SIGNAL PEPTIDE-CONTAINING MOLECULES

Inventors: Preeti Lal, Santa Clara, CA (US); Y. Tom Tang, San Jose, CA (US); Gina A. Gorgone, Earleville, MD (US); Neil C. Corley, Castro Valley, CA (US); Karl J. Guegler, Menlo Park, CA (US); Mariah R. Baughn, Los Angeles, CA (US); Ingrid E. Akerblom, Lansdale, PA (US); Janice Au-Young, Brisbane, CA (US); Henry Yue, Sunnyvale, CA (US); Chandra Patterson, San Diego, CA (US); Roopa Reddy, Fremont, CA (US); Jennifer L. Hillman, Santa Cruz, CA (US); Olga Bandman, Mountain View, CA (US)

Correspondence Address:
FOLEY AND LARDNER
SUITE 500
3000 K STREET NW
WASHINGTON, DC 20007 (US)

Assignee: Incyte Corporation, Palo Alto, CA (US)

Appl. No.: 10/820,474
Filed: Apr. 7, 2004

Related U.S. Application Data

Division of application No. 09/720,533, filed on Mar. 20, 2001, now abandoned, filed as 371 of international application No. PCT/US99/14484, filed on Jun. 25, 1999.

Provisional application No. 60/090,762, filed on Jun. 26, 1998. Provisional application No. 60/094,583, filed on Jul. 31, 1998. Provisional application No. 60/102,686, filed on Oct. 1, 1998. Provisional application No. 60/112,129, filed on Dec. 11, 1998.

Publication Classification

Int. Cl.7 .......................... A01K 67/00; C12Q 1/68;
.......................... C07H 21/04; C12N 9/64;
.......................... C07K 14/47

U.S. Cl. ............ 800/8; 435/6; 435/69.1; 435/320.1;
.......................... 435/325; 530/350; 536/23.5

ABSTRACT

The invention provides human signal peptide-containing proteins (HSPP) and polynucleotides which identify and encode HSPP. 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 expression of HSPP.
SIGNAL PEPTIDE-CONTAINING MOLECULES

[0001] This application is a divisional application of the National Stage application of International Application No. PCT/US99/14484, filed on Jun. 25, 1999, which claims benefit under 35 U.S.C. § 119(e) and is a continuation-in-part of the following applications: provisional application 60/090,762, filed on Jun. 26, 1998, provisional application 60/094,983, filed on Jul. 31, 1998, provisional application 60/102,686, filed on Oct. 1, 1998, and provisional application 60/112,129, filed on Dec. 11, 1998; all of which applications are hereby incorporated herein by reference.

TECHNICAL FIELD

[0002] This invention relates to nucleic acid and amino acid sequences of human signal peptide-containing proteins and to the use of these sequences in the diagnosis, treatment, and prevention of cell proliferative disorders including cancer; inflammation; and cardiovascular, neurological, reproductive, and developmental disorders.

BACKGROUND OF THE INVENTION

[0003] Protein transport is essential for cellular function. Transport of a protein may be mediated by a signal peptide located at the amino terminus of the protein itself. 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. Secreted proteins are often synthesized as inactive precursors that are activated by post-translational processing events during transit through the secretory pathway. Such events include glycosylation, phosphorylation, 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 receptors, extracellular matrix molecules, cytokines, hormones, growth and differentiation factors, neuromodulators, vasomodulators, phosphokinases, phosphatases, phospholipases, phosphodiesterases, G and Ras-related proteins, ion channels, transporters/pumps, proteases, and transcription factors. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, New York, N.Y., pp. 557-560, 582-592.)

[0004] G-protein coupled receptors (GPCRs) comprise a superfamily of integral membrane proteins which transduce extracellular signals. GPCRs include receptors for biogenic amines such as dopamine, epinephrine, histamine, glutamate (metabotropic effect), acetylcholine (muscarinic effect), and serotonin; for lipid mediators of inflammation such as prostaglandins, platelet activating factor, and leukotrienes; for peptide hormones such as calcitonin, C3a anaphylatoxin, follicle stimulating hormone, gonadotropin releasing hormone, neurokinin, oxytocin, and thrombin; and for sensory signal mediators such as retinal photopigments and olfactory stimulatory molecules. The structure of these highly conserved receptors consists of seven hydrophobic transmembrane regions, cysteine disulfide bridges between the second and third extracellular loops, an extracellular N-terminus, and a cytoplasmic C-terminus. The N-terminus interacts with ligands, the disulfide bridges interact with agonists and antagonists, and the large third intracellular loop interacts with G proteins to activate second messengers such as cyclic AMP, phospholipase C, inositol triphosphate, or ion channel. (Reviewed in Watson, S. and Arkinstall, S. (1994) The G-protein Linked Receptor Facts Book, Academic Press, San Diego, Calif., pp. 2-6; and Bolander, E. F. (1994) Molecular Endocrinology, Academic Press, San Diego, Calif., pp. 162-176.)

[0005] Other types of receptors 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 “CD” number. Some of the genes encoding proteins identified by CD antigens have been isolated and 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. (1993) The Leucocyte Antigen Facts Book, Academic Press, San Diego, Calif., pp. 144-145; Noel, L. S. et al. (1998) J. Biol. Chem. 273: 3878-3883.)

[0006] Tetraspanins are a superfamily of membrane proteins which facilitate the formation and stability of cell-surface signaling complexes containing lineage-specific proteins, integrins, and other tetraspanins. They are involved in cell activation, proliferation (including cancer), differentiation, adhesion, and motility. These proteins cross the membrane four times, have conserved intracellular—and C-termini and an extracellular, non-conserved hydrophilic domain. Tetraspanins include, e.g., platelet and endothelial cell membrane proteins, leukocyte surface proteins, tissue specific and tumor antigens, and the retinotropic pigments- associated gene peripherin. (Maecker, H. T. et al. (1997) FASEB J. 11: 428-442.)

[0007] Matrix proteins (MPs) are transmembrane and extracellular proteins which function in 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 domains, EGF-like domains, immunoglobulin-like domains, and fibronectin-like domains. In addition, some MPs are heavily glycosylated. MPs include extracellular proteins such as fibronectin, collagen, and galectin and endocytic and cell adhesion receptors such as cell adhesion molecules (CAMs), cadherins, and integrins. (Reviewed in Ayad, S. et

**[0008]** Lectins are proteins characterized by their ability to bind carbohydrates on cell membranes by means of discrete, modular carbohydrate recognition domains, CRDs. (Kishore, U. et al. (1997) Matrix Biol. 15: 583-592.) Certain cytokines and membrane-spanning proteins have CRDs which may enhance interactions with extracellular or intracellular ligands, with proteins in secretory pathways, or with molecules in signal transduction pathways. The lipocalin superfamily constitutes a phylogenetically conserved group of more than forty proteins that function by binding to and transporting a variety of physiologically important ligands. (Tanaka, T. et al. (1997) J. Biol. Chem. 272: 15789-15795; and van’t Hof, W. et al. (1997) J. Biol. Chem. 272: 1837-1841.) Selectins are a family of calcium ion-dependent lectins expressed on inflamed vascular endothelium and the surface of some leukocytes. (Rossiter, H. et al. (1997) Mol. Med. Today 3: 214-222.)

**[0009]** Protein kinases regulate many different cell prolifer-, differentiation, and signaling processes by adding phosphate groups to proteins. Reversible protein phosphorylation is a key strategy for controlling protein functional activity in eukaryotic cells. The high energy phosphate which drives this activation is generally transferred from adenosine triphosphate molecules (ATP) to a particular protein by protein kinases and removed from that protein by protein phosphatases. Phosphorylation occurs in response to extracellular signals, cell cycle checkpoints, and environmental or nutritional stresses. Protein kinases may be roughly divided into two groups; protein tyrosine kinases (PTKs) which phosphorylate tyrosine residues, and serine/threonine kinases (STKs) which phosphorylate serine or threonine residues. A few protein kinases have dual specificity. A majority of kinases contain a similar 250-300 amino acid catalytic domain. (Hardie, G. and Hanks, S. (1995) *The Protein Kinase Facts Book*, Vol I, pp. 7-47, Academic Press, San Diego, Calif.)

**[0010]** Protein phosphatases remove phosphate groups from molecules previously modified by protein kinases thus participating in cell signaling, proliferation, differentiation, contacts, and oncogenesis. Protein phosphorylation is a key strategy used to control protein functional activity in eukaryotic cells. The high energy phosphate is transferred from ATP to a protein by protein kinases and removed by protein phosphatases. There appear to be three, evolutionarily distinct protein phosphatase gene families: protein phosphatases (PPs); protein tyrosine phosphatases (PTPs); and acid/alkaline phosphatases (APs). PPs dephosphorylate phosphoserine/threonine residues and are an important regulator of many cAMP mediated, hormone responses in cells. PTPs reverse the effects of protein tyrosine kinases and therefore play a significant role in cell cycle and cell signaling processes. Although APs dephosphorylate substrates in vitro, their role in vivo is not well known. (Charbonneau, H. and Tonks, N. K. (1992) Annu. Rev. Cell Biol. 8: 463-493.)

**[0011]** Cyclic nucleotides (cAMP and cGMP) function as intracellular second messengers to transduce a variety of extracellular signals, including hormones, light and neurotransmitters. Cyclic nucleotide phosphodiesterases (PDEs) degrade cyclic nucleotides to their corresponding monophosphates, thereby regulating the intracellular concentrations of cyclic nucleotides and their effects on signal transduction. At least seven families of mammalian PDEs have been identified based on substrate specificity and affinity, sensitivity to cofactors and sensitivity to inhibitory drugs. (Beavo, J. A. (1995) Physiological Reviews 75: 725-748.)

**[0012]** Phospholipases (PLs) are enzymes that catalyze the removal of fatty acid residues from phosphoglycerides. PLs play an important role in transmembrane signal transduction and are named according to the specific ester bond in phosphoglycerides that is hydrolyzed, i.e., A1, A2, C or D. PLA2 cleaves the ester bond at position 2 of the glycerol moiety of membrane phospholipids giving rise to arachidonic acid. Arachidonic acid is the common precursor to four major classes of eicosanoids, namely prostaglandins, prostacyclins, thromboxanes and leukotrienes. Eicosanoids are signaling molecules involved in the contraction of smooth muscle, platelet aggregation, and pain and inflammatory responses. (Alberts, B. et al. (1994) *Molecular Biology of The Cell*, Garland Publishing, Inc., New York, N.Y., pp. 85, 211, 239-240, 642-645.)

**[0013]** The nucleotide cyclases, i.e., adenylate and guanylate cyclase, catalyze the synthesis of the cyclic nucleotides, cAMP and cGMP, from ATP and GTP, respectively. They act in concert with phosphodiesterases, which degrade cAMP and cGMP, to regulate the cellular levels of these molecules and their functions. cAMP and cGMP function as intracellular second messengers to transduce a variety of extracellular signals, e.g., hormones, and light and neurotransmitters. (Stryer, L. (1988) *Biochemistry* W.H. Freeman and Co., New York, pp. 975-980, 1029-1035.)

**[0014]** Cytokines are produced in response to cell perturbation. Some cytokines are produced as precursor forms, and some form multimers in order to become active. They are produced in groups and in patterns characteristic of the particular stimulus or disease, and the members of the group interact with one another and other molecules to produce an overall biological response. Interleukins, neurotrophins, growth factors, interferons, and chemokines are all families of cytokines which work in conjunction with cell receptors to regulate cell proliferation and differentiation and to affect such activities as leukocyte migration and function, hematopoietic cell proliferation, temperature regulation, acute response to infections, tissue remodeling, apoptosis, and cell survival. Studies using antibodies or other drugs that modify the activity of a particular cytokine are used to elucidate the roles of individual cytokines in pathology and physiology.


**[0016]** Growth and differentiation factors are secreted proteins which function in intercellular communication.
Some factors require oligomerization or association with MPs 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 tumors may contribute to vascularization and metastasis of melanotic tumors. During hematopoiesis, growth factor misregulation can result in anemia, 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 oncogenes. In addition, growth factors affect transcriptional regulation of both proto-oncogenes and oncogenes. (Reviewed in Pimentel, E. (1994) Handbook of Growth Factors, CRC Press, Ann Arbor, Mich., pp. 1-9.)

Proteolytic enzymes or proteases either activate or deactivate proteins by hydrolyzing peptide bonds. Proteases are found in the cytosol, in membrane-bound compartments, and in the extracellular space. The major families are the zinc, serine, cysteine, thiol, and carboxylate proteases.

Zinc proteases, e.g., carboxypeptidase A, have a zinc ion bound to the active site. These proteases recognize C-terminal residues that contain an aromatic or bulky aliphatic side chain, and hydrolyze the peptide bond adjacent to the C-terminal residues. Serine proteases have an active site serine residue and include digestive enzymes, e.g., trypsin and chymotrypsin, components of the complement and blood-clotting cascades, and enzymes that control the degradation and turnover of extracellular matrix (ECM) molecules. Cysteine proteases (e.g. cathepsin) are produced by monocytes, macrophages and other immune cells, and are involved in diverse cellular processes ranging from the processing of precursor proteins to intracellular degradation. Overproduction of these enzymes can cause tissue destruction associated with rheumatoid arthritis and asthma. Thiols proteases, e.g., papain, contain an active site cysteine and are widely distributed within tissues. Carboxylate proteases, e.g., pepsin, are active only under acidic conditions (pH 2 to 3).

Guanosine triphosphate-binding proteins (G proteins) can be grouped into two major classes: heterotrimeric G proteins and small G proteins. Heterotrimeric G proteins interact with GPCRs that respond to hormones, growth factors, neuromodulators, or other signaling molecules. The interaction between GPCR and G protein allows the G protein to exchange GTP for guanosine diphosphate (GDP). This exchange activates the G protein, allowing it to dissociate from the receptor and interact with the its cognate second messenger-generating protein, e.g., adenylate cyclase, guanylate cyclase, phospholipase C, or ion channels. The hydrolysis of GTP to GDP by the G protein acts as an on-off switch, terminating the action of the G protein and preventing it to interact with another receptor molecule, thus beginning another round of signal transduction.

[0021] The small G proteins consist of single 21-30 kDa polypeptides. They can be classified into five subfamilies: Ras, Rho, Ran, Rab, and ADP-ribosylation factor. These proteins regulate cell growth, cell cycle control, protein secretion, and intracellular vesicle interaction. In particular, the Ras proteins are essential in transducing signals from receptor tyrosine kinases to serine/threonine kinases which control cell growth and differentiation. Mutant Ras proteins, which bind but cannot hydrolyze GTP, are permanently activated and cause continuous cell proliferation or cancer. All five subfamilies share common structural features and four conserved motifs. Most of the membrane-bound G proteins require a carboxy terminal isoprenyl group (CAAX), added posttranslationally, for membrane association and biological activity. The G proteins also have a variable effector region, located between motifs I and II, which is characterized as the interaction site for guanine nucleotide exchange factors or GTase-activating proteins.

[0022] Eukaryotic cells are bound by a membrane and subdivided into membrane-bound compartments. Membranes are impermeable to many ions and polar molecules, therefore transport of these molecules is mediated by ion channels, ion pumps, transport proteins, or pumps. Symporters and antiporters regulate cytosolic pH by transporting ions and small molecules, e.g., amino acids, glucose, and drugs, across membranes; symporters transport small molecules and ions in the same direction, and antiporters, in the opposite direction. Transporter superfamilies include facilitative transporters and active ATP binding cassette transporters involved in multiple-drug resistance and the targeting of antigenic peptides to MHC Class I molecules. These transporters bind to a specific ion or other molecule and undergo conformational changes in order to transfer the ion or molecule across a membrane. Transport can occur by a passive, concentration-dependent mechanism or can be linked to an energy source such as ATP hydrolysis or an ion gradient.

[0023] Ion channels, ion pumps, and transport proteins mediate the transport of molecules across cellular membranes. Symporters and antiporters regulate cytosolic pH by transporting ions and small molecules such as amino acids, glucose, and drugs. Symporters transport small molecules and ions unidirectionally, and antiporters, bidirectionally. Transporter superfamilies include facilitative transporters and active ATP-binding cassette transporters which are involved in multiple-drug resistance and the targeting of antigenic peptides to MHC Class I molecules. These transporters bind to a specific ion or other molecule and undergo a conformational change in order to transfer the ion or molecule across the membrane. Transport can occur by a
passive, concentration-dependent mechanism or can be linked to an energy source such as ATP hydrolysis. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, New York, N.Y., pp. 523-546.)

[0024] Ion channels are formed by transmembrane proteins which create a lined passageway through the membrane through which water and ions, such as Na⁺, K⁺, Ca²⁺, and Cl⁻, enter and exit the cell. For example, chloride channels are involved in the regulation of the membrane electric potential as well as absorption and secretion of ions across the membrane. Chloride channels also regulate the internal pH of membrane-bound organelles.

[0025] Ion pumps are ATPases which actively maintain membrane gradients. Ion pumps are classified as P, V, or F according to their structure and function. All have one or more binding sites for ATP in their cytosolic domains. The P-class ion pumps include Ca²⁺ ATPase and Na⁺/K⁺ ATPase and function in transporting H⁺, Na⁺, K⁺, and Ca²⁺ ions. P-class pumps consist of two α and two β transmembrane subunits. The V- and F-class ion pumps have similar structures and transport only H⁺. F class H⁺ pumps mediate transport across the membranes of mitochondria and chloroplasts, while V-class H⁺ pumps regulate acidity inside lysosomes, endosomes, and plant vacuoles.


[0028] Proton-coupled, 12 membrane-spanning domain transporters such as PEPT 1 and PEPT 2 are responsible for gastrointestinal absorption and for renal reabsorption of peptides using an electrochemical H⁺ gradient as the driving force. A heterodimeric peptide transporter, consisting of TAP 1 and TAP 2, is associated with antigen processing. Peptide antigens are transported across the membrane of the endoplasmic reticulum so they can be presented to the major histocompatibility complex class I molecules. Each TAP protein consists of multiple hydrophobic membrane spanning segments and a highly conserved ATP-binding cassette. (Boll, M. et al. (1996) Proc. Natl. Acad. Sci. 93: 284-289.)

[0029] 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 compositions and mechanisms of action, hormones can be grouped into two categories. One category consists of 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-steroid hormones such as progesterone, estrogen, testosterone, cortisol, and aldosterone. The second category consists of 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 and peptide hormones such as glucagon, insulin, gastrin, secretin, cholecystokinin, adrenocorticotropic hormone, follicle stimulating hormone, luteinizing hormone, thyroid stimulating hormone, and vasopressin. (See, for example, Lodish et al. (1995) Molecular Cell Biology, Scientific American Books Inc., New York, N.Y.: pp. 856-864.)

[0030] Neuropeptides and vasemodulators (NP/VM) comprise a large family of endogenous signaling molecules. Included in this family are neuropeptides and neuropeptide hormones such as bombesin, neuropeptide Y, neuropepsins, neurenomin, melanoocyte, 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, N.Y., pp. 57-62.)

[0031] Regulatory molecules turn individual genes or groups of genes on and off in response to various inductive mechanisms of the cell or organism; act as transcription factors by determining whether or not transcription is initiated, enhanced, or repressed; and splice transcripts as dictated in a particular cell or tissue. Although they interact with short stretches of DNA scattered throughout the entire genome, most gene expression is regulated near the site at which transcription starts or within the open reading frame of the gene being expressed. Many of the transcription factors incorporate one of a set of DNA-binding structural motifs, each of which contains either α helices or β sheets and binds to the major groove of DNA. (Pabo, C. O. and R. T. Sauer (1992) Annu. Rev. Biochem. 61: 1053-95.) Other domains of transcription factors may form crucial contacts with the DNA. In addition, accessory proteins provide important interactions which may convert a particular protein complex to an activator or a repressor or may prevent binding. (Alberts, B. et al. (1994) Molecular Biology of the Cell, Garland Publishing Co, New York, N.Y. pp. 401-474.)

[0032] The discovery of new human signal peptide-containing 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 disorders including cancer; inflammation; cardiovascular, neurological, reproductive, and developmental disorders.

**SUMMARY OF THE INVENTION**

[0033] The invention features substantially purified polypeptides, proteins with signal peptides, referred to col-

[0034] The invention further provides a substantially purified variant having at least 90% amino acid identity to at least one of the amino acid sequences selected from the group consisting of SEQ ID NO:1-134, and fragments thereof. The invention also provides an isolated and purified polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof. The invention also includes an isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof.

[0035] Additionally, the invention provides an isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof. The invention also provides an isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide encoding the polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof.

The invention also provides a method for treating or preventing a disorder associated with decreased expression or activity of HSPP, the method comprising administering to a subject in need of such treatment an effective amount of a pharmaceutical composition comprising a substantially purified polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

The invention also provides a method for treating or preventing a disorder associated with increased expression or activity of HSPP, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and fragments thereof.

**BRIEF DESCRIPTION OF THE TABLES**

Table 1 shows nucleotide and polypeptide sequence identification numbers (SEQ ID NO), clone identification numbers (clone ID), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding HSPP.

Table 2 shows features of each polypeptide sequence, including predicted signal peptide sequences, and methods and algorithms used for identification of HSPP.

Table 3 shows the tissue-specific expression patterns of each nucleic acid sequence as determined by northern analysis, diseases, disorders, or conditions associated with these tissues, and the vector into which each cDNA was cloned.

Table 4 describes the tissues used to construct the cDNA libraries from which Incyte cDNA clones encoding HSPP were isolated.

Table 5 shows the programs, their descriptions, references, and threshold parameters used to analyze HSPP.

Table 6 shows the regions of the full-length nucleotide sequences of HSPP to which cDNA fragments of Table 1 correspond.

**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.

Unless otherwise indicated, 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 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.

[0053] Definitions

[0054] “HSPP” refers to the amino acid sequences of substantially purified HSPP obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and preferably the human species, from any source, whether natural, synthetic, semi-synthetic, or recombinant.

[0055] The term “agonist” refers to a molecule which, when bound to HSPP, increases or prolongs the duration of the effect of HSPP. Agonists may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to and modulate the effect of HSPP.

[0056] An “allelic variant” is an alternative form of the gene encoding HSPP. 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. Any given natural or recombinant gene may have none, one, or many allelic forms. 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.

[0057] “Altered” nucleic acid sequences encoding HSPP include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polynucleotide the same as HSPP or a polypeptide with at least one functional characteristic of HSPP. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding HSPP, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding HSPP. 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 HSPP. 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 HSPP is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, positively charged amino acids may include lysine and arginine, and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine, and valine; glycine and alanine; asparagine and glutamine; serine and threonine; and phenylalanine and tyrosine.

[0058] The terms “amino acid” or “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. In this context, “fragments,” “immunogenic fragments,” or “antigenic fragments” refer to fragments of HSPP which are preferably at least 5 to about 15 amino acids in length, most preferably at least 14 amino acids, and which retain some biological activity or immunological activity of HSPP. Where “amino acid sequence” is recited to refer to an amino acid 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.

[0059] “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.

[0060] The term “antagonist” refers to a molecule which, when bound to HSPP, decreases the amount or the duration of the effect of the biological or immunological activity of HSPP. Antagonists may include proteins, nucleic acids, carbohydrates, antibodies, or any other molecules which decrease the effect of HSPP.

[0061] The term “antibody” refers to intact molecules as well as to fragments thereof, such as Fab, F(ab)¼, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind HSPP 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, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

[0062] The term “antigenic determinant” refers to that fragment 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 (given regions or three-dimensional structures 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.

[0063] The term “antisense” refers to any composition containing a nucleic acid sequence which is complementary to the “sense” strand of a specific nucleic acid sequence. Antisense molecules may be produced by any method including synthesis or transcription. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form duplexes and to block either transcription or translation. The designation “negative” can refer to the antisense strand, and the designation “positive” can refer to the sense strand.

[0064] The term “biologically active,” refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, “immunologically active” refers to the capability of the natural, recombinant, or synthetic HSPP, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.
The terms “complementary” or “complementarity” refer to the natural binding of polynucleotides by base pairing. For example, the sequence “5’ A-G-T 3’” bonds to the complementary sequence “3’ T-C-A 5’.” Complementarity between two single-stranded molecules may be “partial,” such that only some of the nucleic acids bind, or it may be “complete,” such that total complementarity exists between the single stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands. This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands, and in the design and use of peptide nucleic acid (PNA) molecules.

A “composition comprising a given polynucleotide sequence” or 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 HSPP or fragments of HSPP may be 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 resequenced to resolve uncalled bases, extended using XL-PCR kit (Perkin-Elmer, Norwalk Conn.) in the 5’ and/or the 3’ direction, and resequenced, or which has been assembled from the overlapping sequences of more than one InCyte Clone using a computer program for fragment assembly, such as the GELVIEW Fragment Assembly system (GCG, Madison Wis.). Some sequences have been both extended and assembled to produce the consensus sequence.

The term “correlates with expression of a polynucleotide” indicates that the detection of the presence of nucleic acids, the same or related to a nucleic acid sequence encoding HSPP, by northern analysis is indicative of the presence of nucleic acids encoding HSPP in a sample, and thereby correlates with expression of the transcript from the polynucleotide encoding HSPP.

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 the chemical modification of a polypeptide sequence, or a polynucleotide sequence. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, 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.

The term “similarity” refers to a degree of complementarity. There may be partial similarity or complete similarity. The word “identity” may substitute for the word “similarity.” A partially complementary sequence that at least partially inhibits an identical sequence from hybridizing to a target nucleic acid is referred to as “substantially similar.” The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or northern blot, solution hybridization, and the like) under conditions of reduced stringency. A substantially similar sequence or hybridization probe will compete for and inhibit the binding of a completely similar (identical) sequence to the target sequence under conditions of reduced stringency. This is not to say that conditions of reduced stringency are such that non-specific binding is permitted, as reduced stringency conditions require that the binding of two sequences to one another be a specific (i.e., a selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% similarity or identity). In the absence of non-specific binding, the substantially similar sequence or probe will not hybridize to the second non-complementary target sequence.

The phrases “percent identity” or “% identity” refer to the percentage of sequence similarity found in a comparison of two or more amino acid or nucleic acid sequences. Percent identity can be determined electronically, e.g., by using the MEGALIGN program (DNASTAR, Madison Wis.) which creates alignments between two or more sequences according to methods selected by the user, e.g., the clustal method. (See, e.g., Higgins, D. G. and P. M. Sharp (1988) Gene 73: 237-244.) The clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. The percentage similarity between two amino acid sequences, e.g., sequence A and sequence B, is calculated by dividing the length of sequence A, minus the number of gap residues in sequence A, minus the number of gap residues in sequence B, into the sum of the residue matches between sequence A and sequence B, times one hundred. Gaps of low or of no similarity between the two amino acid sequences are not included in determining percentage similarity. Percent identity between nucleic acid sequences can also be counted or calculated by other methods known in the art, e.g., the Jotun Heim method. (See, e.g., Heim, J. (1990) Methods Enzymol. 183: 626-645.) Identity between sequences can also be determined by other methods known in the art, e.g., by varying hybridization conditions.

“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 stable mitotic chromosome segregation and maintenance.

The term “humanized antibody” refers to antibody molecules 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 any process by which a strand of nucleic acid binds with a complementary strand through base pairing.

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., C\textsubscript{0.5} or R\textsubscript{0.5} analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobiized 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).

[0077] The words “insertion” or “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, to the sequence found in the naturally occurring molecule.

[0078] “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.

[0079] The term “microarray” refers to an arrangement of distinct polynucleotides on a substrate.

