somia (1997) *Nature* 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) *Nature* 335:395-396; Poeschla, E. et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in SECP expression or regulation causes disease, the expression of SECP from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in SECP are treated by constructing mammalian expression vectors encoding SECP and introducing these vectors by mechanical means into SECP-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) *Annu. Rev. Biochem.* 62:191-217; Ivics, Z. (1997) *Cell* 91:501-510; Boulay, J-L. and H. Récipon (1998) *Curr. Opin. Biotechnol.* 9:445-450).

Expression vectors that may be effective for the expression of SECP include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). SECP may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) *Proc. Natl. Acad. Sci. USA* 89:5547-5551; Gossen, M. et al. (1995) *Science* 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) *Curr. Opin. Biotechnol.* 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra)), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding SECP from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID

TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al. (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to SECP expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding SECP under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) *J. Virol.* 61:1647-1650; Bender, M.A. et al. (1987) *J. Virol.* 61:1639-1646; Adam, M.A. and A.D. Miller (1988) *J. Virol.* 62:3802-3806; Dull, T. et al. (1998) *J. Virol.* 72:8463-8471; Zufferey, R. et al. (1998) *J. Virol.* 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) *J. Virol.* 71:7020-7029; Bauer, G. et al. (1997) *Blood* 89:2259-2267; Bonyhadi, M.L. (1997) *J. Virol.* 71:4707-4716; Ranga, U. et al. (1998) *Proc. Natl. Acad. Sci. USA* 95:1201-1206; Su, L. (1997) *Blood* 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding SECP to cells which have one or more genetic abnormalities with respect to the expression of SECP. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) *Transplantation* 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999)

Annu. Rev. Nutr. 19:511-544 and Verma, I.M. and N. Somia (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding SECP to target cells which have one or more genetic abnormalities with respect to the expression of SECP. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing SECP to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) J. Virol. 73:519-532 and Xu, H. et al. (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding SECP to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and K.-J. Li (1998) Curr. Opin. Biotechnol. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting the coding sequence for SECP into the alphavirus genome in place of the capsid-coding region results in the production of a large number of SECP-coding RNAs and the synthesis of high levels of SECP in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will

allow the introduction of SECP into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding SECP.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding SECP. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible

modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding SECP. Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased SECP expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding SECP may be therapeutically useful, and in the treatment of disorders associated with decreased SECP expression or activity, a compound which specifically promotes expression of the polynucleotide encoding SECP may be therapeutically useful.

At least one, and up to a plurality, of test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding SECP is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an *in vitro* cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding SECP are assayed by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding SECP. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to a test compound indicates that the test compound is effective in altering the expression of the

polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a Schizosaccharomyces pombe gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a
5 combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruice, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruice, T.W. et al. (2000) U.S. Patent No. 6,022,691).

10 Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat.
15 Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

An additional embodiment of the invention relates to the administration of a composition
20 which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such compositions may consist of SECP, antibodies to SECP, and mimetics, agonists, antagonists, or inhibitors of SECP.

25 The compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Compositions for pulmonary administration may be prepared in liquid or dry powder form.
30 These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton,
35 J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration

without needle injection, and obviates the need for potentially toxic penetration enhancers.

Compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

5 Specialized forms of compositions may be prepared for direct intracellular delivery of macromolecules comprising SECP or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, SECP or a fragment thereof may be joined to a short cationic N-terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to
10 transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys, or pigs. An animal model may also be used to determine the appropriate concentration
15 range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example SECP or fragments thereof, antibodies of SECP, and agonists, antagonists or inhibitors of SECP, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by
20 standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED₅₀ (the dose therapeutically effective in 50% of the population) or LD₅₀ (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD₅₀/ED₅₀ ratio. Compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are
25 used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED₅₀ with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the
30 subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting compositions may be administered every 3 to 4 days, every week,
35 or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind SECP may be used for the diagnosis of disorders characterized by expression of SECP, or in assays to monitor patients being treated with SECP or agonists, antagonists, or inhibitors of SECP. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for SECP include methods which utilize the antibody and a label to detect SECP in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring SECP, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of SECP expression. Normal or standard values for SECP expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibodies to SECP under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of SECP expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding SECP may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of SECP may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of SECP, and to monitor regulation of SECP levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding SECP or closely related molecules may be used to identify nucleic acid sequences which encode SECP. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding SECP, allelic variants, or related

sequences.

Probes may also be used for the detection of related sequences, and may have at least 50% sequence identity to any of the SECP encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:45-88 or from
5 genomic sequences including promoters, enhancers, and introns of the SECP gene.

Means for producing specific hybridization probes for DNAs encoding SECP include the cloning of polynucleotide sequences encoding SECP or SECP derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA
10 polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding SECP may be used for the diagnosis of disorders associated with expression of SECP. Examples of such disorders include, but are not limited to, a
15 cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall
20 bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune
25 polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis,
30 myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a
35 cardiovascular disorder such as congestive heart failure, ischemic heart disease, angina pectoris,

myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, complications of cardiac transplantation, arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery; congenital lung anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia,

diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia and seizures; and a developmental disorder such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss. The polynucleotide sequences encoding SECP may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered SECP expression. Such qualitative or quantitative methods are well known in the art.

15 In a particular aspect, the nucleotide sequences encoding SECP may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding SECP may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding SECP in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

25 In order to provide a basis for the diagnosis of a disorder associated with expression of SECP, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding SECP, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

35 Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the

patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding SECP may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding SECP, or a fragment of a polynucleotide complementary to the polynucleotide encoding SECP, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding SECP may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from the polynucleotide sequences encoding SECP are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSSCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed *in silico* SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

Methods which may also be used to quantify the expression of SECP include radiolabeling or

biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described below. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

In another embodiment, SECP, fragments of SECP, or antibodies specific for SECP may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect gene expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile the expression of the polynucleotides of the present invention may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed

5 molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain

10 expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of

15 gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in

20 toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present

25 invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of the polypeptide sequences of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global

30 pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the

35 separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are

separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, supra). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for SECP to quantify the levels of SECP expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-111; Mendoze, L.G. et al. (1999) *Biotechniques* 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing

the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are
5 incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

10 Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are
15 well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

In another embodiment of the invention, nucleic acid sequences encoding SECP may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be
20 preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1
25 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP).
30 (See, for example, Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding SECP on a
35 physical map and a specific disorder, or a predisposition to a specific disorder, may help define the

region of DNA associated with that disorder and thus may further positional cloning efforts.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the gene or genes responsible for a disease or syndrome have been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the instant invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, SECP, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between SECP and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with SECP, or fragments thereof, and washed. Bound SECP is then detected by methods well known in the art. Purified SECP can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding SECP specifically compete with a test compound for binding SECP. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with SECP.

In additional embodiments, the nucleotide sequences which encode SECP may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific

embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/214,601, U.S. Ser. No. 60/212,890, U.S. Ser. No. 60/222,372, U.S. Ser.

5 No. 60/213,466, U.S. Ser. No. 60/231,435, and U.S. Ser. No. 60/232,889, are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

10 Incyte cDNAs were derived from cDNA libraries described in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA) and shown in Table 4, column 5. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or
15 extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A)+ RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN,
20 Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP
25 vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, *supra*, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-
30 1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSPORT1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), or pINCY (Incyte Genomics, Palo Alto
35 CA), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells

including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids obtained as described in Example I were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows. Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Applied Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

The polynucleotide sequences derived from Incyte cDNAs were validated by removing vector, linker, and poly(A) sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The Incyte cDNA sequences or translations thereof were then queried against a selection of public

databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and hidden Markov model (HMM)-based protein family databases such as PFAM. (HMM is a probabilistic approach which analyzes consensus primary structures of gene families. See, for example, Eddy, S.R. (1996) Curr. Opin. Struct. Biol. 6:361-365.)

5 The queries were performed using programs based on BLAST, FASTA, BLIMPS, and HMMER. The Incyte cDNA sequences were assembled to produce full length polynucleotide sequences. Alternatively, GenBank cDNAs, GenBank ESTs, stitched sequences, stretched sequences, or Genscan-predicted coding sequences (see Examples IV and V) were used to extend Incyte cDNA assemblages to full length. Assembly was performed using programs based on Phred, Phrap, and

10 Consed, and cDNA assemblages were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length polypeptide sequences. Alternatively, a polypeptide of the invention may begin at any of the methionine residues of the full length translated polypeptide. Full length polypeptide sequences were subsequently analyzed by querying against databases such as the

15 GenBank protein databases (genpept), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and hidden Markov model (HMM)-based protein family databases such as PFAM. Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the

20 CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 7 summarizes the tools, programs, and algorithms used for the analysis and assembly of Incyte cDNA and full length sequences and provides applicable descriptions, references, and threshold parameters. The first column of Table 7 shows the tools, programs, and algorithms used,

25 the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score or the lower the probability value, the greater the identity between two sequences).

30 The programs described above for the assembly and analysis of full length polynucleotide and polypeptide sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:45-88. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies are described in Table 4, column 4.

IV. Identification and Editing of Coding Sequences from Genomic DNA

35 Putative secreted proteins were initially identified by running the Genscan gene identification

program against public genomic sequence databases (e.g., gbpri and gbhtg). Genscan is a general-purpose gene identification program which analyzes genomic DNA sequences from a variety of organisms (See Burge, C. and S. Karlin (1997) J. Mol. Biol. 268:78-94, and Burge, C. and S. Karlin (1998) Curr. Opin. Struct. Biol. 8:346-354). The program concatenates predicted exons to form an assembled cDNA sequence extending from a methionine to a stop codon. The output of Genscan is a FASTA database of polynucleotide and polypeptide sequences. The maximum range of sequence for Genscan to analyze at once was set to 30 kb. To determine which of these Genscan predicted cDNA sequences encode secreted proteins, the encoded polypeptides were analyzed by querying against PFAM models for secreted proteins. Potential secreted proteins were also identified by homology to Incyte cDNA sequences that had been annotated as secreted proteins. These selected Genscan-predicted sequences were then compared by BLAST analysis to the genpept and gbpri public databases. Where necessary, the Genscan-predicted sequences were then edited by comparison to the top BLAST hit from genpept to correct errors in the sequence predicted by Genscan, such as extra or omitted exons. BLAST analysis was also used to find any Incyte cDNA or public cDNA coverage of the Genscan-predicted sequences, thus providing evidence for transcription. When Incyte cDNA coverage was available, this information was used to correct or confirm the Genscan predicted sequence. Full length polynucleotide sequences were obtained by assembling Genscan-predicted coding sequences with Incyte cDNA sequences and/or public cDNA sequences using the assembly process described in Example III. Alternatively, full length polynucleotide sequences were derived entirely from edited or unedited Genscan-predicted coding sequences.

V. Assembly of Genomic Sequence Data with cDNA Sequence Data

"Stitched" Sequences

Partial cDNA sequences were extended with exons predicted by the Genscan gene identification program described in Example IV. Partial cDNAs assembled as described in Example III were mapped to genomic DNA and parsed into clusters containing related cDNAs and Genscan exon predictions from one or more genomic sequences. Each cluster was analyzed using an algorithm based on graph theory and dynamic programming to integrate cDNA and genomic information, generating possible splice variants that were subsequently confirmed, edited, or extended to create a full length sequence. Sequence intervals in which the entire length of the interval was present on more than one sequence in the cluster were identified, and intervals thus identified were considered to be equivalent by transitivity. For example, if an interval was present on a cDNA and two genomic sequences, then all three intervals were considered to be equivalent. This process allows unrelated but consecutive genomic sequences to be brought together, bridged by cDNA sequence. Intervals thus identified were then "stitched" together by the stitching algorithm in the order that they appear along their parent sequences to generate the longest possible sequence, as well as sequence variants.

Linkages between intervals which proceed along one type of parent sequence (cDNA to cDNA or genomic sequence to genomic sequence) were given preference over linkages which change parent type (cDNA to genomic sequence). The resultant stitched sequences were translated and compared by BLAST analysis to the genpept and gbpi public databases. Incorrect exons predicted by Genscan were corrected by comparison to the top BLAST hit from genpept. Sequences were further extended with additional cDNA sequences, or by inspection of genomic DNA, when necessary.

“Stretched” Sequences

Partial DNA sequences were extended to full length with an algorithm based on BLAST analysis. First, partial cDNAs assembled as described in Example III were queried against public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases using the BLAST program. The nearest GenBank protein homolog was then compared by BLAST analysis to either Incyte cDNA sequences or GenScan exon predicted sequences described in Example IV. A chimeric protein was generated by using the resultant high-scoring segment pairs (HSPs) to map the translated sequences onto the GenBank protein homolog. Insertions or deletions may occur in the chimeric protein with respect to the original GenBank protein homolog. The GenBank protein homolog, the chimeric protein, or both were used as probes to search for homologous genomic sequences from the public human genome databases. Partial DNA sequences were therefore “stretched” or extended by the addition of homologous genomic sequences. The resultant stretched sequences were examined to determine whether it contained a complete gene.

VI. Chromosomal Mapping of SECP Encoding Polynucleotides

The sequences which were used to assemble SEQ ID NO:45-88 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:45-88 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon were used to determine if any of the clustered sequences had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location.

Map locations are represented by ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome’s p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation

hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

5 In this manner, SEQ ID NO:48 was mapped to chromosome 15 within the interval from 72.3 to 77.4 centiMorgans.

In this manner, SEQ ID NO:54 was mapped to chromosome 20 within the interval from 6.20 to 9.40 centiMorgans. SEQ ID NO:61 was mapped to chromosome 22 within the interval from 0.00 to 19.50 centiMorgans.

10 In this manner, SEQ ID NO:82 was mapped to chromosome 22 within the interval from 0.0 to 19.5 centiMorgans. SEQ ID NO:85 was mapped to chromosome 12 within the interval from 84.7 to 92.5 centiMorgans and from 137.5 to 145.7 centiMorgans. More than one map location is reported for SEQ ID NO:85, indicating that sequences having different map locations were assembled into a single cluster. This situation occurs, for example, when sequences having strong similarity, but not
15 complete identity, are assembled into a single cluster.

In this manner, SEQ ID NO:66 was mapped to chromosome 16 within the interval from 65.60 to 72.60 centiMorgans. In this manner, SEQ ID NO:67 was mapped to chromosome 11 within the interval from 59.50 to 65.00 centiMorgans. In this manner, SEQ ID NO:69 was mapped to chromosome 6 within the interval from 132.70 to 144.40 centiMorgans.

20 VII. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, *supra*, ch. 7; Ausubel (1995) *supra*, ch. 4 and 16.)

25 Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

30

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum \{length(Seq. 1), length(Seq. 2)\}}}$$

The product score takes into account both the degree of similarity between two sequences and the
35 length of the sequence match. The product score is a normalized value between 0 and 100, and is

calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by
5 gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the
10 other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

Alternatively, polynucleotide sequences encoding SECP are analyzed with respect to the tissue sources from which they were derived. For example, some full length sequences are assembled, at least in part, with overlapping Incyte cDNA sequences (see Example III). Each cDNA
15 sequence is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following organ/tissue categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed;
20 or urinary tract. The number of libraries in each category is counted and divided by the total number of libraries across all categories. Similarly, each human tissue is classified into one of the following disease/condition categories: cancer, cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled, and other, and the number of libraries in each category is counted and divided by the total number of libraries across all categories. The resulting percentages reflect the tissue- and
25 disease-specific expression of cDNA encoding SECP. cDNA sequences and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

VIII. Extension of SECP Encoding Polynucleotides

Full length polynucleotide sequences were also produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One
30 primer was synthesized to initiate 5' extension of the known fragment, and the other primer was synthesized to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would
35 result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and 2-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μ l PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA

recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

5 In like manner, full length polynucleotide sequences are verified using the above procedure or are used to obtain 5' regulatory sequences using the above procedure along with oligonucleotides designed for such extension, and an appropriate genomic library.

IX. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:45-88 are employed to screen cDNAs,
10 genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ -³²P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase
15 (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

20 The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and
25 compared.

X. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, supra), mechanical microspotting technologies, and derivatives thereof. The substrate in each of the
30 aforementioned technologies should be uniform and solid with a non-porous surface (Skena (1999), supra). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to
35 those of ordinary skill in the art and may contain any appropriate number of elements. (See, e.g.,

Schena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645; Marshall, A. and J. Hodgson (1998) Nat. Biotechnol. 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/μl oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/μl RNase inhibitor, 500 μM dATP, 500 μM dGTP, 500 μM dTTP, 40 μM dCTP, 40 μM dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA. After incubation at 37° C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85° C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μl 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 μg. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia

Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR

5 Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 µl of the array element DNA, at an average
10 concentration of 100 ng/µl, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate
15 buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60°C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 µl of sample mixture consisting of 0.2 µg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample
20 mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 µl of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash
25 buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines
30 at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the sample mixture at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

XI. Complementary Polynucleotides

Sequences complementary to the SECP-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring SECP. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of SECP. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the SECP-encoding transcript.

XII. Expression of SECP

Expression and purification of SECP is achieved using bacterial or virus-based expression systems. For expression of SECP in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express SECP upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of SECP in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding SECP by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, SECP is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from SECP at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch. 10 and 16). Purified SECP obtained by these methods can be used directly in the assays shown in Examples XVI and XVII, where applicable.

XIII. Functional Assays

SECP function is assessed by expressing the sequences encoding SECP at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include PCMV SPORT (Life Technologies) and PCR3.1 (Invitrogen, Carlsbad CA), both of which

contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of SECP on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding SECP and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding SECP and other genes of interest can be analyzed by northern analysis or microarray techniques.

XIV. Production of SECP Specific Antibodies

SECP substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the SECP amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, ch. 11.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A

peptide synthesizer (Applied Biosystems) using FMOC chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, supra.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for anti-peptide and anti-SECP activity by, for example, binding the peptide or SECP to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XV. Purification of Naturally Occurring SECP Using Specific Antibodies

Naturally occurring or recombinant SECP is substantially purified by immunoaffinity chromatography using antibodies specific for SECP. An immunoaffinity column is constructed by covalently coupling anti-SECP antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing SECP are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of SECP (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/SECP binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and SECP is collected.

XVI. Identification of Molecules Which Interact with SECP

SECP, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled SECP, washed, and any wells with labeled SECP complex are assayed. Data obtained using different concentrations of SECP are used to calculate values for the number, affinity, and association of SECP with the candidate molecules.

Alternatively, molecules interacting with SECP are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) Nature 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (Clontech).

SECP may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

XVII. Demonstration of SECP Activity

An assay for the determination of SECP activity consists of an enzyme reaction mixture consisting of 25 mM Tris-HCl (pH 7.4), 0.25% Triton X-100, 5 mM MnCl₂, 5 mM CDP-choline, 5

mM 2-mercaptoethanol, 0.05 mM UDP-[¹⁴C]GalNAc (4,000 cpm/nmol), 250 μM peptide, and varying amounts of SECP in a final volume of 100 μl. The reaction mixture is incubated for 10 min. at 37° C followed by Dowex 1 ion exchange (formic acid form) chromatography. Eluted peptide-containing fractions are subjected to scintillation counting. The amount of [¹⁴C]GalNAc present in the peptide-
5 containing fractions is proportional to SECP activity. Confirmation of substrate and SECP source can be evaluated by C-18 chromatography (C2C18 3.2 Smart System, Pharmacia Biotech Inc.) to ensure peptide stability and that incorporated [¹⁴C]GalNAc is associated with the peptide (Sørensen, T. et al. (1995) J. Biol. Chem. 270:24166-24173).

Alternatively, an assay for growth stimulating or inhibiting activity of SECP measures the
10 amount of DNA synthesis in Swiss mouse 3T3 cells (McKay, I. and Leigh, I., eds. (1993) Growth Factors: A Practical Approach, Oxford University Press, New York, NY). In this assay, varying amounts of SECP are added to quiescent 3T3 cultured cells in the presence of [³H]thymidine, a radioactive DNA precursor. SECP for this assay can be obtained by recombinant means or from biochemical preparations. Incorporation of [³H]thymidine into acid-precipitable DNA is measured
15 over an appropriate time interval, and the amount incorporated is directly proportional to the amount of newly synthesized DNA. A linear dose-response curve over at least a hundred-fold SECP concentration range is indicative of growth modulating activity. One unit of activity per milliliter is defined as the concentration of SECP producing a 50% response level, where 100% represents maximal incorporation of [³H]thymidine into acid-precipitable DNA.

20 Alternatively, an assay for SECP activity measures the stimulation or inhibition of neurotransmission in cultured cells. Cultured CHO fibroblasts are exposed to SECP. Following endocytic uptake of SECP, the cells are washed with fresh culture medium, and a whole cell voltage-clamped Xenopus myocyte is manipulated into contact with one of the fibroblasts in SECP-free medium. Membrane currents are recorded from the myocyte. Increased or decreased current relative
25 to control values are indicative of neuromodulatory effects of SECP (Morimoto, T. et al. (1995) Neuron 15:689-696).

Alternatively, an assay for SECP activity measures the amount of SECP in secretory, membrane-bound organelles. Transfected cells as described above are harvested and lysed. The lysate is fractionated using methods known to those of skill in the art, for example, sucrose gradient
30 ultracentrifugation. Such methods allow the isolation of subcellular components such as the Golgi apparatus, ER, small membrane-bound vesicles, and other secretory organelles. Immunoprecipitations from fractionated and total cell lysates are performed using SECP-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The concentration of SECP in secretory organelles relative to SECP in total cell lysate is
35 proportional to the amount of SECP in transit through the secretory pathway.

In another alternative, SECP recognizes and precipitates antigen from serum. This activity can be measured by the quantitative precipitin reaction. (Golub, E. S. et al. (1987) Immunology: A Synthesis, Sinauer Associates, Sunderland, MA, pages 113-115.) SECP is isotopically labeled using methods known in the art. Various serum concentrations are added to constant amounts of labeled SECP. SECP-antigen complexes precipitate out of solution and are collected by centrifugation. The amount of precipitable SECP-antigen complex is proportional to the amount of radioisotope detected in the precipitate. The amount of precipitable SECP-antigen complex is plotted against the serum concentration. For various serum concentrations, a characteristic precipitation curve is obtained, in which the amount of precipitable SECP-antigen complex initially increases proportionately with increasing serum concentration, peaks at the equivalence point, and then decreases proportionately with further increases in serum concentration. Thus, the amount of precipitable SECP-antigen complex is a measure of SECP activity which is characterized by sensitivity to both limiting and excess quantities of antigen.

Alternatively, an assay for SECP activity measures the expression of SECP on the cell surface. cDNA encoding SECP is transfected into a non-leukocytic cell line. Cell surface proteins are labeled with biotin (de la Fuente, M.A. et.al. (1997) *Blood* 90:2398-2405). Immunoprecipitations are performed using SECP-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The ratio of labeled immunoprecipitant to unlabeled immunoprecipitant is proportional to the amount of SECP expressed on the cell surface.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID
2101688	1	2101688CD1	45	2101688CB1
5452330	2	5452330CD1	46	5452330CB1
4362432	3	4362432CD1	47	4362432CB1
5308104	4	5308104CD1	48	5308104CB1
3092736	5	3092736CD1	49	3092736CB1
3580257	6	3580257CD1	50	3580257CB1
3634758	7	3634758CD1	51	3634758CB1
4027923	8	4027923CD1	52	4027923CB1
4348533	9	4348533CD1	53	4348533CB1
4521857	10	4521857CD1	54	4521857CB1
4722253	11	4722253CD1	55	4722253CB1
4878134	12	4878134CD1	56	4878134CB1
5050133	13	5050133CD1	57	5050133CB1
5630124	14	5630124CD1	58	5630124CB1
5677286	15	5677286CD1	59	5677286CB1
6436791	16	6436791CD1	60	6436791CB1
1820972	17	1820972CD1	61	1820972CB1
3286805	18	3286805CD1	62	3286805CB1
3506590	19	3506590CD1	63	3506590CB1
003600	20	003600CD1	64	003600CB1
1251534	21	1251534CD1	65	1251534CB1
1402211	22	1402211CD1	66	1402211CB1
1623474	23	1623474CD1	67	1623474CB1
1706443	24	1706443CD1	68	1706443CB1
1748627	25	1748627CD1	69	1748627CB1
1818332	26	1818332CD1	70	1818332CB1
1822832	27	1822832CD1	71	1822832CB1
1832219	28	1832219CD1	72	1832219CB1
1899010	29	1899010CD1	73	1899010CB1
2008768	30	2008768CD1	74	2008768CB1
2070984	31	2070984CD1	75	2070984CB1
2193240	32	2193240CD1	76	2193240CB1
2235177	33	2235177CD1	77	2235177CB1
2416227	34	2416227CD1	78	2416227CB1
2461076	35	2461076CD1	79	2461076CB1
1957517	36	1957517CD1	80	1957517CB1
866038	37	866038CD1	81	866038CB1
3869704	38	3869704CD1	82	3869704CB1
1415179	39	1415179CD1	83	1415179CB1

Table 1 (cont.)

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID
1664792	40	1664792CD1	84	1664792CB1
2079396	41	2079396CD1	85	2079396CB1
5390115	42	5390115CD1	86	5390115CB1
1403326	43	1403326CD1	87	1403326CB1
7690129	44	7690129CD1	88	7690129CB1

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability Score	GenBank Homolog
1	2101688CD1	g971461	1.50E-141	UDP-GalNAc:polypeptide N-acetyl- galactosaminyl transferase [Homo sapiens] (White, T. et al. J. Biol. Chem. (1995) 270(41):24156-65)
2	5452330CD1	g1139548	0	Seizure-related gene product 6 type 2 precursor [Mus musculus] (Shimizu- Nishikawa, K. et al. (1995) Biochem. Biophys. Res. Commun. 216:382-389)
3	4362432CD1	g4467410	5.20E-40	Lysozyme [Gallus gallus] (Nakano, T. & Graf, T. (1992) Oncogene 7:527-534)
4	5308104CD1	g3878261	2.10E-92	Similarity to S. Pombe BEM1/BUD5 [Caenorhabditis elegans]
16	6436791CD1	g13274582	5.00E-39	Thymus atrophy-related protein [Mus musculus]
17	1820972CD1	g33702	2.20E-106	Immunoglobulin lambda light chain [Homo sapiens]
18	3286805CD1	g431420	1.50E-283	Macrophage specific protein MPS1 [Mus musculus] (Spillsbury, K. et al. (1995) Blood 85:1620-1629)
19	3506590CD1	g577056	1.00E-211	C gamma 3 [Homo sapiens]
29	1899010CD1	g13384378	8.00E-43	Putative phosphate translocator [Oryza sativa]
36	1957517CD1	g1572802	2.90E-65	Enterococcus faecalis TRAB [Caenorhabditis elegans]
37	866038CD1	g849238	1.90E-30	Similar to polyposis locus protein 1 [Caenorhabditis elegans]
38	3869704CD1	g33718	5.20E-114	Immunoglobulin lambda light chain [Homo sapiens]
43	1403326CD1	g3983152	8.10E-56	Schlafen3 Lymphoid growth regulatory protein [Mus musculus] (Schwarz, D.A. et al. (1998) Immunity 9:657-668)
44	7690129CD1	g6715117	3.10E-219	MTR1 [Homo sapiens] Melastatin/TRP related protein found in Beckwith- Wiedemann syndrome chromosomal region 11p15.5 (Prawitt, D. et al. (2000) Hum. Mol. Genet. 9:203-216)

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
1	2101688CD1	552	S200 S241 S313 S387 S399 S433 S45 S507 S84 S89 T130 T196 T237 T27 T35 T355 T41 T467 T5 Y408 Y74		Glycosyl transferase: S114-F292 Glycosyl transferase: I147-D157 (P<0.021) PD003162:NACETYLGALACTOSAMINYLTTRANSFERASE TRANSFERASE POLYPEPTIDE ACETYLGALACTOSAMINYLTTRANSFERASE UDPGALNAC:POLYPEPTIDE GLYCOSYLTTRANSFERASE PROTEINUDP PROTEIN UDP N: Q256-P414 ACETYLGALACTOSAMINYLTTRANSFERASE; POLYPEPTIDE; DM03891 I37405 21-571: V26-W547 Signal peptide: M1-R29 Transmembrane domain: L4-W25 Signal cleavage: M1-R29 Signal peptide: M1-G19 Signal peptide: M1-G19 Transmembrane domain: I930-Y947 Sushi domains (SCR repeats): C357-C412, C532-C589, C710-C765, C771-C830, C838-C895 CUB domains: C416-Y524, C593-F701 SEIZURERELATED GENE PRODUCT PRECURSOR SIGNAL TYPE PD024762:H18-A415 PD028803:V911-G984 SUSHI REPEAT DM04887 P33730 1-610: T735-D901, F381-P450, T548-I631 DM04887 P16581 1-609: T732-Y904, L354-P450, E525-P610 DM04887 P27113 1-551: S722-R896, L354-P450	HMMER_PFAM BLIMPS_PFAM BLAST_PRODUM BLAST_DOMO HMMER HMMER SPSCAN HMMER SPSCAN HMMER HMMER_PFAM HMMER_PFAM BLAST_PRODUM BLAST_DOMO
2	5452330CD1	994	S218 S249 S257 S263 S291 S378 S463 S501 S674 S724 S770 S780 S786 S820 S824 S842 S877 S919 S974 T38 T425 T553 T63 T647 T655 T709 T757 T812	N247 N289 N313 N399 N422 N436 N440 N541 N583 N707		

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
3	4362432CD1	212	S181 S190 S211 S26 T153 T16 T188 T45		Signal_cleavage: M1-G19 Signal_peptide: M1-G19 Transglycosylase SLT domain SLT: T82-A202 Pterin 4 alpha carbinolamine dehydratase PF01329: G124-K130 LYSOZYME G SIGNATURE PR00749: G174-D195, D191-S211, C39-M59, N60-Q81, I84-I102, S103-F123, G124-K142, K157-K173 LYSOZYME G 4BETA-N-ACETYLMURAMIDASE GOOSETYPE HYDROLASE PD016787: G38-F212 LYSOZYME G DM07376 P00718 1-184: C39-F212 DM07376 P27042 27-210: G38-F212 Signal_cleavage: M1-G61 Dienelactone hydrolase family DL: P235-H262 Tonb_Dependent_Receptor protein signature M1-S5 PROTEIN INTERGENIC REGION TRANSMEMBRANE OF TRAXFINO PLASMID SECTION BEM46 KRE1HXT14 PD009919: T113-S216 HYPOTHETICAL 34.9 KD PROTEIN HYPOTHETICAL PROTEIN PD126088: F234-S302 K04G2.2 PROTEIN PD126091: N2-E40 Signal_peptide: M1-A19 Signal_cleavage: M1-G22	SPSCAN HMMER HMMER_PFAM BLIMPS_PFAM BLIMPS_PRINTS BLAST_PRODROM BLAST_DOMO
4	5308104CD1	308	S154 S158 S201 S5 S79 S93 T225 T253 T55 T71 Y163		Signal_cleavage: M1-G61 Dienelactone hydrolase family DL: P235-H262 Tonb_Dependent_Receptor protein signature M1-S5 PROTEIN INTERGENIC REGION TRANSMEMBRANE OF TRAXFINO PLASMID SECTION BEM46 KRE1HXT14 PD009919: T113-S216 HYPOTHETICAL 34.9 KD PROTEIN HYPOTHETICAL PROTEIN PD126088: F234-S302 K04G2.2 PROTEIN PD126091: N2-E40 Signal_peptide: M1-A19 Signal_cleavage: M1-G22	SPSCAN HMMER_PFAM MOTIFS BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM HMMER SPSCAN
5	3092736CD1	328	S116 S121 S148 S155 S159 S221 S278 S317 S52 T57		Signal_cleavage: M1-A21 Signal_cleavage: M1-G17 Signal_peptide: M1-R37	SPSCAN SPSCAN HMMER
6	3580257CD1	69	T58		Signal_cleavage: M1-A21	SPSCAN
7	3634758CD1	158	T34 T55		Signal_cleavage: M1-G17	SPSCAN
8	4027923CD1	463	S113 S175 S360 S45 S86 T132 T157		Signal_peptide: M1-R37	HMMER
9	4348533CD1	648	S179 S244 S265 S303 S327 S329 S337 S389 S551 S571 S586 S620 S639 T276 T425 T470 T49 T496 T599 T606	N161 N310 N313	Signal_cleavage: M1-N68 Leucine_Zipper: L178-L199	SPSCAN MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
10	4521857CD1	130	S10 T75		Signal_cleavage: M1-A38 Transmembrane domain: G20-Y40	SPSCAN HMMER
11	4722253CD1	279	S171 S230 S73 S77 T107 T243 T268	N191 N266 N71	Signal_cleavage: M1-A62	SPSCAN
12	4878134CD1	458	S15 S229 S279 S321 S340 S381 S439 T127 T93	N198 N259 N319	Transmembrane domain: L22-L41 Rgd: R118-D120	HMMER MOTIFS
13	5050133CD1	173	S130 S50		Signal_cleavage: M1-A31	SPSCAN
14	5630124CD1	335	S142 S191 S219 S295 S302 S324 S67 S74 T104 T190 T225 T243 T252 T275 T292 Y332		Signal_peptide: M1-A39 Signal_cleavage: M1-G36	HMMER SPSCAN
15	5677286CD1	71	T42		Signal_peptide: M1-A34	HMMER
16	6436791CD1	148	S143 S16 T18	N31	Signal_cleavage: M1-A66	SPSCAN
17	1820972CD1	231	S140 S206 S219 S74		Transmembrane domain: L109-F126 Signal_peptide: M1-S20 Signal_cleavage: M1-G16 do IMMUNOGLOBULIN; IG; HISTOCOMPATIBILITY; MAJOR DM02680 A39949 1-118: V115-C230 MHC FRAMEWORK DOMAIN DM00397 S24319 1-128: M1-P128 B-cell mu chain associated 8HS20 protein precursor PD174509: L23-V108 Immunoglobulins and MHC protein signature BL00290: T150-S172, Y210-P227 Immunoglobulins and MHC protein signature ig_mhc.prf: K190-S231 Immunoglobulin domain ig: G34-V108, A146-V214 Ig_Mhc: Y210-H216	HMMER HMMER HMMER SPSCAN BLAST_DOMO BLAST_DOMO BLAST_PRODOM BLIMPS_BLOCKS PROFILESKAN HMMER_PFAM MOTIFS
18	3286805CD1	716	S179 S231 S268 S331 S484 S553 S92 T147 T158 T207 T440 T447 T613 T679 T707 S19 T72 Y67 Y78	N185 N255 N269 N272 N375	Signal_peptide: M1-P22 Transmembrane domain: S653-I676 Signal_cleavage: M1-A17	HMMER HMMER SPSCAN

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
19	3506590CD1	519	S104 S144 S339 S36 S396 S426 S75 S82 T234 T371 T509 Y113 Y368	N369	Signal_cleavage: M1-C19 Signal_peptide: M1-C19 MHC HINGE DOMAIN DM01060 P01862 1-329: S142-K275, R285-G518 IG GAMMA3 CHAIN C REGION HEAVY DISEASE PROTEIN HDC IMMUNOGLOBULIN GLYCOPROTEIN PD028815: E241-G309 Immunoglobulins and MHC protein signature BL00290: S436-Q458, F495-S512 Immunoglobulins and MHC protein signature ig_mhc.prf: T371-V420, D473-K519 Immunoglobulin domain ig: G34-R117, G162-V227, S326-V395, K432-V499 Ig_Mhc: Y223-H229, F495-H501 Signal_peptide:M6-L26 Signal_cleavage:M1-A28 Transmembrane domain:L12-N30 Leucine zipper motif:L12-L33 Signal_peptide:M43-M67 Transmembrane domain:A250-I267 Signal_peptide:M345-H366	SPSCAN HMMER BLAST_DOMO BLAST_PRODOM BLIMPS_BLOCKS PROFILESKAN HMMER_PFAM MOTIFS HMMER HMMER HMMER
20	003600CD1	172	T73 T71 T90 S128			
21	1251534CD1	314				
22	1402211CD1	542	S430 S131 S137 S186 T273 S371 S395 T417 T426 S454 T34 S44 T114 S319 T509	N2 N359 N408 N409 N424 N529		
23	1623474CD1	715	T66 S121 T216 T334 S376 S380 S386 T436 T475 T524 S543 S585 S586 S647 T659 S704 T709 S5 T108 T222 T279 S372 S390 S395 S406 S429 S445 S455 S503 S590 S639	N238 N335 N61 N239 N461 N465 N535	Rgd motif:R377-D379 Signal peptide:M187-V211 Transmembrane domain:I49-F67	MOTIFS HMMER HMMER

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
24	1706443CD1	469	Y228 T70 S102 S158 T283 T337 S364 T37 S168 S179 T182 S292 S316 S359 T436 S462 S466		Rgd motif: R119-D121 Signal peptide: M1-G24 Signal cleavage: M1-G24	MOTIFS HMMER SPSCAN
25	1748627CD1	274	T9 T90 T237 S241 S248 S62 S100 S136 S191 T35	N254 N270	Signal cleavage: M1-A59	SPSCAN
26	1818332CD1	154	S120 S136 T41 S56 T76 S98 S138		Signal cleavage: M1-A26	SPSCAN
27	1822832CD1	102	T13 T19	N16	Signal peptide: M34-P57 Rgd motif: R21-D23	HMMER MOTIFS
28	1832219CD1	113			Signal cleavage: M1-G29	SPSCAN
29	1899010CD1	313	S127 S145 S300	N43 N92 N97 N98 N238	Signal peptide: M194-G211 Transmembrane domain: H11-I35, F151-V171, W219-V237	HMMER HMMER
30	2008768CD1	195	S35 S49 T64 S78 S117		Signal peptide: M121-A139 Transmembrane domain: L95-R116, N122-L145	HMMER HMMER
31	2070984CD1	350	T77	N294	Signal cleavage: M1-A66 Transmembrane domain: Y40-G61, M84-C102, V173-V191	SPSCAN HMMER
32	2193240CD1	360	Y327 S220 S221 S7 S38 T135 S318	N159 N207 N218 N142	Signal peptide: M101-S121	HMMER
33	2235177CD1	559	S301 S412 S520 T11 T27 S29 S42 T76 T156 S165 S252 T277 T303 T336 T462 T120 T121 S292 S322 S397 T407 T418	N70 N171 N357 N325 N417	Signal peptide: M191-A209	HMMER
34	2416227CD1	198	S136 S167 S137	N38 N68 N75 N92	Signal peptide: M1-S18 Signal cleavage: M1-S18 Transmembrane domain: F113-L133	HMMER SPSCAN HMMER
35	2461076CD1	73	T40 S25 T41		Signal peptide: M1-G21 Signal cleavage: M1-V19	HMMER SPSCAN

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
36	1957517CD1	376	S87 T94 T196 S257 S326 S38 S224 S280	N36 N307		MOTIFS
37	866038CD1	216	T11 T15 S59 S114 S142 T146 S167 S172 S107 S157 T200 T209 S210 Y68		Leucine zipper motif:L129-L150 Signal cleavage:M1-G45	MOTIFS SPSCAN
38	3869704CD1	233	S112 S142 S208 S221 S74 T15 T36		Signal peptide: M1-A19 Signal cleavage: M1-A19 Immunoglobulins and major histocompatibility domains: Y212-H218 Immunoglobulins and major histocompatibility domains ig_mhc.prf: N191-S233 Immunoglobulins and major histocompatibility domains BL00290: T152-S174, Y212-P229 Immunoglobulin domain ig: G34-S108, A148-V216 IMMUNOGLOBULIN; MAJOR HISTOCOMPATIBILITY DM02680 A39949 1-118: V117-C232 Immunoglobulin framework domain DM00397 S30526S 1-119: S20-F139 IMMUNOGLOBULIN DM00001 S29258 119-206: T137-K225	HMMER SPSCAN MOTIFS PROFILES SCAN BLIMPS_BLOCKS HMMER_PFAM BLAST_DOMO BLAST_DOMO BLAST_DOMO
39	1415179CD1	163	T104 T86		Signal cleavage: M1-S35 Mitochondrial Carrier: P134-M142 ZP receptor-type domain BL00682: C50-L56 Signal peptide M1-D18	SPSCAN MOTIFS BLIMPS_BLOCKS HMMER
40	1664792	235	S33 T70 T93 T94 T121 T224			
41	2079396CD1	94	S21 S45		Signal cleavage: M1-S42 GTP-binding elongation factors signature efactor_gtp.prf: M1-S52 Peroxidases signatures peroxidase_2.prf: I37-W90	SPSCAN PROFILES SCAN PROFILES SCAN
42	5390115CD1	85	S3 S8 T16 T63 T81		Signal cleavage: M1-S47 Transmembrane domain: Y24-I44	SPSCAN HMMER

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
43	1403326CD1	901	S120 S13 S139 S219 S269 S383 S521 S531 S588 S603 S641 S708 S80 S805 S853 S858 T154 T230 T25 T296 T344 T352 T354 T493 T505 T650 T688 T776 T795 T815 Y279 Y311 Y681 Y804 Y824		P-loop Atp_Gtp_A: G599-T606	MOTIFS
44	7690129CD1	1040	S191 S254 S367 S539 S579 S679 S969 S971 S978 T112 T140 T182 T503 T535 T544 T729 T93	N116 N54 N818	Leucine Zipper: L695-L716 Rgd: R40-D42 R241-D243 Transmembrane domain: V606-F623, M753-A773, W844-V862 PROTEIN CHROMOSOME TRANSMEMBRANE MELASTATIN C05C12.3 T01H8.5 I F54D1.5 IV PD151509: V730-A1018 PD018035: K8-W246 PD039592: Q382-E546	MOTIFS MOTIFS HMMER BLAST_PRODOR

Table 4

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
45	2101688CB1	2508	71-123	6735891H1 (LIVRTUT13)	883	1375
				7620180J1 (KIDNTUE01)	1757	2290
				6874586H1 (EPIMUNN04)	1988	2508
				7704542H1 (UTRETUE01)	192	634
				3593046H1 (293TF5T01)	1	304
				6018547H1 (HNT2UNN03)	1327	2033
				6124211H1 (BRAHNON05)	1053	1632
				7700489J1 (KIDPTDE01)	409	938
46	5452330CB1	4034	1493-1673, 1-1081, 2638-2908, 3129-3535	3470968F6 (BRAIDIT01)	1862	2432
				6982855F8 (BRAIFER05)	1	427
				4775091H1 (BRAQNOT01)	3798	4034
				5404047T6 (BRAHNOT01)	3471	4026
				7293087F8 (BRAIFER06)	526	1205
				7583209H1 (BRAIFEC01)	301	861
				6207435H1 (PITUNON01)	3033	3733
				5404047F6 (BRAHNOT01)	2931	3445
				7115489H1 (BRAENOK01)	2298	2745
				6990568H1 (BRAIFER05)	480	1092
				7293087R8 (BRAIFER06)	1078	1790
				7579594H1 (BRAIFEC01)	2446	2962
				7291338F8 (BRAIFER06)	1717	2352
47	4362432CB1	845	1-44, 685-845	4362432F6 (SKIRNOT01)	1	664
				4362432T9 (SKIRNOT01)	228	845
48	5308104CB1	2300	1-807, 2192-2300	71013085V1	1689	2273
				6809635J1 (SKIRNOR01)	1	532
				8044501J1 (OVRTUE01)	214	765
				1550768R6 (PROSNOT06)	1989	2283
				6804176H1 (COLENOR03)	1230	1814
				71014150V1	656	1210
				6880707H1 (BRAHTDR03)	1100	1808
				503680H1 (TMLR3DT02)	2119	2300
49	3092736CB1	1587	1-180	SCGA02766V1	367	1073
				SCGA07870V1	685	1131
				1611754F6 (COLNTUT06)	1153	1587

Table 4 (Cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
49				2823991F6 (ADRETUT06)	1031	1532
				SCGA12762V1	1	524
50	3580257CB1	669	1-24	3580257F6 (293TF3T01)	133	669
				5107219H1 (PROSTUS19)	1	240
				g1496797	1	495
51	3634758CB1	1463	1-51	4719037H1 (BRAIHCT02)	1177	1432
				SXAF05002V1	1	521
				SXAF05483V1	379	868
				3243342H1 (BRAINOT19)	1231	1463
				2729881H1 (OVARUT04)	1095	1333
				SXAF05152V1	604	1131
52	4027923CB1	1686	1-204, 1666-1686	2532289H1 (GBLANOT02)	963	1179
				1281432F6 (COLNNOT16)	620	1173
				2561353H1 (ADRETUT01)	1	276
				664136H1 (SCORNOT01)	1428	1686
				3585158H1 (293TF4T01)	325	639
				1281432T6 (COLNNOT16)	1051	1684
				6772967J1 (BRAUNOR01)	75	607
53	4348533CB1	2497	1556-1848, 1-150, 2371-2497, 762-909	6933091H1 (SINTTMR02)	1346	1901
				g1617775	1	405
				2890155F6 (LUNGFET04)	1	483
				6781002J1 (OVARDIR01)	153	903
				2622331H1 (KERANOT02)	2139	2497
				2507578T6 (CONUTUT01)	1684	2359
				1728133F6 (PROSNOT14)	546	1160
				6945931H1 (FTUBTUR01)	1132	1795
54	4521857CB1	1783	1-733, 805-890	3003172H1 (TLYMNOT06)	900	1194
				4521857F6 (HNT2TXT01)	1	537
				825638T1 (PROSNOT06)	1100	1762
				857689R1 (NGANNT01)	1194	1777
				3644845F6 (LUNGNOT34)	490	903
				362417R6 (PROSNOT01)	1227	1783
55	4722253CB1	1461	1-499	4722253H1 (COLCTUT02)	933	1204
				7018504H1 (KIDNNOC01)	1	668
				2455753F6 (ENDANOT01)	577	1109

Table 4 (Cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
55				g3053012	975	1461
				3028265F6 (HEARFET02)	1292	1461
56	4878134CB1	2116	1-1071	3396235H1 (BRAIDIT01)	1865	2116
				4501019F6 (BRAVXTT02)	544	1119
				SBQA01857D1	467	1044
				3521653T6 (LUNGNON03)	1181	1713
				5021921H1 (OVARNON03)	1745	2041
				3766951H1 (BRSTNOT24)	1553	1851
				4501019T6 (BRAVXTT02)	1050	1704
				70874715V1	1	544
57	5050133CB1	702	1-28, 651-702	g1802638	321	702
				6871022H1 (BRAGNON02)	1	630
				3729290F6 (SMCCNON03)	199	686
58	5630124CB1	2613	1-975	6821390J1 (SINTNOR01)	520	1293
				6431012H1 (LUNGNON07)	1175	1881
				6855495H1 (BRAIFEN08)	1	643
				3878611T6 (SPLNNOT11)	2075	2590
				1358001T6 (LUNGNON09)	1940	2586
				481430R7 (LIVRBCT01)	854	1381
				2252822R6 (OVRTUT01)	2311	2613
				481430T7 (LIVRBCT01)	1371	2013
59	5677286CB1	1778	1736-1778, 1-143, 672-767	70613827V1	1195	1777
				7053934H2 (BRACNOK02)	602	1280
				6340571H1 (BRANDIN01)	669	1324
				3620887T6 (BRSTNOT24)	1	642
				1810961F6 (PROSTUT12)	1421	1778
60	6436791CB1	1234	1-192	1212854T6 (BRSTTUT01)	556	1221
				3510032F6 (CONCNOT01)	1	590
				3943483F6 (SCORNOT04)	764	1234
61	1820972CB1	863	1-228, 843-863	60144357B1	227	833
				70636975V1	253	863
				1820972H1 (GBLATUT01)	1	267
62	3286805CB1	2521	1-155, 1165-2294	5030319F7 (COLCDIT01)	1300	1973
				7168560H1 (MCLRNOC01)	575	1020
				6959075H1 (SKINDIA01)	1	674

Table 4 (Cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
62				3286805F6 (HEAONOT05)	1706	2266
				6466032H1 (PLACFEB01)	764	1319
				71054005V1	1949	2521
63	3506590CB1	1765	1-798	71409670V1	1051	1765
				7710638H1 (TESTTUE02)	524	1080
				70515763V1	1	556
				7733848H2 (COLDDIE01)	543	1266
64	003600CB1	1264	1-699	2718319H1 (THYRNOT09)	195	442
				2397316T6 (THP1AZT01)	714	1264
				003600R6 (HMC1NOT01)	509	1042
				008108H1 (HMC1NOT01)	269	498
				4592276H1 (MASTTXXT01)	398	639
				2911566H1 (KIDNTUT15)	1	265
65	1251534CB1	3415	1-122, 2125-2328, 2982-3415, 834-1643	531771T6 (BRAINOT03)	2338	2967
				4697183F6 (BRALNOT01)	235	863
				487800H1 (HNT2AGT01)	1633	1906
				4740283H1 (THYMNOR02)	1210	1470
				1717327T6 (UCMCNOT02)	2865	3415
				7761153H1 (THYMNOR02)	1	708
				6855869H1 (BRAIFEN08)	1969	2594
				6442673H1 (BRAENOT02)	1814	2453
				3291485F6 (BONRFET01)	798	1410
				5404331H1 (BRAHNOT01)	1669	1969
				1251534H1 (LUNGFET03)	1448	1681
66	1402211CB1	2289	1707-2289	1650008F6 (PROSTUT09)	1296	1912
				429727T6 (BLADNOT01)	1626	2289
				2862734H1 (SININOT03)	1082	1342
				2129033R6 (KIDNNOT05)	1	512
				2499655F7 (ADRETUT05)	564	1084
				5397049H1 (LIVRTUT13)	1031	1293
				826301R1 (PROSNOT06)	1332	1928
				429727R6 (BLADNOT01)	335	862
67	1623474CB1	4480	2411-3066, 1-22, 109-587, 3638-3733	2158031F6 (BRAINOT09)	3973	4480