[0080] The terms “element” or “array element” in a microarray context, refer to hybridizable polynucleotides arranged on the surface of a substrate.

[0081] The term “modulate” refers to a change in the activity of HSPP. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of HSPP.

[0082] The phrases “nucleic acid” or “nucleic acid sequence,” as used herein, 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. In this context, “fragments” refers to those nucleic acid sequences which, comprise a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:135-268, for example, as distinct from other sequences in the same genome. For example, a fragment of SEQ ID NO:135-268 is useful in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:135-268 from related polynucleotide sequences. A fragment of SEQ ID NO:135-268 is at least about 15-20 nucleotides in length. The precise length of the fragment of SEQ ID NO:135-268 and the region of SEQ ID NO:135-268 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment. In some cases, a fragment, when translated, would produce polypeptides retaining some functional characteristic, e.g., antigenicity, or structural domain characteristic, e.g., ATP-binding site, of the full-length polypeptide.

[0083] The terms “operably associated” or “operably linked” refer to functionally related nucleic acid sequences. A promoter is operably associated or operably linked with a coding sequence if the promoter controls the translation of the encoded polypeptide. While operably associated or operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements, e.g., repressor genes, are not contiguously linked to the sequence encoding the polypeptide but still bind to operator sequences that control expression of the polypeptide.

[0084] The term “oligonucleotide” refers to a nucleic acid sequence of at least about 6 nucleotides to 60 nucleotides, preferably about 15 to 30 nucleotides, and most preferably about 20 to 25 nucleotides, which can be used in PCR amplification or in a hybridization assay or microarray. “Oligonucleotide” is substantially equivalent to the terms “amplimer,” “primer,” “oligomer,” and “probe,” as these terms are commonly defined in the art.

[0085] “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 elongation, and may be peglated to extend their lifespan in the cell.

[0086] The term “sample” is used in its broadest sense. A sample suspected of containing nucleic acids encoding HSP, or fragments thereof, or HSPP itself, 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.

[0087] The terms “specific binding” or “specifically binding” refer to that interaction between a protein or peptide and an agonist, an antibody, or an antagonist. 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 containing 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.

[0088] The term “stringent conditions” refers to conditions which permit hybridization between polynucleotides and the claimed polynucleotides. Stringent conditions can be defined by salt concentration, the concentration of organic solvent, e.g., formamide, temperature, and other conditions well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature.

[0089] 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 about 60% free, preferably about 75% free, and most preferably about 90% free from other components with which they are naturally associated.

[0090] A “substitution” refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

[0091] “Substrate” refers to any suitable rigid or semirigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The sub-
strate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

[0092] "Transformation" describes a process by which exogenous DNA enters and changes 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 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, viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" 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.

[0093] A "variant" of HSPP polypeptides refers to an amino acid sequence that is altered by one or more amino acid residues. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties (e.g., replacement of leucine with isoleucine). More rarely, a variant may have "nonconservative" changes (e.g., replacement of glycine with tryptophan). Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE software (DNASTAR).

[0094] The term "variant," when used in the context of a polynucleotide sequence, may encompass a polynucleotide sequence related to HSPP. This definition may also include, for example, "allelic" (as defined above), "splice," "species," or "polymorphic" variants. A splice variant may have significance to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or an absence of domains. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will 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 base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

[0095] The Invention

[0096] The invention is based on the discovery of new human signal peptide-containing proteins (HSPP), the polynucleotides encoding HSPP, and the use of these compositions for the diagnosis, treatment, or prevention of cell proliferative disorders including cancer; inflammation; and cardiovascular, neurological, reproductive, and developmental disorders.

[0097] Table 1 lists the Incyte Clones used to derive full length nucleotide sequences encoding HSPP. Columns 1 and 2 show the sequence identification numbers (SEQ ID NO) of the amino acid and nucleic acid sequences, respectively. Column 3 shows the Clone ID of the Incyte Clone in which nucleic acids encoding each HSPP were identified, and column 4, the cDNA libraries from which these clones were isolated. Column 5 shows Incyte clones, their corresponding cDNA libraries, and shotgun sequences. The clones and shotgun sequences are part of the consensus nucleotide sequence of each HSPP and are useful as fragments in hybridization technologies.

[0098] Table 6 shows the regions of the full-length nucleotide sequences of HSPP to which cDNA fragments of Table 1 correspond. Column 1 lists nucleotide sequence identifiers and column 2 shows the clone ID of the Incyte clone in which nucleic acids encoding each HSPP were identified. Column 3 shows Incyte clones and shotgun sequences which are part of the consensus nucleotide sequence of each HSPP and are useful as fragments in hybridization technologies. Column 4 lists the starting nucleotide position and column 5 the ending nucleotide position of the region of the full-length HSPP to which the cDNA fragment corresponds.

[0099] The columns of Table 2 show various properties of the polypeptides of the invention: column 1 references the SEQ ID NO; column 2 shows the number of amino acid residues in each polypeptide; column 3, potential phosphorylation sites; column 4, potential glycosylation sites; column 5, the amino acid residues comprising signature sequences and motifs; column 6, the identity of each protein; and column 7, analytical methods used to identify each HSPP as a signal peptide-containing protein. Note that in column 5, the first line of each cell lists the amino acid residues comprising predicted signal peptide sequences. Additional identifying motifs or signatures are also listed in column 5. Of particular note is the presence of a glycosyl hydrolase family 9 active site signature in SEQ ID NO:126, a ribosomal protein S18 signature in SEQ ID NO:127, an adrenodoxin family iron-sulfur binding region signature and a cytochrome c family heme-binding site signature in SEQ ID NO:132, and a urotensin II signature sequence in SEQ ID NO:96.

[0100] Using BLAST, SEQ ID NO:68 (HSPP-68) has been identified as a TWIK-related acid-sensitive K+ channel, and SEQ ID NO:92 (HSPP-92) has been identified as a tyrosine-specific protein phosphatase. The tyrosine-specific protein phosphatases signature in SEQ ID NO:92 (HSPP-92) from about V328 through about F340 (including the putative active site cysteine residue at C330) was identified using BLOCKS and PRINTS. Also of note is the identification of SEQ ID NO:66 (HSPP-66) as a steroid binding protein using BLAST.

[0101] The columns of Table 3 show the tissue-specificity and diseases, disorders, or conditions associated with nucleotide sequences encoding HSPP. The first column of Table 3 lists the nucleotide sequence identifiers. The second column lists tissue categories which express HSPP as a fraction of total tissue categories expressing HSPP. The third column lists the diseases, disorders, or conditions associated with those tissues expressing HSPP. The fourth column lists the vectors used to subclone the cDNA library. Of particular note is the expression of SEQ ID NO:200, SEQ ID NO:203, and SEQ ID NO:225 in lung tissues; the expression of SEQ ID NO:212, SEQ ID NO:216, and SEQ ID NO:220 in
reproductive tissues; the expression of SEQ ID NO:223 in cancerous tissues; the expression of SEQ ID NO:232 in gastrointestinal tissue, specifically the small intestine and colon (fifteen out of sixteen (93.8%) cDNA libraries); and the expression of SEQ ID NO:224 in cancerous and proliferating tissues. Also of particular interest is the tissue-specific expression of SEQ ID NO:252 and SEQ ID NO:257. SEQ ID NO:252 is derived from OVARUT01, an ovarian tumor cDNA library and is exclusively expressed in reproductive tumor tissue. SEQ ID NO:252 is derived from THP1/LAZT01, a 5-aza-2'-deoxycytidine treated human promonocytic cDNA library and is exclusively expressed in hematopoietic tissue.

[0102] The following fragments of the nucleotide sequences encoding HSPP are useful in hybridization or amplification technologies to identify SEQ ID NO:135-268 and to distinguish between SEQ ID NO:135-268 and related polynucleotide sequences. The useful fragments are the fragment of SEQ ID NO:230 from about nucleotide 75 to about nucleotide 104; the fragment of SEQ ID NO:231 from about nucleotide 210 to about nucleotide 239; the fragment of SEQ ID NO:232 from about nucleotide 157 to about nucleotide 186; the fragment of SEQ ID NO:233 from about nucleotide 268 to about nucleotide 297; the fragment of SEQ ID NO:234 from about nucleotide 160 to about nucleotide 186; the fragment of SEQ ID NO:235 from about nucleotide 201 to about nucleotide 230; the fragment of SEQ ID NO:236 from about nucleotide 165 to about nucleotide 194; the fragment of SEQ ID NO:237 from about nucleotide 366 to about nucleotide 395; the fragment of SEQ ID NO:238 from about nucleotide 714 to about nucleotide 743; the fragment of SEQ ID NO:239 from about nucleotide 1731 to about nucleotide 1760; the fragment of SEQ ID NO:240 from about nucleotide 419 to about nucleotide 448; the fragment of SEQ ID NO:241 from about nucleotide 494 to about nucleotide 523; the fragment of SEQ ID NO:242 from about nucleotide 100 to about nucleotide 129; the fragment of SEQ ID NO:243 from about nucleotide 104 to about nucleotide 133; the fragment of SEQ ID NO:244 from about nucleotide 136 to about nucleotide 165; the fragment of SEQ ID NO:245 from about nucleotide 140 to about nucleotide 169; the fragment of SEQ ID NO:246 from about nucleotide 125 to about nucleotide 154; the fragment of SEQ ID NO:247 from about nucleotide 687 to about nucleotide 758; the fragment of SEQ ID NO:248 from about nucleotide 327 to about nucleotide 398; the fragment of SEQ ID NO:249 from about nucleotide 741 to about nucleotide 785; the fragment of SEQ ID NO:250 from about nucleotide 184 to about nucleotide 255; the fragment of SEQ ID NO:251 from about nucleotide 165 to about nucleotide 242; the fragment of SEQ ID NO:252 from about nucleotide 271 to about nucleotide 342; the fragment of SEQ ID NO:253 from about nucleotide 1081 to about nucleotide 1152; the fragment of SEQ ID NO:254 from about nucleotide 781 to about nucleotide 852; the fragment of SEQ ID NO:255 from about nucleotide 620 to about nucleotide 691; the fragment of SEQ ID NO:256 from about nucleotide 872 to about nucleotide 916; the fragment of SEQ ID NO:257 from about nucleotide 242 to about nucleotide 313; the fragment of SEQ ID NO:258 from about nucleotide 595 to about nucleotide 648; the fragment of SEQ ID NO:259 from about nucleotide 163 to about nucleotide 216; the fragment of SEQ ID NO:260 from about nucleotide 241 to about nucleotide 315; the fragment of SEQ ID NO:261 from about nucleotide 75 to about nucleotide 128; the fragment of SEQ ID NO:262 from about nucleotide 650 to about nucleotide 703; the fragment of SEQ ID NO:263 from about nucleotide 143 to about nucleotide 214; the fragment of SEQ ID NO:264 from about nucleotide 434 to about nucleotide 487; the fragment of SEQ ID NO:265 from about nucleotide 218 to about nucleotide 271; the fragment of SEQ ID NO:266 from about nucleotide 89 to about nucleotide 145; the fragment of SEQ ID NO:267 from about nucleotide 198 to about nucleotide 254; and the fragment of SEQ ID NO:268 from about nucleotide 10 to about nucleotide 54.

[0103] The invention also encompasses HSPP variants. A preferred HSPP variant is one which has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% amino acid sequence identity to the HSPP amino acid sequence, and which contains at least one functional or structural characteristic of HSPP.

[0104] The invention also encompasses polynucleotides which encode HSPP. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:135-268, which encodes HSPP.

[0105] The invention also encompasses a variant of a polynucleotide sequence encoding HSPP. In particular, such a variant polynucleotide sequence will have at least about 80%, more preferably at least about 90%, and most preferably at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding HSPP. 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:135-268 which has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:135-268. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of HSPP.

[0106] 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 HSPP, 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 HSPP, and all such variations are to be considered as being specifically disclosed.

[0107] Although nucleotide sequences which encode HSPP and its variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring HSPP under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding HSPP 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 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 HSPP 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.

[0108] The invention also encompasses production of DNA sequences which encode HSPP and HSPP 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 HSPP or any fragment thereof.

[0109] 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:135-268 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.) For example, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and most preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, while high stringency hybridization can be obtained in the presence of at least about 5% formamide, and most preferably at least about 50% formamide. Stringent temperature conditions will ordinarily include temperatures of at least about 30°C., more preferably of at least about 37°C., and most preferably of at least about 42°C. Varying additional parameters, such as hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Various levels of stringency are accomplished by combining these various conditions as needed. In a preferred embodiment, hybridization will occur at 30°C. in 750 mM NaCl, 75 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, hybridization will occur at 37°C. in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 μg/ml denatured salmon sperm DNA (ssDNA). In a most preferred embodiment, hybridization will occur at 42°C. in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50% formamide, and 200 μg/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

[0110] The washing steps which follow hybridization can also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include temperature of at least about 25°C., more preferably of at least about 42°C., and most preferably of at least about 68°C. In a preferred embodiment, wash steps will occur at 25°C. in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42°C. in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a most preferred embodiment, wash steps will occur at 68°C. in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art.

[0111] 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 Ohio), Taq polymerase (Perkin-Elmer), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway N.J.), or 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 Hamilton MICROLAB 2200 (Hamilton, Reno Nev.), Peltier Thermal Cycler 200 (PTC200, MJ Research, Watertown Mass.) and the ABI CATALYST 800 (Perkin-Elmer). Sequencing is then carried out using either ABI 373 or 377 DNA sequencing systems (Perkin-Elmer) or the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale Calif.). 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 N.Y., unit 7.7; Meyers, R. A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York N.Y., pp. 856-853.)
[0113] 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 into 5’ non-transcribed regulatory regions.

[0114] 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 emitted wavelengths. Output light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, PerkinElmer), 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.

[0115] In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode HSPP may be cloned in recombinant DNA molecules that direct expression of HSPP 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 HSPP.

[0116] The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter HSPP-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-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.

[0117] In another embodiment, sequences encoding HSPP 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) Nucl. Acids Res. Symp. Ser. 215-223, and Horn, T. et al. (1980) Nucl. Acids Res. Symp. Ser. 225-232.) Alternatively, HSPP itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solid-phase techniques. (See, e.g., Roberge, J. Y. et al. (1993) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A Peptide Synthesizer (Perkin-Elmer). Additionally, the amino acid sequence of HSPP, 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.


[0119] In order to express a biologically active HSPP, the nucleotide sequences encoding HSPP or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains 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 HSPP. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding HSPP. Such signals include the ATG initiation codon and adjacent sequences, e.g., the Kozak sequence. In cases where sequences encoding HSPP 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 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.)

[0120] Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding HSPP 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 N.Y., ch. 4, 8, and 16-17; Ausubel, F. M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York N.Y., ch. 9, 13, and 16.)

[0121] A variety of expression vector/host systems may be utilized to contain and express sequences encoding HSPP. 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. The invention is not limited by the host cell employed.

[0122] In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding HSPP. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding HSPP can be achieved using a multifunctional E. coli vector such as PBR-SCRIPT (Stratagene, La Jolla Calif.) or pSPORT1 plasmid (Life Technologies). Ligation of sequences encoding HSPP
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 deleted derivatives in the cloned sequence. (See, e.g., Van Hecke, G. and S. M. Schuster (1989) J. Biol. Chem. 264: 5503-5509.) When large quantities of HSPP are needed, e.g. for the production of antibodies, vectors which direct high level expression of HSPP may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

[0123] Yeast expression systems may be used for production of HSPP. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGI, 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; Grant et al. (1987) Methods Enzymol. 153: 516-54; and Scorer, C. A. et al. (1994) BioTechnology 12: 181-184.)

[0124] Plant systems may also be used for expression of HSPP. Transcription of sequences encoding HSPP may be driven 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 N.Y., pp. 191-196.)

[0125] 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 HSPP 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 viruses which expresses HSPP in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. 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.

[0126] 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 0.6 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.)

[0127] For long term production of recombinant proteins in mammalian systems, stable expression of HSPP in cell lines is preferred. For example, sequences encoding HSPP 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.

[0128] 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- or 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 or pat confers resistance to chlorosulfuron and phosphonitric acid acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. 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. 85: 8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β-galacturonidase and its substrate β-glucuronide, or luciferase and its substrate 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.)

[0129] 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 sequence encoding HSPP is inserted within a marker gene sequence, transformed cells containing sequences encoding HSPP can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding HSPP 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.

[0130] In general, host cells that contain the nucleic acid sequence encoding HSPP and that express HSPP 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.

[0131] Immunological methods for detecting and measuring the expression of HSPP 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 reac-

[0132] 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 HSPP include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding HSPP, or any fragments thereof, may be cloned into a vector 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 Wis.), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

[0133] Host cells transformed with nucleotide sequences encoding HSPP 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 and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode HSPP may be designed to contain signal sequences which direct secretion of HSPP through a prokaryotic or eukaryotic cell membrane.

[0134] 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 the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" 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 American Type Culture Collection (ATCC, Manassas, Va.) and may be chosen to ensure the correct modification and processing of the foreign protein.

[0135] In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding HSPP 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 HSPP protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of HSPP 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, 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 HSPP encoding sequence and the heterologous protein sequence, so that HSPP 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.

[0136] In a further embodiment of the invention, synthesis of radiolabeled HSPP may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract systems (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, preferably 35S-methionine.

[0137] Fragments of HSPP may be produced not only by recombinant production, but also by direct peptide synthesis using solid-phase techniques. (See, e.g., Creighton, supra, pp. 55-60.) Protein synthesis may be performed by manual techniques or by automation. Automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin-Elmer). Various fragments of HSPP may be synthesized separately and then combined to produce the full length molecule.

[0138] Therapeutics

[0139] Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of HSPP and signal peptide sequences. In addition, chemical and structural similarity, in the context of sequences and motifs, exists between HSPP-66 and prostatic steroid-binding C3 precursor from rat (GI 206453); between HSPP-68 and TWIK-related acid-sensitive K+ channel from human (GI 246554); and between HSPP-92 and tyrosine specific protein phosphatases (PROSITE PDOC00323). In addition, the expression of HSPP is closely associated with proliferative, cancerous, inflamed, cardiovascular, nervous, reproductive, hematopoietic/immune, and developmental tissue. Therefore, HSPP appears to play a role in cell proliferative disorders including cancer; inflammation; and cardiovascular, neurological, reproductive, and developmental disorders. In the treatment of cell proliferative disorders including cancer; inflammation; and cardiovascular, neurological, reproductive, and developmental disorders associated with increased HSPP expression or activity, it is desirable to decrease the expression or activity of HSPP. In the treatment of the above disorders associated with increased HSPP expression or activity, it is desirable to increase the expression or activity of HSPP.

[0140] Therefore, in one embodiment, HSPP 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 HSPP. Examples of such disorders include, but are not limited to, cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, burstitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocytopenia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; inflammatory disorders, 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-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn’s disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroleukosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture’s syndrome, gout, Graves’ disease, Hashimoto’s thyroiditis, hyperesinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter’s syndrome, rheumatoid arthritis, scleroderma, Sjögren’s syndrome, systemic lupus erythematosus, 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; cardiovascular disorders including disorders of the blood vessels such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud’s disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, and vascular tumors; disorders of the heart 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, cardiomypathy, mycarditis, pericarditis, neoplastic heart disease, and congenital heart disease; and disorders of the lungs such as 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, and plural tumors; neurological disorders 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; fetal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebellar hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, 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; akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoiac psychoses, postherpetic neuralgia, and Tourette’s disorder; reproductive disorders such as disorders of prolactin production; infertility, including tubal disease, ovulatory defects, and endometriosis; disruptions of the estrous cycle, disruptions of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumors, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; disruptions of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie’s disease, carcinoma of the male breast, and gynecomastia; and developmental disorders, such as renal tubular acidosis, anemia, Cushing’s syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms’ tumor, aniridia, genourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucopolisaccharidosis, dysplasia, 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.

In another embodiment, a vector capable of expressing HSPP 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 HSPP including, but not limited to, those described above.

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

[0143] In still another embodiment, an agonist which modulates the activity of HSPP may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of HSPP including, but not limited to, those listed above.

[0144] In a further embodiment, an antagonist of HSPP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of HSPP. Examples of such disorders include, but are not limited to, those described above. In one aspect, an antibody which specifically binds HSPP may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express HSPP.

[0145] In an additional embodiment, a vector expressing the complement of the polynucleotide encoding HSPP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of HSPP including, but not limited to, those described above.

[0146] 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 synergestically 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.

[0147] An antagonist of HSPP may be produced using methods which are generally known in the art. In particular, purified HSPP may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind HSPP. Antibodies to HSPP 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 especially preferred for therapeutic use.

[0148] For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with HSPP 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 lysisolcehin, phoronic polyls, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

[0149] It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to HSPP have an amino acid sequence consisting of at least about 5 amino acids, and, more preferably, 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 and contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of HSPP amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.


[0153] Antibody fragments which contain specific binding sites for HSPP may also be generated. For example, such fragments include, but are not limited to, Fab(2)/2 fragments produced by papain digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the Fab(2)/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.)

[0154] 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 HSPP and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering HSPP epitopes is preferred, but a competitive binding assay may also be employed (Pound, supra).

[0155] Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for HSPP. Affinity is
expressed as an association constant, \( K_a \), which is defined as the molar concentration of HSPP-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 HSPP epitopes, represents the average affinity, or avidity, of the antibodies for HSPP. The \( K_a \) determined for a preparation of monoclonal antibodies, which are monospecific for a particular HSPP epitope, represents a true measure of affinity. High-affinity antibody preparations with \( K_a \) ranging from about \( 10^8 \) to \( 10^9 \) L/mole are preferred for use in immunoassays in which the HSPP-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 HSPP, preferably in active form, from the antibody (Catty, D. (1988) Antibodies. Volume I: A Practical Approach, IRL Press, Washington, D.C.; Liddell, J. E. and Cryer, A. (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York N.Y.).

The titer and avidity of polyclonal antibody preparations may be further evaluated to 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 preferred for use in procedures requiring precipitation of HSPP-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., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding HSPP, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, the complement of the polynucleotide encoding HSPP may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding HSPP. Thus, complementary molecules or fragments may be used to modulate HSPP activity, or to achieve regulation of gene function. Such technology is now well known in the art, and sense or antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding HSPP.

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. Methods which are well known to those skilled in the art can be used to construct vectors to express nucleic acid sequences complementary to the polynucleotides encoding HSPP. (See, e.g., Sambrook, supra; Ausubel, 1995, supra.)

Genes encoding HSPP can be turned off by transforming a cell or tissue with expression vectors which express high levels of a polynucleotide, or fragment thereof, encoding HSPP. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector, and may last even longer if appropriate replication elements are part of the vector system.

As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5', or regulatory regions of the gene encoding HSPP. Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, are preferred. 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., Catty, D. (1988) Antibodies. Volume I: A Practical Approach, IRL Press, Washington, D.C.; Liddell, J. E. and Cryer, A. (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York N.Y.).

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 HSPP.

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 HSPP. 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 phosphodiester linkages within the backbone of the molecule. This concept is inherent in the production of PNAAs 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.

[0165] 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) Nature Biotechnology 15: 462-466.)

[0166] Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

[0167] An additional embodiment of the invention relates to the administration of a pharmaceutical or sterile composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of HSP, antibodies to HSP, and mimetics, agonists, antagonists, or inhibitors of HSP. The compositions may be administered alone or in combination with at least one other agent, such as a stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs, or hormones.

[0168] The pharmaceutical 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, transdural, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

[0169] In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton Pa.).

[0170] Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, drages, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

[0171] Pharmaceutical preparations for oral use can be obtained through combining active compounds with solid excipient and processing the resultant mixture of granules (optionally, after grinding) to obtain tablets or dragee cores. Suitable auxiliaries can be added, if desired. Suitable excipients include carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, and sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums, including arabic and tragacanth; and proteins, such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, and alginic acid or a salt thereof, such as sodium alginate.

[0172] Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, t alc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dye-stuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

[0173] Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with fillers or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

[0174] Pharmaceutical formulations suitable for parenteral administration may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks’ solution, Ringer’s solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils, such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate, triglycerides, or liposomes. Non-lipid polycationic amino polymers may also be used for delivery. Optionally, the suspension may also contain suitable stabilizers or agents to increase the solubility of the compounds and allow for the preparation of highly concentrated solutions.

[0175] For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

[0176] The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

[0177] The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, and succinic acid. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1 mM to 50 mM bistidine, 0.1% to 2% sucrose, and 2% to 7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.
[0178] After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of HSPP, such labeling would include amount, frequency, and method of administration.

[0179] Pharmaceutical 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.

[0180] 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, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

[0181] A therapeutically effective dose refers to that amount of active ingredient, for example HSPP or fragments thereof, antibodies of HSPP, and agonists, antagonists or inhibitors of HSPP, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by 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, and it can be expressed as the LD₅₀/ED₅₀ ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are 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.

[0182] The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety 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 pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

[0183] 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.

[0184] Diagnostics

[0185] In another embodiment, antibodies which specifically bind HSPP may be used for the diagnosis of disorders characterized by expression of HSPP, or in assays to monitor patients being treated with HSPP or agonists, antagonists, or inhibitors of HSPP. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for HSPP include methods which utilize the antibody and a label to detect HSPP 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.

[0186] A variety of protocols for measuring HSPP, including ELISAs, RIAs, and FACSs, are known in the art and provide a basis for diagnosing altered or abnormal levels of HSPP expression. Normal or standard values for HSPP expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody to HSPP under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, preferably by photometric means. Quantities of HSPP 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.

[0187] In another embodiment of the invention, the polynucleotides encoding HSPP may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAAs. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which expression of HSPP may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of HSPP, and to monitor regulation of HSPP levels during therapeutic intervention.

[0188] In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding HSPP or closely related molecules may be used to identify nucleic acid sequences which encode HSPP. 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 (maximal, high, intermediate, or low), will determine whether the probe identifies only naturally occurring sequences encoding HSPP, allelic variants, or related sequences.

[0189] Probes may also be used for the detection of related sequences, and should preferably have at least 50% sequence identity to any of the HSPP 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:135-268 or from genomic sequences including promoters, enhancers, and introns of the HSPP gene.

[0190] Means for producing specific hybridization probes for DNAs encoding HSPP include the cloning of polynucleotide sequences encoding HSPP or HSPP 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 polymerases and the appro-
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.

[0191] Polynucleotide sequences encoding HSPP may be used for the diagnosis of disorders associated with expression of HSPP. Examples of such disorders include, but are not limited to, cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thombocytopenia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bronchus, cancer, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; inflammatory disorders, 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-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn’s disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopnea with lymphocyte toxins, erythrolastosis fetalis, erythema nodosum, atopic gastritis, glomerulonephritis, Goodpasture’s syndrome, gout, Graves’ disease, Hashimoto’s thyroiditis, hyperesinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter’s syndrome, rheumatoid arthritis, scleroderma, Sjögren’s syndrome, systemic anaplasticis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extra-corporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; cardiovascular disorders including disorders of the blood vessels such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud’s disease, aneurysms, arterial dissectsions, variocose veins, thrombophlebitis and phlebothrombosis, and vascular tumors; disorders of the heart 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, neonatal heart disease, and congenital heart disease; and disorders of the lungs such as 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, and pleural tumors; neurological disorders 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-Sträussler-Scheinker syndrome; fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebellar hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, 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; akathesia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid, psychoses, postherpetic neuralgia, and Tourette’s disorder; reproductive disorders such as disorders of prolactin production; infertility, including tubal disease, ovaulatory defects, and endometriosis; disruptions of the estrous cycle, disruptions of the menstrual cycle, polycystic ovary syndrome, ovarian hyper-stimulation syndrome, endometrial and ovarian tumors, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; disruptions of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie’s disease, carcinoma of the male breast, and gynecomastia; and developmental disorders, 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 neuropathies, hypothroidism, 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 HSPP 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 HSPP expression. Such qualitative or quantitative methods are well known in the art.

[0192] In a particular aspect, the nucleotide sequences encoding HSPP may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding HSPP 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 quantitated 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 HSPP 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.

[0193] In order to provide a basis for the diagnosis of a disorder associated with expression of HSPP, 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 HSPP, 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.

[0194] 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.

[0195] 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.

[0196] Additional diagnostic uses for oligonucleotides designed from the sequences encoding HSPP 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 HSPP, or a fragment of a polynucleotide complementary to the polynucleotide encoding HSPP, 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 quantitation of closely related DNA or RNA sequences.
mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or syndrome has 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 subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

[0203] In another embodiment of the invention, HSPP, 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 HSPP and the agent being tested may be measured.

[0204] 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 HSPP, or fragments thereof, and washed. Bound HSPP is then detected by methods well known in the art. Purified HSPP 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.

[0205] In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding HSPP specifically compete with a test compound for binding HSPP. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with HSPP.

[0206] In additional embodiments, the nucleotide sequences which encode HSPP 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.

[0207] 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 limiting of the remainder of the disclosure in any way whatsoever.

[0208] The disclosures of all applications, patents, and publications, mentioned above and below, in particular U.S. Ser. No. 60/090,762, U.S. Ser. No. 60/094,983, U.S. Ser. No. 60/102,686, and U.S. Ser. No. 60/112,129, are hereby expressly incorporated by reference.

EXAMPLES

[0209] I. Construction of cDNA Libraries

[0210] RNA was purchased from Clontech or isolated from tissues described in Table 4. 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 monophosphoric solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

[0211] 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), OLI GOTEK latex particles (QIAGEN, Valencia Calif.), or an OLI GOTEK 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 Tex.).

[0212] 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 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 (300-1000 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), or pINCY (Incyte Corporation, Palo Alto Calif.). Recombinant plasmids were transformed into competent E. coli cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5a, DH10B, or ElectroMAX DH10B from Life Technologies.

[0213] II. Isolation of cDNA Clones

[0214] Plasmids were recovered from host cells by in vivo excision, using the UNIZAP vector system (Stratagene) or 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 REAL Prep 96 plasmid kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

[0215] 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 PICO GREEN dye (Molecular Probes, Eugene Ore.) and a Fluoroskan II fluorescence scanner (Labsystems Oy, Helsinki, Finland).
III. Sequencing and Analysis

The cDNAs were prepared for sequencing using the ABI CATALYST 800 (Perkin-Elmer) or the HYDRA microdispenser (Robbins Scientific) or MICROLAB 2200 (Hamilton) systems in combination with the PTC-200 thermal cyclers (MJ Research). The cDNAs were sequenced using the ABI PRISM 373 or 377 sequencing systems (Perkin-Elmer) and standard ABI protocols, base calling software, and kits. In one alternative, cDNAs were sequenced using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics). In another alternative, the cDNAs were amplified and sequenced using the ABI PRISM BIGDYE terminator cycle sequencing ready reaction kit (Perkin-Elmer). In yet another alternative, cDNAs were sequenced using solutions and dyes from Amersham Pharmacia Biotech. Reading frames for the ESTs were determined 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 V.

The polynucleotide sequences derived from cDNA, extension, and shotgun sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the software programs, descriptions, references, and threshold parameters used. The first column of Table 5 shows the tools, programs, and algorithms used, the second column provides a brief description thereof, the third column presents the references which are incorporated by reference herein, 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 probability the greater the homology). Sequences were analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco Calif.) and LASERGENE software (DNASTAR).

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases such as GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS to acquire annotation, using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and 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 amino acid sequences, and these full length sequences were subsequently analyzed by querying against databases such as the GenBank databases (described above), SwissProt, BLOCKS, PRINTS, Prosite, 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, e.g., Eddy, S. R. (1996) Cur. Opin. Str. Biol. 6: 361-365.)

The programs described above for the assembly and analysis of full length polynucleotide and amino acid sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:135-268. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in the Invention section above.

IV. Northern Analysis

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.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in nucleotide databases such as GenBank or LIFSEQ database (Incyte Corporation). 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:

\[ \frac{\% \text{ sequence identity} \times \% \text{ maximum BLAST score}}{100} \]

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1% to 2% error, and, with a product score of 70, the match will be exact. Similar molecules are usually identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding HSPP occurred. Analysis involved the categorization of cDNA libraries by organ/tissue and disease. The organ/tissue categories included cardiovascular, dermatologic, developmental, endocrine, gastrointestinal, hematopoietic/immune, musculoskeletal, nervous, reproductive, and urologic. The disease/condition categories included cancer, inflammation/trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific expression are reported in Table 3.

V. Extension of HSPP Encoding Polynucleotides

Full length nucleic acid sequences of SEQ ID Nos:135-229 were produced by extension of the component fragments described in Table 1, column 5, using oligonucleotide primers based on these fragments. For each nucleic acid sequence, one primer was synthesized to initiate extension of an antisense polynucleotide, and the other was synthesized to initiate extension of a sense polynucleotide. Primers were used to facilitate the extension of the known sequence “outward” generating amplicons containing new unknown nucleotide sequence for the region of interest. The initial primers were designed from the cDNA using Oligo 4.06 (National Biosciences, Plymouth, Minn.), 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 result in hairpin structures and primer-primer dimerizations was avoided.

[0228] Selected human cDNA libraries (GIBCO BRL) were used to extend the sequence. If more than one extension is necessary or desired, additional sets of primers are designed to further extend the known region.

[0229] High fidelity amplification was obtained by following the instructions for the XL-PCR kit (The Perkin-Elmer Corp., Norwalk, Conn.) and thoroughly mixing the enzyme and reaction mix. PCR was performed using the PTC-200 thermal cycler (MJ Research, Inc., Watertown, Mass.), beginning with 40 pmol of each primer and the recommended concentrations of all other components of the kit, with the following parameters:

<table>
<thead>
<tr>
<th>Step</th>
<th>Temperature (C)</th>
<th>Time (min)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Step 1</td>
<td>94</td>
<td>1</td>
</tr>
<tr>
<td>Step 2</td>
<td>65</td>
<td>1</td>
</tr>
<tr>
<td>Step 3</td>
<td>68</td>
<td>6</td>
</tr>
<tr>
<td>Step 4</td>
<td>94</td>
<td>35</td>
</tr>
<tr>
<td>Step 5</td>
<td>65</td>
<td>1</td>
</tr>
<tr>
<td>Step 6</td>
<td>68</td>
<td>7</td>
</tr>
<tr>
<td>Step 7</td>
<td>94</td>
<td>15</td>
</tr>
<tr>
<td>Step 8</td>
<td>65</td>
<td>3</td>
</tr>
<tr>
<td>Step 9</td>
<td>68</td>
<td>7:15</td>
</tr>
<tr>
<td>Step 10</td>
<td>55</td>
<td>30</td>
</tr>
<tr>
<td>Step 11</td>
<td>72</td>
<td>90</td>
</tr>
<tr>
<td>Step 12</td>
<td></td>
<td>90</td>
</tr>
<tr>
<td>Step 13</td>
<td>4</td>
<td></td>
</tr>
</tbody>
</table>

[0230] A 5 μl to 10 μl aliquot of the reaction mixture was analyzed by electrophoresis on a low concentration (about 0.6% to 0.8%) agarose mini-gel to determine which reactions were successful in extending the sequence. Bands thought to contain the largest products were excised from the gel, purified using QIAQUICK (QIAGEN Inc.), and trimmed of overhangs using Klenow enzyme to facilitate religation and cloning.

[0231] After ethanol precipitation, the products were redissolved in 13 μl of ligation buffer, 1 μl T4-DNA ligase (15 units) and 1 μl T4 polynucleotide kinase were added, and the mixture was incubated at room temperature for 2 to 3 hours, or overnight at 16°C. Competent E. coli cells (in 40 μl of appropriate media) were transformed with 3 μl of ligation mixture and cultured in 80 μl of SOC medium. (See, e.g., Sambrook, supra, Appendix A, p. 2.) After incubation for one hour at 37°C, the E. coli mixture was plated on Luria Bertani (LB) agar (see, e.g., Sambrook, supra, Appendix A, p. 1) containing carbocillin (2× carb). The following day, several colonies were randomly picked from each plate and cultured in 150 μl of liquid LB at 2×. The media was plated on an individual well of an appropriate commercially-available sterile 96-well microtiter plate. The following day, 5 μl of each overnight culture was transferred into a non-sterile 96-well plate, and after dilution 1:10 with water, 5 μl from each sample was transferred into a PCR array.

[0232] For PCR amplification, 18 μl of concentrated PCR reaction mix (3.3×) containing 4 units of Tth DNA polymerase, a vector primer, and one or both of the gene specific primers used for the extension reaction were added to each well. Amplification was performed using the following conditions:

<table>
<thead>
<tr>
<th>Step</th>
<th>Conditions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Step 1</td>
<td>94°C for 60 sec</td>
</tr>
<tr>
<td>Step 2</td>
<td>55°C for 20 sec</td>
</tr>
<tr>
<td>Step 3</td>
<td>72°C for 90 sec</td>
</tr>
<tr>
<td>Step 4</td>
<td>Repeat steps 2 through 4 for</td>
</tr>
<tr>
<td></td>
<td>an additional 29 cycles</td>
</tr>
<tr>
<td>Step 5</td>
<td>72°C for 180 sec</td>
</tr>
<tr>
<td>Step 6</td>
<td>4°C (and holding)</td>
</tr>
</tbody>
</table>

[0233] Aliquots of the PCR reactions were run on agarose gels, together with molecular weight markers. The sizes of the PCR products were compared to the original partial cDNAs, and appropriate clones were selected, ligated into plasmid, and sequenced.

[0234] The full length nucleic acid sequences of SEQ ID NO:230-268 were produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5’ extension of the known fragment, and the other primer, to initiate 3’ extension of the known fragment. The initial primers were designed using OLGOS by 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 result in hairpin structures and primer-primer dimerizations was avoided.

[0235] 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.

[0236] 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++, (NH4)2SO4, and β-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELLONGASE 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.

[0237] The concentration of DNA in each well was determined by dispensing 100 μl PICOGREEN quantitation reagent (0.25% [v/v] PICOGREEN; Molecular Probes, Eugene Ore.) dissolved in 1×TE and 0.5 μl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton Mass.), 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 µl to 10 µl aliquot of the reaction mixture was analyzed by electrophoresis on a 1% agarose mini-gel to determine which reactions were successful in extending the sequence.

[0238] The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison Wis.), and sonicated or sheared prior to religation into µUC 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 Mass.) into µUC 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, individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

[0239] 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: 94°C, 3 min; 7 repeated 29 times; Step 6: 72°C, 5 min; Step 7: 72°C, 5 min. The 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 (Perkin-Elmer).

[0240] In like manner, the nucleotide sequences of SEQ ID NO:135-268 are used to obtain 5 regulatory sequences using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

[0241] VI. Labeling and Use of Individual Hybridization Probes

[0242] Hybridization probes derived from SEQ ID NO:135-268 are employed to screen cDNAs, 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 OLIIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 µCi of [α-32P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (Du Pont NEN, Boston Mass.). 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 (Du Pont NEN).

[0243] The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytiran Plus, Schleicher & Schuell, Durham N.H.). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1x saline sodium citrate and 0.5% sodium dodecyl sulfate. After XOMAT-AR film (Eastman Kodak, Rochester N.Y.) is exposed to the blots to film for several hours, hybridization patterns are compared visually.

[0244] VII. Microarrays

[0245] A chemical coupling procedure and an ink jet device can be used to synthesize array elements on the surface of a substrate. (See, e.g., Baldeschweiler, supra.) An array 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 by hand or by using available methods and machines and contain any appropriate number of elements. After hybridization, nonhybridized probes are removed and a scanner used to determine the levels and patterns of fluorescence. The degree of complementarity and the relative abundance of each probe which hybridizes to an element on the microarray may be assessed through analysis of the scanned images.

[0246] Full-length cDNAs, Expressed Sequence Tags (ESTs), or fragments thereof may comprise the elements of the microarray. Fragments suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). Full-length cDNAs, ESTs, or fragments thereof corresponding to one of the nucleotide sequences of the present invention, or selected at random from a cDNA library relevant to the present invention, are arranged on an appropriate substrate, e.g., a glass slide. The cDNA is fixed to the slide using, e.g., UV cross-linking followed by thermal and chemical treatments and subsequent drying. (See, e.g., Schena, M. et al. (1995) Science 270: 467-470; Shalon, D. et al. (1996) Genome Res. 6: 639-645.) Fluorescent probes are prepared and used for hybridization to the elements on the substrate. The substrate is analyzed by procedures described above.

[0247] VIII. Complementary Polynucleotides

[0248] Sequences complementary to the HSPP-encoding sequences, or any part thereof, are used to detect, decrease, or inhibit expression of naturally occurring HSPP. 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 OLIIGO 4.06 software (National Biosciences) and the coding sequence of HSPP. To inhibit transcription, a complementary oligonucleotide is designed to 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 HSPP-encoding transcript.

[0249] IX. Expression of HSPP

[0250] Expression and purification of HSPP is achieved using bacterial or virus-based expression systems. For expression of HSPP 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 HSPP upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of HSPP 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 HSPP 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 (SF) 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.)

[0251] In most expression systems, HSPP 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 HSPP at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunofluorescence with 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 Ausbel (1995, supra, ch 10 and 16). Purified HSPP obtained by these methods can be used directly in the following activity assay.

[0252] X. Demonstration of HSPP Activity

[0253] HSPP-68

[0254] HSPP-68 activity is measured by determining the potassium current using voltage clamp analysis on single Xenopus laevis oocytes injected with HSPP-68 cRNA. HSPP-68 cRNA is synthesized in vitro from linearized HSPP-68 encoding plasmids using the T7 RNA polymerase and injected into oocytes. Injected oocytes are used two to four days after injection. In a 0.3 ml perfusion chamber, a single oocyte is impaled with two standard microelectrodes (1-2.5 MΩ) filled with 3 M KCl. The oocyte is maintained under voltage clamp by using a Dagan TEV 200 amplifier, in buffer containing 96 mM NaCl, 2 mM KCl, 1.8 mM CaCl₂, 2 mM MgCl₂, 5 mM HEPES, pH 7.4 with NaOH. Stimulation of the preparation, data acquisition, and analysis is performed using a computer. All experiments are performed at room temperature (21-22°C). Following a depolarizing pulse, the characteristics of the resulting potassium current are measured via the recording electrode. The amount of potassium current that flows in response to a unit depolarization is proportional to the activity of HSPP-68 in the cell. (Duprat, F. et al. (1997) EMBO J. 16: 5464-5471.)

[0255] HSPP-92

[0256] HSPP-92 protein phosphatase activity is measured by the hydrolysis of P-nitrophenyl phosphate (PNPP). HSPP-92 is incubated together with PNPP in HEPES buffer pH 7.5, in the presence of 0.1% b-mercaptoethanol at 37°C for 60 min. The reaction is stopped by the addition of 6 ml of 10 N NaOH and the increase in light absorbance at 410 nm resulting from the hydrolysis of PNPP is measured using a spectrophotometer. The increase in light absorbance is proportional to the activity of PP in the assay. (Diamond R. H. et al (1994) Mol Cell Biol 14: 3752-62.)

[0257] Alternatively, HSPP, or biologically active fragments thereof, are labeled with 125I Bolton-Hunter reagent. (See, e.g., Bolton et al. (1973) Biochem. J. 133: 529.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled HSPP, washed, and any wells with labeled HSPP complex are assayed. Data obtained using different concentrations of HSPP are used to calculate values for the number, affinity, and association of HSPP with the candidate molecules.

[0258] Alternatively, an assay for HSPP activity measures the expression of HSPP on the cell surface. cDNA encoding HSPP is subcloned into an appropriate mammalian expression vector suitable for high levels of cDNA expression. The resulting construct is transfected into a nonhuman cell line such as NIH3T3. Cell surface proteins are labeled with biotin using methods known in the art. Immunoprecipitations are performed using HSPP-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 HSPP expressed on the cell surface.

[0259] Alternatively, an assay for HSPP activity measures the amount of HSPP 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 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 HSPP-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The concentration of HSPP in secretory organelles relative to HSPP in total cell lysate is proportional to the amount of HSPP in transit through the secretory pathway.

[0260] XI. Functional Assays

[0261] HSPP function is assessed by expressing the sequences encoding HSPP 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 Calif.), both of which contain the cytomegalovirus promoter. 5-10 µg of recombinant vector is transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2 µg 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 non-
transfected cells and is a reliable predictor of cDNA expres-
sion 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 properties, for example, their apoptotic state.
FCM detects and quantifies the uptake of fluorescent mol-
ecules 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-regu-
lation of DNA synthesis as measured by decrease in bromode-
oxuryridine uptake; alterations in expression of cell surface
and intracellular proteins as measured with 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.

[0262] The influence of HSPP on gene expression can be
assessed using highly purified populations of cells trans-
fected with sequences encoding HSPP 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 effi-
ciently 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 to those of skill in
the art. Expression of mRNA encoding HSPP and other
genes of interest can be analyzed by northern analysis or
microarray techniques.

[0263] XII. Production of HSPP Specific Antibodies
[0264] HSPP substantially purified using polyacrylamide
gel electrophoresis (PAGE; see, e.g., Harrington, M. G.
(1990) Methods Enzymol. 182: 488-495), or other purifica-
tion techniques, is used to immunize rabbits and to produce
antibodies using standard protocols.

[0265] Alternatively, the HSPP amino acid sequence is
analyzed using LASERGENE software (DNASTAR) to
determine regions of high immunogenicity, and a corre-
sponding 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.)

[0266] Typically, oligopeptides 15 residues in length are
synthesized using an ABI 431A Peptide Synthesizer (Perkin-
Elmer) using fmoc-chemistry and coupled to KLH (Sigma-
Aldrich, St. Louis Mo.) by reaction with N-maleimidoben-
zoyl-N-hydroxysuccinimide ester (MBS) to increase
immunogenicity. (See, e.g., Ausubel, 1995, supra.) Rabbits
are immunized with the oligopeptide-KLH complex in com-
plete Freund’s adjuvant. Resulting antisera are tested for
antipeptide activity by, for example, binding the peptide to
plastic, blocking with 1% BSA, reacting with rabbit antisera,
washing, and reacting with radio-iodinated goat anti-rabbit
IgG.

[0267] XIII. Purification of Naturally Occurring HSPP
Using Specific Antibodies
[0268] Naturally occurring or recombinant HSPP is sub-
stantially purified by immunoaffinity chromatography using
antibodies specific for HSPP. An immunoaffinity column is
constructed by covalently coupling anti-HSPP 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.

[0269] Media containing HSPP are passed over the immu-
noaffinity column, and the column is washed under condi-
tions that allow the preferential absorbance of HSPP (e.g.,
high ionic strength buffers in the presence of detergent). The
column is eluted under conditions that disrupt antibody/
HSPP 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 HSPP is collected.

[0270] XIV. Identification of Molecules Which Interact
with HSPP
[0271] HSPP, or biologically active fragments thereof, are
labeled with 125I Bolton-Hunter reagent. (See, e.g., Bolton
et al. (1973) Biochem. J. 133: 529.) Candidate molecules
previously arrayed in the wells of a multi-well plate are
incubated with the labeled HSPP, washed, and any wells
with labeled HSPP complex are assayed. Data obtained
using different concentrations of HSPP are used to calculate
values for the number, affinity, and association of HSPP with
the candidate molecules.

[0272] 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 specific preferred
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**

<table>
<thead>
<tr>
<th>Protein Name</th>
<th>Nucleotide SEQ ID No.</th>
<th>Fragment Details</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>135</td>
<td>443531H1 (MPHGNOT03), 443531H5 (MPHGNOT03), 140680F6 (LAIUTUT2), 443531H6 (MPHGNOT03), SBBAB0651F1, SBBAB00651F1</td>
</tr>
<tr>
<td>2</td>
<td>136</td>
<td>63280H1 (NEUTGTM01), 784715R3 (PROSNOT5), 509590H1 (MPHGNOT03)</td>
</tr>
<tr>
<td>3</td>
<td>137</td>
<td>670001H1 (CRBLNOUT1), 669871R1 (CRBLNOUT1), 669871R1 (CRBLNOUT1), 861234F1 (BLADUTU04)</td>
</tr>
<tr>
<td>4</td>
<td>138</td>
<td>726498 (SYNOOAT01), 726498 (SYNOOAT01), 726498 (SYNOOAT01), 866595R3 (BRAITUTO3)</td>
</tr>
</tbody>
</table>