Table 4 (Cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
67				3332425T6 (BRAIFET01)	2946	3643
				6914395J1 (PITUDIR01)	2128	2758
				6918276H1 (PLACFER06)	218	977
				6128115H1 (BRAHNON05)	2348	3030
				70758295V1	1025	1574
				3394074H1 (LUNGNOT28)	1	287
				1864803T6 (PROSNOT19)	3133	3718
				1975441T6 (PANCYTUT02)	3747	4451
				1975441F6 (PANCYTUT02)	3664	4246
				70760953V1	426	1008
				70761097V1	821	1416
				70757930V1	1651	2163
				60205344U1	1374	2060
68	1706443CB1	1568	1-43	6630210U1	438	905
				1858593T6 (PROSNOT18)	1044	1521
				1706443T6 (DUODNOT02)	906	1513
				1858593F6 (PROSNOT18)	686	989
				7062677H1 (PENITMN02)	1	468
				1390249H1 (EOSINOT01)	1342	1568
69	1748627CB1	1887	1-649	5407812F8 (BRAMNOT01)	429	985
				71427502V1	1299	1887
				6886749J1 (BRAHTDR03)	632	1022
				3627391F6 (COLNNOT38)	1	531
				71430251V1	1047	1612
				1979283R6 (LUNGUT03)	997	1556
70	1818332CB1	569	1-35	1255779F2 (MENITUT03)	39	569
				1336021T1 (COLNNOT13)	1	541
71	1822832CB1	2338	529-565, 1332-1369, 1-124, 1488-2338	1289709F6 (BRAINOT11)	1977	2338
				1822832X352U1 (GBLATUT01)	25	655
				g1975312	1	277
				SAOA01720F1	710	1312
				SAOA01416F1	1318	1894
				1452843F6 (PENITUT01)	520	1212
				SAOA01295F1	1707	2338
				SAOA00837F1	1223	1841

Table 4 (Cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
72	1832219CB1	481	1-21	SXAF02203V1 1832219R6 (BRAINON01)	1 44	479 481
73	1899010CB1	1255	1-62	1899010F6 (BLADTUT06) 2174773F6 (ENDCNOT03) 1909527T6 (CONNTTUT01) 1425473H1 (BEPINON01) 1909527F6 (CONNTTUT01)	341 863 569 1 34	824 1255 1233 264 643
74	2008768CB1	875	1-411	2008768T6 (TESTNOT03) 6025379H1 (TESTNOT11) 563323R6 (NEUTLPT01)	159 1 472	858 261 875
75	2070984CB1	2188	1-72, 1579-1656	1273987F1 (TESTTUT02) 7162982H1 (PLACNOR01) SBIA08036D1 SBIA01466D1 6907510J1 (PITUDIR01) 3320716H1 (PROSBPT03)	1769 321 1307 891 112 1	2188 914 1793 1516 851 280
76	2193240CB1	1561	1-624	1624251F6 (BRAITUT13) 2429918R6 (MENTUNON2) 2429918T6 (MENTUNON2) 900981R1 (BRSTTUT03)	1 734 1003 365	472 1174 1561 926
77	2235177CB1	1777	1-32	71113502V1 6993448H1 (BRAQTDOR02) 71264559V1 71113614V1	1140 1 837 679	1777 725 1353 1308
78	2416227CB1	1841	1-482 518-1018	6821668J1 (SINTNOR01) 2416227T6 (HNT3AZT01) 2416227F6 (HNT3AZT01) 854765H1 (NGANNOT01) 7017947H1 (KIDNNOC01) 7154302H1 (HEARNONO3)	194 1210 976 774 1 1446	980 1789 1434 1005 604 1841
79	2461076CB1	1616	835-861, 565-783, 1-219	7039965H1 (UTRSTMR02)	110	673
				219625R6 (STOMNOT01) 6935657H1 (SINTTMR02) 219625T6 (STOMNOT01) 2461076F6 (THYRNOT08) 6073858H1 (UTREDIT09)	948 855 958 484 1	1492 1446 1616 938 273

Table 4 (Cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
80	1957517CB1	1434	1-111	7161288H1 (PLACNOR01)	448	1014
				1233279F1 (LUNGFEET03)	1	537
				6573238H1 (COLHTUS02)	655	1348
				1575944H1 (LNODNOT03)	1214	1434
81	866038CB1	2085	51-124	6913288J1 (PITUDIR01)	272	823
				5964475H1 (BRATNOT05)	1744	2085
				7132506H1 (BRAHTDK01)	816	1499
				6054811H1 (BRAENOT04)	784	1447
				755563R1 (BRAITUT02)	215	753
				5483139H1 (FIBPFEN06)	1	285
				6438276H1 (BRAENOT02)	1420	2083
82	3869704CB1	904	1-36	705156H1 (SYNORAT04)	1	232
				71052048V1	331	904
				3901129R8 (LUNGNON03)	48	697
				3904253R9 (LUNGNON03)	217	837
83	1415179CB1	1496	1-248, 606-836	2042611R6 (HIPONON02)	729	1206
				660950R6 (BRAINOT03)	557	1155
				4713560H1 (BRAIHCOT01)	1	252
				658639F1 (BRAINOT03)	839	1496
				2708523H1 (PONSAT01)	430	732
				2967826F6 (SCORNOT04)	58	686
84	1664792CB1	2837	1-1559	70858742V1	407	959
				4797546H1 (LIVRTUT09)	1248	1524
				2699003T6 (OVARUT010)	2154	2825
				71224728V1	867	1504
				2542259F6 (BONRTUT01)	1859	2386
				7460645H1 (LIVRTUE01)	441	1062
				2260182R6 (UTRSNOT02)	2545	2837
				1664792T6 (BRSTNOT09)	1698	2381
				6988160H1 (BRAIFER05)	1	444
				1664792F6 (BRSTNOT09)	1257	1834
				4179737H1 (SINITUT03)	1589	1863
85	2079396CB1	1123	1-45, 993-1123	6820736H1 (SINTNOR01)	566	1063
				g1401473	1	507
				874769R1 (LUNGAST01)	786	1123
				6819702J1 (OVARDIR01)	54	794
85				6335288H1 (BRANDIN01)	17	509

Table 4 (Cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
86	5390115CB1	1549	1-270	1258145F1 (MENITUT03)	589	1247
				1466677F1 (PANCUTUT02)	1086	1549
				4250616F6 (BRADDIR01)	1	633
				1310308F1 (COLNFET02)	758	1337
87	1403326CB1	4820	1-3502	1306452F6 (PLACNOT02)	1069	1588
				70607520V1	291	789
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				3080429F6 (BRAIUNT01)	2387	3023
				70476331V1	1812	2459
				70604815V1	1	395
				2801448F6 (PENCNOT01)	3054	3590
				4729710H1 (GBLADIT01)	1585	1844
				6245574H1 (TESTNOT17)	3553	4124
				70815905V1	417	793
				5718724H1 (PANCNOT16)	1188	1815
				6863174H1 (BRAGNON02)	4389	4820
				6937903H1 (FTUBTUR01)	3745	4307
				6489460H1 (MIXDUNB01)	2100	2703
				4884473H2 (LUNLTMT01)	2991	3242
				2820527T6 (BRSTNOT14)	4094	4505
				5642645R8 (UTRSTMR01)	603	1080
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				1851125T6 (LUNGFET03)	2986	3599
				7757184J1 (SPLNTUE01)	706	1447
				6800356J1 (COLENOR03)	222	920
				6831480J1 (SINTNOR01)	1821	2515
				6883161H1 (BRAHTDR03)	580	1029
				5868845F8 (COLTDT04)	1644	2425
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Table 5

Polynucleotide SEQ ID NO:	Incyte Project ID	Representative Library
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47	4362432CB1	SKIRNOT01
48	5308104CB1	BRAYDIN03
49	3092736CB1	BRAITUT08
50	3580257CB1	293TF3T01
51	3634758CB1	HUVENOB01
52	4027923CB1	COLNNOT16
53	4348533CB1	LIVRNON08
54	4521857CB1	SPLNNOT04
55	4722253CB1	TESTNOT03
56	4878134CB1	LJUNGNON03
57	5050133CB1	FIBPFEN06
58	5630124CB1	LJUNGNOT09
59	5677286CB1	PROSTUT12
60	6436791CB1	MEGBUNT01
61	1820972CB1	SPLNNOT04
62	3286805CB1	SKINDIA01
63	3506590CB1	COLDDIE01
64	003600CB1	HMC1NOT01
65	1251534CB1	THYMNOT05
66	1402211CB1	CARCTXT02
67	1623474CB1	HMC1NOT01
68	1706443CB1	DUODNOT02
69	1748627CB1	FIBPFEN06
70	1818332CB1	ISLTNOT01
71	1822832CB1	BRAINOT11
72	1832219CB1	TESTNOT03
73	1899010CB1	BLADTUT06
74	2008768CB1	TESTNOT03
75	2070984CB1	PLACNOT07
76	2193240CB1	BRAITUT13
77	2235177CB1	HNT2AGT01

Table 5 (Cont.)

Polynucleotide SEQ ID NO:	Incyte Project ID	Representative Library
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79	2461076CB1	STOMN0T01
80	1957517CB1	OVARTUT01
81	866038CB1	BRAITUT03
82	3869704CB1	LUNGN0T03
83	1415179CB1	BRAIN0T03
84	1664792CB1	BRSTTUT01
85	2079396CB1	CONUTUT01
86	5390115CB1	BRAITUT03
87	1403326CB1	BRSTN0T01
88	7690129CB1	PROSTUT12

Table 6

Library	Vector	Library Description
293TF3T01	pINCY	Library was constructed using RNA isolated from a serum-starved transformed embryonal cell line (293-EBNA) derived from kidney epithelial tissue. The cells were transformed with adenovirus 5 DNA.
BLADTUT06	pINCY	Library was constructed using RNA isolated from bladder tumor tissue removed from the posterior bladder wall of a 58-year-old Caucasian male during a radical cystectomy, radical prostatectomy, and gastrectomy. Pathology indicated grade 3 transitional cell carcinoma in the left lateral bladder wall. The remaining bladder showed marked cystitis with scattered microscopic foci of transitional cell carcinoma in situ. Patient history included angina, emphysema and tobacco use. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.
BRAIDIT01	pINCY	Library was constructed using RNA isolated from diseased brain tissue. Patient history included multiple sclerosis, type II lesion.
BRAINOT03	PSPORT1	Library was constructed using RNA isolated from brain tissue removed from a 26-year-old Caucasian male during cranioplasty and excision of a cerebral meningeal lesion. Pathology for the associated tumor tissue indicated a grade 4 oligoastrocytoma in the right fronto-parietal part of the brain.
BRAINOT11	pINCY	Library was constructed using RNA isolated from brain tissue removed from the right temporal lobe of a 5-year-old Caucasian male during a hemispherectomy. Pathology indicated extensive polymicrogyria and mild to moderate gliosis (predominantly subpial and subcortical), consistent with chronic seizure disorder. Family history included a cervical neoplasm.
BRAITUT02	PSPORT1	Library was constructed using RNA isolated from brain tumor tissue removed from the frontal lobe of a 58-year-old Caucasian male during excision of a cerebral meningeal lesion. Pathology indicated a grade 2 metastatic hypernephroma. Patient history included a grade 2 renal cell carcinoma, insomnia, and chronic airway obstruction. Family history included a malignant neoplasm of the kidney.
BRAITUT03	PSPORT1	Library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 17-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated a grade 4 fibrillary giant and small-cell astrocytoma. Family history included benign hypertension and cerebrovascular disease.
BRAITUT08	pINCY	Library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 47-year-old Caucasian male during excision of cerebral meningeal tissue. Pathology indicated grade 4 fibrillary astrocytoma with focal tumoral radionecrosis. Patient history included cerebrovascular disease, deficiency anemia, hyperlipidemia, epilepsy, and tobacco use. Family history included cerebrovascular disease and a malignant prostate neoplasm.
BRAITUT13	pINCY	Library was constructed using RNA isolated from brain tumor tissue removed from the left frontal lobe of a 68-year-old Caucasian male during excision of a cerebral meningeal lesion. Pathology indicated a meningioma in the left frontal lobe.

Table 6 (Cont.)

Library	Vector	Library Description
BRAYDIN03	PINCY	This normalized library was constructed from 6.7 million independent clones from a brain tissue library. Starting RNA was made from RNA isolated from diseased hypothalamus tissue removed from a 57-year-old Caucasian male who died from a cerebrovascular accident. Patient history included Huntington's disease and emphysema. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228 and Bonaldo et al., Genome Research (1996) 6:791, except that a significantly longer (48 hours/round) reannealing hybridization was used. The library was linearized and recircularized to select for insert containing clones.
BRSTNOT01	PBLUESCRIPT	Library was constructed using RNA isolated from the breast tissue of a 56-year-old Caucasian female who died in a motor vehicle accident.
BRSTTUT01	PSPORT1	Library was constructed using RNA isolated from breast tumor tissue removed from a 55-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated invasive grade 4 mammary adenocarcinoma of mixed lobular and ductal type, extensively involving the left breast. The tumor was identified in the deep dermis near the lactiferous ducts with extracapsular extension. Seven mid and low and five high axillary lymph nodes were positive for tumor. Proliferative fibrocystic changes were characterized by apocrine metaplasia, sclerosing adenosis, cyst formation, and ductal hyperplasia without atypia. Patient history included atrial tachycardia, blood in the stool, and a benign breast neoplasm. Family history included benign hypertension, atherosclerotic coronary artery disease, cerebrovascular disease, and depressive disorder.
CARCTXT02	PSPORT1	Library was constructed using RNA from chondrocytes that were isolated from pooled knee cartilage obtained during total knee joint replacement. The cartilage was removed from the underlying bone, chopped into smaller pieces, and stimulated with 5 ng/ml IL-1 for 18 hours.
COLDDIE01	PCDNA2.1	This 5 prime biased random primed library was constructed using RNA isolated from diseased descending colon tissue removed from a 28-year-old Caucasian male during a total intra-abdominal colectomy and temporary ileostomy. Pathology indicated chronic ulcerative colitis, moderate to severe, actively involving the distal 23 cm of colon. The entire 24 cm segment of rectosigmoid, rectum, and rectal tissue was involved with chronic ulcerative colitis, severely active. The patient presented with blood in the stool, diarrhea, and deficiency anemia. Patient history included shoulder dystonia (sprained rotator cuff), and tobacco abuse. The patient was treated with a transfusion. Patient medications included Asacol, Prednisone, and cortisone enemas. Family history included acute myocardial infarction, upper lobe lung cancer, colon cancer, and type I diabetes in the grandparent(s).
COLNNOT16	PINCY	Library was constructed using RNA isolated from sigmoid colon tissue removed from a 62-year-old Caucasian male during a sigmoidectomy and permanent colostomy.
CONUTUT01	PINCY	Library was constructed using RNA isolated from sigmoid mesentery tumor tissue obtained from a 61-year-old female during a total abdominal hysterectomy and bilateral salpingo-oophorectomy with regional lymph node excision. Pathology indicated a metastatic grade 4 malignant mixed müllerian tumor present in the sigmoid mesentery at two sites.

Table 6 (Cont.)

Library	Vector	Library Description
DUODNOT02	pINCY	Library was constructed using RNA isolated from duodenal tissue of a 8-year-old Caucasian female, who died from head trauma. Serology was positive for cytomegalovirus (CMV).
FIBPFEN06	pINCY	The normalized prostate stromal fibroblast tissue libraries were constructed from 1.56 million independent clones from a prostate fibroblast library. Starting RNA was made from fibroblasts of prostate stroma removed from a male fetus, who died after 26 weeks' gestation. The libraries were normalized in two rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228 and Bonaldo et al., Genome Research (1996) 6:791, except that a significantly longer (48-hours/round) reannealing hybridization was used. The library was then linearized and recircularized to select for insert containing clones as follows: plasmid DNA was prepped from approximately 1 million clones from the normalized prostate stromal fibroblast tissue libraries following soft agar transformation.
HMC1NOT01	PBLUESCRIPT	Library was constructed using RNA isolated from the HMC-1 human mast cell line derived from a 52-year-old female. Patient history included mast cell leukemia.
HNT2AGT01	PBLUESCRIPT	Library was constructed at Stratagene (STR937233), using RNA isolated from the hNT2 cell line derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor. Cells were treated with retinoic acid for 5 weeks and with mitotic inhibitors for two weeks and allowed to mature for an additional 4 weeks in conditioned medium.
HUVENOB01	PBLUESCRIPT	Library was constructed using RNA isolated from HUV-EC-C (ATCC CRL 1730) cells.
ISLTNOT01	pINCY	Library was constructed using RNA isolated from a pooled collection of pancreatic islet cells.

Table 6 (Cont.)

Library	Vector	Library Description
LIVRNON08	pINCY	This normalized library was constructed from 5.7 million independent clones from a pooled liver tissue library. Starting RNA was made from pooled liver tissue removed from a 4-year-old Hispanic male who died from anoxia and a 16 week female fetus who died after 16-weeks gestation from anencephaly. Serologies were positive for cytomegalovirus in the 4-year-old. Patient history included asthma in the 4-year-old. Family history included taking daily prenatal vitamins and mitral valve prolapse in the mother of the fetus. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228 and Bonaldo et al., Genome Research 6 (1996):791, except that a significantly longer (48 hours/round) reannealing hybridization was used.
LUNGNON03	PSPORT1	This normalized library was constructed from 2.56 million independent clones from a lung tissue library. RNA was made from lung tissue removed from the left lobe a 58-year-old Caucasian male during a segmental lung resection. Pathology for the associated tumor tissue indicated a metastatic grade 3 (of 4) osteosarcoma. Patient history included soft tissue cancer, secondary cancer of the lung, prostate cancer, and an acute duodenal ulcer with hemorrhage. Patient also received radiation therapy to the retroperitoneum. Family history included prostate cancer, breast cancer, and acute leukemia. The normalization and hybridization conditions were adapted from Soares et al., PNAS (1994) 91:9228; Swaroop et al., NAR (1991) 19:1954; and Bonaldo et al., Genome Research (1996) 6:791.
LUNGNOT03	PSPORT1	Library was constructed using RNA isolated from lung tissue of a 79-year-old Caucasian male. Pathology for the associated tumor tissue indicated grade 4 carcinoma. Patient history included a benign prostate neoplasm and atherosclerosis.
LUNGNOT09	pINCY	Library was constructed using RNA isolated from the lung tissue of a 23-week-old Caucasian male fetus. The pregnancy was terminated following a diagnosis by ultrasound of infantile polycystic kidney disease.
MEGBUNT01	pINCY	Library was constructed using RNA isolated from an untreated MEG-01 megakaryoblast cell line, derived from bone marrow cells obtained from a 55-year-old male in megakaryoblastic crisis of chronic myelogenous leukemia.
OVARTUT01	PSPORT1	Library was constructed using RNA isolated from ovarian tumor tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology indicated grade 2 mucinous cystadenocarcinoma involving the entire left ovary. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, stress reaction, cerebrovascular disease, breast cancer, and uterine cancer.
PLACNOT07	pINCY	Library was constructed using RNA isolated from placental tissue removed from a Caucasian fetus, who died after 16 weeks' gestation from fetal demise and hydrocephalus. Serology was positive for anti-CMV (cytomegalovirus).

Table 6 (Cont.)

Library	Vector	Library Description
PROSTUT12	pINCY	Library was constructed using RNA isolated from prostate tumor tissue removed from a 65-year-old Caucasian male during a radical prostatectomy. Pathology indicated an adenocarcinoma (Gleason grade 2+2). Adenofibromatous hyperplasia was also present. The patient presented with elevated prostate specific antigen (PSA).
SKINDIA01	PSPORT1	This amplified library was constructed using RNA isolated from diseased skin tissue removed from 1 female and 4 males during skin biopsies. Pathologies indicated tuberculoid and lepromatious leprosy.
SKIRNOT01	pINCY	Library was constructed using RNA isolated from skin tissue removed from the breast of a 26-year-old Caucasian female during bilateral reduction mammoplasty.
SPLNNOT04	pINCY	Library was constructed using RNA isolated from the spleen tissue of a 2-year-old Hispanic male, who died from cerebral anoxia. Past medical history and serologies were negative.
STOMNOT01	PBLUESCRIPT	Library was constructed using RNA isolated from the stomach tissue of a 55-year-old Caucasian male, who died from cardiopulmonary arrest.
TESTNOT03	PBLUESCRIPT	Library was constructed using RNA isolated from testicular tissue removed from a 37-year-old Caucasian male, who died from liver disease. Patient history included cirrhosis, jaundice, and liver failure.
THYMNOT05	pINCY	Library was constructed using RNA isolated from thymus tissue removed from a 3-year-old Hispanic male during a thymectomy and closure of a patent ductus arteriosus. The patient presented with severe pulmonary stenosis and cyanosis. Patient history included a cardiac catheterization and echocardiogram. Previous surgeries included Blalock-Taussig shunt and pulmonary valvotomy. The patient was not taking any medications. Family history included benign hypertension, osteoarthritis, depressive disorder, and extrinsic asthma in the grandparent(s).

Table 7

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	<i>ESTs</i> : Probability value= 1.0E-8 or less <i>Full Length sequences</i> : Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	<i>ESTs</i> : fasta E value=1.06E-6 <i>Assembled ESTs</i> : fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less <i>Full Length sequences</i> : fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	<i>PFAM hits</i> : Probability value= 1.0E-3 or less <i>Signal peptide hits</i> : Score= 0 or greater

Table 7 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score≥GCG-specified “HIGH” value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPSscan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. on Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence Press, Menlo Park, CA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

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Leu	Ala	His	Gly	Leu	Ser	Leu	Glu	Ala	Pro	Thr	Val	Gly	Lys	Gly
				20					25					30
Gln	Ala	Pro	Gly	Ile	Glu	Glu	Thr	Asp	Gly	Glu	Leu	Thr	Ala	Ala
				35					40					45
Pro	Thr	Pro	Glu	Gln	Pro	Glu	Arg	Gly	Val	His	Phe	Val	Thr	Thr
				50					55					60
Ala	Pro	Thr	Leu	Lys	Leu	Leu	Asn	His	His	Pro	Leu	Leu	Glu	Glu
				65					70					75
Phe	Leu	Gln	Glu	Gly	Leu	Glu	Lys	Gly	Asp	Glu	Glu	Leu	Arg	Pro
				80					85					90
Ala	Leu	Pro	Phe	Gln	Pro	Asp	Pro	Pro	Ala	Pro	Phe	Thr	Pro	Ser
				95					100					105
Pro	Leu	Pro	Arg	Leu	Ala	Asn	Gln	Asp	Ser	Arg	Pro	Val	Phe	Thr
				110					115					120
Ser	Pro	Thr	Pro	Ala	Met	Ala	Ala	Val	Pro	Thr	Gln	Pro	Gln	Ser
				125					130					135
Lys	Glu	Gly	Pro	Trp	Ser	Pro	Glu	Ser	Glu	Ser	Pro	Met	Leu	Arg
				140					145					150
Ile	Thr	Ala	Pro	Leu	Pro	Pro	Gly	Pro	Ser	Met	Ala	Val	Pro	Thr
				155					160					165
Leu	Gly	Pro	Gly	Glu	Ile	Ala	Ser	Thr	Thr	Pro	Pro	Ser	Arg	Ala
				170					175					180
Trp	Thr	Pro	Thr	Gln	Glu	Gly	Pro	Gly	Asp	Met	Gly	Arg	Pro	Trp
				185					190					195
Val	Ala	Glu	Val	Val	Ser	Gln	Gly	Ala	Gly	Ile	Gly	Ile	Gln	Gly
				200					205					210
Thr	Ile	Thr	Ser	Ser	Thr	Ala	Ser	Gly	Asp	Asp	Glu	Glu	Thr	Thr
				215					220					225
Thr	Thr	Thr	Thr	Ile	Ile	Thr	Thr	Thr	Ile	Thr	Thr	Val	Gln	Thr
				230					235					240
Pro	Gly	Pro	Cys	Ser	Trp	Asn	Phe	Ser	Gly	Pro	Glu	Gly	Ser	Leu
				245					250					255
Asp	Ser	Pro	Thr	Asp	Leu	Ser	Ser	Pro	Thr	Asp	Val	Gly	Leu	Asp
				260					265					270
Cys	Phe	Phe	Tyr	Ile	Ser	Val	Tyr	Pro	Gly	Tyr	Gly	Val	Glu	Ile
				275					280					285
Lys	Val	Gln	Asn	Ile	Ser	Leu	Arg	Glu	Gly	Glu	Thr	Val	Thr	Val
				290					295					300
Glu	Gly	Leu	Gly	Gly	Pro	Asp	Pro	Leu	Pro	Leu	Ala	Asn	Gln	Ser
				305					310					315
Phe	Leu	Leu	Arg	Gly	Gln	Val	Ile	Arg	Ser	Pro	Thr	His	Gln	Ala
				320					325					330
Ala	Leu	Arg	Phe	Gln	Ser	Leu	Pro	Pro	Pro	Ala	Gly	Pro	Gly	Thr
				335					340					345
Phe	His	Phe	His	Tyr	Gln	Ala	Tyr	Leu	Leu	Ser	Cys	His	Phe	Pro
				350					355					360
Arg	Arg	Pro	Ala	Tyr	Gly	Asp	Val	Thr	Val	Thr	Ser	Leu	His	Pro
				365					370					375
Gly	Gly	Ser	Ala	Arg	Phe	His	Cys	Ala	Thr	Gly	Tyr	Gln	Leu	Lys
				380					385					390
Gly	Ala	Arg	His	Leu	Thr	Cys	Leu	Asn	Ala	Thr	Gln	Pro	Phe	Trp
				395					400					405
Asp	Ser	Lys	Glu	Pro	Val	Cys	Ile	Ala	Ala	Cys	Gly	Gly	Val	Ile
				410					415					420