Jul. 14, 2005
<table>
<thead>
<tr>
<th>Protein Seq ID No.</th>
<th>Nucleotide Seq ID No.</th>
<th>Close ID</th>
<th>Library</th>
<th>Fragments</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>139</td>
<td>795064</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>140</td>
<td>924925</td>
<td>BRAINOT053</td>
<td>1466436F1 (PANCOT02)</td>
</tr>
<tr>
<td>7</td>
<td>141</td>
<td>962390</td>
<td>BRSTUT02</td>
<td>929258</td>
</tr>
<tr>
<td>8</td>
<td>142</td>
<td>1259405</td>
<td>MENITUT04</td>
<td>1429538F1 (PANCOT02)</td>
</tr>
<tr>
<td>9</td>
<td>143</td>
<td>1293738</td>
<td>BRSTUT02</td>
<td>1293738</td>
</tr>
<tr>
<td>10</td>
<td>144</td>
<td>1299627</td>
<td>BRSTUT02</td>
<td>1299627</td>
</tr>
<tr>
<td>11</td>
<td>145</td>
<td>1306026</td>
<td>PLACOT02</td>
<td>1306026</td>
</tr>
<tr>
<td>12</td>
<td>146</td>
<td>1316219</td>
<td>BLADTUT2</td>
<td>1316219</td>
</tr>
<tr>
<td>13</td>
<td>147</td>
<td>1320031</td>
<td>PANCOT02</td>
<td>1320031</td>
</tr>
<tr>
<td>14</td>
<td>148</td>
<td>1483050</td>
<td>CORPNOT02</td>
<td>1483050</td>
</tr>
<tr>
<td>15</td>
<td>149</td>
<td>1514160</td>
<td>PANCOT01</td>
<td>1514160</td>
</tr>
<tr>
<td>16</td>
<td>150</td>
<td>1603403</td>
<td>LUNGNOT5</td>
<td>1603403</td>
</tr>
<tr>
<td>17</td>
<td>151</td>
<td>1652303</td>
<td>PROSTOT08</td>
<td>1652303</td>
</tr>
<tr>
<td>18</td>
<td>152</td>
<td>1693358</td>
<td>COLNOT23</td>
<td>1693358</td>
</tr>
<tr>
<td>19</td>
<td>153</td>
<td>1707710</td>
<td>DUODNOT2</td>
<td>1707710</td>
</tr>
<tr>
<td>20</td>
<td>154</td>
<td>1738735</td>
<td>COLNOT22</td>
<td>1738735</td>
</tr>
<tr>
<td>21</td>
<td>155</td>
<td>1749147</td>
<td>STOMTUT2</td>
<td>1749147</td>
</tr>
<tr>
<td>22</td>
<td>156</td>
<td>1817722</td>
<td>PROSNOT02</td>
<td>1817722</td>
</tr>
<tr>
<td>23</td>
<td>157</td>
<td>1831290</td>
<td>THPAPZ01</td>
<td>1831290</td>
</tr>
<tr>
<td>24</td>
<td>158</td>
<td>1831477</td>
<td>THPAPZ01</td>
<td>1831477</td>
</tr>
<tr>
<td>25</td>
<td>159</td>
<td>1841607</td>
<td>COLNOT7</td>
<td>1841607</td>
</tr>
<tr>
<td>26</td>
<td>160</td>
<td>1855291</td>
<td>LUNGFE02</td>
<td>1855291</td>
</tr>
<tr>
<td>27</td>
<td>161</td>
<td>1854555</td>
<td>HINTAZ02</td>
<td>1854555</td>
</tr>
<tr>
<td>28</td>
<td>162</td>
<td>1855755</td>
<td>PROSNOT8</td>
<td>1855755</td>
</tr>
<tr>
<td>29</td>
<td>163</td>
<td>1861434</td>
<td>PROSNOT9</td>
<td>1861434</td>
</tr>
<tr>
<td>30</td>
<td>164</td>
<td>1872334</td>
<td>LEUKNOT2</td>
<td>1872334</td>
</tr>
<tr>
<td>31</td>
<td>165</td>
<td>1877230</td>
<td>LEUKNOT3</td>
<td>1877230</td>
</tr>
<tr>
<td>32</td>
<td>166</td>
<td>1877885</td>
<td>LEUKNOT3</td>
<td>1877885</td>
</tr>
<tr>
<td>33</td>
<td>167</td>
<td>1889269</td>
<td>BLADTUT7</td>
<td>1889269</td>
</tr>
<tr>
<td>34</td>
<td>168</td>
<td>1900243</td>
<td>BLADTUT7</td>
<td>1900243</td>
</tr>
<tr>
<td>35</td>
<td>169</td>
<td>1900433</td>
<td>BLADTUT6</td>
<td>1900433</td>
</tr>
<tr>
<td>36</td>
<td>170</td>
<td>1909441</td>
<td>CONNOT1</td>
<td>1909441</td>
</tr>
<tr>
<td>Protein Seq ID NO:</td>
<td>Nucleotide Seq ID NO:</td>
<td>Clone ID</td>
<td>Library</td>
<td>Fragments</td>
</tr>
<tr>
<td>------------------</td>
<td>----------------------</td>
<td>----------</td>
<td>---------</td>
<td>-----------</td>
</tr>
<tr>
<td>37</td>
<td>192226</td>
<td>COLN0T1b</td>
<td>(COLN0T1b, 192226)</td>
<td></td>
</tr>
<tr>
<td>38</td>
<td>192364</td>
<td>COLN0T1c</td>
<td>(COLN0T1c, 192364)</td>
<td></td>
</tr>
<tr>
<td>39</td>
<td>192424</td>
<td>BRST0T7</td>
<td>(BRST0T7, 192424)</td>
<td></td>
</tr>
<tr>
<td>40</td>
<td>192839</td>
<td>PROSN01</td>
<td>(PROSN01, 192839)</td>
<td></td>
</tr>
<tr>
<td>41</td>
<td>229236</td>
<td>BRAIN0N1</td>
<td>(BRAIN0N1, 229236)</td>
<td></td>
</tr>
<tr>
<td>42</td>
<td>234830</td>
<td>COLSUC0T</td>
<td>(COLSUC0T, 234830)</td>
<td></td>
</tr>
<tr>
<td>43</td>
<td>237322</td>
<td>ADREN0T7</td>
<td>(ADREN0T7, 237322)</td>
<td></td>
</tr>
<tr>
<td>44</td>
<td>245768</td>
<td>ENDAN0T1</td>
<td>(ENDAN0T1, 245768)</td>
<td></td>
</tr>
<tr>
<td>45</td>
<td>248042</td>
<td>SMCAN0T1</td>
<td>(SMCAN0T1, 248042)</td>
<td></td>
</tr>
<tr>
<td>46</td>
<td>250374</td>
<td>CONUT0T1</td>
<td>(CONUT0T1, 250374)</td>
<td></td>
</tr>
<tr>
<td>47</td>
<td>253768</td>
<td>BONUT0T1</td>
<td>(BONUT0T1, 253768)</td>
<td></td>
</tr>
<tr>
<td>48</td>
<td>259385</td>
<td>OVART0T2</td>
<td>(OVART0T2, 259385)</td>
<td></td>
</tr>
<tr>
<td>49</td>
<td>264137</td>
<td>LUNG0T8</td>
<td>(LUNG0T8, 264137)</td>
<td></td>
</tr>
<tr>
<td>50</td>
<td>267487</td>
<td>KIDN0T19</td>
<td>(KIDN0T19, 267487)</td>
<td></td>
</tr>
<tr>
<td>51</td>
<td>275848</td>
<td>THP1AZ0S8</td>
<td>(THP1AZ0S8, 275848)</td>
<td></td>
</tr>
<tr>
<td>52</td>
<td>276329</td>
<td>BRST0T12</td>
<td>(BRST0T12, 276329)</td>
<td></td>
</tr>
<tr>
<td>53</td>
<td>277946</td>
<td>OVART0T3</td>
<td>(OVART0T3, 277946)</td>
<td></td>
</tr>
<tr>
<td>54</td>
<td>280852</td>
<td>BLADT08</td>
<td>(BLADT08, 280852)</td>
<td></td>
</tr>
<tr>
<td>55</td>
<td>280928</td>
<td>BLADT09</td>
<td>(BLADT09, 280928)</td>
<td></td>
</tr>
<tr>
<td>56</td>
<td>292136</td>
<td>SINN0T4</td>
<td>(SINN0T4, 292136)</td>
<td></td>
</tr>
<tr>
<td>57</td>
<td>292488</td>
<td>KIDN0T2</td>
<td>(KIDN0T2, 292488)</td>
<td></td>
</tr>
<tr>
<td>58</td>
<td>294922</td>
<td>KIDN0T1</td>
<td>(KIDN0T1, 294922)</td>
<td></td>
</tr>
<tr>
<td>59</td>
<td>299219</td>
<td>BRAIN0T2</td>
<td>(BRAIN0T2, 299219)</td>
<td></td>
</tr>
<tr>
<td>60</td>
<td>304471</td>
<td>HEAN0T1</td>
<td>(HEAN0T1, 304471)</td>
<td></td>
</tr>
<tr>
<td>61</td>
<td>312041</td>
<td>LUNG0T13</td>
<td>(LUNG0T13, 312041)</td>
<td></td>
</tr>
<tr>
<td>62</td>
<td>126758</td>
<td>LUNG0T11</td>
<td>(LUNG0T11, 126758)</td>
<td></td>
</tr>
<tr>
<td>63</td>
<td>674760</td>
<td>CRBLNO1T</td>
<td>(CRBLNO1T, 674760)</td>
<td></td>
</tr>
<tr>
<td>64</td>
<td>122948</td>
<td>BRAIT0T1</td>
<td>(BRAIT0T1, 122948)</td>
<td></td>
</tr>
<tr>
<td>65</td>
<td>123695</td>
<td>LUNG0T3</td>
<td>(LUNG0T3, 123695)</td>
<td></td>
</tr>
<tr>
<td>66</td>
<td>135928</td>
<td>LUNG0T12</td>
<td>(LUNG0T12, 135928)</td>
<td></td>
</tr>
<tr>
<td>67</td>
<td>145070</td>
<td>PENIT01</td>
<td>(PENIT01, 145070)</td>
<td></td>
</tr>
<tr>
<td>68</td>
<td>191068</td>
<td>CONN0T1</td>
<td>(CONN0T1, 191068)</td>
<td></td>
</tr>
<tr>
<td>69</td>
<td>195514</td>
<td>CONN0T1</td>
<td>(CONN0T1, 195514)</td>
<td></td>
</tr>
<tr>
<td>70</td>
<td>196137</td>
<td>BRST0T04</td>
<td>(BRST0T04, 196137)</td>
<td></td>
</tr>
<tr>
<td>Protein SEQ ID NO:</td>
<td>Nucleotide SEQ ID NO:</td>
<td>Clone ID</td>
<td>Library</td>
<td>Fragments</td>
</tr>
<tr>
<td>------------------</td>
<td>-----------------------</td>
<td>---------</td>
<td>---------</td>
<td>-----------</td>
</tr>
<tr>
<td>75</td>
<td>209</td>
<td>CORPNT02</td>
<td>1990762H (CORPNT02), 1990762T (CORPNT02), SBGA0491F1, SBGA0220S1F1</td>
<td></td>
</tr>
<tr>
<td>76</td>
<td>210</td>
<td>CORPNT02</td>
<td>1994133H (CORPNT02), 2645984G6 (OVARUT04)</td>
<td></td>
</tr>
<tr>
<td>77</td>
<td>211</td>
<td>BRSTUT03</td>
<td>1997745H (BNTS3AT01), 1997745H (BRSTUT03), SAZA0059F1</td>
<td></td>
</tr>
<tr>
<td>78</td>
<td>212</td>
<td>TESTN03</td>
<td>2009358H (TESTN03), 2009358S (TESTN03)</td>
<td></td>
</tr>
<tr>
<td>79</td>
<td>213</td>
<td>TESTN03</td>
<td>2009152S (TESTN03), 2009152S (TESTN03), 2783261H (BRSTN013)</td>
<td></td>
</tr>
<tr>
<td>80</td>
<td>214</td>
<td>OVARUT03</td>
<td>2061752H (OVARUT03), 2061752T (OVARUT03), 2732805H (OVARUT03), SAZA0063F1, SAZA0068F1</td>
<td></td>
</tr>
<tr>
<td>81</td>
<td>215</td>
<td>OVARUT03</td>
<td>2061933H (OVARUT03), 2061933H (OVARUT03), 2061933H (OVARUT03), SAZA0069F1</td>
<td></td>
</tr>
<tr>
<td>82</td>
<td>216</td>
<td>UTRSN08</td>
<td>2081422F6 (UTRSN08), 2081422H (UTRSN08), SBGA0497F1, SBGA0657F1, SBGA0068F1</td>
<td></td>
</tr>
<tr>
<td>83</td>
<td>217</td>
<td>BRAINT02</td>
<td>210129F1 (BRAINT02), 2000939F1, 2000939H1, 2000939H1, 2000939H1, 2000939H1</td>
<td></td>
</tr>
<tr>
<td>84</td>
<td>218</td>
<td>BRAINT02</td>
<td>2123155H (BRAINT02), 2123155H (BRAINT02), 2123155H (BRAINT02), 2123155H (BRAINT02)</td>
<td></td>
</tr>
<tr>
<td>85</td>
<td>219</td>
<td>PANCUT02</td>
<td>2241736H (PANCUT02), 2241736H (PANCUT02), 2241736H (PANCUT02), 2241736H (PANCUT02)</td>
<td></td>
</tr>
<tr>
<td>86</td>
<td>220</td>
<td>PANCUT02</td>
<td>2271935F1 (PANCUT02), 2271935H1 (PANCUT02), 2271935H1 (PANCUT02)</td>
<td></td>
</tr>
<tr>
<td>87</td>
<td>221</td>
<td>PANCUT02</td>
<td>2295344H (PANCUT02), 2295344F6 (PANCUT02), 2295344F6 (PANCUT02), 2295344F6 (PANCUT02)</td>
<td></td>
</tr>
<tr>
<td>88</td>
<td>222</td>
<td>PANCUT02</td>
<td>2329994H (PANCUT02), 2329994H (PANCUT02), 2329994H (PANCUT02), 2329994H (PANCUT02)</td>
<td></td>
</tr>
<tr>
<td>89</td>
<td>223</td>
<td>PANCUT02</td>
<td>2497805G8 (PANCUT02), 2497805H1 (PANCUT02), 2497805H1 (PANCUT02), 2497805H1 (PANCUT02)</td>
<td></td>
</tr>
<tr>
<td>90</td>
<td>224</td>
<td>LUNGT01</td>
<td>2646362H (LUNGT01), 2646362H (LUNGT01), 2646362H (LUNGT01)</td>
<td></td>
</tr>
<tr>
<td>91</td>
<td>225</td>
<td>LUNGT01</td>
<td>2657146H (LUNGT01), 2657146H (LUNGT01), 2657146H (LUNGT01)</td>
<td></td>
</tr>
<tr>
<td>92</td>
<td>226</td>
<td>LUNGT01</td>
<td>2755785H (LUNGT01), 2755785H (LUNGT01), 2755785H (LUNGT01)</td>
<td></td>
</tr>
<tr>
<td>93</td>
<td>227</td>
<td>LUNGT01</td>
<td>2631245H (LUNGT01), 2631245H (LUNGT01), 2631245H (LUNGT01)</td>
<td></td>
</tr>
<tr>
<td>94</td>
<td>228</td>
<td>LUNGT01</td>
<td>3116250H (LUNGT01), 3116250H (LUNGT01), 3116250H (LUNGT01)</td>
<td></td>
</tr>
<tr>
<td>95</td>
<td>229</td>
<td>LUNGT01</td>
<td>3219630H (LUNGT01), 3219630H (LUNGT01), 3219630H (LUNGT01)</td>
<td></td>
</tr>
<tr>
<td>96</td>
<td>230</td>
<td>LUNGT01</td>
<td>3076320H (LUNGT01), 3076320H (LUNGT01), 3076320H (LUNGT01)</td>
<td></td>
</tr>
<tr>
<td>97</td>
<td>231</td>
<td>LUNGT01</td>
<td>3269698H (LUNGT01), 3269698H (LUNGT01), 3269698H (LUNGT01)</td>
<td></td>
</tr>
<tr>
<td>98</td>
<td>232</td>
<td>LUNGT01</td>
<td>3345135H (LUNGT01), 3345135H (LUNGT01), 3345135H (LUNGT01)</td>
<td></td>
</tr>
<tr>
<td>99</td>
<td>233</td>
<td>LUNGT01</td>
<td>3196975B (LUNGT01), 3196975B (LUNGT01), 3196975B (LUNGT01)</td>
<td></td>
</tr>
<tr>
<td>100</td>
<td>234</td>
<td>SINTB01</td>
<td>1501749H (SINTB01), 1501749H (SINTB01), 1501749H (SINTB01)</td>
<td></td>
</tr>
<tr>
<td>101</td>
<td>235</td>
<td>LINODN03</td>
<td>1575520H (LINODN03), 1575520H (LINODN03), 1575520H (LINODN03)</td>
<td></td>
</tr>
<tr>
<td>102</td>
<td>236</td>
<td>PROSTN09</td>
<td>1647996H (PROSTN09), 1647996H (PROSTN09), 1647996H (PROSTN09)</td>
<td></td>
</tr>
<tr>
<td>103</td>
<td>237</td>
<td>BRSTN09</td>
<td>1661144H (BRSTN09), 1661144H (BRSTN09), 1661144H (BRSTN09)</td>
<td></td>
</tr>
<tr>
<td>104</td>
<td>238</td>
<td>PROSTN15</td>
<td>1685490H (PROSTN15), 1685490H (PROSTN15), 1685490H (PROSTN15)</td>
<td></td>
</tr>
<tr>
<td>105</td>
<td>239</td>
<td>BRSTN08</td>
<td>1731491F1 (BRSTN08), 1731491F1 (BRSTN08), 1731491F1 (BRSTN08)</td>
<td></td>
</tr>
<tr>
<td>106</td>
<td>240</td>
<td>BRSTN04</td>
<td>180316H (BRSTN04), 180316H (BRSTN04), 180316H (BRSTN04)</td>
<td></td>
</tr>
<tr>
<td>107</td>
<td>241</td>
<td>KIDNNT09</td>
<td>1927159F1 (KIDNNT09), 2440868H (KIDNNT09), 2440868H (KIDNNT09)</td>
<td></td>
</tr>
<tr>
<td>108</td>
<td>242</td>
<td>ADREN04</td>
<td>3150731H (ADREN04), 3150731H (ADREN04), 3150731H (ADREN04)</td>
<td></td>
</tr>
<tr>
<td>109</td>
<td>243</td>
<td>BRSTN18</td>
<td>3170958H (BRSTN18), 3170958H (BRSTN18), 3170958H (BRSTN18)</td>
<td></td>
</tr>
<tr>
<td>110</td>
<td>244</td>
<td>LUNGT07</td>
<td>3475168H (LUNGT07), 3475168H (LUNGT07), 3475168H (LUNGT07)</td>
<td></td>
</tr>
<tr>
<td>111</td>
<td>245</td>
<td>DENTIT01</td>
<td>4465463H (DENTIT01), 4465463H (DENTIT01), 4465463H (DENTIT01)</td>
<td></td>
</tr>
<tr>
<td>112</td>
<td>246</td>
<td>KIDNNT26</td>
<td>4072159F1 (KIDNNT26), 4072159F1 (KIDNNT26), 4072159F1 (KIDNNT26)</td>
<td></td>
</tr>
<tr>
<td>113</td>
<td>247</td>
<td>BRSTN03</td>
<td>620937B6 (BRSTN03), 620937B6 (BRSTN03), 620937B6 (BRSTN03)</td>
<td></td>
</tr>
<tr>
<td>114</td>
<td>248</td>
<td>PANCUT04</td>
<td>2093492H (PANCUT04), 2093492H (PANCUT04), 2093492H (PANCUT04)</td>
<td></td>
</tr>
</tbody>
</table>

**TABLE 1-continued**
**TABLE 1—continued**

<table>
<thead>
<tr>
<th>Protein Seq ID No:</th>
<th>Nucleotide Seq ID No:</th>
<th>Close ID</th>
<th>Library</th>
<th>Fragments</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>115</strong> 249</td>
<td>2108789</td>
<td>BRAUITU03</td>
<td></td>
<td>2108789/H1 and 2108789/R6 (BRAUITU03), 2182008T6 (SININOT01), 3255751R6 and 3255751T5 (OVARUTUN01)</td>
</tr>
<tr>
<td><strong>116</strong> 250</td>
<td>2171401</td>
<td>ENDCNOT03</td>
<td></td>
<td>032741F1 (HUVENOB01), 1821492F6 (GLUTU01), 2055814T6 (BEPPNOT03), 2171401F6 and 2171401H1 (ENDCNOT03), 2668925F6 (ESOGTUT02), 3140315H1 and 3140315T (SMCCNOT02), 2933175H1 (EPPBXT01)</td>
</tr>
<tr>
<td><strong>117</strong> 251</td>
<td>2212530</td>
<td>SINTFET03</td>
<td></td>
<td>187559H6 and 187559T5 (CARDNOT01), 919634F6 (BRAINOT02), 1902331H1 (COMNOT02), 2062384H (OVARNOT03), 2212530F6 and 2212530H1 (SINTFET03), 2520479H1 (BRAINUT01), 2878284F6 (THYRNOT01), 2992534H1 (KIDNET01), 4020710F6 (BRAXNOT02)</td>
</tr>
<tr>
<td><strong>119</strong> 252</td>
<td>2253036</td>
<td>OVARUTU01</td>
<td></td>
<td>2253036H1 and 2253036R6 (OVARUTU01)</td>
</tr>
<tr>
<td><strong>119</strong> 253</td>
<td>2280161</td>
<td>PROSNO01</td>
<td></td>
<td>48232H (BINT2RAT01), 934345H (CEVRNOT01), 1379535F1 and 1379538T1 (LUNGNOT01), 1428562T (PANCNOT08), 1467511F6 (PANCNOT02), 1586138F6 (UTRNOT05), 1636105T5 (UTRNOT06), 2154934F6 (ENDCNOT02), 2208161H1 and 2208161X1F1 (PROSNO01), 2789845F6 (COLNOT16), 3069348H1 (CEVRNOT03), 3774621F6 (BRSTNOT05), 4229271H1 (PANCNOT07), 5111693H1 (ENDITX01), 5324177H1 (FBBPEN06)</td>
</tr>
<tr>
<td><strong>120</strong> 254</td>
<td>2287485</td>
<td>BRAIN01</td>
<td></td>
<td>1454589F6 (PEN1T01), 1593326F6 (BRAIN1T04), 2287485H1 and 2287485R6 (BRAIN01), 3765921H1 (BRSTNOT04), 457429H1 (COMNOT03), 4937933H1 (PROSTUS18), SBCA01722F1</td>
</tr>
<tr>
<td><strong>121</strong> 255</td>
<td>2380344</td>
<td>ISLNOT01</td>
<td></td>
<td>2380344F6 and 2380344H1 (ISLNOT01), 2885556T3 (LUNGFT04), SASA0344F6, SASA0344F6</td>
</tr>
<tr>
<td><strong>122</strong> 256</td>
<td>2383171</td>
<td>ISLNOT01</td>
<td></td>
<td>956269H1 (KIDNOT03), 1342259F1 (COLNOT15), 1468046F1 and 1468046T1 (PANCNOT02), 2383171H1 (ISLNOT01), SBCA05452U1, SBCA03166F1</td>
</tr>
<tr>
<td><strong>123</strong> 257</td>
<td>2396046</td>
<td>THP1AZT01</td>
<td></td>
<td>2396046F6 and 2396046H1 and 239611T6 (THP1AZT01)</td>
</tr>
<tr>
<td><strong>124</strong> 258</td>
<td>2456587</td>
<td>ENDANOT01</td>
<td></td>
<td>2456586H1 and 2456587T6 (ENDANOT01), 287589H1 (THYRNOT01), SBCA03779F1, SBCA01135F1, SBCA02404F1, SBCA01351F1, SBCA01841F1, SBCA04783F1, SBCA0155F1, SBCA0441F1</td>
</tr>
<tr>
<td><strong>125</strong> 259</td>
<td>2484813</td>
<td>BONRITU03</td>
<td></td>
<td>1234070T1 (LUNGFT03), 1338909F6 (COLNOT13), 2484813H1 (BONRITU03), SBCA02305F1, SBCA02064F1, SBCA02151F1, SBCA03370F1, SBCA04866F1, SBCA0340F1</td>
</tr>
<tr>
<td><strong>126</strong> 260</td>
<td>2493851</td>
<td>ADRETO05</td>
<td></td>
<td>2493851H1 (ADRETO05), 380516F6 (BLADITU05), 4500439H1 and 4500748H1 (BRAVXT02), 512080H1 (SMBCBNT01)</td>
</tr>
<tr>
<td><strong>126</strong> 261</td>
<td>2495719</td>
<td>ADRETO05</td>
<td></td>
<td>603447R1 (BRSTU0101), 2495719H1 (ADRETO05), 2014793F6 (THYMFT03), 4647103H1 (PROSTU02), SBCA04041F1</td>
</tr>
<tr>
<td><strong>128</strong> 262</td>
<td>2614153</td>
<td>GBLANOT01</td>
<td></td>
<td>1833158F6 (BRAIN01), 1966515R6 (BRSTNOT04), 2331103R6 (COLNOT11), 2614153H1 (GBLANOT01), 2656691F6 (LUNGFT09), 2651276H1 (DROCS01)</td>
</tr>
<tr>
<td><strong>129</strong> 263</td>
<td>2655184</td>
<td>THYMFT04</td>
<td></td>
<td>2655184H1 (THYMFT04), SBCA05215F1, SBCA06215F1, SBCA0154F6</td>
</tr>
<tr>
<td><strong>130</strong> 264</td>
<td>2684362</td>
<td>BRSTITU03</td>
<td></td>
<td>1297974F1 and 1297974T6 (BRSTITU03), 2684362H1 (BRSTITU3)</td>
</tr>
<tr>
<td><strong>131</strong> 265</td>
<td>2684906</td>
<td>BRSTITU3</td>
<td></td>
<td>1541167F1 and 1541167T1 (SINTT0101), 2684906F6 and 2684906F6 (LUNGNOT02), 2756805H1 (PNLNOT01), 2849006F6 (BRSTITU3)</td>
</tr>
<tr>
<td><strong>132</strong> 266</td>
<td>2689137</td>
<td>DRGNCNOT01</td>
<td></td>
<td>2889137H1 (DRGNCNOT01), 3026490F6 and 3026490F6 (HEART02), 3483359H1 (KIDNOT01)</td>
</tr>
<tr>
<td><strong>133</strong> 267</td>
<td>2996229</td>
<td>CARGDIT01</td>
<td></td>
<td>2996229H1 (HIPPON01), 2996229H1 (CARGDIT01)</td>
</tr>
<tr>
<td><strong>134</strong> 268</td>
<td>3222001</td>
<td>COLNN003</td>
<td></td>
<td>1740070F6 (LRVITU01), 3222201H1 (COLNN003), 4053813T6 (SPLNOT13), 4230282H1 (BRAMITU01), SBDAA07299F3</td>
</tr>
</tbody>
</table>

**TABLE 2**

<table>
<thead>
<tr>
<th>Protein Seq ID No:</th>
<th>Amino Acid Residues</th>
<th>Potential Phosphorylation Sites</th>
<th>Potential Glycosylation Sites</th>
<th>Signature Sequences</th>
<th>Identification</th>
<th>Analytical Methods</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>88</td>
<td>TRS338 T76</td>
<td>M1—A21</td>
<td>Signal Peptide</td>
<td>HMM</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>128</td>
<td>S30 S40 T47 T119</td>
<td>M1—P28</td>
<td>Signal Peptide</td>
<td>HMM</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>111</td>
<td>T70</td>
<td>M1—T18</td>
<td>Signal Peptide</td>
<td>HMM</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>110</td>
<td>S32 T64</td>
<td>N58</td>
<td>M1—A29</td>
<td>Signal Peptide</td>
<td>HMM</td>
</tr>
<tr>
<td>5</td>
<td>78</td>
<td>T27 S39 S49 S44</td>
<td>S22 T27 S28 S57</td>
<td>M1—R24</td>
<td>Signal Peptide</td>
<td>HMM</td>
</tr>
<tr>
<td>6</td>
<td>88</td>
<td>T55 S30 S40 T55</td>
<td>N34</td>
<td>M1—N21</td>
<td>Signal Peptide</td>
<td>HMM</td>
</tr>
<tr>
<td>Protein Seq ID NO:</td>
<td>Amino Acid Residues</td>
<td>Potential Phosphorylation Sites</td>
<td>Potential Glycosylation Sites</td>
<td>Signature Sequences</td>
<td>Identification</td>
<td>Analytical Methods</td>
</tr>
<tr>
<td>------------------</td>
<td>----------------------</td>
<td>-------------------------------</td>
<td>-------------------------------</td>
<td>---------------------</td>
<td>---------------</td>
<td>-------------------</td>
</tr>
<tr>
<td>7</td>
<td>227</td>
<td>S220 S70 S83 T131 S134 S141 T158 Y123</td>
<td>N100</td>
<td>M1–Q20</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>198</td>
<td>S62 T223 S142 S189 S62 T100 Y85</td>
<td>N60</td>
<td>M1–A28</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>65</td>
<td>T48</td>
<td>M1–A29</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>154</td>
<td></td>
<td>M1–A29</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>237</td>
<td>T136 T26 T79 T85 T182 T388 T194 T206 S60 S123 S176 S213</td>
<td>N128</td>
<td>M1–A19</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>225</td>
<td>T158 S128</td>
<td>N166</td>
<td>M1–G27</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>13</td>
<td>117</td>
<td>S41</td>
<td>M1–A23</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>14</td>
<td>253</td>
<td>S49 T63 S92 T110 S127 T239</td>
<td>N42 N47 N72 N207</td>
<td>M1–T20</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>15</td>
<td>171</td>
<td>S43 S94 T114</td>
<td>M88–R312</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>78</td>
<td>S38 S43</td>
<td>N37</td>
<td>M1–G19</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>17</td>
<td>71</td>
<td>T64 T67</td>
<td>M1–C19</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>18</td>
<td>188</td>
<td>S36 T58 T133 Y31</td>
<td>N121 N171</td>
<td>M1–A21</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>19</td>
<td>80</td>
<td>S76</td>
<td>M1–C19</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>20</td>
<td>80</td>
<td></td>
<td>M1–G25</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>21</td>
<td>84</td>
<td>S39 S53 S60</td>
<td>M1–G21</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>22</td>
<td>171</td>
<td>S41 T150</td>
<td>M3–A21</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>23</td>
<td>243</td>
<td>S3 S44 T75 S86 S183 S223 S36 S92 S205 Y40 Y110 T5 S76 T82 T93 T109 S121 T137 T170 S184 S11 T53 S75 S84 T132 S223 S274 Y69</td>
<td>N97</td>
<td>M1–C25</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>24</td>
<td>311</td>
<td>S40 N91 N108 N128 N135 N190</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>25</td>
<td>57</td>
<td></td>
<td>M1–L29</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>26</td>
<td>82</td>
<td>S46 Y26</td>
<td>M1–S18</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>27</td>
<td>115</td>
<td></td>
<td>M1–G34</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>28</td>
<td>327</td>
<td>S93 S50 S167 S233 S89 T205 T214 S302 T318</td>
<td>N138 N206</td>
<td>M1–E28</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>29</td>
<td>133</td>
<td>S63</td>
<td>N105</td>
<td>M1–E29</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>30</td>
<td>129</td>
<td>S21 S65 T93</td>
<td>M1–G20</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>32</td>
<td>93</td>
<td>T21</td>
<td>M1–A18</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>33</td>
<td>92</td>
<td>S57 S8</td>
<td>M1–G47</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>34</td>
<td>143</td>
<td>T6 T14 T135</td>
<td>M9–G40</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>35</td>
<td>89</td>
<td>T15 S58 S66</td>
<td>M1–A19</td>
<td>Signal Peptide HMM</td>
<td></td>
<td></td>
</tr>
<tr>
<td>36</td>
<td>501</td>
<td>T7 T76 S150 T224 S228 S257 S358</td>
<td>N163 N184 N379</td>
<td>M1–E34</td>
<td>Signal Peptide HMM SFScan</td>
<td></td>
</tr>
<tr>
<td>Protein Seq ID NO:</td>
<td>Amino Acid Residues</td>
<td>Potential Phosphorylation Sites</td>
<td>Potential Glycosylation Sites</td>
<td>Signature Sequences</td>
<td>Identification</td>
<td>Analytical Methods</td>
</tr>
<tr>
<td>------------------</td>
<td>---------------------</td>
<td>-------------------------------</td>
<td>-------------------------------</td>
<td>--------------------</td>
<td>---------------</td>
<td>------------------</td>
</tr>
<tr>
<td>37</td>
<td>197</td>
<td>S474 S529 S539 T186 S239 S368</td>
<td>Y523</td>
<td>M1–G28</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>38</td>
<td>437</td>
<td>T47 T146 S233 S391 S403 T43 S130 S273</td>
<td>S339 S364</td>
<td>N46 N189 N382</td>
<td>M1–A21</td>
<td>Signal Peptide HMM</td>
</tr>
<tr>
<td>40</td>
<td>148</td>
<td>T73 S141</td>
<td>N29 N58 N71 N103</td>
<td>M1–R24</td>
<td>receptor-activity-modifying protein (RAMP; g4165368)</td>
<td>Signal Peptide HMM</td>
</tr>
<tr>
<td>41</td>
<td>188</td>
<td>S49</td>
<td>M1–V25</td>
<td></td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>42</td>
<td>222</td>
<td>S89 S165 T174 T182 T38 S158</td>
<td>M1–S24</td>
<td></td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>43</td>
<td>111</td>
<td>S54 S29 S98 S50 S57 T104</td>
<td>M1–T23</td>
<td></td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>45</td>
<td>148</td>
<td>S21 T63 T63 A146</td>
<td>N40</td>
<td>M1–G23</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>46</td>
<td>87</td>
<td>S65</td>
<td>M1–P18</td>
<td></td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>48</td>
<td>109</td>
<td>S25 S22</td>
<td>M1–L18</td>
<td></td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>49</td>
<td>185</td>
<td>S62</td>
<td>M1–A20</td>
<td></td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>50</td>
<td>110</td>
<td>T100 T73 S97 Y48</td>
<td>N71</td>
<td>M1–C21</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>51</td>
<td>126</td>
<td>S17 S110</td>
<td>M1–G18</td>
<td></td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>52</td>
<td>488</td>
<td>S205 T31 S86 T33 S7 T447</td>
<td>N250 N321 N463</td>
<td>M1–L25</td>
<td>putative involvement in cell wall structure or biosynthesis (g3738170)</td>
<td>Signal Peptide HMM</td>
</tr>
<tr>
<td>53</td>
<td>197</td>
<td>T35 S34 S46 S69 T98 S108 T19 T167</td>
<td>S154 S2 S34 T355</td>
<td>M1–A26</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>54</td>
<td>84</td>
<td>S65 S36 T41 S51 S69 S83</td>
<td>N39</td>
<td>M1–G25</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>55</td>
<td>97</td>
<td>S86</td>
<td>M1–A22</td>
<td></td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>56</td>
<td>140</td>
<td>S29</td>
<td>M1–P23</td>
<td></td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>58</td>
<td>262</td>
<td>S62 T166 S62 S71 Y246</td>
<td>N190</td>
<td>M1–G28</td>
<td>3-acylating enzyme (Q44440)</td>
<td>Signal Peptide HMM</td>
</tr>
<tr>
<td>59</td>
<td>189</td>
<td>S120 T154 T34 T37 S174</td>
<td>M1–C22</td>
<td></td>
<td>Signal Peptide HMM</td>
<td>SPSscan</td>
</tr>
<tr>
<td>60</td>
<td>257</td>
<td>S98 T136 T67 S112 S234 S237</td>
<td>M55–E84β</td>
<td></td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>61</td>
<td>82</td>
<td>T66</td>
<td>N67</td>
<td>M1–G18</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>62</td>
<td>202</td>
<td>T21 S117 S120</td>
<td>M1–G27</td>
<td></td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>63</td>
<td>450</td>
<td>S107 S97 S46 S339 S440 S245 T303 S304 S309</td>
<td>3-acylating enzyme (Q44440)</td>
<td>M1–G18</td>
<td>Signal Peptide HMM</td>
<td></td>
</tr>
<tr>
<td>64</td>
<td>322</td>
<td>T145 T214 T16 S24 S35 S45 T145 T269</td>
<td>S297 T300 T314 Y87</td>
<td>N53 N130 N289</td>
<td>M1–G23</td>
<td>Signal Peptide HMM</td>
</tr>
<tr>
<td>Protein SEQ ID NO:</td>
<td>Amino Acid Residues</td>
<td>Potential Glycosylation Sites</td>
<td>Potential Phosphorylation Sites</td>
<td>Signature Sequences</td>
<td>Identification</td>
<td>Analytical Methods</td>
</tr>
<tr>
<td>------------------</td>
<td>---------------------</td>
<td>-----------------------------</td>
<td>--------------------------------</td>
<td>---------------------</td>
<td>---------------</td>
<td>------------------</td>
</tr>
<tr>
<td>65</td>
<td>104</td>
<td>S38 S25 S75</td>
<td></td>
<td>M1-A18</td>
<td></td>
<td>Signal Peptide HMM</td>
</tr>
<tr>
<td>66</td>
<td>93</td>
<td></td>
<td>M1 through about S18 Transmembrane:</td>
<td>M1 through about Y17 Transmembrane:</td>
<td>M1 through about A24 Transmembrane:</td>
<td>SPScan HMM</td>
</tr>
<tr>
<td>67</td>
<td>71</td>
<td>S23 S64</td>
<td>N53</td>
<td>M1 through about S31 Transmembrane: about M159 through about F178 about F309 through about S27 about F225 about V243</td>
<td></td>
<td>MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>68</td>
<td>394</td>
<td>S392 S393 S31 S127 S179 S334 T338 S358 T383 Y323</td>
<td></td>
<td>M1 through about S23 Transmembrane: M1 through about L16 Transmembrane: M1 through about Q18 Transmembrane:</td>
<td>M1 through about S25 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>69</td>
<td>72</td>
<td>S59</td>
<td>N69</td>
<td>M1 through about S23 Transmembrane:</td>
<td></td>
<td>SPScan HMM</td>
</tr>
<tr>
<td>70</td>
<td>71</td>
<td>S11 T26</td>
<td>M1 through about G27 Transmembrane:</td>
<td>M1 through about G20 Transmembrane:</td>
<td>M1 through about G30 Transmembrane:</td>
<td>SPScan HMM</td>
</tr>
<tr>
<td>71</td>
<td>247</td>
<td>S41 T79</td>
<td>M1 through about G26 Transmembrane:</td>
<td>M1 through about S19 Transmembrane:</td>
<td>M1 through about W79 through about H97 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>72</td>
<td>73</td>
<td>S56</td>
<td>M1 through about G27 Transmembrane:</td>
<td>M1 through about G20 Transmembrane:</td>
<td>M1 through about G30 Transmembrane:</td>
<td>SPScan HMM</td>
</tr>
<tr>
<td>73</td>
<td>70</td>
<td></td>
<td>M1 through about S23 Transmembrane:</td>
<td>M1 through about L16 Transmembrane:</td>
<td>M1 through about Q18 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>74</td>
<td>67</td>
<td></td>
<td>M1 through about S23 Transmembrane:</td>
<td>M1 through about L16 Transmembrane:</td>
<td>M1 through about Q18 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>75</td>
<td>91</td>
<td>T29 S46 T51</td>
<td>M1 through about G26 Transmembrane:</td>
<td>M1 through about S19 Transmembrane:</td>
<td>M1 through about W79 through about H97 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>76</td>
<td>56</td>
<td></td>
<td>M1 through about G26 Transmembrane:</td>
<td>M1 through about S19 Transmembrane:</td>
<td>M1 through about W79 through about H97 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>77</td>
<td>112</td>
<td>S62 S65</td>
<td>M1 through about A31 Transmembrane: about L38 through about F55</td>
<td>M1 through about A31 Transmembrane:</td>
<td>M1 through about A38 Transmembrane: about L38 through about T41</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>78</td>
<td>54</td>
<td>N48</td>
<td>M1 through about N34 Transmembrane:</td>
<td>M1 through about N34 Transmembrane:</td>
<td>M1 through about N34 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>79</td>
<td>57</td>
<td>T33 R55</td>
<td>M1 through about C18 Transmembrane:</td>
<td>M1 through about C18 Transmembrane:</td>
<td>M1 through about C18 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>80</td>
<td>52</td>
<td>S34</td>
<td>M1 through about S30 Transmembrane:</td>
<td>M1 through about S30 Transmembrane:</td>
<td>M1 through about S30 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>81</td>
<td>64</td>
<td>T43 Y27</td>
<td>M1 through about S41 Transmembrane:</td>
<td>M1 through about S41 Transmembrane:</td>
<td>M1 through about S41 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>82</td>
<td>65</td>
<td>S45</td>
<td>M1 through about A31 Transmembrane: about L38 through about F55</td>
<td>M1 through about A31 Transmembrane:</td>
<td>M1 through about A38 Transmembrane: about L38 through about T41</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>83</td>
<td>56</td>
<td></td>
<td>M1 through about E23 Transmembrane:</td>
<td>M1 through about E23 Transmembrane:</td>
<td>M1 through about E23 Transmembrane:</td>
<td>SPScan HMM</td>
</tr>
<tr>
<td>84</td>
<td>120</td>
<td>S69 S109 N89 N95</td>
<td>M1 through about A38 Transmembrane: about L38 through about T41</td>
<td>M1 through about A38 Transmembrane: about L38 through about T41</td>
<td>M1 through about A38 Transmembrane: about L38 through about T41</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>85</td>
<td>67</td>
<td>S28</td>
<td>M1 through about K30 Microbodies C-terminal targeting signal: A65KV</td>
<td>M1 through about K30 Microbodies C-terminal targeting signal: A65KV</td>
<td>M1 through about K30 Microbodies C-terminal targeting signal: A65KV</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>86</td>
<td>62</td>
<td>S29 S42 S46</td>
<td>N40</td>
<td>M1 through about S29 Transmembrane:</td>
<td>M1 through about L19 Transmembrane: about I3 through about G20 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
<tr>
<td>87</td>
<td>75</td>
<td>S25 S46</td>
<td>M1 through about L19 Transmembrane: about I3 through about G20 Transmembrane:</td>
<td>M1 through about L19 Transmembrane: about I3 through about G20 Transmembrane:</td>
<td>M1 through about L19 Transmembrane: about I3 through about G20 Transmembrane:</td>
<td>SPScan MOTIFS SPScan HMM</td>
</tr>
</tbody>
</table>
TABLE 2-continued

<table>
<thead>
<tr>
<th>Protein SEQ ID NO:</th>
<th>Amino Acid Residues</th>
<th>Potential Phosphorylation Sites</th>
<th>Potential Glycosylation Sites</th>
<th>Signature Sequences</th>
<th>Identification</th>
<th>Analytical Methods</th>
</tr>
</thead>
<tbody>
<tr>
<td>88</td>
<td>80</td>
<td>T28</td>
<td></td>
<td>M1 through about A20</td>
<td>SPscan</td>
<td>HMM MOTIFS</td>
</tr>
<tr>
<td>89</td>
<td>50</td>
<td>S11</td>
<td></td>
<td>M1 through about C48</td>
<td>SPscan</td>
<td>HMM MOTIFS</td>
</tr>
<tr>
<td>90</td>
<td>116</td>
<td>S38</td>
<td></td>
<td>M1 through about G22</td>
<td>SPscan</td>
<td>HMM MOTIFS</td>
</tr>
<tr>
<td>91</td>
<td>67</td>
<td>S43</td>
<td></td>
<td>M1 through about P21</td>
<td>SPscan</td>
<td>HMM MOTIFS</td>
</tr>
<tr>
<td>92</td>
<td>538</td>
<td>S415 S52 T77 S97 T178 T228 S282 S320 S332 S384 T401 T424 S483 S207 S280 S357 T410 Y263 Y365</td>
<td>N226</td>
<td>M1 through about S18 Tyrosine specific protein phosphatases signature: about V52 through about P340</td>
<td>SPscan</td>
<td>BLOCKS MOTIFS PRINTS</td>
</tr>
<tr>
<td>93</td>
<td>58</td>
<td></td>
<td></td>
<td>M1 through about S25</td>
<td>SPscan</td>
<td>HMM MOTIFS</td>
</tr>
<tr>
<td>94</td>
<td>119</td>
<td>S39</td>
<td></td>
<td>M1 through about S22 Transmembrane: about V3 through about S22</td>
<td>SPscan</td>
<td>HMM MOTIFS</td>
</tr>
<tr>
<td>95</td>
<td>128</td>
<td>S91</td>
<td></td>
<td>M1 through about G31 Transmembrane: about F18 through about L26</td>
<td>SPscan</td>
<td>HMM MOTIFS</td>
</tr>
<tr>
<td>96</td>
<td>124</td>
<td>T115 T43 S91</td>
<td></td>
<td>M1–S20 P116–V124 (urotensin II signature)</td>
<td>SPScan</td>
<td>HMM Motifs BLOCKS BLAST</td>
</tr>
<tr>
<td>97</td>
<td>182</td>
<td>S26 T70 S172 S25 S32 S48 S108 S133</td>
<td></td>
<td>M1–S23, M1–S25</td>
<td>SPscan</td>
<td>HMM Motifs BLOCKS BLAST</td>
</tr>
<tr>
<td>98</td>
<td>237</td>
<td>S55 S89 S121 S135 N45 N73 N107 N118 N132 N172 N175 N185</td>
<td></td>
<td>M1–A16, M1–S21 C40–C198 (cysteine spacing pattern similar to that of RoBo-1)</td>
<td>SPScan</td>
<td>HMM Motifs BLOCKS BLAST</td>
</tr>
<tr>
<td>99</td>
<td>160</td>
<td>S36 S59 T143</td>
<td></td>
<td>M1–A27</td>
<td>SPScan</td>
<td>HMM Motifs</td>
</tr>
<tr>
<td>100</td>
<td>148</td>
<td>T76 S64 Y103</td>
<td></td>
<td>M1–S30, M1–G31</td>
<td>SPScan</td>
<td>HMM Motifs</td>
</tr>
<tr>
<td>101</td>
<td>170</td>
<td>S78 T4 T30 S130 S25 S29 T122</td>
<td></td>
<td>M1–A23, M1–L28</td>
<td>SPScan</td>
<td>HMM Motifs</td>
</tr>
<tr>
<td>102</td>
<td>150</td>
<td>S50 S78 S91</td>
<td></td>
<td>M1–A26, M1–S28</td>
<td>SPScan</td>
<td>HMM Motifs</td>
</tr>
<tr>
<td>103</td>
<td>142</td>
<td>T37 T80</td>
<td></td>
<td>M1–A25, M1–G26</td>
<td>SPScan</td>
<td>HMM Motifs</td>
</tr>
<tr>
<td>104</td>
<td>110</td>
<td>T3</td>
<td></td>
<td>M1–G18, M1–T25</td>
<td>SPScan</td>
<td>HMM Motifs</td>
</tr>
<tr>
<td>105</td>
<td>120</td>
<td>T29 S40 S72</td>
<td></td>
<td>M1–G22, M1–A20</td>
<td>SPScan</td>
<td>HMM Motifs</td>
</tr>
<tr>
<td>106</td>
<td>135</td>
<td>T115 S38 T41</td>
<td>N32 N101</td>
<td>M1–G26, M1–C25</td>
<td>SPScan</td>
<td>HMM Motifs</td>
</tr>
<tr>
<td>107</td>
<td>301</td>
<td>S53 S217 S240 S283 T224</td>
<td></td>
<td>M1–A22</td>
<td>SPScan</td>
<td>HMM Motifs</td>
</tr>
<tr>
<td>108</td>
<td>103</td>
<td>S88 T73 S84</td>
<td></td>
<td>M1–P19, M1–L22</td>
<td>SPScan</td>
<td>HMM Motifs</td>
</tr>
<tr>
<td>Protein Seq ID No.</td>
<td>Amino Acid Residues</td>
<td>Potential Phosphorylation Sites</td>
<td>Potential Glycosylation Sites</td>
<td>Signature Sequences</td>
<td>Identification</td>
<td>Analytical Methods</td>
</tr>
<tr>
<td>-------------------</td>
<td>---------------------</td>
<td>--------------------------------</td>
<td>-----------------------------</td>
<td>--------------------</td>
<td>---------------</td>
<td>-------------------</td>
</tr>
<tr>
<td>109</td>
<td>95</td>
<td>T82 S52 S77</td>
<td>N50</td>
<td>M1-T15, M1-P19</td>
<td>SPScan HMM Motifs</td>
<td></td>
</tr>
<tr>
<td>110</td>
<td>113</td>
<td>T84 S4</td>
<td>M1-P19, M1-A24</td>
<td>SPScan HMM Motifs</td>
<td></td>
<td></td>
</tr>
<tr>
<td>111</td>
<td>234</td>
<td>S179 S184 S51 T70 T158 S168 T228 Y29</td>
<td>N146 N191 N194</td>
<td>M1-A20</td>
<td>NK cell activating receptor (g4403702) SPScan HMM Motifs</td>
<td></td>
</tr>
<tr>
<td>112</td>
<td>119</td>
<td>S39 T61</td>
<td>M1-G30, M1-G27</td>
<td>SPScan HMM Motifs</td>
<td></td>
<td></td>
</tr>
<tr>
<td>113</td>
<td>200</td>
<td>S51 T46 S191</td>
<td>M1-G26 Signal Peptide</td>
<td>Signal Peptide Containing Protein, Homology with KIAA0206 SPScan Motifs</td>
<td></td>
<td></td>
</tr>
<tr>
<td>114</td>
<td>225</td>
<td>S29</td>
<td>M1-Q29 Signal Peptide</td>
<td>Signal Peptide Containing Protein SPScan</td>
<td></td>
<td></td>
</tr>
<tr>
<td>115</td>
<td>155</td>
<td>S40</td>
<td>M1-A20 Signal Peptide</td>
<td>Signal Peptide Containing Protein HMM Motifs</td>
<td></td>
<td></td>
</tr>
<tr>
<td>116</td>
<td>468</td>
<td>S143 T156 T227 S235 T271 T293 T436 S453 S117 T418 T123 S263 S417 Y73</td>
<td>N280 N384</td>
<td>M1-G13 Signal Peptide</td>
<td>Signal Peptide Containing Protein SPScan Motifs</td>
<td></td>
</tr>
<tr>
<td>117</td>
<td>403</td>
<td>S19 S20 S69 S151 T171 T97 S393 Y193 Y378</td>
<td>N87</td>
<td>M1-A24 Signal Peptide</td>
<td>Signal Peptide Containing Protein HMM Motifs</td>
<td></td>
</tr>
<tr>
<td>118</td>
<td>331</td>
<td>T131 S24 T70 T118 T212 T127</td>
<td>M1-G25 Signal Peptide</td>
<td>Signal Peptide Containing Protein SPScan Motifs</td>
<td></td>
<td></td>
</tr>
<tr>
<td>120</td>
<td>514</td>
<td>T457 T80 S86 T141 T372 T432 S474 S94 T102 S112 T340 S297 S553 S470 T46 S78 T12</td>
<td>N100 N168 N319</td>
<td>M1-G24 Signal Peptide</td>
<td>Signal Peptide Containing Protein SPScan Motifs</td>
<td></td>
</tr>
<tr>
<td>121</td>
<td>109</td>
<td>T46 S78 T12</td>
<td>M1-S15 Signal Peptide</td>
<td>Signal Peptide Containing Protein SPScan Motifs</td>
<td></td>
<td></td>
</tr>
<tr>
<td>122</td>
<td>431</td>
<td>S57 T230 S339 S396 S100 S239</td>
<td>M1-L25 Signal Peptide</td>
<td>Signal Peptide Containing Protein, Weakly similar to OXAIL SPScan Motifs</td>
<td></td>
<td></td>
</tr>
<tr>
<td>123</td>
<td>342</td>
<td>S5 T0 S26 T70 S91 T343 T165 S222 S248 S262 T300 T334 S380 S46 T164 T165 S222</td>
<td>N251</td>
<td>M1-W16 Signal Peptide</td>
<td>Signal Peptide Containing Protein SPScan Motifs</td>
<td></td>
</tr>
<tr>
<td>125</td>
<td>588</td>
<td>S510 T24 T30 S91 T153 T165 S222 S248 S262 T300 T334 S380 S46 T164 T165 S222</td>
<td>N322</td>
<td>M1-T39 Signal Peptide</td>
<td>Signal Peptide Containing Protein SPScan Motifs</td>
<td></td>
</tr>
<tr>
<td>126</td>
<td>125</td>
<td>T165 T47 T56 S158</td>
<td>M1-R32 Signal Peptide, V4-L53 Glycosyl Hydrolase Family 9 Active Site</td>
<td>Signal Peptide Containing Protein, Glycosyl Hydrolase Protein SPScan Motifs</td>
<td></td>
<td></td>
</tr>
<tr>
<td>127</td>
<td>196</td>
<td>T165 T47 T56 S158</td>
<td>M1-S26 Signal Peptide, H78-H123 Ribosomal Protein</td>
<td>Signal Peptide Containing Protein, Ribosomal Protein SPScan Motifs</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Protein SEQ ID NO:</td>
<td>Amino Acid Residues</td>
<td>Potential Phosphorylation Sites</td>
<td>Potential Glycosylation Sites</td>
<td>Signature Sequences</td>
<td>Identification</td>
<td>Analytical Methods</td>
</tr>
<tr>
<td>------------------</td>
<td>---------------------</td>
<td>-------------------------------</td>
<td>-------------------------------</td>
<td>---------------------</td>
<td>---------------</td>
<td>-------------------</td>
</tr>
<tr>
<td>128</td>
<td>S122 S123</td>
<td>N37 N92</td>
<td>M1-S35 Signal Peptide</td>
<td>S18 Signature</td>
<td>Signal Peptide Containing Protein, Homology with GTP Binding Protein</td>
<td>Pfam</td>
</tr>
<tr>
<td></td>
<td>129</td>
<td>88</td>
<td>M1-S24 Signal Peptide</td>
<td>S18 Signature</td>
<td>Signal Peptide Containing Protein</td>
<td>HMM</td>
</tr>
<tr>
<td>130</td>
<td>S146 S179 S192 S239 S70 T126 T150</td>
<td>N50 N109</td>
<td>M1-A48 Signal Peptide, G59-S142 Immunoglobulin Domain</td>
<td>S18 Signature</td>
<td>Signal Peptide Containing Protein, Immunoglobulin</td>
<td>Pfam</td>
</tr>
<tr>
<td>131</td>
<td>T176 T56 S72 S179 S256 S87</td>
<td>S183</td>
<td>S11 T41 T42 S83</td>
<td>M1-A30 Signal Peptide</td>
<td>S18 Signature</td>
<td>Pfam</td>
</tr>
<tr>
<td></td>
<td>133</td>
<td>113</td>
<td>S93 T89 Y9</td>
<td>M1-G30 Signal Peptide, V32-L47 PP0664 F-Box Domain</td>
<td>S18 Signature</td>
<td>Pfam</td>
</tr>
<tr>
<td></td>
<td>134</td>
<td>160</td>
<td>T46 T55 S65 S124 T125 T46</td>
<td>M1-A27 Signal Peptide</td>
<td>Signal Peptide Containing Protein, Pfam</td>
<td></td>
</tr>
</tbody>
</table>