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Arg	Asn	Ala	Thr	Thr	Gly	Arg	Ile	Val	Ser	Pro	Gly	Phe	Pro	Gly
				425					430					435
Asn	Tyr	Ser	Asn	Asn	Leu	Thr	Cys	His	Trp	Leu	Leu	Glu	Ala	Pro
				440					445					450
Glu	Gly	Gln	Arg	Leu	His	Leu	His	Phe	Glu	Lys	Val	Ser	Leu	Ala
				455					460					465
Glu	Asp	Asp	Asp	Arg	Leu	Ile	Ile	Arg	Asn	Gly	Asp	Asn	Val	Glu
				470					475					480
Ala	Pro	Pro	Val	Tyr	Asp	Ser	Tyr	Glu	Val	Glu	Tyr	Leu	Pro	Ile
				485					490					495
Glu	Gly	Leu	Leu	Ser	Ser	Gly	Lys	His	Phe	Phe	Val	Glu	Leu	Ser
				500					505					510
Thr	Asp	Ser	Ser	Gly	Ala	Ala	Ala	Gly	Met	Ala	Leu	Arg	Tyr	Glu
				515					520					525
Ala	Phe	Gln	Gln	Gly	His	Cys	Tyr	Glu	Pro	Phe	Val	Lys	Tyr	Gly
				530					535					540
Asn	Phe	Ser	Ser	Ser	Thr	Pro	Thr	Tyr	Pro	Val	Gly	Thr	Thr	Val
				545					550					555
Glu	Phe	Ser	Cys	Asp	Pro	Gly	Tyr	Thr	Leu	Glu	Gln	Gly	Ser	Ile
				560					565					570
Ile	Ile	Glu	Cys	Val	Asp	Pro	His	Asp	Pro	Gln	Trp	Asn	Glu	Thr
				575					580					585
Glu	Pro	Ala	Cys	Arg	Ala	Val	Cys	Ser	Gly	Glu	Ile	Thr	Asp	Ser
				590					595					600
Ala	Gly	Val	Val	Leu	Ser	Pro	Asn	Trp	Pro	Glu	Pro	Tyr	Gly	Arg
				605					610					615
Gly	Gln	Asp	Cys	Ile	Trp	Gly	Val	His	Val	Glu	Glu	Asp	Lys	Arg
				620					625					630
Ile	Met	Leu	Asp	Ile	Arg	Val	Leu	Arg	Ile	Gly	Pro	Gly	Asp	Val
				635					640					645
Leu	Thr	Phe	Tyr	Asp	Gly	Asp	Asp	Leu	Thr	Ala	Arg	Val	Leu	Gly
				650					655					660
Gln	Tyr	Ser	Gly	Pro	Arg	Ser	His	Phe	Lys	Leu	Phe	Thr	Ser	Met
				665					670					675
Ala	Asp	Val	Thr	Ile	Gln	Phe	Gln	Ser	Asp	Pro	Gly	Thr	Ser	Val
				680					685					690
Leu	Gly	Tyr	Gln	Gln	Gly	Phe	Val	Ile	His	Phe	Phe	Glu	Val	Pro
				695					700					705
Arg	Asn	Asp	Thr	Cys	Pro	Glu	Leu	Pro	Glu	Ile	Pro	Asn	Gly	Trp
				710					715					720
Lys	Ser	Pro	Ser	Gln	Pro	Glu	Leu	Val	His	Gly	Thr	Val	Val	Thr
				725					730					735
Tyr	Gln	Cys	Tyr	Pro	Gly	Tyr	Gln	Val	Val	Gly	Ser	Ser	Val	Leu
				740					745					750
Met	Cys	Gln	Trp	Asp	Leu	Thr	Trp	Ser	Glu	Asp	Leu	Pro	Ser	Cys
				755					760					765
Gln	Arg	Val	Thr	Ser	Cys	His	Asp	Pro	Gly	Asp	Val	Glu	His	Ser
				770					775					780
Arg	Arg	Leu	Ile	Ser	Ser	Pro	Lys	Phe	Pro	Val	Gly	Ala	Thr	Val
				785					790					795
Gln	Tyr	Ile	Cys	Asp	Gln	Gly	Phe	Val	Leu	Met	Gly	Ser	Ser	Ile
				800					805					810
Leu	Thr	Cys	His	Asp	Arg	Gln	Ala	Gly	Ser	Pro	Lys	Trp	Ser	Asp
				815					820					825
Arg	Ala	Pro	Lys	Cys	Leu	Leu	Glu	Gln	Leu	Lys	Pro	Cys	His	Gly
				830					835					840
Leu	Ser	Ala	Pro	Glu	Asn	Gly	Ala	Arg	Ser	Pro	Glu	Lys	Gln	Leu
				845					850					855
His	Pro	Ala	Gly	Ala	Thr	Ile	His	Phe	Ser	Cys	Ala	Pro	Gly	Tyr
				860					865					870
Val	Leu	Lys	Gly	Gln	Ala	Ser	Ile	Lys	Cys	Val	Pro	Gly	His	Pro
				875					880					885
Ser	His	Trp	Ser	Asp	Pro	Pro	Pro	Ile	Cys	Arg	Ala	Ala	Ser	Leu

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Asp Gly Phe Tyr	890	Asp Val Ala Lys Ala	900
Asn Ser Arg Ser Leu	905	His Ile Ala Ala Ala	915
Ala Ala Ser Ser Thr	920	Leu Val Gly Gly Val	930
Phe Leu Pro Leu Val	935	Ser Ser Leu Gln Leu	945
Phe Tyr Phe Ser Arg	950	Ile Thr Ile Glu Ser	960
Arg Pro Arg Pro Arg	965	Ser Leu Ser Phe Ala	975
Phe Asp Asn Pro Thr	980		990
Asp Glu Arg Ile			

<210> 3

<211> 212

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4362432CD1

<400> 3

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

<210> 4

<211> 308

<212> PRT

<213> Homo sapiens

<220>

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<221> misc_feature

<223> Incyte ID No: 5308104CD1

<400> 4

Met	Asn	Gly	Leu	Ser	Leu	Ser	Glu	Leu	Cys	Cys	Leu	Phe	Cys	Cys	
1				5					10					15	
Pro	Pro	Cys	Pro	Gly	Arg	Ile	Ala	Ala	Lys	Leu	Ala	Phe	Leu	Pro	
				20					25					30	
Pro	Glu	Ala	Thr	Tyr	Ser	Leu	Val	Pro	Glu	Pro	Glu	Pro	Gly	Pro	
				35					40					45	
Gly	Gly	Ala	Gly	Ala	Ala	Pro	Leu	Gly	Thr	Leu	Arg	Ala	Ser	Ser	
				50					55					60	
Gly	Ala	Pro	Gly	Arg	Trp	Lys	Leu	His	Leu	Thr	Glu	Arg	Ala	Asp	
				65					70					75	
Phe	Gln	Tyr	Ser	Gln	Arg	Glu	Leu	Asp	Thr	Ile	Glu	Val	Phe	Pro	
				80					85					90	
Thr	Lys	Ser	Ala	Arg	Gly	Asn	Arg	Val	Ser	Cys	Met	Tyr	Val	Arg	
				95					100					105	
Cys	Val	Pro	Gly	Ala	Arg	Tyr	Thr	Val	Leu	Phe	Ser	His	Gly	Asn	
				110					115					120	
Ala	Val	Asp	Leu	Gly	Gln	Met	Ser	Ser	Phe	Tyr	Ile	Gly	Leu	Gly	
				125					130					135	
Ser	Arg	Leu	His	Cys	Asn	Ile	Phe	Ser	Tyr	Asp	Tyr	Ser	Gly	Tyr	
				140					145					150	
Gly	Ala	Ser	Ser	Gly	Arg	Pro	Ser	Glu	Arg	Asn	Leu	Tyr	Ala	Asp	
				155					160					165	
Ile	Asp	Ala	Ala	Trp	Gln	Ala	Leu	Arg	Thr	Arg	Tyr	Gly	Ile	Ser	
				170					175					180	
Pro	Asp	Ser	Ile	Ile	Leu	Tyr	Gly	Gln	Ser	Ile	Gly	Thr	Val	Pro	
				185					190					195	
Thr	Val	Asp	Leu	Ala	Ser	Arg	Tyr	Glu	Cys	Ala	Ala	Val	Ile	Leu	
				200					205					210	
His	Ser	Pro	Leu	Met	Ser	Gly	Leu	Arg	Val	Ala	Phe	Pro	Asp	Thr	
				215					220					225	
Arg	Lys	Thr	Tyr	Cys	Phe	Asp	Ala	Phe	Pro	Ser	Ile	Asp	Lys	Ile	
				230					235					240	
Ser	Lys	Val	Thr	Ser	Pro	Val	Leu	Val	Ile	His	Gly	Thr	Glu	Asp	
				245					250					255	
Glu	Val	Ile	Asp	Phe	Ser	His	Gly	Leu	Ala	Met	Tyr	Glu	Arg	Cys	
				260					265					270	
Pro	Arg	Ala	Val	Glu	Pro	Leu	Trp	Val	Glu	Gly	Ala	Gly	His	Asn	
				275					280					285	
Asp	Ile	Glu	Leu	Tyr	Ala	Gln	Tyr	Leu	Glu	Arg	Leu	Lys	Gln	Phe	
				290					295					300	
Ile	Ser	His	Glu	Leu	Pro	Asn	Ser								
				305											

<210> 5

<211> 328

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3092736CD1

<400> 5

Met	Trp	Cys	Ser	Phe	Leu	Ala	Pro	Val	Ser	Ser	Ser	Cys	Leu	Cys	
1				5					10					15	
Trp	Val	Trp	Ala	Cys	Trp	Gly	Glu	Gly	His	Cys	Cys	Gln	Arg	Gly	
				20					25					30	
Thr	Asp	Phe	Leu	Met	Val	Leu	Pro	Lys	Val	Asn	Val	Gly	Asp	Thr	
				35					40					45	

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Val	Ala	Met	Leu	Pro	Lys	Ser	Arg	Arg	Ala	Leu	Thr	Ile	Gln	Glu	
				50					55					60	
Ile	Ala	Ala	Leu	Ala	Arg	Ser	Ser	Leu	His	Gly	Ile	Ser	Gln	Val	
				65					70					75	
Val	Lys	Asp	His	Val	Thr	Lys	Pro	Thr	Ala	Met	Ala	Gln	Gly	Arg	
				80					85					90	
Val	Ala	His	Leu	Ile	Glu	Trp	Lys	Gly	Trp	Ser	Lys	Pro	Ser	Asp	
				95					100					105	
Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala	Phe	Ser	Ser	Tyr	Ser	Asp	Leu	
				110					115					120	
Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg	Phe	Ala	Ala	Gly	Val	Ala	Glu	
				125					130					135	
Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys	Leu	Arg	Ala	Trp	Ser	Ser	Val	
				140					145					150	
Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp	Ser	Tyr	Asp	Glu	Asp	Phe	Ala	
				155					160					165	
Gly	Gly	Met	Asp	Thr	Asp	Met	Ala	Gly	Gln	Leu	Pro	Leu	Gly	Pro	
				170					175					180	
His	Leu	Gln	Asp	Leu	Phe	Thr	Gly	His	Arg	Phe	Ser	Arg	Pro	Val	
				185					190					195	
Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu	Ser	Asp	Cys	Ser	Gln	Thr	Val	
				200					205					210	
Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser	Leu	Cys	Ser	Leu	Glu	Asp	Gly	
				215					220					225	
Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu	Ala	Ser	Gln	Leu	Leu	Gly	Asp	
				230					235					240	
Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro	Pro	Ser	Arg	Glu	Ser	Ala	Phe	
				245					250					255	
Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala	Gln	Asp	Ser	Leu	Tyr	Asn	Ser	
				260					265					270	
Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser	Pro	Ala	Glu	Glu	Glu	Pro	Ala	
				275					280					285	
Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu	Cys	Pro	Pro	Leu	Thr	Gly	Ser	
				290					295					300	
Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser	Asp	Leu	Ala	Ser	Ser	Gly	Val	
				305					310					315	
Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala	Glu	Pro	Glu	Glu	Gln			
				320					325						

<210> 6

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3580257CD1

<400> 6

Met	Ala	Met	Ala	Val	Asp	Val	Ala	Ala	Ser	Ala	Asp	Gly	Val	Leu	
1				5					10					15	
Ala	Val	Ala	Met	Glu	Ala	Thr	Asp	Met	Ala	Leu	Ala	Leu	Glu	Ala	
				20					25					30	
Thr	Asp	Met	Ala	Leu	Ala	Leu	Glu	Ala	Thr	Asp	Met	Ala	Leu	Ala	
				35					40					45	
Leu	Glu	Ala	Met	Asp	Met	Ala	Ala	Ala	Ala	His	Arg	Thr	Met	Glu	
				50					55					60	
Asp	Thr	Asp	Ser	Leu	Ala	Phe	Ile	Lys							
				65											

<210> 7

<211> 158

<212> PRT

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<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3634758CD1

<400> 7

Met	Ala	Asp	Glu	Ala	Leu	Phe	Leu	Leu	Leu	His	Asn	Glu	Met	Val
1				5					10					15
Ser	Gly	Val	Tyr	Lys	Ser	Ala	Glu	Gln	Gly	Glu	Val	Glu	Asn	Gly
				20					25					30
Arg	Cys	Ile	Thr	Lys	Leu	Glu	Asn	Met	Gly	Phe	Arg	Val	Gly	Gln
				35					40					45
Gly	Leu	Ile	Glu	Arg	Phe	Thr	Lys	Asp	Thr	Ala	Arg	Phe	Lys	Asp
				50					55					60
Glu	Leu	Asp	Ile	Met	Lys	Phe	Ile	Cys	Lys	Asp	Phe	Trp	Thr	Thr
				65					70					75
Val	Phe	Lys	Lys	Gln	Ile	Asp	Asn	Leu	Arg	Thr	Asn	His	Gln	Gly
				80					85					90
Ile	Tyr	Val	Leu	Gln	Asp	Asn	Lys	Phe	Arg	Leu	Leu	Thr	Gln	Met
				95					100					105
Ser	Ala	Gly	Lys	Gln	Tyr	Leu	Glu	His	Ala	Ser	Lys	Tyr	Leu	Ala
				110					115					120
Phe	Thr	Cys	Gly	Leu	Ile	Arg	Gly	Gly	Leu	Ser	Asn	Leu	Gly	Ile
				125					130					135
Lys	Ser	Ile	Val	Thr	Ala	Glu	Val	Ser	Ser	Met	Pro	Ala	Cys	Lys
				140					145					150
Phe	Gln	Val	Met	Ile	Gln	Lys	Leu							
				155										

<210> 8

<211> 463

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4027923CD1

<400> 8

Met	Arg	Ala	Gly	Pro	Glu	Pro	Gln	Ala	Leu	Val	Gly	Gln	Lys	Arg
1				5					10					15
Gly	Ala	Leu	Arg	Leu	Leu	Val	Pro	Arg	Leu	Val	Leu	Thr	Val	Ser
				20					25					30
Ala	Pro	Ala	Glu	Val	Arg	Arg	Arg	Val	Leu	Arg	Pro	Val	Leu	Ser
				35					40					45
Trp	Met	Asp	Arg	Glu	Thr	Arg	Ala	Leu	Ala	Asp	Ser	His	Phe	Arg
				50					55					60
Gly	Leu	Gly	Val	Asp	Val	Pro	Gly	Val	Gly	Gln	Ala	Pro	Gly	Arg
				65					70					75
Val	Ala	Phe	Val	Ser	Glu	Pro	Gly	Ala	Phe	Ser	Tyr	Ala	Asp	Phe
				80					85					90
Val	Arg	Gly	Phe	Leu	Leu	Pro	Asn	Leu	Pro	Cys	Val	Phe	Ser	Ser
				95					100					105
Ala	Phe	Thr	Gln	Gly	Trp	Gly	Ser	Arg	Arg	Arg	Trp	Val	Thr	Pro
				110					115					120
Ala	Gly	Arg	Pro	Asp	Phe	Asp	His	Leu	Leu	Arg	Thr	Tyr	Gly	Asp
				125					130					135
Val	Val	Val	Pro	Val	Ala	Asn	Cys	Gly	Val	Gln	Glu	Tyr	Asn	Ser
				140					145					150
Asn	Pro	Lys	Glu	His	Met	Thr	Leu	Arg	Asp	Tyr	Ile	Thr	Tyr	Trp
				155					160					165
Lys	Glu	Tyr	Ile	Gln	Ala	Gly	Tyr	Ser	Ser	Pro	Arg	Gly	Cys	Leu

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				170					175					180
Tyr	Leu	Lys	Asp	Trp	His	Leu	Cys	Arg	Asp	Phe	Pro	Val	Glu	Asp
				185					190					195
Val	Phe	Thr	Leu	Pro	Val	Tyr	Phe	Ser	Ser	Asp	Trp	Leu	Asn	Glu
				200					205					210
Phe	Trp	Asp	Ala	Leu	Asp	Val	Asp	Asp	Tyr	Arg	Phe	Val	Tyr	Ala
				215					220					225
Gly	Pro	Ala	Gly	Ser	Trp	Ser	Pro	Phe	His	Ala	Asp	Ile	Phe	Arg
				230					235					240
Ser	Phe	Ser	Trp	Ser	Val	Asn	Val	Cys	Gly	Arg	Lys	Lys	Trp	Leu
				245					250					255
Leu	Phe	Pro	Pro	Gly	Gln	Glu	Glu	Ala	Leu	Arg	Asp	Arg	His	Gly
				260					265					270
Asn	Leu	Pro	Tyr	Asp	Val	Thr	Ser	Pro	Ala	Leu	Cys	Asp	Thr	His
				275					280					285
Leu	His	Pro	Arg	Asn	Gln	Leu	Ala	Gly	Pro	Pro	Leu	Glu	Ile	Thr
				290					295					300
Gln	Glu	Ala	Gly	Glu	Met	Val	Phe	Val	Pro	Ser	Gly	Trp	His	His
				305					310					315
Gln	Val	His	Asn	Leu	Asp	Asp	Thr	Ile	Ser	Ile	Asn	His	Asn	Trp
				320					325					330
Val	Asn	Gly	Phe	Asn	Leu	Ala	Asn	Met	Trp	Arg	Phe	Leu	Gln	Gln
				335					340					345
Glu	Leu	Cys	Ala	Val	Gln	Glu	Glu	Val	Ser	Glu	Trp	Arg	Asp	Ser
				350					355					360
Met	Pro	Asp	Trp	His	His	His	Cys	Gln	Val	Ile	Met	Arg	Ser	Cys
				365					370					375
Ser	Gly	Ile	Asn	Phe	Glu	Glu	Phe	Tyr	His	Phe	Leu	Lys	Val	Ile
				380					385					390
Ala	Glu	Lys	Arg	Leu	Leu	Val	Leu	Arg	Glu	Ala	Ala	Ala	Glu	Asp
				395					400					405
Gly	Ala	Gly	Leu	Gly	Phe	Glu	Gln	Ala	Ala	Phe	Asp	Val	Gly	Arg
				410					415					420
Ile	Thr	Glu	Val	Leu	Ala	Ser	Leu	Val	Ala	His	Pro	Asp	Phe	Gln
				425					430					435
Arg	Val	Asp	Thr	Ser	Ala	Phe	Ser	Pro	Gln	Pro	Lys	Glu	Leu	Leu
				440					445					450
Gln	Gln	Leu	Arg	Glu	Ala	Val	Asp	Ala	Ala	Ala	Ala	Pro		
				455					460					

<210> 9

<211> 648

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4348533CD1

<400> 9

Met	Glu	Lys	Ala	Arg	Arg	Gly	Gly	Asp	Gly	Val	Pro	Arg	Gly	Pro
1				5					10					15
Val	Leu	His	Ile	Val	Val	Val	Gly	Phe	His	His	Lys	Lys	Gly	Cys
				20					25					30
Gln	Val	Glu	Phe	Ser	Tyr	Pro	Pro	Leu	Ile	Pro	Gly	Asp	Gly	His
				35					40					45
Asp	Ser	His	Thr	Leu	Pro	Glu	Glu	Trp	Lys	Tyr	Leu	Pro	Phe	Leu
				50					55					60
Ala	Leu	Pro	Asp	Gly	Ala	His	Asn	Tyr	Gln	Glu	Asp	Thr	Val	Phe
				65					70					75
Phe	His	Leu	Pro	Pro	Arg	Asn	Gly	Asn	Gly	Ala	Thr	Val	Phe	Gly
				80					85					90
Ile	Ser	Cys	Tyr	Arg	Gln	Ile	Glu	Ala	Lys	Ala	Leu	Lys	Val	Arg

				95					100					105
Gln	Ala	Asp	Ile	Thr	Arg	Glu	Thr	Val	Gln	Lys	Ser	Val	Cys	Val
				110					115					120
Leu	Ser	Lys	Leu	Pro	Leu	Tyr	Gly	Leu	Leu	Gln	Ala	Lys	Leu	Gln
				125					130					135
Leu	Ile	Thr	His	Ala	Tyr	Phe	Glu	Glu	Lys	Asp	Phe	Ser	Gln	Ile
				140					145					150
Ser	Ile	Leu	Lys	Glu	Leu	Tyr	Glu	His	Met	Asn	Ser	Ser	Leu	Gly
				155					160					165
Gly	Ala	Ser	Leu	Glu	Gly	Ser	Gln	Val	Tyr	Leu	Gly	Leu	Ser	Pro
				170					175					180
Arg	Asp	Leu	Val	Leu	His	Phe	Arg	His	Lys	Val	Leu	Ile	Leu	Phe
				185					190					195
Lys	Leu	Ile	Leu	Leu	Glu	Lys	Lys	Val	Leu	Phe	Tyr	Ile	Ser	Pro
				200					205					210
Val	Asn	Lys	Leu	Val	Gly	Ala	Leu	Met	Thr	Val	Leu	Ser	Leu	Phe
				215					220					225
Pro	Gly	Met	Ile	Glu	His	Gly	Leu	Ser	Asp	Cys	Ser	Gln	Tyr	Arg
				230					235					240
Pro	Arg	Lys	Ser	Met	Ser	Glu	Asp	Gly	Gly	Leu	Gln	Glu	Ser	Asn
				245					250					255
Pro	Cys	Ala	Asp	Asp	Phe	Val	Ser	Ala	Ser	Thr	Ala	Asp	Val	Ser
				260					265					270
His	Thr	Asn	Leu	Gly	Thr	Ile	Arg	Lys	Val	Met	Ala	Gly	Asn	His
				275					280					285
Gly	Glu	Asp	Ala	Ala	Met	Lys	Thr	Glu	Glu	Pro	Leu	Phe	Gln	Val
				290					295					300
Glu	Asp	Ser	Ser	Lys	Gly	Gln	Glu	Pro	Asn	Asp	Thr	Asn	Gln	Tyr
				305					310					315
Leu	Lys	Pro	Pro	Ser	Arg	Pro	Ser	Pro	Asp	Ser	Ser	Glu	Ser	Asp
				320					325					330
Trp	Glu	Thr	Leu	Asp	Pro	Ser	Val	Leu	Glu	Asp	Pro	Asn	Leu	Lys
				335					340					345
Glu	Arg	Glu	Gln	Leu	Gly	Ser	Asp	Gln	Thr	Asn	Leu	Phe	Pro	Lys
				350					355					360
Asp	Ser	Val	Pro	Ser	Glu	Ser	Leu	Pro	Ile	Thr	Val	Gln	Pro	Gln
				365					370					375
Ala	Asn	Thr	Gly	Gln	Val	Val	Leu	Ile	Pro	Gly	Leu	Ile	Ser	Gly
				380					385					390
Leu	Glu	Glu	Asp	Gln	Tyr	Gly	Met	Pro	Leu	Ala	Ile	Phe	Thr	Lys
				395					400					405
Gly	Tyr	Leu	Cys	Leu	Pro	Tyr	Met	Ala	Leu	Gln	Gln	His	His	Leu
				410					415					420
Leu	Ser	Asp	Val	Thr	Val	Arg	Gly	Phe	Val	Ala	Gly	Ala	Thr	Asn
				425					430					435
Ile	Leu	Phe	Arg	Gln	Gln	Lys	His	Leu	Ser	Asp	Ala	Ile	Val	Glu
				440					445					450
Val	Glu	Glu	Ala	Leu	Ile	Gln	Ile	His	Asp	Pro	Glu	Leu	Arg	Lys
				455					460					465
Leu	Leu	Asn	Pro	Thr	Thr	Ala	Asp	Leu	Arg	Phe	Ala	Asp	Tyr	Leu
				470					475					480
Val	Arg	His	Val	Thr	Glu	Asn	Arg	Asp	Asp	Val	Phe	Leu	Asp	Gly
				485					490					495
Thr	Gly	Trp	Glu	Gly	Gly	Asp	Glu	Trp	Ile	Arg	Ala	Gln	Phe	Ala
				500					505					510
Val	Tyr	Ile	His	Ala	Leu	Leu	Ala	Ala	Thr	Leu	Gln	Leu	Asp	Asn
				515					520					525
Glu	Lys	Ile	Leu	Ser	Asp	Tyr	Gly	Thr	Thr	Phe	Val	Thr	Ala	Trp
				530					535					540
Lys	Asn	Thr	His	Asn	Tyr	Arg	Val	Trp	Asn	Ser	Asn	Lys	His	Pro
				545					550					555
Ala	Leu	Ala	Glu	Ile	Asn	Pro	Asn	His	Pro	Phe	Gln	Gly	Gln	Tyr
				560					565					570