**TABLE 3**

<table>
<thead>
<tr>
<th>Nucleotide SEQ ID NO:</th>
<th>Tissue Expression (Fraction of Total)</th>
<th>Disease/Condition-Specific Expression (Total of Fraction)</th>
<th>Vector</th>
</tr>
</thead>
<tbody>
<tr>
<td>135</td>
<td>Hematopoietic/Immune (1.000)</td>
<td>Inflammation (1.000)</td>
<td>pBLUESCRIPT</td>
</tr>
<tr>
<td>136</td>
<td>Hematopoietic/Immune (0.750) Cardiovascular (0.250)</td>
<td>Inflammation (0.750) Cancer (0.250)</td>
<td>pSPORT1</td>
</tr>
<tr>
<td>137</td>
<td>Nervous (1.000)</td>
<td>Trauma (1.000)</td>
<td>pSPORT1</td>
</tr>
<tr>
<td>138</td>
<td>Musculoskeletal (1.000)</td>
<td>Inflammation (1.000)</td>
<td>pSPORT1</td>
</tr>
<tr>
<td>139</td>
<td>Gastrointestinal (0.714) Cardiovascular (0.143) Reproductive (0.143)</td>
<td>Cancer (0.714) Trauma (0.143)</td>
<td>pSPORT1</td>
</tr>
<tr>
<td>140</td>
<td>Nervous (1.000)</td>
<td>Neurological (0.500) Trauma (0.500)</td>
<td>pSPORT1</td>
</tr>
<tr>
<td>141</td>
<td>Reproductive (0.203) Gastrointestinal (0.146) Hematopoietic/Immune (0.146)</td>
<td>Cancer (0.479) Inflammation (0.256) Fetal (0.146)</td>
<td>pNCY</td>
</tr>
<tr>
<td>142</td>
<td>Reproductive (0.206) Gastrointestinal (0.170) Neurological (0.180)</td>
<td>Cancer (0.479) Inflammation (0.277) Fetal (0.181)</td>
<td>pNCY</td>
</tr>
<tr>
<td>143</td>
<td>Reproductive (0.417) Nervous (0.292) Developmental (0.125)</td>
<td>Cancer (0.417) Inflammation (0.250) Fetal (0.167)</td>
<td>pNCY</td>
</tr>
<tr>
<td>144</td>
<td>Reproductive (0.321) Cardiovascular (0.143) Developmental (0.143)</td>
<td>Cancer (0.464) Fetal (0.214) Inflammation (0.143)</td>
<td>pNCY</td>
</tr>
<tr>
<td>145</td>
<td>Reproductive (0.600) Gastrointestinal (0.400)</td>
<td>Cancer (0.400) Trauma (0.400)</td>
<td>pNCY</td>
</tr>
<tr>
<td>146</td>
<td>Cardiovascular (0.400) Dermatologic (0.200) Nervous (0.200)</td>
<td>Cancer (0.600) Fetal (0.600)</td>
<td>pNCY</td>
</tr>
<tr>
<td>147</td>
<td>Developmental (0.667) Gastrointestinal (0.333)</td>
<td>Fetal (0.667) Cancer (0.335)</td>
<td>pNCY</td>
</tr>
<tr>
<td>148</td>
<td>Reproductive (0.259) Nervous (0.246) Cardiovascular (0.137)</td>
<td>Cancer (0.479) Inflammation (0.214) Fetal (0.145)</td>
<td>pNCY</td>
</tr>
<tr>
<td>149</td>
<td>Reproductive (0.244) Nervous (0.178) Hematopoietic/Immune (0.167)</td>
<td>Cancer (0.433) Inflammation (0.322) Fetal (0.156)</td>
<td>pNCY</td>
</tr>
<tr>
<td>150</td>
<td>Cardiovascular (0.523) Developmental (0.077)</td>
<td>Cancer (0.692) Fetal (0.154) Inflammation (0.154)</td>
<td>pNCY</td>
</tr>
<tr>
<td>Nucleotide Seq ID NO:</td>
<td>Tissue Expression (Fraction of Total)</td>
<td>Disease/Condition-Specific Expression (Total of Fraction)</td>
<td>Vector</td>
</tr>
<tr>
<td>-------------------</td>
<td>--------------------------------------</td>
<td>-------------------------------------------------------</td>
<td>--------</td>
</tr>
<tr>
<td>151</td>
<td>Reproductive (0.215) Nervous (0.190)</td>
<td>Cancer (0.494) Inflammation (0.278)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>152</td>
<td>Gastrointestinal (0.177)</td>
<td>Trauma (0.152)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>153</td>
<td>Reproductive (0.200) Nervous (0.171)</td>
<td>Inflammation (0.371) Cancer (0.229)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>154</td>
<td>Hematopoietic/Immune (0.143)</td>
<td>Fetal (0.200)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>155</td>
<td>Gastrointestinal (0.429) Reproductive (0.286) Nervous (0.143)</td>
<td>Inflammation (0.429) Cancer (0.286)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>156</td>
<td>Reproductive (1.000)</td>
<td>Trauma (0.143)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>157</td>
<td>Hematopoietic/Immune (0.346) Reproductive (0.154) Gastrointestinal (0.115)</td>
<td>Cancer (0.500) Inflammation (0.500)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>158</td>
<td>Reproductive (0.236) Hematopoietic/Immune (0.217) Gastrointestinal (0.132)</td>
<td>Fetal (0.212)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>159</td>
<td>Gastrointestinal (1.000)</td>
<td>Cancer (0.415) Inflammation (0.388)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>160</td>
<td>Developmental (0.500) Hematopoietic/Immune (0.250) Nervous (0.250)</td>
<td>Cancer (0.142)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>161</td>
<td>Hematopoietic/Immune (0.250) Reproductive (0.250) Nervous (0.208)</td>
<td>Cancer (1.000)</td>
<td>pSPORT1</td>
</tr>
<tr>
<td>162</td>
<td>Gastrointestinal (0.412) Reproductive (0.412) Cardiovascular (0.088)</td>
<td>Reproductive (0.994) Fetal (0.292)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>163</td>
<td>Reproductive (0.208) Cardiovascular (0.170) Nervous (0.149)</td>
<td>Cancer (0.572) Inflammation (0.213)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>164</td>
<td>Gastrointestinal (0.333) Hematopoietic/Immune (0.333) Reproductive (0.333)</td>
<td>Cancer (0.667) Inflammation (0.333)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>165</td>
<td>Reproductive (0.205) Gastrointestinal (0.159) Nervous (0.148)</td>
<td>Cancer (0.534) Inflammation (0.284)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>166</td>
<td>Hematopoietic/Immune (0.538) Cardiovascular (0.077) Reproductive (0.077)</td>
<td>Fetal (0.091)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>167</td>
<td>Reproductive (0.483) Gastrointestinal (0.121) Nervous (0.103)</td>
<td>Inflammation (0.731) Cancer (0.154)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>168</td>
<td>Gastrointestinal (0.222) Hematopoietic/Immune (0.222) Nervous (0.148)</td>
<td>Cancer (0.672) Inflammation (0.155)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>169</td>
<td>Urologic (1.000)</td>
<td>Cancer (0.519) Inflammation (0.370)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>170</td>
<td>Reproductive (0.214) Gastrointestinal (0.179) Nervous (0.145)</td>
<td>Fetal (0.250)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>171</td>
<td>Reproductive (0.261) Developmental (0.174) Nervous (0.174)</td>
<td>Cancer (0.643) Inflammation (0.143)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>172</td>
<td>Reproductive (0.367) Gastrointestinal (0.321) Cardiovascular (0.073)</td>
<td>Fetal (0.107)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>173</td>
<td>Reproductive (0.306) Nervous (0.161) Cardiovascular (0.129)</td>
<td>Inflammation (0.217) Cancer (0.286)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>174</td>
<td>Reproductive (0.229) Nervous (0.188) Cardiovascular (0.167)</td>
<td>Cancer (0.519) Inflammation (0.223)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>175</td>
<td>Reproductive (0.444) Developmental (0.167) Cardiovascular (0.111)</td>
<td>Trauma (0.111)</td>
<td>pSPORT1</td>
</tr>
<tr>
<td>176</td>
<td>Reproductive (0.294) Gastrointestinal (0.176) Cardiovascular (0.138)</td>
<td>Cancer (0.765) Fetal (0.118)</td>
<td>pSPORT1</td>
</tr>
<tr>
<td>177</td>
<td>Gastrointestinal (1.000)</td>
<td>Cancer (0.667) Inflammation (0.333)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>178</td>
<td>Reproductive (0.385) Nervous (0.231)</td>
<td>Cancer (0.385) Inflammation (0.385)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>179</td>
<td>Gastrointestinal (1.054)</td>
<td>Cancer (0.667) Fetal (0.167)</td>
<td>pBLUESCRIPT</td>
</tr>
<tr>
<td>180</td>
<td>Cardiovascular (0.223) Reproductive (0.231) Gastrointestinal (0.154)</td>
<td>Cancer (0.615) Inflammation (0.308)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>181</td>
<td>Reproductive (0.324) Gastrointestinal (0.176) Cardiovascular (0.130)</td>
<td>Fetal (0.154)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>182</td>
<td>Reproductive (0.320) Nervous (0.180)</td>
<td>Cancer (0.519) Inflammation (0.160)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>183</td>
<td>Gastrointestinal (0.120)</td>
<td>Fetal (0.101)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>184</td>
<td>Gastrointestinal (0.667) Reproductive (0.333) Urologic (0.107)</td>
<td>Cancer (1.000)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>185</td>
<td>Cardiovascular (0.500) Reproductive (0.500)</td>
<td>Cancer (0.667) Fetal (0.179)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>186</td>
<td>Reproductive (0.393) Developmental (0.107) Urologic (0.107)</td>
<td>Inflammation (0.107)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>187</td>
<td>Cardiovascular (0.400) Reproductive (0.333) Gastrointestinal (0.135)</td>
<td>Inflammation (0.467) Cancer (0.267)</td>
<td>pSPORT1</td>
</tr>
<tr>
<td>188</td>
<td>Nervous (0.318) Reproductive (0.227) Urologic (0.136)</td>
<td>Fetal (0.267)</td>
<td>pSPORT1</td>
</tr>
<tr>
<td>189</td>
<td>Cardiovascular (0.500) Reproductive (0.500)</td>
<td>Cancer (0.636) Inflammation (0.136)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>190</td>
<td>Reproductive (0.518) Nervous (0.227) Hematopoietic/Immune (0.136)</td>
<td>Fetal (0.091)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>191</td>
<td>Reproductive (0.518) Nervous (0.227) Hematopoietic/Immune (0.136)</td>
<td>Cancer (1.000)</td>
<td>pNCRY</td>
</tr>
<tr>
<td>Nucleotide</td>
<td>Disease/Condition-Specific Expression (Total of Fraction)</td>
<td>Vector</td>
<td></td>
</tr>
<tr>
<td>------------</td>
<td>--------------------------------------------------------</td>
<td>--------</td>
<td></td>
</tr>
<tr>
<td>SEQ ID NO:</td>
<td>Tissue Expression (Fraction of Total)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.255) Cardiovascular (0.158)</td>
<td>Cancer (0.463) Inflammation (0.232)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Gastrointestinal (0.147)</td>
<td>Fetal (0.201)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.333) Gastrointestinal (0.286)</td>
<td>Cancer (0.571) Inflammation (0.333)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.055)</td>
<td>Fetal (0.095)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.304) Cardiovascular (0.217)</td>
<td>Cancer (0.435) Inflammation (0.391)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Gastrointestinal (0.136)</td>
<td>Fetal (0.174)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.312) Nervous (0.188)</td>
<td>Cancer (0.438) Inflammation (0.250)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.125)</td>
<td>Fetal (0.188)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Developmental (1.000)</td>
<td>Fetal (1.000)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.233) Cardiovascular (0.209)</td>
<td>Cancer (0.605) Fetal (0.136)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nervous (0.140)</td>
<td>Inflammation (0.116)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.182) Gastrointestinal (0.136)</td>
<td>Cancer (0.477) Inflammation (0.341)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Hematopoietic/Immune (0.136)</td>
<td>Fetal (0.182)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gastrointestinal (0.205) Reproductive (0.205)</td>
<td>Inflammation (0.341) Cancer (0.250)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.114)</td>
<td>Fetal (0.227)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.520) Reproductive (0.280)</td>
<td>Cancer (0.720) Fetal (0.200)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Developmental (0.160)</td>
<td>Inflammation (0.080)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lung (0.958) Developmental (0.25)</td>
<td>Cancer (0.583) Fetal or Proliferating (0.292) Inflammation (0.167)</td>
<td>pBLUESCRIPT</td>
<td></td>
</tr>
<tr>
<td>Musculoskeletal (0.042)</td>
<td>Cancer (0.429) Inflammation (0.571)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.571) Musculoskeletal (0.143)</td>
<td>Cancer (0.450) Inflammation (0.400)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Nervous (0.143) Urologic (0.143)</td>
<td>Cancer (0.375) Inflammation (0.625)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.125) Developmental (0.125) Gastrointestinal (0.125)</td>
<td>Fetal or Proliferating (0.125)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.125)</td>
<td>Cancer (0.590) Urologic (0.250)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lung (1.000)</td>
<td>Cancer (0.500)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Lung (0.500) Perinatal (0.500)</td>
<td>Fetal or Proliferating (0.385)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.231)</td>
<td>Fetal or Proliferating (0.385)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.231)</td>
<td>Fetal or Proliferating (0.154)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.231)</td>
<td>Fetal or Proliferating (0.250)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Nervous (0.596) Reproductive (0.154)</td>
<td>Cancer (0.442) Neurological (0.192)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Gastrointestinal (0.077)</td>
<td>Inflammation (0.251)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.100)</td>
<td>Fetal (0.080)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.300) Hematopoietic/Immune (0.200)</td>
<td>Cancer (0.485) Inflammation (0.400)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Nervous (0.150)</td>
<td>Neurological (0.500) Inflammation (0.500)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Heart (0.500) Brachial (0.500)</td>
<td>Neurological (0.500) Inflammation (0.500)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Nervous (0.625) Reproductive (0.250)</td>
<td>Cancer (0.780) Fetal or Proliferating (0.285) Neurological (0.125)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Musculoskeletal (0.125)</td>
<td>Cancer (0.522) Fetal or Proliferating (0.174) Inflammation (0.130)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Nervous (0.263) Reproductive (0.304)</td>
<td>Cancer (0.522) Fetal or Proliferating (0.174) Inflammation (0.130)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Gastrointestinal (0.174)</td>
<td>Cancer (0.322) Fetal or Proliferating (0.174) Inflammation (0.130)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Testis (1.000)</td>
<td>Inflammation (1.000)</td>
<td>pBLUESCRIPT</td>
<td></td>
</tr>
<tr>
<td>Nervous (0.400) Reproductive (0.400)</td>
<td>Cancer (0.400) Inflammation (0.400)</td>
<td>pBLUESCRIPT</td>
<td></td>
</tr>
<tr>
<td>Gastrointestinal (0.200)</td>
<td>Neurological (0.200)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.476) Gastrointestinal (0.286)</td>
<td>Cancer (0.714) Inflammation (0.286)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.095)</td>
<td>Neurological (0.048)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.284) Gastrointestinal (0.216)</td>
<td>Cancer (0.486) Inflammation (0.351)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Nervous (0.176) Hematopoietic/Immune (0.108)</td>
<td>Cancer (0.656) Inflammation (0.344)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.108)</td>
<td>Fetal or Proliferating (0.122)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Urethra (0.500) Prostate (0.500)</td>
<td>Cancer (0.500) Inflammation (0.500)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Nervous (0.429) Cardiovascular (0.143)</td>
<td>Cancer (0.571) Inflammation (0.429)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Gastrointestinal (0.143) Hematopoietic/Immune (0.143)</td>
<td>Fetal or Proliferating (0.285)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.143)</td>
<td>Cancer (0.650) Inflammation (0.200)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.450) Hematopoietic/Immune (0.200)</td>
<td>Fetal or Proliferating (0.050)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Nervous (0.100) Gastrointestinal (0.100)</td>
<td>Cancer (0.636) Inflammation (0.182)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Nervous (0.182)</td>
<td>Fetal or Proliferating (0.182) Inflammation (0.273)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Prostate (1.000)</td>
<td>Inflammation (1.000)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Nervous (0.333) Nervous (0.333)</td>
<td>Cancer (0.588) Inflammation (0.344)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.098)</td>
<td>Fetal or Proliferating (0.066)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.133) Gastrointestinal (0.333)</td>
<td>Cancer (1.000)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.333)</td>
<td>Cancer (0.800) Fetal or Proliferating (0.200)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.200) Developmental (0.200)</td>
<td>Cancer (1.000)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Gastrointestinal (0.200) Reproductive (0.200) Urologic (0.200)</td>
<td>Cancer (0.800) Fetal or Proliferating (0.200)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Lung (1.000)</td>
<td>Cancer (0.381) Inflammation (0.381)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>Reproductive (0.302) Hematopoietic/Immune (0.254)</td>
<td>Fetal or Proliferating (0.286)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.111)</td>
<td>Inflammation (1.000)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Lymphocytes (1.000)</td>
<td>Cancer (0.656) Inflammation (0.250)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular (0.531) Reproductive (0.250)</td>
<td>Fetal or Proliferating (0.094)</td>
<td>pINCY</td>
<td></td>
</tr>
<tr>
<td>Nucleotide</td>
<td>Disease/Condition-Specific Expression (Fraction of Total)</td>
<td>Vector</td>
<td></td>
</tr>
<tr>
<td>------------</td>
<td>-------------------------------------------------------</td>
<td>--------</td>
<td></td>
</tr>
<tr>
<td>229</td>
<td>Reproductive (0.333)</td>
<td>Cancer (0.500) Fetal or Proliferating (0.167) Inflammation (0.333)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Cardiovascular (0.167)</td>
<td>pNCY</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Gastrointestinal (0.167) Endocrine (0.167)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Hematopoietic/Immune (0.167)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>230</td>
<td>Hematopoietic/Immune (0.500) Reproductive (0.500)</td>
<td>Cell Proliferation (0.500) Inflammation (0.500)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Cancer (0.500) Proliferating (0.333) Inflammation (0.167)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>231</td>
<td>Cardiovascular (0.333) Nervous (0.333)</td>
<td>Cancer (0.500) Proliferation (0.333) Inflammation (0.167)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Developmental (0.167)</td>
<td>pNCY</td>
<td></td>
</tr>
<tr>
<td>232</td>
<td>Gastrointestinal (0.062) Reproductive (0.255)</td>
<td>Cancer (0.500) Inflammation (0.500)</td>
<td></td>
</tr>
<tr>
<td>233</td>
<td>Nervous (0.254) Reproductive (0.255)</td>
<td>Cancer (0.456) Inflammation (0.235)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Hematopoietic/Immune (0.118)</td>
<td>pNCY</td>
<td></td>
</tr>
<tr>
<td>234</td>
<td>Nervous (0.255) Reproductive (0.255)</td>
<td>Cancer (0.545) Inflammation (0.255)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Musculoskeletal (0.182) Reproductive (0.251)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>235</td>
<td>Musculoskeletal (0.388)</td>
<td>Cancer (0.538) Inflammation (0.231)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Gastrointestinal (0.154) Reproductive (0.251)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>236</td>
<td>Nervous (1.000)</td>
<td>Cancer (1.000)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Gastrointestinal (0.429) Reproductive (0.254)</td>
<td>Cancer (0.571) Proliferation (0.143) Trauma (0.143)</td>
<td></td>
</tr>
<tr>
<td>237</td>
<td>Hematopoietic/Immune (0.143) Nervous (0.143)</td>
<td>Cancer (0.453) Inflammation (0.241)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Nervous (0.128)</td>
<td>pNCY</td>
<td></td>
</tr>
<tr>
<td>238</td>
<td>Nervous (0.333) Dermatologic (0.167) Reproductive (0.227)</td>
<td>Trauma (0.333) Cancer (0.167)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Endocrine (0.167)</td>
<td>Cancer (0.167)</td>
<td></td>
</tr>
<tr>
<td>239</td>
<td>Nervous (0.273) Endocrine (0.136)</td>
<td>Cancer (0.545) Proliferation (0.182) Inflammation (0.182)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Reproductive (0.273)</td>
<td>pNCY</td>
<td></td>
</tr>
<tr>
<td>240</td>
<td>Hematopoietic/Immune (0.182) Urologic (0.182)</td>
<td>Cancer (0.455) Proliferation (0.273) Inflammation (0.273)</td>
<td></td>
</tr>
<tr>
<td>241</td>
<td>Endocrine (1.000)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>242</td>
<td>Reproductive (1.000)</td>
<td>Cancer (1.000)</td>
<td></td>
</tr>
<tr>
<td>243</td>
<td>Hematopoietic/Immune (0.545) Musculoskeletal (0.182)</td>
<td>Inflammation (0.636) Trauma (0.182)</td>
<td></td>
</tr>
<tr>
<td>244</td>
<td>Hematopoietic/Immune (0.400) Musculoskeletal (0.300)</td>
<td>Cancer (0.091)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Cardiovascular (0.091)</td>
<td>Inflammation (0.650) Cancer (0.300)</td>
<td></td>
</tr>
<tr>
<td>245</td>
<td>Nervous (0.128)</td>
<td>pNCY</td>
<td></td>
</tr>
<tr>
<td>246</td>
<td>Urologic (1.000)</td>
<td>Cancer (0.500) Proliferation (0.500)</td>
<td></td>
</tr>
<tr>
<td>247</td>
<td>Nervous (0.292) Reproductive (0.222)</td>
<td>Cell Proliferation (0.625) Inflammation/Trauma (0.181)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Musculoskeletal (0.125)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>248</td>
<td>Reproductive (0.211) Developmental (0.132)</td>
<td>Cell Proliferation (0.658) Inflammation/Trauma (0.134)</td>
<td></td>
</tr>
<tr>
<td>249</td>
<td>Nervous (0.803) Gastrointestinal (0.300) Hematopoietic/Immune (0.000)</td>
<td>Cell Proliferation (0.930) Inflammation/Trauma (0.300)</td>
<td></td>
</tr>
<tr>
<td>250</td>
<td>Cardiovascular (0.209) Gastrointestinal (0.140)</td>
<td>Cancer (0.605)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Hematopoietic/Immune (0.140)</td>
<td>pNCY</td>
<td></td>
</tr>
<tr>
<td>251</td>
<td>Nervous (0.508) Cardiovascular (0.154) Gastrointestinal (0.154)</td>
<td>Cell Proliferation (0.616) Inflammation/Trauma (0.269)</td>
<td></td>
</tr>
<tr>
<td>252</td>
<td>Reproductive (1.000)</td>
<td>Cancer (1.000)</td>
<td></td>
</tr>
<tr>
<td>253</td>
<td>Reproductive (0.324) Nervous (0.162)</td>
<td>Cell Proliferation (1.000)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Gastrointestinal (0.113)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>254</td>
<td>Reproductive (0.315) Nervous (0.296)</td>
<td>Cancer (0.630)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Developmental (0.093)</td>
<td>pSPORT1</td>
<td></td>
</tr>
<tr>
<td>255</td>
<td>Nervous (0.211) Reproductive (0.211)</td>
<td>Cell Proliferation (0.579) Inflammation/Trauma (0.298)</td>
<td></td>
</tr>
<tr>
<td>256</td>
<td>Reproductive (0.250) Gastrointestinal (0.148)</td>
<td>Cell Proliferation (0.708)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Hematopoietic/Immune (0.148)</td>
<td>pNCY</td>
<td></td>
</tr>
<tr>
<td>257</td>
<td>Hematopoietic/Immune (1.500)</td>
<td>Cell Proliferation (0.833) Inflammation/Trauma (0.333)</td>
<td></td>
</tr>
<tr>
<td>258</td>
<td>Cardiovascular (0.333) Reproductive (0.333) Developmental (0.167)</td>
<td>Cell Proliferation (0.883) Inflammation/Trauma (0.600)</td>
<td></td>
</tr>
<tr>
<td>259</td>
<td>Cardiovascular (0.333) Reproductive (0.250) Developmental (0.167)</td>
<td>Cell Proliferation (0.625) Inflammation/Trauma (0.208)</td>
<td></td>
</tr>
<tr>
<td>260</td>
<td>Endocrine (0.500) Cardiovascular (0.250) Nervous (0.250)</td>
<td>Cell Proliferation (0.750) Inflammation/Trauma (0.194)</td>
<td></td>
</tr>
<tr>
<td>261</td>
<td>Reproductive (0.252) Cardiovascular (0.155) Hematopoietic/Immune (0.126)</td>
<td>Cell Proliferation (0.728) Inflammation/Trauma (0.210)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Reproductive (0.274) Cardiovascular (0.177) Nervous (0.145)</td>
<td>Cell Proliferation (0.742) Inflammation/Trauma (0.210)</td>
<td></td>
</tr>
<tr>
<td>262</td>
<td>Reproductive (0.267) Cardiovascular (0.160) Hematopoietic/Immune (0.127)</td>
<td>Cell Proliferation (0.654) Inflammation/Trauma (0.193)</td>
<td></td>
</tr>
<tr>
<td>263</td>
<td>Nervous (0.229) Endogenous Hematopoietic/Immune (0.200) Reproductive (0.200)</td>
<td>Cell Proliferation (0.743) Inflammation/Trauma (0.286)</td>
<td></td>
</tr>
<tr>
<td>264</td>
<td>Nervous (1.000) Hematopoietic/Immune (0.033) Gastrointestinal (0.167)</td>
<td>Cell Proliferation (0.600) Inflammation/Trauma (0.333)</td>
<td></td>
</tr>
<tr>
<td>265</td>
<td>Nervous (0.133)</td>
<td>pNCY</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Nervous (0.290) Reproductive (0.258)</td>
<td>Cell Proliferation (0.677) Inflammation/Trauma (0.194)</td>
<td></td>
</tr>
<tr>
<td>266</td>
<td>Cardiovascular (0.129)</td>
<td>pNCY</td>
<td></td>
</tr>
</tbody>
</table>
### TABLE 3-continued

<table>
<thead>
<tr>
<th>Nucleotide</th>
<th>Disease/Condition-Specific Expression (Fraction of Total)</th>
<th>Vector</th>
</tr>
</thead>
<tbody>
<tr>
<td>267 Reproductive (0.201)</td>
<td>Cell Proliferation (0.652)</td>
<td>pNCY</td>
</tr>
<tr>
<td></td>
<td>Inflammation/Trauma (0.391)</td>
<td></td>
</tr>
<tr>
<td>268 Gastrointestinal (0.227) Reproductive (0.193)</td>
<td>Cell Proliferation (0.731)</td>
<td>pSPORT1</td>
</tr>
<tr>
<td></td>
<td>Inflammation/Trauma (0.227)</td>
<td></td>
</tr>
</tbody>
</table>