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Ser	Val	Ser	Asp	Met	Lys	Leu	Arg	Phe	Ser	His	Ser	Val	Gln	Asn
				575					580					585
Ser	Glu	Arg	Gly	Lys	Lys	Ile	Gly	Asn	Val	Met	Val	Thr	Thr	Ser
				590					595					600
Arg	Asn	Val	Val	Gln	Thr	Gly	Lys	Ala	Val	Gly	Gln	Ser	Val	Gly
				605					610					615
Gly	Ala	Phe	Ser	Ser	Ala	Lys	Thr	Ala	Met	Ser	Ser	Trp	Leu	Ser
				620					625					630
Thr	Phe	Thr	Thr	Ser	Thr	Ser	Gln	Ser	Leu	Thr	Glu	Pro	Pro	Asp
				635					640					645
Glu	Lys	Pro												

<210> 10
 <211> 130
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 4521857CD1

Met	Tyr	Leu	Gln	Val	Glu	Thr	Arg	Thr	Ser	Ser	Arg	Leu	His	Leu
1				5					10					15
Lys	Arg	Ala	Pro	Gly	Ile	Arg	Ser	Trp	Ser	Leu	Leu	Val	Gly	Ile
				20					25					30
Leu	Ser	Ile	Gly	Leu	Ala	Ala	Ala	Tyr	Tyr	Ser	Gly	Asp	Ser	Leu
				35					40					45
Gly	Trp	Lys	Leu	Phe	Tyr	Val	Thr	Gly	Cys	Leu	Phe	Val	Ala	Val
				50					55					60
Gln	Asn	Leu	Glu	Asp	Trp	Glu	Glu	Ala	Ile	Phe	Asp	Lys	Ser	Thr
				65					70					75
Gly	Lys	Val	Val	Leu	Lys	Thr	Phe	Ser	Leu	Tyr	Lys	Lys	Leu	Leu
				80					85					90
Thr	Leu	Phe	Arg	Ala	Gly	His	Asp	Gln	Val	Val	Val	Leu	Leu	His
				95					100					105
Val	Val	Pro	Asp	Thr	Ala	Ser	Ser	Pro	Trp	Trp	Thr	Ser	Pro	Ala
				110					115					120
Val	Arg	Cys	Phe	Pro	Lys	Gly	Ser	Glu	Gly					
				125					130					

<210> 11
 <211> 279
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 4722253CD1

Met	Gly	Arg	Gly	Leu	Arg	Trp	Trp	Gly	Gly	Arg	Gly	Arg	Arg	His
1				5					10					15
Gly	Gln	Ala	Pro	Glu	Trp	Gly	Pro	Leu	Val	Gly	Ala	Arg	Leu	Lys
				20					25					30
Gly	Val	Ala	Arg	Ala	Ala	Ser	Leu	Val	Gly	Arg	Arg	Arg	Ala	Gly
				35					40					45
Thr	Gly	Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala
				50					55					60
Leu	Ala	His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys
				65					70					75
Phe	Ser	Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val

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

<210> 12

<211> 458

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4878134CD1

<400> 12

Met	Pro	Thr	Ile	Leu	Trp	Leu	Met	Asp	Trp	Ser	Asp	Met	Asn	Ser
1				5					10					15
Asn	Leu	Asp	Leu	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Ile	Ser	Ser	Phe
				20					25					30
Val	Leu	Ile	Thr	Gly	Cys	Ala	Asn	Met	Leu	Leu	Met	Ala	Ala	Leu
				35					40					45
Trp	Gly	Leu	Tyr	Met	Ser	Leu	Val	Asn	Val	Gly	His	Val	Trp	Tyr
				50					55					60
Ser	Phe	Gly	Trp	Glu	Ser	Gln	Leu	Leu	Glu	Thr	Gly	Phe	Leu	Gly
				65					70					75
Ile	Phe	Leu	Cys	Pro	Leu	Trp	Thr	Leu	Ser	Arg	Leu	Pro	Gln	His
				80					85					90
Thr	Pro	Thr	Ser	Arg	Ile	Val	Leu	Trp	Gly	Phe	Arg	Trp	Leu	Ile
				95					100					105
Phe	Arg	Ile	Met	Leu	Gly	Ala	Gly	Leu	Ile	Lys	Ile	Arg	Gly	Asp
				110					115					120
Arg	Cys	Trp	Arg	Asp	Leu	Thr	Cys	Met	Asp	Phe	His	Tyr	Glu	Thr
				125					130					135
Gln	Pro	Met	Pro	Asn	Pro	Val	Ala	Tyr	Tyr	Leu	His	His	Ser	Pro
				140					145					150
Trp	Trp	Phe	His	Arg	Phe	Glu	Thr	Leu	Ser	Asn	His	Phe	Ile	Glu
				155					160					165
Leu	Leu	Val	Pro	Phe	Phe	Leu	Phe	Leu	Gly	Arg	Arg	Ala	Cys	Ile
				170					175					180
Ile	His	Gly	Val	Leu	Gln	Ile	Leu	Phe	Gln	Ala	Val	Leu	Ile	Val

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	185		190		195
Ser Gly Asn Leu	Ser Phe Leu Asn Trp	Leu Thr Met Val Pro	Ser		
	200		205		210
Leu Ala Cys Phe	Asp Asp Ala Thr Leu	Gly Phe Leu Phe Pro	Ser		
	215		220		225
Gly Pro Gly Ser	Leu Lys Asp Arg Val	Leu Gln Met Gln Arg	Asp		
	230		235		240
Ile Arg Gly Ala	Arg Pro Glu Pro Arg	Phe Gly Ser Val Val	Arg		
	245		250		255
Arg Ala Ala Asn	Val Ser Leu Gly Val	Leu Leu Ala Trp Leu	Ser		
	260		265		270
Val Pro Val Val	Leu Asn Leu Leu Ser	Ser Arg Gln Val Met	Asn		
	275		280		285
Thr His Phe Asn	Ser Leu His Ile Val	Asn Thr Tyr Gly Ala	Phe		
	290		295		300
Gly Ser Ile Thr	Lys Glu Arg Ala Glu	Val Ile Leu Gln Gly	Thr		
	305		310		315
Ala Ser Ser Asn	Ala Ser Ala Pro Asp	Ala Met Trp Glu Asp	Tyr		
	320		325		330
Glu Phe Lys Cys	Lys Pro Gly Asp Pro	Ser Arg Arg Pro Cys	Leu		
	335		340		345
Ile Ser Pro Tyr	His Tyr Arg Leu Asp	Trp Leu Met Trp Phe	Ala		
	350		355		360
Ala Phe Gln Thr	Tyr Glu His Asn Asp	Trp Ile Ile His Leu	Ala		
	365		370		375
Gly Lys Leu Leu	Ala Ser Asp Ala Glu	Ala Leu Ser Leu Leu	Ala		
	380		385		390
His Asn Pro Phe	Ala Gly Arg Pro Pro	Pro Arg Trp Val Arg	Gly		
	395		400		405
Glu His Tyr Arg	Tyr Lys Phe Ser Arg	Pro Gly Gly Arg His	Ala		
	410		415		420
Ala Glu Gly Lys	Trp Trp Val Arg Lys	Arg Ile Gly Ala Tyr	Phe		
	425		430		435
Pro Pro Leu Ser	Leu Glu Glu Leu Arg	Pro Tyr Phe Arg Asp	Arg		
	440		445		450
Gly Trp Pro Leu	Pro Gly Pro Leu				
	455				

<210> 13

<211> 173

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5050133CD1

<400> 13

Met Leu Leu Val	Asp Ala Asp Gln Pro	Glu Pro Met Arg Ser	Gly
1	5	10	15
Ala Arg Glu Leu	Ala Leu Phe Leu Thr	Pro Glu Pro Gly Ala	Glu
	20	25	30
Ala Lys Glu Val	Glu Glu Thr Ile Glu	Gly Met Leu Leu Arg	Leu
	35	40	45
Glu Glu Phe Cys	Ser Leu Ala Asp Leu	Ile Arg Ser Asp Thr	Ser
	50	55	60
Gln Ile Leu Glu	Glu Asn Ile Pro Val	Leu Lys Ala Lys Leu	Thr
	65	70	75
Glu Met Arg Gly	Ile Tyr Ala Lys Val	Asp Arg Leu Glu Ala	Phe
	80	85	90
Val Lys Met Val	Gly His His Val Ala	Phe Leu Glu Ala Asp	Val
	95	100	105
Leu Gln Ala Glu	Arg Asp His Gly Ala	Phe Pro Gln Ala Leu	Arg

<400>	14														
Met	Gly	Ala	Ser	Ser	Ser	Ser	Ala	Leu	Ala	Arg	Leu	Gly	Leu	Pro	
1				5					10					15	
Ala	Arg	Pro	Trp	Pro	Arg	Trp	Leu	Gly	Val	Ala	Ala	Leu	Gly	Leu	
				20					25					30	
Ala	Ala	Val	Ala	Leu	Gly	Thr	Val	Ala	Trp	Arg	Arg	Ala	Trp	Pro	
				35					40					45	
Arg	Arg	Arg	Arg	Arg	Leu	Gln	Gln	Val	Gly	Thr	Val	Ala	Lys	Leu	
				50					55					60	
Trp	Ile	Tyr	Pro	Val	Lys	Ser	Cys	Lys	Gly	Val	Pro	Val	Ser	Glu	
				65					70					75	
Ala	Glu	Cys	Thr	Ala	Met	Gly	Leu	Arg	Ser	Gly	Asn	Leu	Arg	Asp	
				80					85					90	
Arg	Phe	Trp	Leu	Val	Ile	Lys	Glu	Asp	Gly	His	Met	Val	Thr	Ala	
				95					100					105	
Arg	Gln	Glu	Pro	Arg	Leu	Val	Leu	Ile	Ser	Ile	Ile	Tyr	Glu	Asn	
				110					115					120	
Asn	Cys	Leu	Ile	Phe	Arg	Ala	Pro	Asp	Met	Asp	Gln	Leu	Val	Leu	
				125					130					135	
Pro	Ser	Lys	Gln	Pro	Ser	Ser	Asn	Lys	Leu	His	Asn	Cys	Arg	Ile	
				140					145					150	
Phe	Gly	Leu	Asp	Ile	Lys	Gly	Arg	Asp	Cys	Gly	Asn	Glu	Ala	Ala	
				155					160					165	
Lys	Trp	Phe	Thr	Asn	Phe	Leu	Lys	Thr	Glu	Ala	Tyr	Arg	Leu	Val	
				170					175					180	
Gln	Phe	Glu	Thr	Asn	Met	Lys	Gly	Arg	Thr	Ser	Arg	Lys	Leu	Leu	
				185					190					195	
Pro	Thr	Leu	Asp	Gln	Asn	Phe	Gln	Val	Ala	Tyr	Pro	Asp	Tyr	Cys	
				200					205					210	
Pro	Leu	Leu	Ile	Met	Thr	Asp	Ala	Ser	Leu	Val	Asp	Leu	Asn	Thr	
				215					220					225	
Arg	Met	Glu	Lys	Lys	Met	Lys	Met	Glu	Asn	Phe	Arg	Pro	Asn	Ile	
				230					235					240	
Val	Val	Thr	Gly	Cys	Asp	Ala	Phe	Glu	Glu	Asp	Thr	Trp	Asp	Glu	
				245					250					255	
Leu	Leu	Ile	Gly	Ser	Val	Glu	Val	Lys	Lys	Val	Met	Ala	Cys	Pro	
				260					265					270	
Arg	Cys	Ile	Leu	Thr	Thr	Val	Asp	Pro	Asp	Thr	Gly	Val	Ile	Asp	
				275					280					285	
Arg	Lys	Gln	Pro	Leu	Asp	Thr	Leu	Lys	Ser	Tyr	Arg	Leu	Cys	Asp	
				290					295					300	
Pro	Ser	Glu	Arg	Glu	Leu	Tyr	Lys	Leu	Ser	Pro	Leu	Phe	Gly	Ile	
				305					310					315	
Tyr	Tyr	Ser	Val	Glu	Lys	Ile	Gly	Ser	Leu	Arg	Val	Gly	Asp	Pro	

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	320	325	330
Val Tyr Arg Met Val			
	335		

<210> 15
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 5677286CD1

<400> 15
 Met His Ser Pro Ala Ser Gly Pro Leu Leu Pro Pro Leu Arg Val
 1 5 10 15
 Pro Trp Leu Pro Pro Val Val Leu Gly Asn Leu Gly Pro Ser Pro
 20 25 30
 Ala Ser Pro Ala Ser His Ser Ser Ser Leu Val Thr Leu Arg Glu
 35 40 45
 Leu Arg Ala Arg Leu Val Ala Gly Leu Leu Cys Phe Cys Pro Arg
 50 55 60
 Leu Leu Trp Ser Leu Ala Gly Asn Ser Met Ile
 65 70

<210> 16
 <211> 148
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 6436791CD1

<400> 16
 Met Leu Pro Arg Gly Leu Lys Met Ala Pro Arg Gly Lys Arg Leu
 1 5 10 15
 Ser Ser Thr Pro Leu Glu Ile Leu Phe Phe Leu Asn Gly Trp Tyr
 20 25 30
 Asn Ala Thr Tyr Phe Leu Leu Glu Leu Phe Ile Phe Leu Tyr Lys
 35 40 45
 Gly Val Leu Leu Pro Tyr Pro Thr Ala Asn Leu Val Leu Asp Val
 50 55 60
 Val Met Leu Leu Leu Tyr Leu Gly Ile Glu Val Ile Arg Leu Phe
 65 70 75
 Phe Gly Thr Lys Gly Asn Leu Cys Gln Arg Lys Met Pro Leu Ser
 80 85 90
 Ile Ser Val Ala Leu Thr Phe Pro Ser Ala Met Met Ala Ser Tyr
 95 100 105
 Tyr Leu Leu Leu Gln Thr Tyr Val Leu Arg Leu Glu Ala Ile Met
 110 115 120
 Asn Gly Ile Leu Leu Phe Phe Cys Gly Ser Glu Leu Leu Leu Glu
 125 130 135
 Val Leu Thr Leu Ala Ala Phe Ser Ser Met Asp Thr Ile
 140 145

<210> 17
 <211> 231
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature

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Met	Lys	Thr	Leu	125	Gln	Val	Lys	Asp	Gln	130	Ala	Ile	Thr	Thr	Arg	Val	135
				140						145							150
Gln	Val	Arg	Asn	155	Leu	Val	Tyr	Thr	Val	160	Lys	Ile	Asn	Pro	Thr	Leu	165
				170						175							180
Glu	Leu	Ser	Ser	185	Gly	Phe	Arg	Lys	Glu	190	Leu	Leu	Asp	Ile	Ser	Asp	195
				200						205							210
Arg	Leu	Glu	Asn	215	Asn	Gln	Thr	Arg	Met	220	Ala	Thr	Tyr	Leu	Ala	Glu	225
				230						235							240
Leu	Leu	Val	Leu	245	Asn	Tyr	Gly	Thr	His	250	Val	Thr	Thr	Ser	Val	Asp	255
				260						265							270
Ala	Gly	Ala	Ala	275	Leu	Ile	Gln	Glu	Asp	280	His	Leu	Arg	Ala	Ser	Phe	285
				290						295							300
Leu	Gln	Asp	Ser	305	Gln	Ser	Ser	Arg	Ser	310	Ala	Val	Thr	Ala	Ser	Ala	315
				320						325							330
Gly	Leu	Ala	Phe	335	Gln	Asn	Thr	Val	Asn	340	Phe	Lys	Phe	Glu	Glu	Asn	345
				350						355							360
Tyr	Thr	Ser	Gln	365	Asn	Val	Leu	Thr	Lys	370	Ser	Tyr	Leu	Ser	Asn	Arg	375
				380						385							390
Thr	Asn	Ser	Arg	395	Val	Gln	Ser	Ile	Gly	400	Gly	Val	Pro	Phe	Tyr	Pro	405
				410						415							420
Gly	Ile	Thr	Leu	425	Gln	Ala	Trp	Gln	Gln	430	Gly	Ile	Thr	Asn	His	Leu	435
				440						445							450
Val	Ala	Ile	Asp	455	Arg	Ser	Gly	Leu	Pro	460	Leu	His	Phe	Phe	Ile	Asn	465
				470						475							480
Pro	Asn	Met	Leu	485	Pro	Asp	Leu	Pro	Gly	490	Pro	Leu	Val	Lys	Lys	Val	495
				500						505							510
Ser	Lys	Thr	Val	515	Glu	Thr	Ala	Val	Lys	520	Arg	Tyr	Tyr	Thr	Phe	Asn	525
				530						535							540
Thr	Tyr	Pro	Gly	545	Cys	Thr	Asp	Leu	Asn	550	Ser	Pro	Asn	Phe	Asn	Phe	555
				560						565							570
Gln	Ala	Asn	Thr	575	Asp	Asp	Gly	Ser	Cys	580	Glu	Gly	Lys	Met	Thr	Asn	585
				590						595							600
Phe	Ser	Phe	Gly		Gly	Val	Tyr	Gln	Glu		Cys	Thr	Gln	Leu	Ser	Gly	
Asn	Arg	Asp	Val		Leu	Leu	Cys	Gln	Lys		Leu	Glu	Gln	Lys	Asn	Pro	
Leu	Thr	Gly	Asp		Phe	Ser	Cys	Pro	Ser		Gly	Tyr	Ser	Pro	Val	His	
Leu	Leu	Ser	Gln		Ile	His	Glu	Glu	Gly		Tyr	Asn	His	Leu	Glu	Cys	
His	Arg	Lys	Cys		Thr	Leu	Leu	Val	Phe		Cys	Lys	Thr	Val	Cys	Glu	
Asp	Val	Phe	Gln		Val	Ala	Lys	Ala	Glu		Phe	Arg	Ala	Phe	Trp	Cys	
Val	Ala	Ser	Ser		Gln	Val	Pro	Glu	Asn		Ser	Gly	Leu	Leu	Phe	Gly	
Gly	Leu	Phe	Ser		Ser	Lys	Ser	Ile	Asn		Pro	Met	Thr	Asn	Ala	Gln	
Ser	Cys	Pro	Ala		Gly	Tyr	Phe	Pro	Leu		Arg	Leu	Phe	Glu	Asn	Leu	
Lys	Val	Cys	Val		Ser	Gln	Asp	Tyr	Glu		Leu	Gly	Ser	Arg	Phe	Ala	
Val	Pro	Phe	Gly		Gly	Phe	Phe	Ser	Cys		Thr	Val	Gly	Asn	Pro	Leu	
Val	Asp	Pro	Ala		Ile	Ser	Arg	Asp	Leu		Gly	Ala	Pro	Ser	Leu	Lys	
Lys	Cys	Pro	Gly		Gly	Phe	Ser	Gln	His		Pro	Ala	Leu	Ile	Ser	Asp	
Gly	Cys	Gln	Val		Ser	Tyr	Cys	Val	Lys		Ser	Gly	Leu	Phe	Thr	Gly	
Gly	Ser	Leu	Pro		Pro	Ala	Arg	Leu	Pro		Pro	Phe	Thr	Arg	Pro	Pro	

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Leu	Met	Ser	Gln	Ala	Ala	Thr	Asn	Thr	Val	Ile	Val	Thr	Asn	Ser
				605					610					615
Glu	Asn	Ala	Arg	Ser	Trp	Ile	Lys	Asp	Ser	Gln	Thr	His	Gln	Trp
				620					625					630
Arg	Leu	Gly	Glu	Pro	Ile	Glu	Leu	Arg	Arg	Ala	Met	Asn	Val	Ile
				635					640					645
His	Gly	Asp	Gly	Gly	Gly	Leu	Ser	Gly	Gly	Ala	Ala	Ala	Gly	Val
				650					655					660
Thr	Val	Gly	Val	Thr	Thr	Ile	Leu	Ala	Val	Val	Ile	Thr	Leu	Ala
				665					670					675
Ile	Tyr	Gly	Thr	Arg	Lys	Phe	Lys	Lys	Lys	Ala	Tyr	Gln	Ala	Ile
				680					685					690
Glu	Glu	Arg	Gln	Ser	Leu	Val	Pro	Gly	Thr	Ala	Ala	Thr	Gly	Asp
				695					700					705
Thr	Thr	Tyr	Gln	Glu	Gln	Gly	Gln	Ser	Pro	Ala				
				710					715					

<210> 19

<211> 519

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3506590CD1

<400> 19

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

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Cys	Pro	Glu	Pro	Lys	Ser	Cys	Asp	Thr	Pro	Pro	Pro	Cys	Pro	Arg
				275					280					285
Cys	Pro	Glu	Pro	Lys	Ser	Cys	Asp	Thr	Pro	Pro	Pro	Cys	Pro	Arg
				290					295					300
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
				305					310					315
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
				320					325					330
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
				335					340					345
Gln	Phe	Lys	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
				350					355					360
Thr	Lys	Leu	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Phe	Arg	Val	Val
				365					370					375
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu
				380					385					390
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu
				395					400					405
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
				410					415					420
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val
				425					430					435
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala
				440					445					450
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Asn	Thr
				455					460					465
Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
				470					475					480
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Ile	Phe
				485					490					495
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	Arg	Tyr	Thr	Gln
				500					505					510
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
				515										

<210> 20

<211> 172

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 003600CD1

<400> 20

Met	Leu	Thr	Glu	Val	Met	Glu	Val	Trp	His	Gly	Leu	Val	Ile	Ala
1				5					10					15
Val	Val	Ser	Leu	Phe	Leu	Gln	Ala	Cys	Phe	Leu	Thr	Ala	Ile	Asn
				20					25					30
Tyr	Leu	Leu	Ser	Arg	His	Met	Ala	His	Lys	Ser	Glu	Gln	Ile	Leu
				35					40					45
Lys	Ala	Ala	Ser	Leu	Gln	Val	Pro	Arg	Pro	Ser	Pro	Gly	His	His
				50					55					60
His	Pro	Pro	Ala	Val	Lys	Glu	Met	Lys	Glu	Thr	Gln	Thr	Glu	Arg
				65					70					75
Asp	Ile	Pro	Met	Ser	Asp	Ser	Leu	Tyr	Arg	His	Asp	Ser	Asp	Thr
				80					85					90
Pro	Ser	Asp	Ser	Leu	Asp	Ser	Ser	Cys	Ser	Ser	Pro	Pro	Ala	Cys
				95					100					105
Gln	Ala	Thr	Glu	Asp	Val	Asp	Tyr	Thr	Gln	Val	Val	Phe	Ser	Asp
				110					115					120
Pro	Gly	Glu	Leu	Lys	Asn	Asp	Ser	Pro	Leu	Asp	Tyr	Glu	Asn	Ile
				125					130					135

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Lys	Glu	Ile	Thr	Asp	Tyr	Val	Asn	Val	Asn	Pro	Glu	Arg	His	Lys
				140					145					150
Pro	Ser	Phe	Trp	Tyr	Phe	Val	Asn	Pro	Ala	Leu	Ser	Glu	Pro	Ala
				155					160					165
Glu	Tyr	Asp	Gln	Val	Ala	Met								
				170										

<210> 21

<211> 314

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1251534CD1

<400> 21

Met	Gly	Leu	Leu	Asp	Ser	Glu	Pro	Gly	Ser	Val	Leu	Asn	Val	Val
1				5					10					15
Ser	Thr	Ala	Leu	Asn	Asp	Thr	Val	Glu	Phe	Tyr	Arg	Trp	Thr	Trp
				20					25					30
Ser	Ile	Ala	Asp	Lys	Arg	Val	Glu	Asn	Trp	Pro	Leu	Met	Gln	Ser
				35					40					45
Pro	Trp	Pro	Thr	Leu	Ser	Ile	Ser	Thr	Leu	Tyr	Leu	Leu	Phe	Val
				50					55					60
Trp	Leu	Gly	Pro	Lys	Trp	Met	Lys	Asp	Arg	Glu	Pro	Phe	Gln	Met
				65					70					75
Arg	Leu	Val	Leu	Ile	Ile	Tyr	Asn	Phe	Gly	Met	Val	Leu	Leu	Asn
				80					85					90
Leu	Phe	Ile	Phe	Arg	Glu	Leu	Phe	Met	Gly	Ser	Tyr	Asn	Ala	Gly
				95					100					105
Tyr	Ser	Tyr	Ile	Cys	Gln	Ser	Val	Asp	Tyr	Ser	Asn	Asn	Val	His
				110					115					120
Glu	Val	Arg	Ile	Ala	Ala	Ala	Leu	Trp	Trp	Tyr	Phe	Val	Ser	Lys
				125					130					135
Gly	Val	Glu	Tyr	Leu	Asp	Thr	Val	Phe	Phe	Ile	Leu	Arg	Lys	Lys
				140					145					150
Asn	Asn	Gln	Val	Ser	Phe	Leu	His	Val	Tyr	His	His	Cys	Thr	Met
				155					160					165
Phe	Thr	Leu	Trp	Trp	Ile	Gly	Ile	Lys	Trp	Val	Ala	Gly	Gly	Gln
				170					175					180
Ala	Phe	Phe	Gly	Ala	Gln	Leu	Asn	Ser	Phe	Ile	His	Val	Ile	Met
				185					190					195
Tyr	Ser	Tyr	Tyr	Gly	Leu	Thr	Ala	Phe	Gly	Pro	Trp	Ile	Gln	Lys
				200					205					210
Tyr	Leu	Trp	Trp	Lys	Arg	Tyr	Leu	Thr	Met	Leu	Gln	Leu	Ile	Gln
				215					220					225
Phe	His	Val	Thr	Ile	Gly	His	Thr	Ala	Leu	Ser	Leu	Tyr	Thr	Asp
				230					235					240
Cys	Pro	Phe	Pro	Lys	Trp	Met	His	Trp	Ala	Leu	Ile	Ala	Tyr	Ala
				245					250					255
Ile	Ser	Phe	Ile	Phe	Leu	Phe	Leu	Asn	Phe	Tyr	Ile	Arg	Thr	Tyr
				260					265					270
Lys	Glu	Pro	Lys	Lys	Pro	Lys	Ala	Gly	Lys	Thr	Ala	Met	Asn	Gly
				275					280					285
Ile	Ser	Ala	Asn	Gly	Val	Ser	Lys	Ser	Glu	Lys	Gln	Leu	Met	Ile
				290					295					300
Glu	Asn	Gly	Lys	Lys	Gln	Lys	Asn	Gly	Lys	Ala	Lys	Gly	Asp	
				305					310					

<210> 22

<211> 542

<212> PRT

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<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1402211CD1

<400> 22

Met	Asn	Gly	Lys	Arg	Pro	Ala	Glu	Pro	Gly	Pro	Ala	Arg	Val	Gly	1	5	10	15
Lys	Lys	Gly	Lys	Lys	Glu	Val	Met	Ala	Glu	Phe	Ser	Asp	Ala	Val	20	25	30	
Thr	Glu	Glu	Thr	Leu	Lys	Lys	Gln	Val	Ala	Glu	Ala	Trp	Ser	Arg	35	40	45	
Arg	Thr	Pro	Phe	Ser	His	Glu	Val	Ile	Val	Met	Asp	Met	Asp	Pro	50	55	60	
Phe	Leu	His	Cys	Val	Ile	Pro	Asn	Phe	Ile	Gln	Ser	Gln	Asp	Phe	65	70	75	
Leu	Glu	Gly	Leu	Gln	Lys	Glu	Leu	Met	Asn	Leu	Asp	Phe	His	Glu	80	85	90	
Lys	Tyr	Asn	Asp	Leu	Tyr	Lys	Phe	Gln	Gln	Ser	Asp	Asp	Leu	Lys	95	100	105	
Lys	Arg	Arg	Glu	Pro	His	Ile	Ser	Thr	Leu	Arg	Lys	Ile	Leu	Phe	110	115	120	
Glu	Asp	Phe	Arg	Ser	Trp	Leu	Ser	Asp	Ile	Ser	Lys	Ile	Asp	Leu	125	130	135	
Glu	Ser	Thr	Ile	Asp	Met	Ser	Cys	Ala	Lys	Tyr	Glu	Phe	Thr	Asp	140	145	150	
Ala	Leu	Leu	Cys	His	Asp	Asp	Glu	Leu	Glu	Gly	Arg	Arg	Ile	Ala	155	160	165	
Phe	Ile	Leu	Tyr	Leu	Val	Pro	Pro	Trp	Asp	Arg	Ser	Met	Gly	Gly	170	175	180	
Thr	Leu	Asp	Leu	Tyr	Ser	Ile	Asp	Glu	His	Phe	Gln	Pro	Lys	Gln	185	190	195	
Ile	Val	Lys	Ser	Leu	Ile	Pro	Ser	Trp	Asn	Lys	Leu	Val	Phe	Phe	200	205	210	
Glu	Val	Ser	Pro	Val	Ser	Phe	His	Gln	Val	Ser	Glu	Val	Leu	Ser	215	220	225	
Glu	Glu	Lys	Ser	Arg	Leu	Ser	Ile	Ser	Gly	Trp	Phe	His	Gly	Pro	230	235	240	
Ser	Leu	Thr	Arg	Pro	Pro	Asn	Tyr	Phe	Glu	Pro	Pro	Ile	Pro	Arg	245	250	255	
Ser	Pro	His	Ile	Pro	Gln	Asp	His	Glu	Ile	Leu	Tyr	Asp	Trp	Ile	260	265	270	
Asn	Pro	Thr	Tyr	Leu	Asp	Met	Asp	Tyr	Gln	Val	Gln	Ile	Gln	Glu	275	280	285	
Glu	Phe	Glu	Glu	Ser	Ser	Glu	Ile	Leu	Leu	Lys	Glu	Phe	Leu	Lys	290	295	300	
Pro	Glu	Lys	Phe	Thr	Lys	Val	Cys	Glu	Ala	Leu	Glu	His	Gly	His	305	310	315	
Val	Glu	Trp	Ser	Ser	Arg	Gly	Pro	Pro	Asn	Lys	Arg	Phe	Tyr	Glu	320	325	330	
Lys	Ala	Glu	Glu	Ser	Lys	Leu	Pro	Glu	Ile	Leu	Lys	Glu	Cys	Met	335	340	345	
Lys	Leu	Phe	Arg	Ser	Glu	Ala	Leu	Phe	Leu	Leu	Leu	Ser	Asn	Phe	350	355	360	
Thr	Gly	Leu	Lys	Leu	His	Phe	Leu	Ala	Pro	Ser	Glu	Glu	Asp	Glu	365	370	375	
Met	Asn	Asp	Lys	Lys	Glu	Ala	Glu	Thr	Thr	Asp	Ile	Thr	Glu	Glu	380	385	390	
Gly	Thr	Ser	His	Ser	Pro	Pro	Glu	Pro	Glu	Asn	Asn	Gln	Met	Ala	395	400	405	
Ile	Ser	Asn	Asn	Ser	Gln	Gln	Ser	Asn	Glu	Gln	Thr	Asp	Pro	Glu	410	415	420	

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Pro	Glu	Glu	Asn	Glu	Thr	Lys	Lys	Glu	Ser	Ser	Val	Pro	Met	Cys
				425					430					435
Gln	Gly	Glu	Leu	Arg	His	Trp	Lys	Thr	Gly	His	Tyr	Thr	Leu	Ile
				440					445					450
His	Asp	His	Ser	Lys	Ala	Glu	Phe	Ala	Leu	Asp	Leu	Ile	Leu	Tyr
				455					460					465
Cys	Gly	Cys	Glu	Gly	Trp	Glu	Pro	Glu	Tyr	Gly	Gly	Phe	Thr	Ser
				470					475					480
Tyr	Ile	Ala	Lys	Gly	Glu	Asp	Glu	Glu	Leu	Leu	Thr	Val	Asn	Pro
				485					490					495
Glu	Ser	Asn	Ser	Leu	Ala	Leu	Val	Tyr	Arg	Asp	Arg	Glu	Thr	Leu
				500					505					510
Lys	Phe	Val	Lys	His	Ile	Asn	His	Arg	Ser	Leu	Glu	Gln	Lys	Lys
				515					520					525
Thr	Phe	Pro	Asn	Arg	Thr	Gly	Phe	Trp	Asp	Phe	Ser	Phe	Ile	Tyr
				530					535					540
Tyr	Glu													

<210> 23

<211> 715

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1623474CD1

<400> 23

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

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Pro	Lys	Lys	Glu	Lys	Thr	Ile	Val	Ile	Arg	Pro	Pro	Phe	Leu	Arg	
				260					265					270	
Pro	Glu	Val	Ser	Asp	Gly	Gln	Ile	Thr	Val	Lys	Ile	Met	Asp	Asn	
				275					280					285	
Gly	Ile	Gln	Gly	Glu	Leu	Arg	Arg	Thr	Lys	Ser	Lys	Gly	Ser	Leu	
				290					295					300	
Glu	Ile	Thr	Glu	Ser	Gln	Ser	Ala	Asp	Ala	Glu	Pro	Pro	Pro	Pro	
				305					310					315	
Pro	Lys	Pro	Asp	Leu	Ser	Arg	Tyr	Thr	Gly	Leu	Arg	Thr	His	Leu	
				320					325					330	
Gly	Leu	Ala	Thr	Asn	Glu	Asp	Ser	Ser	Leu	Leu	Ala	Lys	Asp	Ser	
				335					340					345	
Pro	Pro	Thr	Pro	Thr	Met	Tyr	Lys	Tyr	Arg	Pro	Gly	Tyr	Ser	Ser	
				350					355					360	
Ser	Ser	Thr	Ser	Ala	Ala	Met	Pro	His	Ser	Ser	Ser	Ala	Lys	Leu	
				365					370					375	
Ser	Arg	Gly	Asp	Ser	Leu	Lys	Glu	Pro	Thr	Ser	Ile	Ala	Glu	Ser	
				380					385					390	
Ser	Arg	His	Pro	Ser	Tyr	Arg	Ser	Glu	Pro	Ser	Leu	Glu	Pro	Glu	
				395					400					405	
Ser	Phe	Arg	Ser	Pro	Thr	Phe	Gly	Lys	Ser	Phe	His	Phe	Asp	Pro	
				410					415					420	
Leu	Ser	Ser	Gly	Ser	Arg	Ser	Ser	Ser	Leu	Lys	Ser	Ala	Gln	Gly	
				425					430					435	
Thr	Gly	Phe	Glu	Leu	Gly	Gln	Leu	Gln	Ser	Ile	Arg	Ser	Glu	Gly	
				440					445					450	
Thr	Thr	Ser	Thr	Ser	Tyr	Lys	Ser	Leu	Ala	Asn	Gln	Thr	Arg	Asn	
				455					460					465	
Gly	Ser	Leu	Ser	Tyr	Asp	Ser	Leu	Leu	Thr	Pro	Ser	Asp	Ser	Pro	
				470					475					480	
Asp	Phe	Glu	Ser	Val	Gln	Ala	Gly	Pro	Glu	Pro	Asp	Pro	Pro	Leu	
				485					490					495	
Gly	Tyr	Thr	Ser	Pro	Phe	Leu	Ser	Ala	Arg	Leu	Ala	Gln	Gln	Arg	
				500					505					510	
Glu	Ala	Glu	Arg	His	Pro	Arg	Leu	Val	Pro	Thr	Gly	Pro	Thr	His	
				515					520					525	
Arg	Glu	Pro	Ser	Pro	Val	Arg	Tyr	Asp	Asn	Leu	Ser	Arg	His	Ile	
				530					535					540	
Val	Ala	Ser	Leu	Gln	Glu	Arg	Glu	Lys	Leu	Leu	Arg	Gln	Ser	Pro	
				545					550					555	
Pro	Leu	Pro	Gly	Arg	Glu	Glu	Glu	Pro	Gly	Leu	Gly	Asp	Ser	Gly	
				560					565					570	
Ile	Gln	Ser	Thr	Pro	Gly	Ser	Gly	His	Ala	Pro	Arg	Thr	Ser	Ser	
				575					580					585	
Ser	Ser	Asp	Asp	Ser	Lys	Arg	Ser	Pro	Leu	Gly	Lys	Thr	Pro	Leu	
				590					595					600	
Gly	Arg	Pro	Ala	Val	Pro	Arg	Phe	Gly	Lys	Pro	Asp	Gly	Leu	Arg	
				605					610					615	
Gly	Arg	Gly	Val	Gly	Ser	Pro	Glu	Pro	Gly	Pro	Thr	Ala	Pro	Tyr	
				620					625					630	
Leu	Gly	Arg	Ser	Met	Ser	Tyr	Ser	Ser	Gln	Lys	Ala	Gln	Pro	Gly	
				635					640					645	
Val	Ser	Glu	Thr	Glu	Glu	Val	Ala	Leu	Gln	Pro	Leu	Leu	Thr	Pro	
				650					655					660	
Lys	Asp	Glu	Val	Gln	Leu	Lys	Thr	Thr	Tyr	Ser	Lys	Ser	Asn	Gly	
				665					670					675	
Gln	Pro	Lys	Ser	Leu	Gly	Ser	Ala	Ser	Pro	Gly	Pro	Gly	Gln	Pro	
				680					685					690	
Pro	Leu	Ser	Ser	Pro	Thr	Arg	Gly	Gly	Val	Lys	Lys	Val	Ser	Gly	
				695					700					705	
Val	Gly	Gly	Thr	Thr	Tyr	Glu	Ile	Ser	Val						
				710					715						

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<210> 24
 <211> 469
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1706443CD1

<400> 24

Met	Gly	Arg	Val	Arg	Arg	Ile	Tyr	Pro	Gln	Leu	Leu	Leu	Ala	Leu
1				5					10					15
Leu	Ile	Gln	Val	His	Tyr	His	Ile	Gly	Leu	Asn	Leu	Pro	Gly	Cys
				20					25					30
Val	Ala	Pro	Pro	Lys	Asp	Thr	Lys	Lys	Gly	Ala	Gln	Pro	Ser	Pro
				35					40					45
Phe	Val	Pro	Val	Arg	Trp	Val	Val	Lys	Val	Val	Lys	Thr	Leu	Leu
				50					55					60
Leu	Arg	Met	Gly	Cys	Ser	Tyr	Glu	Thr	Thr	Phe	Leu	Glu	Asp	Gln
				65					70					75
Gly	Gly	Trp	Glu	Leu	Met	Glu	Gln	Val	Glu	Ser	His	His	Arg	Gly
				80					85					90
Val	Ala	Leu	Leu	Ala	Arg	Ala	Met	Val	Gln	Tyr	Ser	Cys	Gln	Glu
				95					100					105
Leu	Cys	Arg	Ile	Leu	Tyr	Leu	Leu	Ile	Pro	Leu	Leu	Glu	Arg	Gly
				110					115					120
Asp	Glu	Lys	His	Arg	Ile	Thr	Ala	Thr	Ala	Phe	Phe	Val	Glu	Leu
				125					130					135
Leu	Gln	Met	Glu	Gln	Val	Arg	Arg	Ile	Pro	Glu	Glu	Tyr	Ser	Leu
				140					145					150
Gly	Arg	Met	Ala	Glu	Gly	Leu	Ser	His	His	Asp	Pro	Ile	Met	Lys
				155					160					165
Val	Leu	Ser	Ile	Arg	Gly	Leu	Val	Ile	Leu	Ala	Arg	Arg	Ser	Glu
				170					175					180
Lys	Thr	Ala	Lys	Val	Lys	Ala	Leu	Leu	Pro	Ser	Met	Val	Lys	Gly
				185					190					195
Leu	Lys	Asn	Met	Asp	Gly	Met	Leu	Val	Val	Glu	Ala	Val	His	Asn
				200					205					210
Leu	Lys	Ala	Val	Phe	Lys	Gly	Arg	Asp	Gln	Lys	Leu	Met	Asp	Ser
				215					220					225
Ala	Val	Tyr	Val	Glu	Met	Leu	Gln	Ile	Leu	Leu	Pro	His	Phe	Ser
				230					235					240
Asp	Ala	Arg	Glu	Asp	Val	Arg	Ser	Ser	Cys	Ile	Asn	Leu	Tyr	Gly
				245					250					255
Lys	Val	Val	Gln	Lys	Leu	Arg	Ala	Pro	Arg	Thr	Gln	Ala	Met	Glu
				260					265					270
Glu	Gln	Leu	Val	Ser	Thr	Leu	Val	Pro	Leu	Leu	Leu	Thr	Met	Gln
				275					280					285
Glu	Gly	Asn	Ser	Lys	Val	Ser	Gln	Lys	Cys	Val	Lys	Thr	Leu	Leu
				290					295					300
Arg	Cys	Ser	Tyr	Phe	Met	Ala	Trp	Glu	Leu	Pro	Lys	Arg	Ala	Tyr
				305					310					315
Ser	Arg	Lys	Pro	Trp	Asp	Asn	Gln	Gln	Gln	Thr	Val	Ala	Lys	Ile
				320					325					330
Cys	Lys	Cys	Leu	Val	Asn	Thr	His	Arg	Asp	Ser	Ala	Phe	Ile	Phe
				335					340					345
Leu	Ser	Gln	Ser	Leu	Glu	Tyr	Ala	Lys	Asn	Ser	Arg	Ala	Ser	Leu
				350					355					360
Arg	Lys	Cys	Ser	Val	Met	Phe	Ile	Gly	Ser	Leu	Val	Pro	Cys	Met
				365					370					375
Glu	Ser	Ile	Met	Thr	Glu	Asp	Arg	Leu	Asn	Glu	Val	Lys	Ala	Ala
				380					385					390
Leu	Asp	Asn	Leu	Arg	His	Asp	Pro	Glu	Ala	Ser	Val	Cys	Ile	Tyr

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				395					400					405
Ala	Ala	Gln	Val	Gln	Asp	His	Ile	Leu	Ala	Ser	Cys	Trp	Gln	Asn
				410					415					420
Ser	Trp	Leu	Pro	His	Gly	Asn	Ser	Trp	Val	Cys	Tyr	Ser	Ala	Thr
				425					430					435
Thr	His	Arg	Trp	Ser	Pro	Ser	Cys	Glu	Asn	Leu	Pro	Thr	Ser	His
				440					445					450
Gln	Arg	Arg	Ser	Trp	Ile	Met	Gln	Ala	Leu	Gly	Ser	Trp	Lys	Met
				455					460					465
Ser	Leu	Lys	Lys											

<210> 25

<211> 274

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1748627CD1

<400> 25

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

<210> 26

<211> 154

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<212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1818332CD1

<400> 26
 Met Ala Gly Pro Val Lys Asp Arg Glu Ala Phe Gln Arg Leu Asn
 1 5 10 15
 Phe Leu Tyr Gln Ala Ala His Cys Val Leu Ala Gln Asp Pro Glu
 20 25 30
 Asn Gln Ala Leu Ala Arg Phe Tyr Cys Tyr Thr Glu Arg Thr Ile
 35 40 45
 Ala Lys Arg Leu Val Leu Arg Arg Asp Pro Ser Val Lys Arg Thr
 50 55 60
 Leu Cys Arg Gly Cys Ser Ser Leu Leu Val Pro Gly Leu Thr Cys
 65 70 75
 Thr Gln Arg Gln Arg Arg Cys Arg Gly Gln Arg Trp Thr Val Gln
 80 85 90
 Thr Cys Leu Thr Cys Gln Arg Ser Gln Arg Phe Leu Asn Asp Pro
 95 100 105
 Gly His Leu Leu Trp Gly Asp Arg Pro Glu Ala Gln Leu Gly Ser
 110 115 120
 Gln Ala Asp Ser Lys Pro Leu Gln Pro Leu Pro Asn Thr Ala His
 125 130 135
 Ser Ile Ser Asp Arg Leu Pro Glu Glu Lys Met Gln Thr Gln Gly
 140 145 150
 Ser Ser Asn Gln

<210> 27
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1822832CD1

<400> 27
 Met Lys Phe Asp Trp Val Met Gly Leu Arg Ser Ile Thr Leu Lys
 1 5 10 15
 Asn Ser Ser Thr Gly Arg Gly Asp Gly Pro Lys Gln His Leu Gln
 20 25 30
 Ala Asp Pro Met Leu Ile Ile Arg Ala Arg Thr Leu Ser Leu Ser
 35 40 45
 Val Ser Leu Ser Val Ser Pro Leu Gly Leu Thr Pro His Trp Thr
 50 55 60
 Pro Leu His Pro Cys Pro Ser His Asn Thr Ala Ala Val Ser Ser
 65 70 75
 Ala Cys Leu Trp Glu Ser Pro Leu Phe Ser Ser Val Phe Phe Ser
 80 85 90
 Ser Cys Pro Ile Thr Pro Cys Thr Ser Pro Phe Pro
 95 100

<210> 28
 <211> 113
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature

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<223> Incyte ID No: 1832219CD1

<400> 28

Met	Ala	Gly	Pro	Ala	Ala	Ala	Phe	Arg	Arg	Leu	Gly	Ala	Leu	Ser
1				5					10					15
Gly	Ala	Ala	Ala	Leu	Gly	Phe	Ala	Ser	Tyr	Gly	Ala	His	Gly	Ala
				20					25					30
Gln	Phe	Pro	Asp	Ala	Tyr	Gly	Lys	Glu	Leu	Phe	Asp	Lys	Ala	Asn
				35					40					45
Lys	His	His	Phe	Leu	His	Ser	Leu	Ala	Leu	Leu	Gly	Val	Pro	His
				50					55					60
Cys	Arg	Lys	Pro	Leu	Trp	Ala	Gly	Leu	Leu	Leu	Ala	Ser	Gly	Thr
				65					70					75
Thr	Leu	Phe	Cys	Thr	Ser	Phe	Tyr	Tyr	Gln	Ala	Leu	Ser	Gly	Asp
				80					85					90
Pro	Ser	Ile	Gln	Thr	Leu	Ala	Pro	Ala	Gly	Gly	Thr	Leu	Leu	Leu
				95					100					105
Leu	Gly	Trp	Leu	Ala	Leu	Ala	Leu							
				110										

<210> 29

<211> 313

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1899010CD1

<400> 29

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

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				245					250					255
Phe	Gly	His	Phe	Lys	Phe	Cys	Ile	Thr	Leu	Phe	Gly	Gly	Tyr	Val
				260					265					270
Leu	Phe	Lys	Asp	Pro	Leu	Ser	Ile	Asn	Gln	Ala	Leu	Gly	Ile	Leu
				275					280					285
Cys	Thr	Leu	Phe	Gly	Ile	Leu	Ala	Tyr	Thr	His	Phe	Lys	Leu	Ser
				290					295					300
Glu	Gln	Glu	Gly	Ser	Arg	Ser	Lys	Leu	Ala	Gln	Arg	Pro		
				305					310					

<210> 30

<211> 195

<212> PRT

<213> Homo, sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2008768CD1

<400> 30

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

<210> 31

<211> 350

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2070984CD1

<400> 31

Met	Asn	Leu	Arg	Gly	Leu	Phe	Gln	Asp	Phe	Asn	Pro	Ser	Lys	Phe
1				5					10					15
Leu	Ile	Tyr	Ala	Cys	Leu	Leu	Leu	Phe	Ser	Val	Leu	Leu	Ala	Leu
				20					25					30
Arg	Leu	Asp	Gly	Ile	Ile	Gln	Trp	Ser	Tyr	Trp	Ala	Val	Phe	Ala