### TABLE 4

<table>
<thead>
<tr>
<th>Polynucleotide</th>
<th>Seq ID NO:</th>
<th>Clone ID</th>
<th>Library</th>
<th>Library Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>135 MPHIGNOT03</td>
<td>443531</td>
<td></td>
<td></td>
<td>The library was constructed using RNA isolated from plastic adherent mononuclear cells isolated from buffy coat units obtained from unrelated male and female donors.</td>
</tr>
<tr>
<td>136 NEUTGMT01</td>
<td>632860</td>
<td></td>
<td></td>
<td>The library was constructed using RNA isolated from peripheral blood granulocytes collected by density gradient centrifugation through Ficoll-Hypaque. The cells were isolated from buffy coat units obtained from 20 unrelated male and female donors. Cells were cultured in 10 nM GM-CSF for 1 hour before washing and harvesting for RNA preparation.</td>
</tr>
<tr>
<td>137 CRBLNOT01</td>
<td>670010</td>
<td></td>
<td></td>
<td>The library was constructed using RNA isolated from the cerebellum tissue of a 69-year-old Caucasian male who died from chronic obstructive pulmonary disease. Patient history included myocardial infarction, hypertension, and osteoarthritis. osteoarthritis.</td>
</tr>
<tr>
<td>138 SYNOOAT01</td>
<td>726498</td>
<td></td>
<td></td>
<td>The library was constructed using RNA isolated from the knee synovial membrane tissue of an 82-year-old female with osteoarthritis.</td>
</tr>
<tr>
<td>139 OVISION603</td>
<td>795064</td>
<td></td>
<td></td>
<td>The library was constructed using RNA isolated from ovarian tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology for the associated tumor tissue indicated grade 2 mucinous cystadenocarcinoma. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, cerebrovascular disease, breast cancer, and uterine cancer.</td>
</tr>
<tr>
<td>140 BRAINOT04</td>
<td>924925</td>
<td></td>
<td></td>
<td>The library was constructed using RNA isolated from the brain tissue of a 44-year-old Caucasian male with a cerebral hemorrhage. The tissue, which contained clotted blood, came from the choroid plexus of the right anterior temporal lobe. Family history included coronary artery disease and myocardial infarction.</td>
</tr>
<tr>
<td>141 BRSTTUT03</td>
<td>962390</td>
<td></td>
<td></td>
<td>The library was constructed using RNA isolated from breast tumor tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated multicentric invasive grade 4 lobular carcinoma. The mass was identified in the upper outer quadrant, and three separate nodules were found in the lower outer quadrant of the left breast. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular disease, coronary artery aneurysm, breast cancer, prostate cancer, atherosclerotic coronary artery disease, and type I diabetes.</td>
</tr>
<tr>
<td>142 MUNITU03</td>
<td>1259405</td>
<td></td>
<td></td>
<td>The library was constructed using RNA isolated from brain meningioma tissue removed from a 55-year-old Caucasian female during excision of a cerebral meningioma lesion. Pathology indicated a benign neoplasm in the right cerebellar pontine angle of the brain. Patient history included hypothyroidism. Family history included myocardial infarction and breast cancer.</td>
</tr>
<tr>
<td>143 BRSTNOT07</td>
<td>1297384</td>
<td></td>
<td></td>
<td>The library was constructed using RNA isolated from diseased breast tissue removed from a 43-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated mild proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive...</td>
</tr>
<tr>
<td>Polynucleotide</td>
<td>SEQ ID NO:</td>
<td>Clone ID</td>
<td>Library</td>
<td>Library Description</td>
</tr>
<tr>
<td>---------------</td>
<td>-----------</td>
<td>---------</td>
<td>---------</td>
<td>---------------------</td>
</tr>
<tr>
<td></td>
<td>144</td>
<td>1299627</td>
<td>BRSTNOT07</td>
<td>The library was constructed using RNA isolated from diseased breast tissue removed from a 45-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, atherosclerotic coronary artery disease, and type II diabetes.</td>
</tr>
<tr>
<td></td>
<td>145</td>
<td>1306026</td>
<td>PLACNOT02</td>
<td>The library was constructed using RNA isolated from the placental tissue of a Hispanic female fetus, who was prematurely delivered at 21 weeks gestation. Serologies of the mother’s blood were positive for CMV (cytomegalovirus).</td>
</tr>
<tr>
<td></td>
<td>146</td>
<td>1316219</td>
<td>BLADTUT02</td>
<td>The library was constructed using RNA isolated from bladder tumor tissue removed from an 80-year-old Caucasian female during a radical cystectomy and lymph node excision. Pathology indicated grade 3 invasive transitional cell carcinoma. Family history included osteoarthritis and atherosclerosis.</td>
</tr>
<tr>
<td></td>
<td>147</td>
<td>1329031</td>
<td>PANCNOT07</td>
<td>The library was constructed using RNA isolated from the pancreatic tissue of a Caucasian male fetus, who died at 23 weeks gestation.</td>
</tr>
<tr>
<td></td>
<td>148</td>
<td>1483050</td>
<td>CORPNOT02</td>
<td>The library was constructed using RNA isolated from diseased corpus callosum tissue removed from the brain of a 74-year-old Caucasian male who died from Alzheimer’s disease.</td>
</tr>
<tr>
<td></td>
<td>149</td>
<td>1514100</td>
<td>PANCUT01</td>
<td>The library was constructed using RNA isolated from pancreatic tumor tissue removed from a 65-year-old Caucasian female during radical subtotal pancreatectomy. Pathology indicated an invasive grade 2 adenocarcinoma. Patient history included type II diabetes, osteoarthritis, cardiovascular disease, benign neoplasm in the large bowel, and a uterine cancer. Family history included cardiovascular disease, type II diabetes, and stomach cancer.</td>
</tr>
<tr>
<td></td>
<td>150</td>
<td>1603403</td>
<td>LUNGNOT15</td>
<td>The library was constructed using RNA isolated from lung tissue removed from a 69-year-old Caucasian male during a segmental lung resection. Pathology for the associated tumor tissue indicated residual grade 3 invasive squamous cell carcinoma. Patient history included acute myocardial infarction, prostatic hyperplasia, and malignant skin neoplasm. Family history included cerebrovascular disease, type I diabetes, acute myocardial infarction, and atherosclerotic coronary disease.</td>
</tr>
<tr>
<td></td>
<td>151</td>
<td>1652303</td>
<td>PROSTUT08</td>
<td>The library was constructed using RNA isolated from prostate tumor tissue removed from a 69-year-old Caucasian male during radical prostatectomy and regional lymph node excision. Pathology indicated an adenocarcinoma (Gleason grade 3 + 4). Adenofibromatous hyperplasia was also present. The patient presented with elevated prostate specific antigen (PSA). Patient history included a kidney cyst. Family history included tuberculosis, cerebrovascular disease, and atherosclerotic coronary artery disease.</td>
</tr>
<tr>
<td></td>
<td>152</td>
<td>1693358</td>
<td>COLNOT23</td>
<td>The library was constructed using RNA isolated from diseased colon tissue removed from a 16-year-old Caucasian male during a total colectomy with abdominal/perineal resection. Pathology indicated gastritis and pancolitis consistent with the acute phase of ulcerative colitis. There was only mild involvement of the ascending and sigmoid colon, and no significant involvement of the cecum, rectum, or terminal ileum. Family history included irritable bowel syndrome.</td>
</tr>
<tr>
<td></td>
<td>153</td>
<td>1707711</td>
<td>DUODNOT02</td>
<td>The library was constructed using RNA isolated from duodenal tissue of a 6-year-old Caucasian female, who died from head trauma. Serology was positive for cytomegalovirus (CMV).</td>
</tr>
<tr>
<td></td>
<td>154</td>
<td>1738735</td>
<td>COLNOT22</td>
<td>The library was constructed using RNA isolated from colon tissue removed from a 56-year-old Caucasian female with Crohn’s disease during a partial resection of the small intestine. Pathology indicated Crohn’s disease of the ileum and ileal-colonic anastomosis, causing a fistula at the anastomotic site that extended into pericolonic fat. The ileal mucosa showed linear and punctate ulcers with intervening normal tissue. Previous surgeries included a partial ileal resection.</td>
</tr>
<tr>
<td>Polynucleotide Seq ID NO:</td>
<td>Clone ID</td>
<td>Library</td>
<td>Library Description</td>
<td></td>
</tr>
<tr>
<td>-------------------------</td>
<td>----------</td>
<td>---------</td>
<td>---------------------</td>
<td></td>
</tr>
<tr>
<td>155 1749147</td>
<td>STOMITU2</td>
<td></td>
<td>The library was constructed using RNA isolated from stomach tumor tissue obtained from a 68-year-old Caucasian female during a partial gastrectomy. Pathology indicated a malignant lymphoma of diffuse large-cell type. Patient history included thalassemia. Family history included acute leukemia, malignant neoplasm of the esophagus, malignant stomach neoplasm, and atherosclerotic coronary artery disease.</td>
<td></td>
</tr>
<tr>
<td>156 1817722</td>
<td>PROSNOT20</td>
<td></td>
<td>The library was constructed using RNA isolated from diseased prostate tissue removed from a 65-year-old Caucasian male during a radical prostatectomy. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated an adenocarcinoma.</td>
<td></td>
</tr>
<tr>
<td>157 1831200</td>
<td>THP1AZTO1</td>
<td></td>
<td>The library was constructed using 1 microgram of polyA RNA isolated from THP-1 monocytes treated for three days with 0.8 micromolar 5-aza-2'-deoxycytidine. THP-1 (ATCC TIB 202) is a human monocyte line derived from peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia.</td>
<td></td>
</tr>
<tr>
<td>158 1831477</td>
<td>THP1AZTO1</td>
<td></td>
<td>The library was constructed using 1 microgram of polyA RNA isolated from THP-1 monocytes treated for three days with 0.8 micromolar 5-aza-2'-deoxycytidine. THP-1 (ATCC TIB 202) is a human monocyte line derived from peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia.</td>
<td></td>
</tr>
<tr>
<td>159 1841607</td>
<td>COLNOT07</td>
<td></td>
<td>The library was constructed using RNA isolated from colon tissue removed from a 60-year-old Caucasian male during a left hemicolectomy.</td>
<td></td>
</tr>
<tr>
<td>160 1852391</td>
<td>LUNGFET03</td>
<td></td>
<td>The library was constructed using RNA isolated from lung tissue removed from a Caucasian female fetus, who died at 20 weeks’ gestation.</td>
<td></td>
</tr>
<tr>
<td>161 1854555</td>
<td>HNT3AZTO1</td>
<td></td>
<td>The library was constructed 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 for three days with 0.35 micromolar 5-aza-2'-deoxycytidine (AZT).</td>
<td></td>
</tr>
<tr>
<td>162 1855755</td>
<td>PROSNOT38</td>
<td></td>
<td>The library was constructed using RNA isolated from diseased prostate tissue removed from a 58-year-old Caucasian male during a radical cystectomy, radical prostatectomy, and gastrectomy. Pathology indicated adenofibromatous hyperplasia. This tissue was associated with a grade 3 transitional cell carcinoma. Patient history included angina and emphysema. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.</td>
<td></td>
</tr>
<tr>
<td>163 1861434</td>
<td>PROSNOT19</td>
<td></td>
<td>The library was constructed using RNA isolated from diseased prostate tissue removed from a 59-year-old Caucasian male during a radical prostatectomy with regional lymph node excision. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue indicated an adenocarcinoma (Gleason grade 3 + 3). The patient presented with elevated prostate-specific antigen (PSA). Patient history included colon diverticulitis and thrombophlebitis. Family history included benign hypertension, multiple myeloma, hyperlipidemia and rheumatoid arthritis.</td>
<td></td>
</tr>
<tr>
<td>164 1872334</td>
<td>LEUKNOT02</td>
<td></td>
<td>The library was constructed using RNA isolated from white blood cells of a 45-year-old female with blood type O+. The donor tested positive for cytomegalovirus (CMV).</td>
<td></td>
</tr>
<tr>
<td>165 1877230</td>
<td>LEUKNOT03</td>
<td></td>
<td>The library was constructed using RNA isolated from white blood cells of a 27-year-old female with blood type A+. The donor tested negative for cytomegalovirus (CMV).</td>
<td></td>
</tr>
<tr>
<td>166 1877885</td>
<td>LEUKNOT03</td>
<td></td>
<td>The library was constructed using RNA isolated from white blood cells of a 27-year-old female with blood type A+. The donor tested negative for cytomegalovirus (CMV).</td>
<td></td>
</tr>
</tbody>
</table>

Jul. 14, 2005
<table>
<thead>
<tr>
<th>Polynucleotide</th>
<th>SEQ ID NO:</th>
<th>Clone ID</th>
<th>Library</th>
<th>Library Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>167</td>
<td>1889269</td>
<td>BLADTUT07</td>
<td></td>
<td>The library was constructed using RNA isolated from bladder tumor tissue removed from the anterior bladder wall of a 58-year-old Caucasian male during a radical cystectomy, radical prostatectomy, and gastrectomy. Pathology indicated a grade 3 transitional cell carcinoma in the left lateral bladder. Patient history included angina and emphysema. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.</td>
</tr>
<tr>
<td>168</td>
<td>1890243</td>
<td>BLADTUT07</td>
<td></td>
<td>The library was constructed using RNA isolated from bladder tumor tissue removed from the anterior bladder wall of a 58-year-old Caucasian male during a radical cystectomy, radical prostatectomy, and gastrectomy. Pathology indicated a grade 3 transitional cell carcinoma in the left lateral bladder. Patient history included angina and emphysema. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.</td>
</tr>
<tr>
<td>169</td>
<td>1900433</td>
<td>BLADTUT06</td>
<td></td>
<td>The 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 a grade 3 transitional cell carcinoma in the left lateral bladder. Patient history included angina and emphysema. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.</td>
</tr>
<tr>
<td>170</td>
<td>1909441</td>
<td>CONNTUT01</td>
<td></td>
<td>The library was constructed using RNA isolated from a soft tissue tumor removed from the cervical area of the skull of a 30-year-old Caucasian female. Pathology indicated chondroid chondroma with neoplastic cells reactive for keratin.</td>
</tr>
<tr>
<td>171</td>
<td>1932226</td>
<td>COLNOT16</td>
<td></td>
<td>The library was constructed using RNA isolated from sigmoid colon tissue removed from a 62-year-old Caucasian male during a sigmoidectomy and permanent colostomy.</td>
</tr>
<tr>
<td>172</td>
<td>1932647</td>
<td>COLNOT16</td>
<td></td>
<td>The library was constructed using RNA isolated from sigmoid colon tissue removed from a 62-year-old Caucasian male during a sigmoidectomy and permanent colostomy.</td>
</tr>
<tr>
<td>173</td>
<td>2124245</td>
<td>BRSTNOT07</td>
<td></td>
<td>The library was constructed using RNA isolated from diseased breast tissue removed from a 43-year-old Caucasian female during unilateral extended simple mastectomy. Pathology indicated mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, atherosclerotic coronary artery disease, and type II diabetes.</td>
</tr>
<tr>
<td>174</td>
<td>2132626</td>
<td>OVARNOT3</td>
<td></td>
<td>The library was constructed using RNA isolated from ovarian tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology for the associated tumor tissue indicated grade 2 mucinous cystadenocarcinoma. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, cerebrovascular disease, breast cancer, and uterine cancer.</td>
</tr>
<tr>
<td>175</td>
<td>2286039</td>
<td>PROSNON01</td>
<td></td>
<td>The library was constructed and normalized from 4.4 million independent clones from the PROSNOT01 library. Starting RNA was made from prostate tissue removed from a 28-year-old Caucasian male who died from a gunshot wound. The normalization and hybridization conditions were adapted from Soares, M. B. et al. (1994).</td>
</tr>
<tr>
<td>Polynucleotide SEQ ID NO:</td>
<td>Clone ID</td>
<td>Library</td>
<td>Library Description</td>
<td></td>
</tr>
<tr>
<td>---------------------------</td>
<td>----------</td>
<td>---------</td>
<td>---------------------</td>
<td></td>
</tr>
<tr>
<td>176 2202356</td>
<td>BRAINON01</td>
<td></td>
<td>Proc. Natl. Acad. Sci. USA 91: 9228-9232, using a longer (19 hour) reannealing hybridization period. The library was constructed and normalized from 4.88 million independent clones from the BRAINNOT03 library. Starting RNA was made 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.</td>
<td></td>
</tr>
<tr>
<td>177 2349310</td>
<td>COLSUCT01</td>
<td></td>
<td>The library was constructed using RNA isolated from diseased sigmoid colon tissue obtained from a 70-year-old Caucasian male during colectomy with permanent ileostomy. Pathology indicated chronic ulcerative colitis. Patient history included benign neoplasm of the colon. Family history included atherosclerotic coronary artery disease and myocardial infarctions.</td>
<td></td>
</tr>
<tr>
<td>178 2373272</td>
<td>ADRENOT07</td>
<td></td>
<td>The library was constructed using RNA isolated from adrenal tissue removed from a 61-year-old female during a bilateral adrenalectomy. Patient history included an unspecified disorder of the adrenal glands.</td>
<td></td>
</tr>
<tr>
<td>179 2457682</td>
<td>ENDANOT01</td>
<td></td>
<td>The library was constructed using RNA isolated from aortic endothelial cell tissue from an explanted heart removed from a male during a heart transplant.</td>
<td></td>
</tr>
<tr>
<td>180 2480426</td>
<td>SMCANOT01</td>
<td></td>
<td>The library was constructed using RNA isolated from aortic smooth muscle cell line derived from the explanted heart of a male during a heart transplant.</td>
<td></td>
</tr>
<tr>
<td>181 2503743</td>
<td>CONUTUT01</td>
<td></td>
<td>The 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 Mullerian tumor present in the sigmoid mesentery at two sites.</td>
<td></td>
</tr>
<tr>
<td>182 2537684</td>
<td>BONRITU02</td>
<td></td>
<td>The library was constructed using RNA isolated from rib tumor tissue removed from a 16-year-old Caucasian male during a rib osteotomy and a wedge resection of the lung. Pathology indicated a metastatic grade 3 (of 4) osteosarcoma, forming a mass involving the chest wall.</td>
<td></td>
</tr>
<tr>
<td>183 2593853</td>
<td>OVARUT02</td>
<td></td>
<td>The library was constructed using RNA isolated from ovarian tumor tissue removed from a 51-year-old Caucasian female during an exploratory laparotomy, total abdominal hysterectomy, salpingo-oophorectomy, and an incidental appendectomy. Pathology indicated mucinous cystadenoma presenting as a multiloculated neoplasm involving the entire left ovary. The right ovary contained a follicular cyst and a hemorrhagic corpus luteum. The uterus showed proliferative endometrium and a single intramural leiomyoma. The peritoneal biopsy indicated benign glandular inclusions consistent with endosalpingiosis. Family history included atherosclerotic coronary artery disease, benign hyperthyroidism, breast cancer, and uterine cancer.</td>
<td></td>
</tr>
<tr>
<td>184 2622354</td>
<td>KERANOT02</td>
<td></td>
<td>The library was constructed using RNA isolated from epidermal breast keratinocytes (NHEK). NHEK (Clontech #CC-2501) is a human breast keratinocyte cell line derived from a 30-year-old black female during breast-reduction surgery.</td>
<td></td>
</tr>
<tr>
<td>185 2641377</td>
<td>LUNGTUT08</td>
<td></td>
<td>The library was constructed using RNA isolated from lung tumor tissue removed from a 63-year-old Caucasian male during a right upper lobectomy with fiberoptic bronchoscopy. Pathology indicated a grade 3 adenocarcinoma. Patient history included atherosclerotic coronary artery disease, an acute myocardial infarction, rectal cancer, an asymptomatic abdominal aortic aneurysm,</td>
<td></td>
</tr>
<tr>
<td>Polynucleotide</td>
<td>SEQ ID NO:</td>
<td>Clone ID</td>
<td>Library</td>
<td>Description</td>
</tr>
<tr>
<td>---------------</td>
<td>-------------</td>
<td>----------</td>
<td>---------</td>
<td>-------------</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>and cardiac dysrhythmia. Family history included congestive heart failure, stomach cancer, and lung cancer; type II diabetes, atherosclerotic coronary artery disease, and an acute myocardial infarction. The library was constructed using RNA isolated from kidney tissue removed a 65-year-old Caucasian male during an exploratory laparotomy and nephroureterectomy. Pathology for the associated tumor tissue indicated a grade 1 renal cell carcinoma within the upper pole of the left kidney. Patient history included malignant melanoma of the abdominal skin, benign neoplasm of colon, cerebrovascular disease, and umbilical hernia. Family history included myocardial infarction, atherosclerotic coronary artery disease, cerebrovascular disease, prostate cancer, myocardial infarction, and atherosclerotic coronary artery disease.</td>
</tr>
<tr>
<td>186</td>
<td>2674857</td>
<td>KIDNOT19</td>
<td></td>
<td></td>
</tr>
<tr>
<td>187</td>
<td>2758485</td>
<td>THP1AZ58</td>
<td></td>
<td>The subtracted THP-1 promonocyte cell line library was constructed using 5.76 million clones from a 5-aza-2’-deoxycytidine (AZT) treated THP-1 cell library. Starting RNA was made from THP-1 promonocyte cells treated for three days with 0.8 micromolar AZT. The library was oligo(dT)-primed, and cDNAs were cloned directionally into the pSPORTI vectoring system using SalI (5’) and NotI (3’). The hybridization procedure was derived from a similarly constructed library, made from 1 microgram of polyA RNA isolated from untreated THP-1 cells. 5.76 million clones from the AZT-treated THP-1 cell library were then subjected to two rounds of subtractive hybridization with 5 million clones from the untreated THP-1 cell library. Subtractive hybridization conditions were based on the methodologies of Swaroop et al. (Nucl Acids Res. 1991) 19: 3524 and Bonaldo et al. (Genome Res 1996) 6: 791-806.</td>
</tr>
<tr>
<td>188</td>
<td>2763296</td>
<td>BRSTNOT12</td>
<td></td>
<td>The library was constructed using RNA isolated from diseased breast tissue removed from a 52-year-old Caucasian female during a bilateral reduction mammoplasty. Pathology indicated nonproliferative fibrocystic disease. Family history included benign hypertension and atherosclerotic coronary artery disease.</td>
</tr>
<tr>
<td>189</td>
<td>2779436</td>
<td>OVARTU08</td>
<td></td>
<td>The library was constructed using RNA isolated from ovarian tumor tissue removed from the left ovary of a 52-year-old mixed ethnicity female during a total abdominal hysterectomy, bilateral salpingo-oophorectomy, peritoneal and lymphatic structure biopsy, regional lymph node excision, and peritoneal tissue destruction. Pathology indicated an invasive grade 3 (of 4) serousplastic carcinoma forming a mass in the left ovary. The endometrium was atrophic. Multiple (2) leiomyomata were identified, one subserosal and 1 intramural. Pathology also indicated a menestatic grade 3 serousplastic carcinoma involving the omentum, cul-de-sac peritoneum, left broad ligament peritoneum, and massentery colon. Patient history included breast cancer, chronic peptic ulcer, and joint pain. Family history included colon cancer, cerebrovascular disease, breast cancer, type II diabetes, celiac disease, and depressive disorder.</td>
</tr>
<tr>
<td>190</td>
<td>2808528</td>
<td>BLADTU08</td>
<td></td>
<td>The library was constructed using RNA isolated from bladder tumor tissue removed from a 72-year-old Caucasian male during a radical cystectomy and prostatectomy. Pathology indicated an invasive grade 3 (of 3) transitional cell carcinoma in the right bladder base. Family history included myocardial infarction, cerebrovascular disease, brain cancer, and myocardial infarction.</td>
</tr>
<tr>
<td>191</td>
<td>2809230</td>
<td>BLADTU08</td>
<td></td>
<td>The library was constructed using RNA isolated from bladder tumor tissue removed from a 72-year-old Caucasian male during a radical cystectomy and prostatectomy. Pathology indicated an</td>
</tr>
</tbody>
</table>
TABLE 4-continued

<table>
<thead>
<tr>
<th>Polynucleotide</th>
<th>SEQ ID NO:</th>
<th>Clone ID</th>
<th>Library</th>
<th>Library Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>192</td>
<td>2816821</td>
<td>BRSTNOT14</td>
<td></td>
<td>invasive grade 3 (of 3) transitional cell carcinoma in the right bladder base. Patient history included pure hypercholesterolemia and tobacco abuse. Family history included myocardial infarction, cerebrovascular disease, brain cancer, and myocardial infarction. The library was constructed using RNA isolated from breast tissue removed from a 62-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive grade 3 (of 4), nuclear grade 3 (of 3) adenocarcinoma, ductal type. Ductal carcinoma in situ, comedo type, comprised 60% of the tumor mass. Metastatic adenocarcinoma was identified in one (of 14) axillary lymph nodes with no perinodal extension. The tumor cells were strongly positive for estrogen receptors and weakly positive for progesterone receptors. Patient history included a benign colon neoplasm, hyperlipidemia, and cardiac dysrhythmia. Family history included atherosclerotic coronary artery disease, myocardial infarction, colon cancer, ovarian cancer, lung cancer, and cerebrovascular disease.</td>
</tr>
<tr>
<td>193</td>
<td>2817268</td>
<td>BRSTNOT14</td>
<td></td>
<td>The library was constructed using RNA isolated from breast tissue removed from a 62-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive grade 3 (of 4), nuclear grade 3 (of 3) adenocarcinoma, ductal type. Ductal carcinoma in situ, comedo type, comprised 60% of the tumor mass. Metastatic adenocarcinoma was identified in one (of 14) axillary lymph nodes with no perinodal extension. The tumor cells were strongly positive for estrogen receptors and weakly positive for progesterone receptors. Patient history included a benign colon neoplasm, hyperlipidemia, and cardiac dysrhythmia. Family history included atherosclerotic coronary artery disease, myocardial infarction, colon cancer, ovarian cancer, lung cancer, and cerebrovascular disease.</td>
</tr>
<tr>
<td>194</td>
<td>2923165</td>
<td>SININOT04</td>
<td></td>
<td>The library was constructed using RNA isolated from diseased ileum tissue obtained from a 26-year-old Caucasian male during a partial colectomy, permanent colostomy, and an incidental appendectomy. Pathology indicated moderately to severely active Crohn’s disease. Family history included enteritis of the small intestine.</td>
</tr>
<tr>
<td>195</td>
<td>2949822</td>
<td>KIDNFETO1</td>
<td></td>
<td>The library was constructed using RNA isolated from kidney tissue removed from a Caucasian female fetus, who died at 17 weeks’ gestation from anencephalus.</td>
</tr>
<tr>
<td>196</td>
<td>2992192</td>
<td>KIDNFETO2</td>
<td></td>
<td>The library was constructed using RNA isolated from kidney tissue removed from a Caucasian male fetus, who was stillborn with a hypoplastic left heart and died at 23 weeks’ gestation.</td>
</tr>
<tr>
<td>197</td>
<td>2992458</td>
<td>KIDNFETO2</td>
<td></td>
<td>The library was constructed using RNA isolated from kidney tissue removed from a Caucasian male fetus, who was stillborn with a hypoplastic left heart and died at 23 weeks’ gestation.</td>
</tr>
<tr>
<td>198</td>
<td>3044730</td>
<td>HEAANOT01</td>
<td></td>
<td>The library was constructed using RNA isolated from right coronary and right circumflex coronary artery tissue removed from the explanted heart of a 46-year-old Caucasian male during a heart transplantation. Patient history included myocardial infarction from total occlusion of the left anterior descending coronary artery, atherosclerotic coronary artery disease, hyperlipidemia, myocardial ischemia, dilated cardiomyopathy, and left ventricular dysfunction. Previous surgeries included cardiac catheterization. Family history included atherosclerotic coronary artery disease.</td>
</tr>
<tr>
<td>199</td>
<td>3120415</td>
<td>LUNGTUT13</td>
<td></td>
<td>The library was constructed using RNA isolated from tumorous lung tissue removed from the right upper lobe of a 47-year-old Caucasian male during...</td>
</tr>
<tr>
<td>Polynucleotide</td>
<td>SEQ ID NO:</td>
<td>Clone ID</td>
<td>Library</td>
<td>Library Description</td>
</tr>
<tr>
<td>----------------</td>
<td>------------</td>
<td>------------</td>
<td>--------------</td>
<td>---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>200</td>
<td>126758</td>
<td>LUNGNOT01</td>
<td>The library was constructed at Stratagene using RNA isolated from the lung tissue of a 72-year-old male.</td>
<td></td>
</tr>
<tr>
<td>201</td>
<td>674760</td>
<td>CRBLNOT01</td>
<td>The library was constructed using RNA isolated from the cerebellum tissue of a 69-year-old Caucasian male who died from chronic obstructive pulmonary disease. Patient history included myocardial infarction, hypertension, and osteoarthritis.</td>
<td></td>
</tr>
<tr>
<td>202</td>
<td>1292438</td>
<td>BRAITUT01</td>
<td>The library was constructed using RNA isolated from brain tumor tissue removed from a 50-year-old Caucasian female during a frontal lobectomy. Pathology indicated recurrent grade 3 oligosarcoma with focal necrosis and extensive calcification. Patient history included a speech disturbance and epilepsy. The patient’s brain had also been irradiated with a total dose of 5,082 cGy (Fraction 8). Family history included a brain tumor.</td>
<td></td>
</tr>
<tr>
<td>203</td>
<td>1236935</td>
<td>LUNGFEIT03</td>
<td>The library was constructed using RNA isolated from lung tissue removed from a Caucasian female fetus who died at 20 weeks' gestation.</td>
<td></td>
</tr>
<tr>
<td>204</td>
<td>1359283</td>
<td>LUNGNOT12</td>
<td>The library was constructed using RNA isolated from lung tissue removed from a 78-year-old Caucasian male during a segmental lung resection and regional lymph node resection. Pathology indicated fibrosis pleura was puckered, but not invaded. Pathology for the associated tumor tissue indicated an invasive pulmonary grade 3 adenocarcinoma. Patient history included cerebrovascular disease, arteriosclerotic coronary artery disease, thrombophlebitis, chronic obstructive pulmonary disease, and asthma. Family history included intracranial hematomas, cerebrovascular disease, arteriosclerotic coronary artery disease, and type 1 diabetes.</td>
<td></td>
</tr>
<tr>
<td>205</td>
<td>1450703</td>
<td>PENITUT01</td>
<td>The library was constructed using RNA isolated from tumor tissue removed from the penis of a 64-year-old Caucasian male during penile amputation. Pathology indicated a fungating invasive grade 4 squamous cell carcinoma involving the inner wall of the foreskin and extending onto the glans penis. Patient history included benign neoplasm of the large bowel, arteriosclerotic coronary artery disease, angina pectoris, gout, and obesity. Family history included malignant pharyngeal neoplasm, chronic lymphocytic leukemia, and chronic liver disease.</td>
<td></td>
</tr>
<tr>
<td>206</td>
<td>1910668</td>
<td>CONNTUT01</td>
<td>The library was constructed using RNA isolated from a soft tissue tumor removed from the erial area of the skull of a 30-year-old Caucasian female. Pathology indicated chondroid chordoma with neoplastic cells reactive for keratin.</td>
<td></td>
</tr>
<tr>
<td>207</td>
<td>1955143</td>
<td>CONNNOT01</td>
<td>The library was constructed using RNA isolated from mesentery fat tissue obtained from a 71-year-old Caucasian male during a partial colectomy and permanent colostomy. Family history included arteriosclerotic coronary artery disease, myocardial infarction, and extrinsic asthma.</td>
<td></td>
</tr>
<tr>
<td>208</td>
<td>1961637</td>
<td>BRSTNOT04</td>
<td>The library was constructed using RNA isolated from breast tissue removed from a 62-year-old East Indian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive grade 3 ductal carcinoma. Patient history included benign hypertension, hyperlipidemia, and hematuria. Family history included cerebrovascular and cardiovascular disease, hyperlipidemia, and liver cancer.</td>
<td></td>
</tr>
<tr>
<td>209</td>
<td>1990762</td>
<td>CORPNOT02</td>
<td>The library was constructed using RNA isolated from diseased corpus callosum tissue removed from a 72-year-old man during a partial callosotomy. Pathology indicated a segmental lung resection. Pathology indicated invasive grade 3 (of 4) adenocarcinoma. Family history included arteriosclerotic coronary artery disease, and type II diabetes.</td>
<td></td>
</tr>
<tr>
<td>Polynucleotide</td>
<td>SEQ ID NO:</td>
<td>Clone ID</td>
<td>Library Description</td>
<td></td>
</tr>
<tr>
<td>---------------</td>
<td>-----------</td>
<td>---------</td>
<td>---------------------</td>
<td></td>
</tr>
<tr>
<td>210</td>
<td>1994131</td>
<td>CORPNOT02</td>
<td>The library was constructed using RNA isolated from diseased corpus cullosum tissue removed from the brain of a 74-year-old Caucasian male who died from Alzheimer’s disease.</td>
<td></td>
</tr>
<tr>
<td>211</td>
<td>1997745</td>
<td>BRSTUT03</td>
<td>The library was constructed using RNA isolated from breast tumor tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated multicentric invasive grade 4 lobular carcinoma. The mass was identified in the upper outer quadrant, and three separate nodules were found in the lower outer quadrant of the left breast. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular disease, coronary artery aneurysm, breast cancer, prostate cancer, atherosclerotic coronary artery disease, and type 1 diabetes.</td>
<td></td>
</tr>
<tr>
<td>212</td>
<td>2009035</td>
<td>TESTNOT03</td>
<td>The library was constructed using polyA 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.</td>
<td></td>
</tr>
<tr>
<td>213</td>
<td>2009152</td>
<td>TESTNOT03</td>
<td>The library was constructed using polyA 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.</td>
<td></td>
</tr>
<tr>
<td>214</td>
<td>2061752</td>
<td>OVARNOT03</td>
<td>The library was constructed using RNA isolated from ovarian tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology for the associated tumor tissue indicated grade 2 mucinous cystadenocarcinoma. 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.</td>
<td></td>
</tr>
<tr>
<td>215</td>
<td>2061933</td>
<td>OVARNOT03</td>
<td>The library was constructed using RNA isolated from ovarian tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology for the associated tumor tissue indicated grade 2 mucinous cystadenocarcinoma. 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.</td>
<td></td>
</tr>
<tr>
<td>216</td>
<td>2081422</td>
<td>UTRSNOT08</td>
<td>The library was constructed using RNA isolated from uterine tissue removed from a 35-year-old Caucasian female during a vaginal hysterectomy with dilatation and curettage. Pathology indicated that the endometrium was secretory phase with benign endometrial polyp 1 cm in diameter. The cervix showed mild chronic cervicitis. Family history included atherosclerotic coronary artery disease and type II diabetes.</td>
<td></td>
</tr>
<tr>
<td>217</td>
<td>2101278</td>
<td>BRAITUT02</td>
<td>The 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 meningioma. Patient history included a grade 2 renal cell carcinoma, insomnia, and chronic airway obstruction. Family history included a malignant neoplasm of the kidney.</td>
<td></td>
</tr>
<tr>
<td>218</td>
<td>2121353</td>
<td>BRSTNOT07</td>
<td>The library was constructed using RNA isolated from diseased breast tissue removed from a 45-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated</td>
<td></td>
</tr>
<tr>
<td>Polynucleotide</td>
<td>SEQ ID NO:</td>
<td>Clone ID</td>
<td>Library</td>
<td>Library Description</td>
</tr>
<tr>
<td>---------------</td>
<td>-----------</td>
<td>---------</td>
<td>---------</td>
<td>---------------------</td>
</tr>
<tr>
<td>mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.</td>
<td>2241736</td>
<td>PANCTUT02</td>
<td>THP1 promonocyte</td>
<td>RNA was made from THP-1 promonocyte cells treated for three days with 0.8 micromolar AZ. The hybridization probe for...</td>
</tr>
<tr>
<td>mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.</td>
<td>2271935</td>
<td>PROSNON01</td>
<td>THP1 promonocyte</td>
<td>This normalized prostate library was constructed from 4.4 M independent clones from the PROSNON01 library. Starting RNA was made from prostate tissue removed from a 26-year-old Caucasian male who died from a self-inflicted gunshot wound. The normalization and hybridization conditions were adapted from Searles, M. B. et al. (1994) Proc. Natl. Acad. Sci. USA 91: 9226-9232, using a longer (19 hour) renamelling hybridization period.</td>
</tr>
<tr>
<td>mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.</td>
<td>2295344</td>
<td>BRSTNOT05</td>
<td>THP1 promonocyte</td>
<td>The library was constructed using RNA isolated from breast tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated multicentric invasive grade 4 lobular carcinoma. Patient history included skin cancer, rheumatic heart disease, osteoarthrosis, and tuberculosis. Family history included cerebrovascular and cardiovascular disease, breast and prostate cancer, and type I diabetes.</td>
</tr>
<tr>
<td>mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.</td>
<td>2303994</td>
<td>BRSTNOT05</td>
<td>THP1 promonocyte</td>
<td>The library was constructed using RNA isolated from breast tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated multicentric invasive grade 4 lobular carcinoma. Patient history included skin cancer, rheumatic heart disease, osteoarthrosis, and tuberculosis. Family history included cerebrovascular and cardiovascular disease, breast and prostate cancer, and type I diabetes.</td>
</tr>
<tr>
<td>mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.</td>
<td>2497805</td>
<td>ADRETUT05</td>
<td>THP1 promonocyte</td>
<td>The library was constructed using RNA isolated from adrenal tumor tissue removed from a 55-year-old Caucasian female during a unilateral adrenalectomy. Pathology indicated a pheochromocytoma.</td>
</tr>
<tr>
<td>mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.</td>
<td>2646362</td>
<td>LUNGUT11</td>
<td>THP1 promonocyte</td>
<td>The library was constructed using RNA isolated from lung tumor tissue removed from the right lower lobe of a 57-year-old Caucasian male during a segmental lung resection. Pathology indicated an infiltrating grade 2 squamous cell carcinoma. Multiple intrapleural perihilar lymph nodes showed metastatic squamous cell carcinoma. Patient history included a benign brain neoplasm and tobacco abuse. Family history included spinal cord cancer, type II diabetes, cerebrovascular disease, and malignant prostate neoplasm.</td>
</tr>
<tr>
<td>mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.</td>
<td>2657146</td>
<td>LUNGUT09</td>
<td>THP1 promonocyte</td>
<td>The library was constructed using RNA isolated from lung tumor tissue removed from a 68-year-old Caucasian male during segmental lung resection. Pathology indicated invasive grade 3 squamous cell carcinoma and a metastatic tumor. Patient history included type II diabetes, thyroid disorder, depressive disorder, hyperlipidemia, esophageal ulcer, and tobacco use.</td>
</tr>
<tr>
<td>mildly proliferative fibrocystic changes with epithelial hyperplasia, papillomatosis, and duct ectasia. Pathology for the associated tumor tissue indicated invasive grade 4, nuclear grade 3 mammary adenocarcinoma with extensive comedo necrosis. Family history included epilepsy, cardiovascular disease, and type II diabetes.</td>
<td>2735766</td>
<td>THP1AZS08</td>
<td>THP1 promonocyte</td>
<td>This subtracted THP-1 promonocyte cell line library was constructed using 5.76 million clones from a 5-aza-2-deoxycytidine (AZ) treated THP-1 cell library. Starting RNA was made from THP-1 promonocyte cells treated for three days with 0.8 micromolar AZ. The hybridization probe for...</td>
</tr>
<tr>
<td>Polynucleotide</td>
<td>SEQ ID NO:</td>
<td>Clone ID</td>
<td>Library</td>
<td>Library Description</td>
</tr>
<tr>
<td>---------------</td>
<td>-----------</td>
<td>---------</td>
<td>---------</td>
<td>---------------------</td>
</tr>
</tbody>
</table>