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Pro	Ile	Trp	Leu	Trp	Lys	Leu	Met	Val	Ile	Val	Gly	Ala	Ser	Val	35	40	45
Gly	Thr	Gly	Val	Trp	Ala	Arg	Asn	Pro	Gln	Tyr	Arg	Ala	Glu	Gly	50	55	60
Glu	Thr	Cys	Val	Glu	Phe	Lys	Ala	Met	Leu	Ile	Ala	Val	Gly	Ile	65	70	75
His	Leu	Leu	Leu	Leu	Met	Phe	Glu	Val	Leu	Val	Cys	Asp	Arg	Ile	80	85	90
Glu	Arg	Gly	Ser	His	Phe	Trp	Leu	Leu	Val	Phe	Met	Pro	Leu	Phe	95	100	105
Phe	Val	Ser	Pro	Val	Ser	Val	Ala	Ala	Cys	Val	Trp	Gly	Phe	Arg	110	115	120
His	Asp	Arg	Ser	Leu	Glu	Leu	Glu	Ile	Leu	Cys	Ser	Val	Asn	Ile	125	130	135
Leu	Gln	Phe	Ile	Phe	Ile	Ala	Leu	Arg	Leu	Asp	Lys	Ile	Ile	His	140	145	150
Trp	Pro	Trp	Leu	Val	Val	Cys	Val	Pro	Leu	Trp	Ile	Leu	Met	Ser	155	160	165
Phe	Leu	Cys	Leu	Val	Val	Leu	Tyr	Tyr	Ile	Val	Trp	Ser	Val	Leu	170	175	180
Phe	Leu	Arg	Ser	Met	Asp	Val	Ile	Ala	Glu	Gln	Arg	Arg	Thr	His	185	190	195
Ile	Thr	Met	Ala	Leu	Ser	Trp	Met	Thr	Ile	Val	Val	Pro	Leu	Leu	200	205	210
Thr	Phe	Glu	Ile	Leu	Leu	Val	His	Lys	Leu	Asp	Gly	His	Asn	Ala	215	220	225
Phe	Ser	Cys	Ile	Pro	Ile	Phe	Val	Pro	Leu	Trp	Leu	Ser	Leu	Ile	230	235	240
Thr	Leu	Met	Ala	Thr	Thr	Phe	Gly	Gln	Lys	Gly	Gly	Asn	His	Trp	245	250	255
Trp	Phe	Gly	Ile	Arg	Lys	Asp	Phe	Cys	Gln	Phe	Leu	Leu	Glu	Ile	260	265	270
Phe	Pro	Phe	Leu	Arg	Glu	Tyr	Gly	Asn	Ile	Ser	Tyr	Asp	Leu	His	275	280	285
His	Glu	Asp	Asn	Glu	Glu	Thr	Glu	Glu	Thr	Pro	Val	Pro	Glu	Pro	290	295	300
Pro	Lys	Ile	Ala	Pro	Met	Phe	Arg	Lys	Lys	Ala	Arg	Val	Val	Ile	305	310	315
Thr	Gln	Ser	Pro	Gly	Lys	Tyr	Val	Leu	Pro	Pro	Pro	Lys	Leu	Asn	320	325	330
Ile	Glu	Met	Pro	Asp											335	340	345
															350		

<210> 32

<211> 360

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2193240CD1

<400> 32

Met	Ser	Leu	Leu	Ala	Val	Ser	Arg	Arg	Ala	Gln	Lys	His	Ala	Leu	1	5	10	15
Lys	Ala	Asn	Leu	Ile	Asp	Asn	Cys	Met	Glu	Gln	Met	Lys	His	Ile	20	25	30	35
Asn	Ala	Gln	Leu	Asn	Leu	Asp	Ser	Leu	Arg	Pro	Gly	Lys	Ala	Ala	40	45	50	55
Leu	Lys	Lys	Lys	Glu	Asp	Gly	Val	Ile	Lys	Glu	Leu	Ser	Ile	Ala	60	65	70	75
Met	Gln	Leu	Leu	Arg	Asn	Cys	Leu	Tyr	Gln	Asn	Glu	Glu	Cys	Lys	80	85	90	95

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	65		70		75									
Glu	Ala	Ala	Leu	Glu	Ala	His	Leu	Val	Pro	Val	Leu	His	Ser	Leu
	80		85		90									
Trp	Pro	Trp	Ile	Leu	Met	Asp	Asp	Ser	Leu	Met	Gln	Ile	Ser	Leu
	95		100		105									
Gln	Leu	Leu	Cys	Val	Tyr	Thr	Ala	Asn	Phe	Pro	Asn	Gly	Cys	Ser
	110		115		120									
Ser	Leu	Cys	Trp	Ser	Ser	Cys	Gly	Gln	His	Pro	Val	Gln	Ala	Thr
	125		130		135									
His	Arg	Gly	Ala	Val	Ser	Asn	Ser	Leu	Met	Leu	Cys	Ile	Leu	Lys
	140		145		150									
Leu	Ala	Ser	Gln	Met	Pro	Leu	Glu	Asn	Thr	Thr	Val	Gln	Gln	Met
	155		160		165									
Val	Phe	Met	Leu	Leu	Ser	Asn	Leu	Ala	Leu	Ser	His	Asp	Cys	Lys
	170		175		180									
Gly	Val	Ile	Gln	Lys	Ser	Asn	Phe	Leu	Gln	Asn	Phe	Leu	Ser	Leu
	185		190		195									
Ala	Leu	Pro	Lys	Gly	Gly	Asn	Lys	His	Leu	Ser	Asn	Leu	Thr	Ile
	200		205		210									
Leu	Trp	Leu	Lys	Leu	Leu	Leu	Asn	Ile	Ser	Ser	Gly	Glu	Asp	Gly
	215		220		225									
Gln	Gln	Met	Ile	Leu	Arg	Leu	Asp	Gly	Cys	Leu	Asp	Leu	Leu	Thr
	230		235		240									
Glu	Met	Ser	Lys	Tyr	Lys	His	Lys	Ser	Ser	Pro	Leu	Leu	Pro	Leu
	245		250		255									
Leu	Ile	Phe	His	Asn	Val	Cys	Phe	Ser	Pro	Ala	Asn	Lys	Pro	Lys
	260		265		270									
Ile	Leu	Ala	Asn	Glu	Lys	Val	Ile	Thr	Val	Leu	Ala	Ala	Cys	Leu
	275		280		285									
Glu	Ser	Glu	Asn	Gln	Asn	Ala	Gln	Arg	Ile	Gly	Ala	Ala	Ala	Leu
	290		295		300									
Trp	Ala	Leu	Ile	Tyr	Asn	Tyr	Gln	Lys	Ala	Lys	Thr	Ala	Leu	Lys
	305		310		315									
Ser	Pro	Ser	Val	Lys	Arg	Arg	Val	Asp	Glu	Ala	Tyr	Ser	Leu	Ala
	320		325		330									
Lys	Lys	Thr	Phe	Pro	Asn	Ser	Glu	Ala	Asn	Pro	Leu	Asn	Ala	Tyr
	335		340		345									
Tyr	Leu	Lys	Cys	Leu	Glu	Asn	Leu	Val	Gln	Leu	Leu	Asn	Ser	Ser
	350		355		360									

<210> 33

<211> 559

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2235177CD1

<400> 33

Met	Gly	Ser	Arg	Ile	Lys	Gln	Asn	Pro	Glu	Thr	Thr	Phe	Glu	Val
1				5					10					15
Tyr	Val	Glu	Val	Ala	Tyr	Pro	Arg	Thr	Gly	Gly	Thr	Leu	Ser	Asp
				20					25					30
Pro	Glu	Val	Gln	Arg	Gln	Phe	Pro	Glu	Asp	Tyr	Ser	Asp	Gln	Glu
				35					40					45
Val	Leu	Gln	Thr	Leu	Thr	Lys	Phe	Cys	Phe	Pro	Phe	Tyr	Val	Asp
				50					55					60
Ser	Leu	Thr	Val	Ser	Gln	Val	Gly	Gln	Asn	Phe	Thr	Phe	Val	Leu
				65					70					75
Thr	Asp	Ile	Asp	Ser	Lys	Gln	Arg	Phe	Gly	Phe	Cys	Arg	Leu	Ser
				80					85					90

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Ser	Gly	Ala	Lys	Ser	Cys	Phe	Cys	Ile	Leu	Ser	Tyr	Leu	Pro	Trp
				95					100					105
Phe	Glu	Val	Phe	Tyr	Lys	Leu	Leu	Asn	Ile	Leu	Ala	Asp	Tyr	Thr
				110					115					120
Thr	Lys	Arg	Gln	Glu	Asn	Gln	Trp	Asn	Glu	Leu	Leu	Glu	Thr	Leu
				125					130					135
His	Lys	Leu	Pro	Ile	Pro	Asp	Pro	Gly	Val	Ser	Val	His	Leu	Ser
				140					145					150
Val	His	Ser	Tyr	Phe	Thr	Val	Pro	Asp	Thr	Arg	Glu	Leu	Pro	Ser
				155					160					165
Ile	Pro	Glu	Asn	Arg	Asn	Leu	Thr	Glu	Tyr	Phe	Val	Ala	Val	Asp
				170					175					180
Val	Asn	Asn	Met	Leu	His	Leu	Tyr	Ala	Ser	Met	Leu	Tyr	Glu	Arg
				185					190					195
Arg	Ile	Leu	Ile	Ile	Cys	Ser	Lys	Leu	Ser	Thr	Leu	Thr	Ala	Cys
				200					205					210
Ile	His	Gly	Ser	Ala	Ala	Met	Leu	Tyr	Pro	Met	Tyr	Trp	Gln	His
				215					220					225
Val	Tyr	Ile	Pro	Val	Leu	Pro	Pro	His	Leu	Leu	Asp	Tyr	Cys	Cys
				230					235					240
Ala	Pro	Met	Pro	Tyr	Leu	Ile	Gly	Ile	His	Leu	Ser	Leu	Met	Glu
				245					250					255
Lys	Val	Arg	Asn	Met	Ala	Leu	Asp	Asp	Val	Val	Ile	Leu	Asn	Val
				260					265					270
Asp	Thr	Asn	Thr	Leu	Glu	Thr	Pro	Phe	Asp	Asp	Leu	Gln	Ser	Leu
				275					280					285
Pro	Asn	Asp	Val	Ile	Ser	Ser	Leu	Lys	Asn	Arg	Leu	Lys	Lys	Val
				290					295					300
Ser	Thr	Thr	Thr	Gly	Asp	Gly	Val	Ala	Arg	Ala	Phe	Leu	Lys	Ala
				305					310					315
Gln	Ala	Ala	Phe	Phe	Gly	Ser	Tyr	Arg	Asn	Ala	Leu	Lys	Ile	Glu
				320					325					330
Pro	Glu	Glu	Pro	Ile	Thr	Phe	Cys	Glu	Glu	Ala	Phe	Val	Ser	His
				335					340					345
Tyr	Arg	Ser	Gly	Ala	Met	Arg	Gln	Phe	Leu	Gln	Asn	Ala	Thr	Gln
				350					355					360
Leu	Gln	Leu	Phe	Lys	Gln	Phe	Ile	Asp	Gly	Arg	Leu	Asp	Leu	Leu
				365					370					375
Asn	Ser	Gly	Glu	Gly	Phe	Ser	Asp	Val	Phe	Glu	Glu	Glu	Ile	Asn
				380					385					390
Met	Gly	Glu	Tyr	Ala	Gly	Ser	Asp	Lys	Leu	Tyr	His	Gln	Trp	Leu
				395					400					405
Ser	Thr	Val	Arg	Lys	Gly	Ser	Gly	Ala	Ile	Leu	Asn	Thr	Val	Lys
				410					415					420
Thr	Lys	Ala	Asn	Pro	Ala	Met	Lys	Thr	Val	Tyr	Lys	Phe	Ala	Lys
				425					430					435
Asp	His	Ala	Lys	Met	Gly	Ile	Lys	Glu	Val	Lys	Asn	Arg	Leu	Lys
				440					445					450
Gln	Lys	Asp	Ile	Ala	Glu	Asn	Gly	Cys	Ala	Pro	Thr	Pro	Glu	Glu
				455					460					465
Gln	Leu	Pro	Lys	Thr	Ala	Pro	Ser	Pro	Leu	Val	Glu	Ala	Lys	Asp
				470					475					480
Pro	Lys	Leu	Arg	Glu	Asp	Arg	Arg	Pro	Ile	Thr	Val	His	Phe	Gly
				485					490					495
Gln	Val	Arg	Pro	Pro	Arg	Pro	His	Val	Val	Lys	Arg	Pro	Lys	Ser
				500					505					510
Asn	Ile	Ala	Val	Glu	Gly	Arg	Arg	Thr	Ser	Val	Pro	Ser	Pro	Glu
				515					520					525
Gln	Asn	Thr	Ile	Ala	Thr	Pro	Ala	Thr	Leu	His	Ile	Leu	Gln	Lys
				530					535					540
Ser	Ile	Thr	His	Phe	Ala	Ala	Lys	Phe	Pro	Thr	Arg	Gly	Trp	Thr
				545					550					555
Ser	Ser	Ser	His											

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<210> 34
 <211> 198
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2416227CD1

<400> 34
 Met Ala Leu Arg His Leu Ala Leu Leu Ala Gly Leu Leu Val Gly
 1 5 10 15
 Val Ala Ser Lys Ser Met Glu Asn Thr Ala Gln Leu Pro Glu Cys
 20 25 30
 Cys Val Asp Val Val Gly Val Asn Ala Ser Cys Pro Gly Ala Ser
 35 40 45
 Leu Cys Gly Pro Gly Cys Tyr Arg Arg Trp Asn Ala Asp Gly Ser
 50 55 60
 Ala Ser Cys Val Arg Cys Gly Asn Gly Thr Leu Pro Ala Tyr Asn
 65 70 75
 Gly Ser Glu Cys Arg Ser Phe Ala Gly Pro Gly Ala Pro Phe Pro
 80 85 90
 Met Asn Arg Ser Ser Gly Thr Pro Gly Arg Pro His Pro Gly Ala
 95 100 105
 Pro Arg Val Ala Ala Ser Leu Phe Leu Gly Thr Phe Phe Ile Ser
 110 115 120
 Ser Gly Leu Ile Leu Ser Val Ala Gly Phe Phe Tyr Leu Lys Arg
 125 130 135
 Ser Ser Lys Leu Pro Arg Ala Cys Tyr Arg Arg Asn Lys Ala Pro
 140 145 150
 Ala Leu Gln Pro Gly Glu Ala Ala Ala Met Ile Pro Pro Pro Gln
 155 160 165
 Ser Ser Val Arg Lys Pro Arg Tyr Val Arg Arg Glu Arg Pro Leu
 170 175 180
 Asp Arg Ala Thr Asp Pro Ala Ala Phe Pro Gly Glu Ala Arg Ile
 185 190 195
 Ser Asn Val

<210> 35
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 2461076CD1

<400> 35
 Met Lys Leu Pro Leu Ser Leu Leu Phe Leu Arg Thr Leu Gly Phe
 1 5 10 15
 Tyr Ile Pro Val Lys Gly Asp Leu Ser Ser Gly Cys Glu Asp Lys
 20 25 30
 Ala Cys Leu Tyr Val Leu Lys Arg Val Thr Thr Asp Lys Val Phe
 35 40 45
 Phe Asp Pro Phe Lys Ile Tyr Phe Arg Pro Val Ile Pro Gly Leu
 50 55 60
 Trp Glu Ala Glu Ala Gly Gly Ser Leu Gly Leu Gly Val
 65 70

<210> 36

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<211> 376

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1957517CD1

<400> 36

Met	Asp	Gly	Glu	Glu	Gln	Gln	Pro	Pro	His	Glu	Ala	Asn	Val	Glu
1				5					10					15
Pro	Val	Val	Pro	Ser	Glu	Ala	Ser	Glu	Pro	Val	Pro	Arg	Val	Leu
				20					25					30
Ser	Gly	Asp	Pro	Gln	Asn	Leu	Ser	Asp	Val	Asp	Ala	Phe	Asn	Leu
				35					40					45
Leu	Leu	Glu	Met	Lys	Leu	Lys	Arg	Arg	Arg	Gln	Arg	Pro	Asn	Leu
				50					55					60
Pro	Arg	Thr	Val	Thr	Gln	Leu	Val	Ala	Glu	Asp	Gly	Ser	Arg	Val
				65					70					75
Tyr	Val	Val	Gly	Thr	Ala	His	Phe	Ser	Asp	Asp	Ser	Lys	Arg	Asp
				80					85					90
Val	Val	Lys	Thr	Ile	Arg	Glu	Val	Gln	Pro	Asp	Val	Val	Val	Val
				95					100					105
Glu	Leu	Cys	Gln	Tyr	Arg	Val	Ser	Met	Leu	Lys	Met	Asp	Glu	Ser
				110					115					120
Thr	Leu	Leu	Arg	Glu	Ala	Gln	Glu	Leu	Ser	Leu	Glu	Lys	Leu	Gln
				125					130					135
Gln	Ala	Val	Arg	Gln	Asn	Gly	Leu	Met	Ser	Gly	Leu	Met	Gln	Met
				140					145					150
Leu	Leu	Leu	Lys	Val	Ser	Ala	His	Ile	Thr	Glu	Gln	Leu	Gly	Met
				155					160					165
Ala	Pro	Gly	Gly	Glu	Phe	Arg	Glu	Ala	Phe	Lys	Glu	Ala	Ser	Lys
				170					175					180
Val	Pro	Phe	Cys	Lys	Phe	His	Leu	Gly	Asp	Arg	Pro	Ile	Pro	Val
				185					190					195
Thr	Phe	Lys	Arg	Ala	Ile	Ala	Ala	Leu	Ser	Phe	Trp	Gln	Lys	Val
				200					205					210
Arg	Leu	Ala	Trp	Gly	Leu	Cys	Phe	Leu	Ser	Asp	Pro	Ile	Ser	Lys
				215					220					225
Asp	Asp	Val	Glu	Arg	Cys	Lys	Gln	Lys	Asp	Leu	Leu	Glu	Gln	Met
				230					235					240
Met	Ala	Glu	Met	Ile	Gly	Glu	Phe	Pro	Asp	Leu	His	Arg	Thr	Ile
				245					250					255
Val	Ser	Glu	Arg	Asp	Val	Tyr	Leu	Thr	Tyr	Met	Leu	Arg	Gln	Ala
				260					265					270
Ala	Arg	Arg	Leu	Glu	Leu	Pro	Arg	Ala	Ser	Asp	Ala	Glu	Pro	Arg
				275					280					285
Lys	Cys	Val	Pro	Ser	Val	Val	Val	Gly	Val	Val	Gly	Met	Gly	His
				290					295					300
Val	Pro	Gly	Ile	Glu	Lys	Asn	Trp	Ser	Thr	Asp	Leu	Asn	Ile	Gln
				305					310					315
Glu	Ile	Met	Thr	Val	Pro	Pro	Pro	Ser	Val	Ser	Gly	Arg	Val	Ser
				320					325					330
Arg	Leu	Ala	Val	Lys	Ala	Ala	Phe	Phe	Gly	Leu	Leu	Gly	Tyr	Ser
				335					340					345
Leu	Tyr	Trp	Met	Gly	Arg	Arg	Thr	Ala	Ser	Leu	Val	Leu	Ser	Leu
				350					355					360
Pro	Ala	Ala	Gln	Tyr	Cys	Leu	Gln	Arg	Val	Thr	Glu	Ala	Arg	His
				365					370					375
Lys														

<210> 37

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<211> 216
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 866038CD1

<400> 37
 Met Met Tyr Trp Ile Val Phe Ala Phe Phe Thr Thr Ala Glu Thr
 1 5 10 15
 Leu Thr Asp Ile Val Leu Ser Trp Phe Pro Phe Tyr Phe Glu Leu
 20 25 30
 Lys Ile Ala Phe Val Ile Trp Leu Leu Ser Pro Tyr Thr Lys Gly
 35 40 45
 Ser Ser Val Leu Tyr Arg Lys Phe Val His Pro Thr Leu Ser Asn
 50 55 60
 Lys Glu Lys Glu Ile Asp Glu Tyr Ile Thr Gln Ala Arg Asp Lys
 65 70 75
 Ser Tyr Glu Thr Met Met Arg Val Gly Lys Arg Gly Leu Asn Leu
 80 85 90
 Ala Ala Asn Ala Ala Val Thr Ala Ala Ala Lys Gly Gln Gly Val
 95 100 105
 Leu Ser Glu Lys Leu Arg Ser Phe Ser Met Gln Asp Leu Thr Leu
 110 115 120
 Ile Arg Asp Glu Asp Ala Leu Pro Leu Gln Arg Pro Asp Gly Arg
 125 130 135
 Leu Arg Pro Ser Pro Gly Ser Leu Leu Asp Thr Ile Glu Asp Leu
 140 145 150
 Gly Asp Asp Pro Ala Leu Ser Leu Arg Ser Ser Thr Asn Pro Ala
 155 160 165
 Asp Ser Arg Thr Glu Ala Ser Glu Asp Asp Met Gly Asp Lys Ala
 170 175 180
 Pro Lys Arg Ala Lys Pro Ile Lys Lys Ala Pro Lys Ala Glu Pro
 185 190 195
 Leu Ala Ser Lys Thr Leu Lys Thr Arg Pro Lys Lys Lys Thr Ser
 200 205 210
 Gly Gly Gly Asp Ser Ala
 215

<210> 38
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 3869704CD1

<400> 38
 Met Ala Trp Thr Pro Leu Leu Leu Pro Leu Leu Thr Phe Cys Thr
 1 5 10 15
 Val Ser Glu Ala Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser
 20 25 30
 Val Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala
 35 40 45
 Leu Pro Lys Lys Tyr Ala Tyr Trp Tyr Gln Gln Lys Ser Gly Gln
 50 55 60
 Ala Pro Val Leu Val Ile Tyr Glu Asp Asn Lys Arg Pro Ser Gly
 65 70 75
 Ile Pro Glu Arg Phe Phe Gly Ser Ser Ser Gly Thr Met Ala Thr
 80 85 90
 Leu Thr Ile Ser Gly Ala Gln Val Glu Asp Glu Ala Asp Tyr Tyr

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				95					100					105
Cys	Tyr	Ser	Thr	Asp	Ser	Ser	Gly	Asn	Asp	Arg	Val	Phe	Gly	Gly
				110					115					120
Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser
				125					130					135
Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu	Glu	Leu	Gln	Ala	Asn	Lys
				140					145					150
Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe	Tyr	Pro	Gly	Ala	Val
				155					160					165
Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val	Lys	Ala	Gly	Val
				170					175					180
Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys	Tyr	Ala	Ala
				185					190					195
Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	His	Lys
				200					205					210
Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu	Lys
				215					220					225
Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser							
				230										

<210> 39
 <211> 163
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1415179CD1

<400> 39														
Met	Leu	Cys	Pro	Leu	Ser	His	Ala	Arg	Val	Val	Arg	Gly	Ala	Gly
1				5					10					15
Ser	Glu	Gly	Gly	Arg	Ile	Leu	Leu	Ser	Leu	Cys	Phe	Ser	Phe	Cys
				20					25					30
Pro	Ser	Gly	Leu	Ser	Cys	Trp	Cys	Ser	Arg	His	Cys	Leu	Pro	Ala
				35					40					45
Leu	Ala	Pro	Arg	Cys	Ser	Pro	Gln	Pro	Tyr	Leu	Ser	Cys	Phe	Pro
				50					55					60
Gly	Ala	Thr	His	Pro	Cys	Pro	Thr	Pro	Ser	Ala	Cys	Ser	His	Gly
				65					70					75
Arg	Gly	Arg	Thr	His	Ser	Leu	His	Thr	His	Thr	Pro	Arg	Leu	His
				80					85					90
Pro	Val	Ser	Ile	Tyr	Lys	His	Val	Arg	Ala	Arg	Val	His	Thr	Ser
				95					100					105
Arg	Phe	Ser	Thr	Ala	Tyr	Gln	Ala	Leu	Leu	Leu	Pro	Cys	Leu	Ser
				110					115					120
Ala	Trp	Arg	Gly	Pro	Pro	Leu	Leu	Thr	Pro	Ser	Val	Pro	Pro	Pro
				125					130					135
Glu	Leu	Ile	Arg	Met	Arg	Met	Val	Val	Pro	Ala	Ser	Glu	Gly	Leu
				140					145					150
Leu	Gly	Leu	Leu	Gly	Ala	Lys	Pro	Leu	Cys	Pro	Lys	Gln		
				155					160					

<210> 40
 <211> 235
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1664792CD1

<400> 40

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

<210> 41

<211> 94

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2079396CD1

<400> 41

Met	Ser	Pro	Leu	Ser	Pro	Thr	Gly	Leu	Asn	Leu	Trp	Gly	Gly	Glu
1				5					10					15
Gly	Ser	Ser	Leu	His	Ser	Ala	Leu	Asp	His	Gln	Gly	Arg	Gly	Ile
				20					25					30
Thr	Leu	Ala	Ile	Gly	Ile	Ile	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Ser
				35					40					45
Pro	Arg	Ile	Arg	Pro	Ser	Ser	Gln	His	Cys	Val	Gly	Leu	Ile	Leu
				50					55					60
Arg	Ile	Leu	Tyr	His	His	Pro	Gly	Leu	Gly	Gly	Cys	Arg	Ser	Trp
				65					70					75
Val	Leu	Leu	Leu	Arg	Asp	Arg	Val	Ser	Leu	Cys	His	Pro	Gly	Trp
				80					85					90
Ser	Ala	Val	Ala											

<210> 42

<211> 85

<212> PRT

<213> Homo sapiens

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<220>

<221> misc_feature

<223> Incyte ID No: 5390115CD1

<400> 42

Met	Ala	Ser	Asp	Leu	Asp	Phe	Ser	Pro	Pro	Glu	Val	Pro	Glu	Pro
1				5					10					15
Thr	Phe	Leu	Glu	Asn	Leu	Leu	Arg	Tyr	Gly	Leu	Phe	Leu	Gly	Ala
			20						25					30
Ile	Phe	Gln	Leu	Ile	Cys	Val	Leu	Ala	Ile	Ile	Val	Pro	Ile	Pro
			35						40					45
Lys	Ser	His	Glu	Ala	Glu	Ala	Glu	Pro	Ser	Glu	Pro	Arg	Ser	Ala
			50						55					60
Glu	Val	Thr	Arg	Lys	Pro	Lys	Ala	Ala	Val	Pro	Ser	Val	Asn	Lys
			65						70					75
Arg	Pro	Lys	Lys	Glu	Thr	Lys	Lys	Lys	Arg					
			80						85					

<210> 43

<211> 901

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1403326CD1

<400> 43

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

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Arg Arg Lys Ile	260	Arg Arg Lys Ile	265	Arg Arg Lys Ile	270
Glu Gln Ala Ile Tyr	275	Lys Leu Pro Cys Val His	280	Lys Leu Pro Cys Val His	285
Phe Cys Gln Pro	290	Phe Thr Leu Lys Ile Val	295	Phe Thr Leu Lys Ile Val	300
Asp Val Leu Lys	305	Gly Tyr Ala Cys Met Ile	310	Gly Tyr Ala Cys Met Ile	315
Arg Val Asn Pro	320	Phe Ser Glu Ala Pro Asn	325	Phe Ser Glu Ala Pro Asn	330
Ser Trp Ile Val	335	Cys Ser Leu Thr Thr Glu	340	Cys Ser Leu Thr Thr Glu	345
Lys Trp Val Gly	350	Asp Pro Asp Leu Leu Gln	355	Asp Pro Asp Leu Leu Gln	360
Leu Ser Glu Asp	365	Ser Leu Ser Ser Gly Pro	370	Ser Leu Ser Ser Gly Pro	375
Pro Leu Ser Arg	380	Lys Gly Leu Glu His Lys	385	Lys Gly Leu Glu His Lys	390
Ala Asp Leu Gln	395	Val Pro Pro Gly His Leu	400	Val Pro Pro Gly His Leu	405
Glu Cys Thr Pro	410	Glu Leu Ser Leu Gln His	415	Glu Leu Ser Leu Gln His	420
Glu Gly Leu Lys	425	Gln Met Arg Pro Phe Ser	430	Gln Met Arg Pro Phe Ser	435
Gln Gly Ile Val	440	Trp Ala Val Asp Leu Asn	445	Trp Ala Val Asp Leu Asn	450
Leu Gln Glu Lys	455	Asp Ala Leu Leu Ile Ala	460	Asp Ala Leu Leu Ile Ala	465
Gln Asn Ser Thr	470	Ile Leu Arg Glu Gln Asp	475	Ile Leu Arg Glu Gln Asp	480
Ala Glu Gly Gln	485	Thr Ala Phe Thr Leu Lys	490	Thr Ala Phe Thr Leu Lys	495
Gln Lys Leu Val	500	Thr Gly Lys Val Cys Val	505	Thr Gly Lys Val Cys Val	510
Arg Ala Lys Val	515	Glu Ser Ser Ala Glu Ala	520	Glu Ser Ser Ala Glu Ala	525
Leu Glu Ala Ala	530	Tyr Pro Ala Ser Tyr Ser	535	Tyr Pro Ala Ser Tyr Ser	540
Leu Ala Gly Thr	545	Leu Leu Gln Ser Leu Val	550	Leu Leu Gln Ser Leu Val	555
Ile Val Leu Leu	560	Leu Ser Asp Gln Leu Gly	565	Leu Ser Asp Gln Leu Gly	570
Cys Glu Val Leu	575	Gln Gln Tyr Glu Ile Phe	580	Gln Gln Tyr Glu Ile Phe	585
Ser Arg Ser Leu	590	Leu Phe Val His Gly Leu	595	Leu Phe Val His Gly Leu	600
Pro Gly Ser Gly	605	Met Lys Ile Met Glu Lys	610	Met Lys Ile Met Glu Lys	615
Ile Arg Asn Val	620	His Arg Ile Leu Tyr Val	625	His Arg Ile Leu Tyr Val	630
Cys Glu Asn Gln	635	Ile Ser Asp Arg Asn Ile	640	Ile Ser Asp Arg Asn Ile	645
Cys Arg Ala Glu	650	Leu Arg Glu Asn Phe Glu	655	Leu Arg Glu Asn Phe Glu	660
His Ile Gln His	665	Ala Gln Asn Phe Arg Thr	670	Ala Gln Asn Phe Arg Thr	675
Glu Asp Gly Asp	680	Lys Ser Ile Thr Arg Arg	685	Lys Ser Ile Thr Arg Arg	690
Ala Lys Gly Gly	695	Ile Phe Leu Asp Tyr Phe	700	Ile Phe Leu Asp Tyr Phe	705
Gln Thr Ser His	710	Leu Pro Pro Leu Ser Asp	715	Leu Pro Pro Leu Ser Asp	720
Gln Tyr Pro Arg	725	Ile Val Arg Asn Ala Asp	730	Ile Val Arg Asn Ala Asp	735

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Pro	Ile	Ala	Lys	Tyr	Leu	Gln	Lys	Glu	Met	Gln	Val	Ile	Arg	Ser
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Asn	Pro	Ser	Phe	Asn	Ile	Pro	Thr	Gly	Cys	Leu	Glu	Val	Phe	Pro
				755					760					765
Glu	Ala	Glu	Trp	Ser	Gln	Gly	Val	Gln	Gly	Thr	Leu	Arg	Ile	Lys
				770					775					780
Lys	Tyr	Leu	Thr	Val	Glu	Gln	Ile	Met	Thr	Cys	Val	Ala	Asp	Thr
				785					790					795
Cys	Arg	Arg	Phe	Phe	Asp	Arg	Gly	Tyr	Ser	Pro	Lys	Asp	Val	Ala
				800					805					810
Val	Leu	Val	Ser	Thr	Ala	Lys	Glu	Val	Glu	His	Tyr	Lys	Tyr	Glu
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Leu	Leu	Lys	Ala	Met	Arg	Lys	Lys	Arg	Val	Val	Gln	Leu	Ser	Asp
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Ala	Cys	Asp	Met	Leu	Gly	Asp	His	Ile	Val	Leu	Asp	Ser	Val	Arg
				845					850					855
Arg	Phe	Ser	Gly	Leu	Glu	Arg	Ser	Ile	Val	Phe	Gly	Ile	His	Pro
				860					865					870
Arg	Thr	Ala	Asp	Pro	Ala	Ile	Leu	Pro	Asn	Val	Leu	Ile	Cys	Leu
				875					880					885
Ala	Ser	Arg	Ala	Lys	Gln	His	Leu	Tyr	Ile	Phe	Pro	Trp	Gly	Gly
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His

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<211> 1040

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7690129CD1

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Pro	Trp	Gly	Val	Val	Arg	Asn	Arg	Asp	Thr	Leu	Ile	Asn	Pro	Lys
				20					25					30
Gly	Ser	Phe	Pro	Ala	Arg	Tyr	Arg	Trp	Arg	Gly	Asp	Pro	Glu	Asp
				35					40					45
Gly	Val	Gln	Phe	Pro	Leu	Asp	Tyr	Asn	Tyr	Ser	Ala	Phe	Phe	Leu
				50					55					60
Val	Asp	Asp	Gly	Thr	His	Gly	Cys	Leu	Gly	Gly	Glu	Asn	Arg	Phe
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Arg	Leu	Arg	Leu	Glu	Ser	Tyr	Ile	Ser	Gln	Gln	Lys	Thr	Gly	Val
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Gly	Gly	Thr	Gly	Ile	Asp	Ile	Pro	Val	Leu	Leu	Leu	Leu	Ile	Asp
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Gly	Asp	Glu	Lys	Met	Leu	Thr	Arg	Ile	Glu	Asn	Ala	Thr	Gln	Ala
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Gln	Leu	Pro	Cys	Leu	Leu	Val	Ala	Gly	Ser	Gly	Gly	Ala	Ala	Asp
				125					130					135
Cys	Leu	Ala	Glu	Thr	Leu	Glu	Asp	Thr	Leu	Ala	Pro	Gly	Ser	Gly
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Gly	Ala	Arg	Gln	Gly	Glu	Ala	Arg	Asp	Arg	Ile	Arg	Arg	Phe	Phe
				155					160					165
Pro	Lys	Gly	Asp	Leu	Glu	Val	Leu	Gln	Ala	Gln	Val	Glu	Arg	Ile
				170					175					180
Met	Thr	Arg	Lys	Glu	Leu	Leu	Thr	Val	Tyr	Ser	Ser	Glu	Asp	Gly
				185					190					195
Ser	Glu	Glu	Phe	Glu	Thr	Ile	Val	Leu	Lys	Ala	Leu	Val	Lys	Ala
				200					205					210

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Cys	Gly	Ser	Ser	Glu	Ala	Ser	Ala	Tyr	Leu	Asp	Glu	Leu	Arg	Leu
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Ala	Val	Ala	Trp	Asn	Arg	Val	Asp	Ile	Ala	Gln	Ser	Glu	Leu	Phe
				230					235					240
Arg	Gly	Asp	Ile	Gln	Trp	Arg	Ser	Phe	His	Leu	Glu	Ala	Ser	Leu
				245					250					255
Met	Asp	Ala	Leu	Leu	Asn	Asp	Arg	Pro	Glu	Phe	Val	Arg	Leu	Leu
				260					265					270
Ile	Ser	His	Gly	Leu	Ser	Leu	Gly	His	Phe	Leu	Thr	Pro	Met	Arg
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Leu	Ala	Gln	Leu	Tyr	Ser	Ala	Ala	Pro	Ser	Asn	Ser	Leu	Ile	Arg
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Ala	Leu	Lys	Gly	Gly	Ala	Ala	Glu	Leu	Arg	Pro	Pro	Asp	Val	Gly
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His	Val	Leu	Arg	Met	Leu	Leu	Gly	Lys	Met	Cys	Ala	Pro	Arg	Tyr
				335					340					345
Pro	Ser	Gly	Gly	Ala	Trp	Asp	Pro	His	Pro	Gly	Gln	Gly	Phe	Gly
				350					355					360
Glu	Ser	Met	Tyr	Leu	Leu	Ser	Asp	Lys	Ala	Thr	Ser	Pro	Leu	Ser
				365					370					375
Leu	Asp	Ala	Gly	Leu	Gly	Gln	Ala	Pro	Trp	Ser	Asp	Leu	Leu	Leu
				380					385					390
Trp	Ala	Leu	Leu	Leu	Asn	Arg	Ala	Gln	Met	Ala	Met	Tyr	Phe	Trp
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Glu	Met	Gly	Ser	Asn	Ala	Val	Ser	Ser	Ala	Leu	Gly	Ala	Cys	Leu
				410					415					420
Leu	Leu	Arg	Val	Met	Ala	Arg	Leu	Glu	Pro	Asp	Ala	Glu	Glu	Ala
				425					430					435
Ala	Arg	Arg	Lys	Asp	Leu	Ala	Phe	Lys	Phe	Glu	Gly	Met	Gly	Val
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Asp	Leu	Phe	Gly	Glu	Cys	Tyr	Arg	Ser	Ser	Glu	Val	Arg	Ala	Ala
				455					460					465
Arg	Leu	Leu	Leu	Arg	Arg	Cys	Pro	Leu	Trp	Gly	Asp	Ala	Thr	Cys
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Leu	Gln	Leu	Ala	Met	Gln	Ala	Asp	Ala	Arg	Ala	Phe	Phe	Ala	Gln
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Asp	Gly	Val	Gln	Ser	Leu	Leu	Thr	Gln	Lys	Trp	Trp	Gly	Asp	Met
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Ala	Ser	Thr	Thr	Pro	Ile	Trp	Ala	Leu	Val	Leu	Ala	Phe	Phe	Cys
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Pro	Pro	Leu	Ile	Tyr	Thr	Arg	Leu	Ile	Thr	Phe	Arg	Lys	Ser	Glu
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Glu	Glu	Pro	Thr	Arg	Glu	Glu	Leu	Glu	Phe	Asp	Met	Asp	Ser	Val
				545					550					555
Ile	Asn	Gly	Glu	Gly	Pro	Val	Gly	Thr	Ala	Asp	Pro	Ala	Glu	Lys
				560					565					570
Thr	Pro	Leu	Gly	Val	Pro	Arg	Gln	Ser	Gly	Arg	Pro	Gly	Cys	Cys
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Gly	Gly	Arg	Cys	Gly	Gly	Arg	Arg	Cys	Leu	Arg	Arg	Trp	Phe	His
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Phe	Trp	Gly	Ala	Pro	Val	Thr	Ile	Phe	Met	Gly	Asn	Val	Val	Ser
				605					610					615
Tyr	Leu	Leu	Phe	Leu	Leu	Leu	Phe	Ser	Arg	Val	Leu	Leu	Val	Asp
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Phe	Gln	Pro	Ala	Pro	Pro	Gly	Ser	Leu	Glu	Leu	Leu	Leu	Tyr	Phe
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Trp	Ala	Phe	Thr	Leu	Leu	Cys	Glu	Glu	Leu	Arg	Gln	Gly	Leu	Ser
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Gly	Gly	Gly	Gly	Ser	Leu	Ala	Ser	Gly	Gly	Pro	Gly	Pro	Gly	His
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Ala	Ser	Leu	Ser	Gln	Arg	Leu	Arg	Leu	Tyr	Leu	Ala	Asp	Ser	Trp

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Asn	Gln	Cys	Asp	680	Leu	Val	Ala	Leu	Thr	685	Cys	Phe	Leu	Leu	Gly	690	Val
Gly	Cys	Arg	Leu	695	Thr	Pro	Gly	Leu	Tyr	700	His	Leu	Gly	Arg	Thr	705	Val
Leu	Cys	Ile	Asp	710	Phe	Met	Val	Phe	Thr	715	Val	Arg	Leu	Leu	His	720	Ile
Phe	Thr	Val	Asn	725	Lys	Gln	Leu	Gly	Pro	730	Lys	Ile	Val	Ile	Val	735	Ser
Lys	Met	Met	Lys	740	Asp	Val	Phe	Phe	Phe	745	Leu	Phe	Phe	Leu	Gly	750	Val
Trp	Leu	Val	Ala	755	Tyr	Gly	Val	Ala	Thr	760	Glu	Gly	Leu	Leu	Arg	765	Pro
Arg	Asp	Ser	Asp	770	Phe	Pro	Ser	Ile	Leu	775	Arg	Arg	Val	Phe	Tyr	780	Arg
Pro	Tyr	Leu	Gln	785	Ile	Phe	Gly	Gln	Ile	790	Pro	Gln	Glu	Asp	Met	795	Asp
Val	Ala	Leu	Met	800	Glu	His	Ser	Asn	Cys	805	Ser	Ser	Glu	Pro	Gly	810	Phe
Trp	Ala	His	Pro	815	Pro	Gly	Ala	Gln	Ala	820	Gly	Thr	Cys	Val	Ser	825	Gln
Tyr	Ala	Asn	Trp	830	Leu	Val	Val	Leu	Leu	835	Leu	Val	Ile	Phe	Leu	840	Leu
Val	Ala	Asn	Ile	845	Leu	Leu	Val	Asn	Leu	850	Leu	Ile	Ala	Met	Phe	855	Ser
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Ala	Gln	Arg	Tyr	875	Arg	Leu	Ile	Arg	Glu	880	Phe	His	Ser	Arg	Pro	885	Ala
Leu	Ala	Pro	Pro	890	Phe	Ile	Val	Ile	Ser	895	His	Leu	Arg	Leu	Leu	900	Leu
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Ala	Leu	Glu	His	920	Phe	Arg	Val	Tyr	Leu	925	Ser	Lys	Glu	Ala	Glu	930	Arg
Lys	Leu	Leu	Thr	935	Trp	Glu	Ser	Val	His	940	Lys	Glu	Asn	Phe	Leu	945	Leu
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Ile	Arg	Glu	Tyr	980	Glu	Gln	Arg	Leu	Lys	985	Val	Leu	Glu	Arg	Glu	990	Val
Gln	Gln	Cys	Ser	995	Arg	Val	Leu	Gly	Trp	1000	Val	Ala	Glu	Ala	Leu	1005	Ser
Arg	Ser	Ala	Leu	1010	Leu	Pro	Pro	Gly	Gly	1015	Pro	Pro	Pro	Pro	Asp	1020	Leu
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<211> 2508

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<400> 45

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<211> 4034

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<210> 47

<211> 845

<212> DNA

<213> Homo sapiens

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<221> misc_feature

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<223> Incyte ID No: 4362432CB1

<400> 47

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<210> 48

<211> 2300

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5308104CB1

<400> 48

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<210> 49

<211> 1587

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3092736CB1

<400> 49

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<210> 50

<211> 669

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3580257CB1

<400> 50

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<210> 51

<211> 1463

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 3634758CB1

<400> 51

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<210> 52

<211> 1686

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4027923CB1

<400> 52

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<210> 53

<211> 2497

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 4348533CB1

<400> 53

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<211> 1783

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 4878134CB1

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<211> 863

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 1820972CB1

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<221> misc_feature

WO 01/98353

PCT/US01/19862

<223> Incyte ID No: 3286805CB1

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<211> 1765

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3506590CB1

<400> 63

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<211> 1264

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte ID No: 003600CB1

<400> 64

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<213> Homo sapiens

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<220>

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 <213> Homo sapiens

<220>
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<220>
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<210> 68

<211> 1568

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1706443CB1

<400> 68

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<210> 69

<211> 1887

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1748627CB1

<400> 69

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<210> 70

<211> 569

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1818332CB1

<400> 70

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<210> 71

<211> 2338

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1822832CB1

<400> 71

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<210> 72

<211> 481

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1832219CB1

<400> 72

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<210> 73

<211> 1255

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> Incyte ID No: 1899010CB1

<400> 73

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<210> 74

<211> 875

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte ID No: 2008768CB1

<400> 74

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<210> 75

<211> 2188

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2070984CB1

<400> 75

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<210> 76

<211> 1561

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2193240CB1

<400> 76

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<210> 77

<211> 1777

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2235177CB1

<400> 77

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<210> 78

<211> 1841

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<400> 78

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<210> 79

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2461076CB1

<400> 79

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<210> 80

<211> 1434

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 1957517CB1

<400> 80

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<210> 81

<211> 2085

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 866038CB1

<400> 81

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<210> 82

<211> 904

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3869704CB1

<400> 82

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<211> 1496

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1415179CB1

<400> 83

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<211> 2837

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1664792CB1

<400> 84

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<210> 85

<211> 1123

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2079396CB1

<400> 85

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<210> 86

<211> 1549

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5390115CB1

<400> 86

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<210> 87

<211> 4820

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<223> Incyte ID No: 1403326CB1

<400> 87

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WO 01/98353

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What is claimed is:

1. An isolated polypeptide selected from the group consisting of:

a) a polypeptide comprising an amino acid sequence selected from the group consisting of
5 SEQ ID NO:1-44,

b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-44,

c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, and

10 d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44.

2. An isolated polypeptide of claim 1 selected from the group consisting of SEQ ID NO:1-44.

15 3. An isolated polynucleotide encoding a polypeptide of claim 1.

4. An isolated polynucleotide encoding a polypeptide of claim 2.

20 5. An isolated polynucleotide of claim 4 selected from the group consisting of SEQ ID NO:45-88.

6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.

25 7. A cell transformed with a recombinant polynucleotide of claim 6.

8. A transgenic organism comprising a recombinant polynucleotide of claim 6.

30 9. A method for producing a polypeptide of claim 1, the method comprising:

a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and

b) recovering the polypeptide so expressed.

10. An isolated antibody which specifically binds to a polypeptide of claim 1.

5 11. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:45-88,

b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:45-88,

10 c) a polynucleotide complementary to a polynucleotide of a),

d) a polynucleotide complementary to a polynucleotide of b), and

e) an RNA equivalent of a)-d).

12. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a
15 polynucleotide of claim 11.

13. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides
20 comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

25

14. A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.

15. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

30 a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

16. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

17. A composition of claim 16, wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:1-44.

18. A method for treating a disease or condition associated with decreased expression of functional SECP, comprising administering to a patient in need of such treatment the composition of claim 16.

10

19. A method for screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

15

20. A composition comprising an agonist compound identified by a method of claim 19 and a pharmaceutically acceptable excipient.

21. A method for treating a disease or condition associated with decreased expression of functional SECP, comprising administering to a patient in need of such treatment a composition of claim 20.

22. A method for screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

- 25
- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
 - b) detecting antagonist activity in the sample.

23. A composition comprising an antagonist compound identified by a method of claim 22 and a pharmaceutically acceptable excipient.

30

24. A method for treating a disease or condition associated with overexpression of functional SECP, comprising administering to a patient in need of such treatment a composition of claim 23.

25. A method of screening for a compound that specifically binds to the polypeptide of claim 1, said method comprising the steps of:

35

a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and

b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a compound that specifically binds to the polypeptide of claim 1.

5

26. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, said method comprising:

a) combining the polypeptide of claim 1 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 1,

10 b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound, and

c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a
15 compound that modulates the activity of the polypeptide of claim 1.

27. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

20 a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

25

28. A method for assessing toxicity of a test compound, said method comprising:

a) treating a biological sample containing nucleic acids with the test compound;

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific
30 hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof;

c) quantifying the amount of hybridization complex; and

d) comparing the amount of hybridization complex in the treated biological sample with the
35 amount of hybridization complex in an untreated biological sample, wherein a difference in the

amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

29. A diagnostic test for a condition or disease associated with the expression of SECP in a biological sample comprising the steps of:

a) combining the biological sample with an antibody of claim 10, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex; and

b) detecting the complex, wherein the presence of the complex correlates with the presence of the polypeptide in the biological sample.

10

30. The antibody of claim 10, wherein the antibody is:

a) a chimeric antibody,

b) a single chain antibody,

c) a Fab fragment,

15

d) a F(ab')₂ fragment, or

e) a humanized antibody.

31. A composition comprising an antibody of claim 10 and an acceptable excipient.

20

32. A method of diagnosing a condition or disease associated with the expression of SECP in a subject, comprising administering to said subject an effective amount of the composition of claim 31.

33. A composition of claim 31, wherein the antibody is labeled.

25

34. A method of diagnosing a condition or disease associated with the expression of SECP in a subject, comprising administering to said subject an effective amount of the composition of claim 33.

30

35. A method of preparing a polyclonal antibody with the specificity of the antibody of claim 10 comprising:

a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, or an immunogenic fragment thereof, under conditions to elicit an antibody response;

b) isolating antibodies from said animal; and

c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44.

5

36. An antibody produced by a method of claim 35.

37. A composition comprising the antibody of claim 36 and a suitable carrier.

10 38. A method of making a monoclonal antibody with the specificity of the antibody of claim 10 comprising:

a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44, or an immunogenic fragment thereof, under conditions to elicit an antibody response;

15 b) isolating antibody producing cells from the animal;

c) fusing the antibody producing cells with immortalized cells to form monoclonal antibody-producing hybridoma cells;

d) culturing the hybridoma cells; and

20 e) isolating from the culture monoclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44.

39. A monoclonal antibody produced by a method of claim 38.

40. A composition comprising the antibody of claim 39 and a suitable carrier.

25

41. The antibody of claim 10, wherein the antibody is produced by screening a Fab expression library.

30 42. The antibody of claim 10, wherein the antibody is produced by screening a recombinant immunoglobulin library.

43. A method for detecting a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44 in a sample, comprising the steps of:

a) incubating the antibody of claim 10 with a sample under conditions to allow specific

binding of the antibody and the polypeptide; and

b) detecting specific binding, wherein specific binding indicates the presence of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44 in the sample.

5

44. A method of purifying a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44 from a sample, the method comprising:

a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide; and

10 b) separating the antibody from the sample and obtaining the purified polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-44.

45. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

15 46. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

47. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:3.

48. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:4.

20

49. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:5.

50. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:6.

25

51. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:7.

52. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:8.

53. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:9.

30

54. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:10.

55. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.

56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.

57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.

5 58. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:14.

59. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:15.

60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:16.

10

61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.

62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.

15

63. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:19.

64. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:20.

65. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:21.

20

66. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:22.

67. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:23.

25

68. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:24.

69. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:25.

70. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:26.

30

71. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:27.

72. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:28.

73. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:29.

74. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:30.

5 75. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:31.

76. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:32.

77. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:33.

10

78. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:34.

79. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:35.

15

80. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:36.

81. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:37.

82. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:38.

20

83. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:39.

84. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:40.

25

85. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:41.

86. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:42.

87. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:43.

30

88. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:44.

89. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:45.

90. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:46.

5 91. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:47.

92. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:48.

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93. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:49.

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94. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:50.

95. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:51.

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96. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:52.

97. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:53.

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98. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:54.

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99. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:55.

100. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:56.

101. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:57.

102. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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103. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:59.

104. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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105. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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15 106. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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107. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
20 NO:63.

108. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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25 109. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:65.

110. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:66.

30 111. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:67.

112. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:68.

113. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:69.

5

114. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:70.

10

115. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:71.

116. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:72.

15

117. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:73.

118. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:74.

20

119. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:75.

25

120. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:76.

121. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:77.

30

122. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:78.

123. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
NO:79.

124. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:80.

5 125. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:81.

126. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:82.

10

127. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:83.

128. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:84.

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129. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:85.

20 130. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:86.

131. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:87.

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132. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:88.