subtraction was derived from a similarly constructed library, made from RNA isolated from untreated THP-1 cells. 5.76 million clones from the AZ-treated THP-1 cell library were then subjected to two rounds of subtractive hybridization with 5 million clones from the untreated THP-1 cell library. Subtractive hybridization conditions were based on the methodologies of Swaroop et al., NAR (1991) 19: 1954, and Bonaldo et al., Genome Research (1996) 6: 791. THP-1 (ATCC TIB 202) is a human promonocyte line derived from peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia.

227 2831245 TLYMNOT03 The library was constructed using RNA isolated from nonseparated Th1 cells. These cells were differentiated from umbilical cord CD4 T cells with IL-12 and B7-transfected COS cells.

228 3116250 LUNGUT13 The library was constructed using RNA isolated from tumorous lung tissue removed from the right upper lobe of a 47-year-old Caucasian male during a segmental lung resection. Pathology indicated invasive grade 3 (of 4) adenocarcinoma. Family history included atherosclerotic coronary artery disease, and type II diabetes.

229 3129630 LUNGUT12 The library was constructed using RNA isolated from tumorous lung tissue removed from a 70-year-old Caucasian female during a lung lobectomy of the left upper lobe. Pathology indicated grade 3 (of 4) adenocarcinoma and vascular invasion. Patient history included tobacco abuse, depressive disorder, anxiety state, and skin cancer. Family history included cerebrovascular disease, congestive heart failure, colon cancer, depressive disorder, and primary liver.

230 007632 IMM1NOT01 The 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.

231 1236968 LUNGFE13 The library was constructed using RNA isolated from lung tissue removed from a Caucasian female fetus who died at 20 weeks’ gestation.

232 1334153 COLNOT13 The library was constructed using RNA isolated from ascending colon tissue of a 28-year-old Caucasian male with moderate chronic ulcerative colitis.

233 1396975 BRAITUT08 The 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 meningioma tissue. Pathology indicated grade 4 fibrillary astrocytoma with focal tumorial multinecrosis. Patient history included cerebrovascular disease, deficiency anemia, hyperlipidemia, epilepsy, and tobacco use. Family history included cerebrovascular disease and malignant prostatic neoplasm.

234 1501749 SINTBST01 The library was constructed using RNA isolated from ileum tissue removed from an 18-year-old Caucasian female during bowel anastomosis. Pathology indicated Crohn’s disease of the ileum. Family history included cerebrovascular disease and atherosclerotic coronary artery disease.

235 1575240 LNOQDNOT03 The library was constructed using RNA isolated from lymph node tissue removed from a 67-year-old Caucasian male during a segmental lung resection and bronchoscopy. This tissue was extensively necrotic with 50% viable tumor. Pathology for the associated tumor tissue indicated invasive grade 3-4 squamous cell carcinoma. Patient history included hemangioema. Family history included atherosclerotic coronary artery disease, benign hypertension, and congestive heart failure.

236 1647884 PROSTUT09 The library was constructed using RNA isolated from prostate tumor tissue removed from a 66-
<table>
<thead>
<tr>
<th>Polynucleotide</th>
<th>SEQ ID NO:</th>
<th>Clone ID</th>
<th>Library</th>
<th>Library Description</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>237</td>
<td>1661144</td>
<td>BRSTNOT09</td>
<td>The library was constructed using RNA isolated from breast tissue removed from a 45-year-old Caucasian female during unilateral extended simple mastectomy. Pathology indicated invasive nuclear grade 2–3 adenocarcinoma. Patient history included valvuloplasty of mitral valve and rheumatic heart disease. Family history included cardiovascular disease and type II diabetes.</td>
</tr>
<tr>
<td></td>
<td>238</td>
<td>1685409</td>
<td>PROSNOT15</td>
<td>The library was constructed using RNA isolated from breast tissue removed from a 57-year-old Caucasian male during a radical prostatectomy, radical cystectomy, and urinary diversion. Pathology indicated grade 3 transitional cell carcinoma. Patient history included lung neoplasm, and benign hypertension. Family history included malignant breast neoplasm, tuberculosis, cerebrovascular disease, atherosclerotic coronary artery disease, and lung cancer.</td>
</tr>
<tr>
<td></td>
<td>239</td>
<td>1731419</td>
<td>BRSTUT08</td>
<td>The library was constructed using RNA isolated from breast tumor tissue removed from a 45-year-old Caucasian female during unilateral extended simple mastectomy. Pathology indicated invasive nuclear grade 2–3 adenocarcinoma. Patient history included valvuloplasty of mitral valve and rheumatic heart disease. Family history included prostate cancer, secondary bone cancer, and benign hypertension.</td>
</tr>
<tr>
<td></td>
<td>240</td>
<td>2650265</td>
<td>BRSTNOT14</td>
<td>The library was constructed using RNA isolated from breast tissue removed from a 62-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive grade 3 (of 4), nuclear grade 3 (of 3) adenocarcinoma. Patient history included a benign colon neoplasm, hyperlipidemia, cardiac dysrhythmia, and obesity. Family history included cardiovascular and cerebrovascular disease and colon, ovary and lung cancer.</td>
</tr>
<tr>
<td></td>
<td>241</td>
<td>2677129</td>
<td>KIDNNOT19</td>
<td>The library was constructed using RNA isolated from kidney tissue removed from a 65-year-old Caucasian male during an exploratory laparotomy and nephroureterectomy. Pathology for the associated tumor tissue indicated grade 1 renal cell carcinoma within the upper pole of the left kidney. Patient history included malignant melanoma of the abdominal skin, benign neoplasm of colon, cerebrovascular disease, and umbilical hernia. Family history included myocardial infarction, atherosclerotic coronary artery disease, cerebrovascular disease, and prostate cancer.</td>
</tr>
<tr>
<td></td>
<td>242</td>
<td>3151073</td>
<td>ADRENON04</td>
<td>The normalized adrenal gland library was constructed from 1.36 × 10^6 independent clones from an adrenal tissue library. Starting RNA was made from adrenal gland tissue removed from a 20-year-old Caucasian male who died from head trauma. The library was normalized in two rounds using conditions adopted from Soares et al. (PNAS 1994 91: 9228–9232) and Bonaldo et al. (Genome Res (1996) 6: 791–808) using a significantly longer (40-hours/round) reannealing hybridization period.</td>
</tr>
<tr>
<td></td>
<td>243</td>
<td>3170095</td>
<td>BRSTNOT18</td>
<td>The library was constructed using RNA isolated from diseased breast tissue removed from a 57-year-old Caucasian female during a unilateral...</td>
</tr>
<tr>
<td>Polynucleotide</td>
<td>SEQ ID NO:</td>
<td>Clone ID</td>
<td>Library</td>
<td>Library Description</td>
</tr>
<tr>
<td>---------------</td>
<td>-----------</td>
<td>----------</td>
<td>---------</td>
<td>---------------------</td>
</tr>
<tr>
<td>244</td>
<td>3475168</td>
<td>LUNGNOT27</td>
<td>The library was constructed using RNA isolated from lung tissue removed from a 17-year-old Hispanic female.</td>
<td></td>
</tr>
<tr>
<td>245</td>
<td>3836893</td>
<td>DENDINT01</td>
<td>The library was constructed using RNA isolated from treated dendritic cells from peripheral blood.</td>
<td></td>
</tr>
<tr>
<td>246</td>
<td>4072159</td>
<td>KIDNNOT26</td>
<td>The library was constructed using RNA isolated from left kidney medulla and cortex tissue removed from a 53-year-old Caucasian female during a nephrectomy. Pathology for the associated tumor tissue included grade 2 renal cell carcinoma involving the lower pole of the kidney. Pathological history included hyperlipidemia, cardiac dysrhythmia, menorrhagia, cerebrovascular disease, atherosclerotic coronary artery disease, and tobacco abuse. Family history included cerebrovascular disease and atherosclerotic coronary artery disease.</td>
<td></td>
</tr>
<tr>
<td>247</td>
<td>1003916</td>
<td>BRSTNOT03</td>
<td>The library was constructed using RNA isolated from diseased breast tissue removed from a 54-year-old Caucasian female during a bilateral radical mastectomy. Pathology indicated grade 3 mammary ductal adenocarcinoma. Patient history included kidney infection and endometrial atresia. Family history included benign hypertension, hyperlipidemia and a malignant neoplasm of the colon.</td>
<td></td>
</tr>
<tr>
<td>248</td>
<td>2093492</td>
<td>PANCNOT04</td>
<td>The library was constructed using RNA isolated from the pancreatic tissue of a 5-year-old Caucasian male who died in a motor vehicle accident.</td>
<td></td>
</tr>
<tr>
<td>249</td>
<td>2108789</td>
<td>BRAITUT03</td>
<td>The 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 meningioma. Pathology indicated a grade 4 fibrillary giant and small-cell astrocytoma. Family history included benign hypertension and cerebrovascular disease.</td>
<td></td>
</tr>
<tr>
<td>250</td>
<td>2171401</td>
<td>ENDCNOT03</td>
<td>The library was constructed using RNA isolated from dermal microvascular endothelial cells removed from a neonatal Caucasian male.</td>
<td></td>
</tr>
<tr>
<td>251</td>
<td>2212530</td>
<td>SINTFET03</td>
<td>The library was constructed using RNA isolated from small intestine tissue removed from a Caucasian female fetus, who died at 20 weeks’ gestation.</td>
<td></td>
</tr>
<tr>
<td>252</td>
<td>2253636</td>
<td>OVARITUT01</td>
<td>The 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.</td>
<td></td>
</tr>
<tr>
<td>253</td>
<td>2280161</td>
<td>PROSNON01</td>
<td>The normalized prostate library was constructed from 4.4 M independent clones from the PROSNOT11 library. Starting RNA was made from prostate tissue removed from a 26-year-old Caucasian male who died from a self-inflicted gunshot wound. The normalization and hybridization conditions were adapted from Soares, M. B. et al. (1994) Proc. Natl. Acad. Sci. USA 91: 9226-9232, using a longer (19 hour) renaturation hybridization period.</td>
<td></td>
</tr>
</tbody>
</table>
| 254 | 2287485 | BRAINON01 | The library was constructed and normalized from 4.88 million independent clones from the BRAINOT03 library. RNA was made from brain tissue...
<table>
<thead>
<tr>
<th>Polynucleotide SEQ ID NO:</th>
<th>Clone ID</th>
<th>Library</th>
<th>Library Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>255 2380344</td>
<td>ISLNOT01</td>
<td></td>
<td>removed from a 26-year-old Caucasian male during cranioplasty and excision of a cerebral meningioma lesion. Pathology for the associated tumor tissue indicated a grade 4 oligoastrocytoma in the right fronto-parietal part of the brain.</td>
</tr>
<tr>
<td>256 2383171</td>
<td>ISLNOT01</td>
<td></td>
<td>The library was constructed using RNA isolated from a pooled collection of pancreatic islet cells.</td>
</tr>
<tr>
<td>257 2396046</td>
<td>THPLAZJ01</td>
<td></td>
<td>The library was constructed using RNA isolated from THP-1 promonocyte cells treated for three days with 0.8 micromolar 5-aza-2’-deoxycytidine. THP-1 (ATCC TIB 202) is a human promonocyte line derived from peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia.</td>
</tr>
<tr>
<td>258 2456587</td>
<td>ENDANOT01</td>
<td></td>
<td>The library was constructed using RNA isolated from aortic endothelial cell tissue from an explanted heart removed from a male during a heart transplant.</td>
</tr>
<tr>
<td>259 2484813</td>
<td>BONRTUT01</td>
<td></td>
<td>The library was constructed using RNA isolated from rib tumor tissue removed from a 10-year-old Caucasian male during a rib osteotomy and a wedge resection of the lung. Pathology indicated a metastatic grade 3 (of 4) osteosarcoma, forming a mass involving the chest wall.</td>
</tr>
<tr>
<td>260 2493851</td>
<td>ADREITUT05</td>
<td></td>
<td>The library was constructed using RNA isolated from adrenal tumor tissue removed from a 52-year-old Caucasian female during a unilateral adrenalectomy. Pathology indicated a pheochromocytoma.</td>
</tr>
<tr>
<td>261 2495719</td>
<td>ADREITUT05</td>
<td></td>
<td>The library was constructed using RNA isolated from adrenal tumor tissue removed from a 52-year-old Caucasian female during a unilateral adrenalectomy. Pathology indicated a pheochromocytoma.</td>
</tr>
<tr>
<td>262 2614153</td>
<td>GBLANOT01</td>
<td></td>
<td>The library was constructed using RNA isolated from diseased gallbladder tissue removed from a 53-year-old Caucasian female during a cholecystectomy. Pathology indicated mild chronic cholecystitis and cholelithiasis with approximately 150 mixed gallstones. Family history included benign hypertension.</td>
</tr>
<tr>
<td>263 2655184</td>
<td>THYMNOT04</td>
<td></td>
<td>The library was constructed using RNA isolated from thymus tissue removed from a 3-year-old Caucasian male, who died from anoxia. Serologies were negative. The patient was not taking any medications.</td>
</tr>
<tr>
<td>264 2848362</td>
<td>BRSTTUT13</td>
<td></td>
<td>The library was constructed using RNA isolated from breast tumor tissue removed from the right breast of a 46-year-old Caucasian female during a unilateral extended simple mastectomy with breast reconstruction. Pathology indicated an invasive grade 3 adenocarcinoma, ductal type with apocrine features and greater than 50% intraductal component. Patient history included breast cancer.</td>
</tr>
<tr>
<td>265 2849906</td>
<td>BRSTTUT13</td>
<td></td>
<td>The library was constructed using RNA isolated from breast tumor tissue removed from the right breast of a 46-year-old Caucasian female during a unilateral extended simple mastectomy with breast reconstruction. Pathology indicated an invasive grade 3 adenocarcinoma, ductal type with apocrine features and greater than 50% intraductal component. Patient history included breast cancer.</td>
</tr>
<tr>
<td>266 2899137</td>
<td>DRCNNOT01</td>
<td></td>
<td>The library was constructed using RNA isolated from dorsal root ganglion tissue removed from the cervical spine of a 32-year-old Caucasian male who died from acute pulmonary edema and bronchopneumonia, bilateral pleural and pericardial effusions, and malignant lymphoma (natural killer cell type). Patient history included probable cytomegalovirus, infection, hepatic congestion and stenosis, splenomegaly, hemorrhagic cystitis, thyroid hemorrhage, and Bell’s palsy. Surgeries included coloscopy, large intestine biopsy, adenotonsillectomy, and</td>
</tr>
</tbody>
</table>
TABLE 4-continued

<table>
<thead>
<tr>
<th>Polynucleotide SEQ ID NO:</th>
<th>Clone ID</th>
<th>Library</th>
<th>Library Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>267 2986229</td>
<td>CARQGDT01</td>
<td>The library was constructed using RNA isolated from diseased cartilage tissue. Patient history included osteoarthritis.</td>
<td></td>
</tr>
<tr>
<td>268 3222081</td>
<td>COLNNON03</td>
<td>The normalized cDNA library was constructed from 2.84 x 10^6 independent clones from the COLNNOT07 library. Starting RNA was made from colon tissue removed from a 60-year-old Caucassian male during a left hemicolectomy. The normalization and hybridization conditions were adapted from Soares et al. (PNAS (1994) 91: 9228-9232), Swaroop et al. (Nucl. Acids Res. (1991) 19: 1954), and Bonaldo et al. (Genome Res (1996) 6: 791-806), using a significantly longer (48 hour) reannealing hybridization period.</td>
<td></td>
</tr>
</tbody>
</table>

[0276]

**TABLE 5**

<table>
<thead>
<tr>
<th>Program</th>
<th>Description</th>
<th>Reference</th>
<th>Parameter Threshold</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABI FACTURA</td>
<td>A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.</td>
<td>Perkin-Elmer Applied Biosystems, Foster City, CA.</td>
<td></td>
</tr>
<tr>
<td>ABUPARACEL FDF</td>
<td>A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.</td>
<td>Perkin-Elmer Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.</td>
<td>Mismatch &lt;50%</td>
</tr>
<tr>
<td>ABI AutoAssembler</td>
<td>A program that assembles nucleic acid sequences.</td>
<td>Perkin-Elmer Applied Biosystems, Foster City, CA.</td>
<td></td>
</tr>
<tr>
<td>BLAST</td>
<td>A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastx, tblastn, and tblastx.</td>
<td>Altschul, S. F. et al. (1990) J. Mol. Biol. 215: 403-410; Altschul, S. F. et al. (1997) Nucleic Acids Res. 25: 3389-3402.</td>
<td>ESTs: Probability value = 1.0E-8 or less Full Length sequences: Probability value = 1.0E-10 or less</td>
</tr>
</tbody>
</table>
### TABLE 5-continued

<table>
<thead>
<tr>
<th>Program</th>
<th>Description</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Motifs</td>
<td>A program that searches amino acid sequences for patterns that matched those defined in Prosite.</td>
<td>Bairoch et al. supr; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.</td>
</tr>
</tbody>
</table>

### TABLE 6-continued

<table>
<thead>
<tr>
<th>Nucleotide SEQ ID NO:</th>
<th>Clone ID</th>
<th>Fragment of SEQ ID NO</th>
<th>Starting Nucleotide of Fragment</th>
<th>Ending Nucleotide of Fragment</th>
</tr>
</thead>
<tbody>
<tr>
<td>135 443531 443531H1</td>
<td>1 253</td>
<td>140607F6 140607F6</td>
<td>152 336</td>
<td>140607F6 140607F6</td>
</tr>
<tr>
<td>136 632680 632680H1</td>
<td>13 253</td>
<td>78471F3 78471F3</td>
<td>17 666</td>
<td>78471F3 78471F3</td>
</tr>
<tr>
<td>137 670100 670100H1</td>
<td>1 263</td>
<td>660791R1 660791R1</td>
<td>1 633</td>
<td>660791R1 660791R1</td>
</tr>
<tr>
<td>138 726498 726498H1</td>
<td>13 263</td>
<td>726498R6 726498R6</td>
<td>13 489</td>
<td>726498R6 726498R6</td>
</tr>
<tr>
<td>139 795064 795064H1</td>
<td>86 323</td>
<td>433045H1 433045H1</td>
<td>4 284</td>
<td>433045H1 433045H1</td>
</tr>
<tr>
<td>140 924925 924925H1</td>
<td>111 412</td>
<td>924925F1 924925F1</td>
<td>112 478</td>
<td>924925F1 924925F1</td>
</tr>
<tr>
<td>140 326383 326383H1</td>
<td>2 239</td>
<td>326383R2 326383R2</td>
<td>111 629</td>
<td>326383R2 326383R2</td>
</tr>
<tr>
<td>141 962390 962390F1</td>
<td>1 478</td>
<td>100755F1 100755F1</td>
<td>1 790</td>
<td>100755F1 100755F1</td>
</tr>
<tr>
<td>142 1259405 1259405F1</td>
<td>46 277</td>
<td>247242H1 247242H1</td>
<td>331 354</td>
<td>247242H1 247242H1</td>
</tr>
<tr>
<td>143 1297384 1297384H1</td>
<td>402 641</td>
<td>1297384F1 1297384F1</td>
<td>1 492</td>
<td>1297384F1 1297384F1</td>
</tr>
<tr>
<td>144 1299627 1299627H1</td>
<td>1 250</td>
<td>1299627F1 1299627F1</td>
<td>1 614</td>
<td>1299627F1 1299627F1</td>
</tr>
<tr>
<td>150 1609396 1609396H1</td>
<td>1 250</td>
<td>1609396F1 1609396F1</td>
<td>1 614</td>
<td>1609396F1 1609396F1</td>
</tr>
</tbody>
</table>

### TABLE 6

<table>
<thead>
<tr>
<th>Nucleotide SEQ ID NO:</th>
<th>Clone ID</th>
<th>Fragment of SEQ ID NO</th>
<th>Starting Nucleotide of Fragment</th>
<th>Ending Nucleotide of Fragment</th>
</tr>
</thead>
<tbody>
<tr>
<td>135 1349224F1 1349224F1</td>
<td>1330 1731</td>
<td>1350143F1 1350143F1</td>
<td>46 297</td>
<td>1350143F1 1350143F1</td>
</tr>
<tr>
<td>145 13360626 13360626H1</td>
<td>1 223</td>
<td>13360626H1 13360626H1</td>
<td>1 223</td>
<td>13360626H1 13360626H1</td>
</tr>
<tr>
<td>146 13361219 13361219H1</td>
<td>246 491</td>
<td>13361219H1 13361219H1</td>
<td>246 491</td>
<td>13361219H1 13361219H1</td>
</tr>
<tr>
<td>147 13329031 13329031H1</td>
<td>1 264</td>
<td>13329031H1 13329031H1</td>
<td>1 264</td>
<td>13329031H1 13329031H1</td>
</tr>
<tr>
<td>148 1483050 1483050H1</td>
<td>722 931</td>
<td>1483050H1 1483050H1</td>
<td>722 931</td>
<td>1483050H1 1483050H1</td>
</tr>
</tbody>
</table>

[0277]
<table>
<thead>
<tr>
<th>Nucleotide SEQ ID NO:</th>
<th>Clone ID</th>
<th>Fragment of SEQ ID NO:</th>
<th>Starting Nucleotide of Fragment</th>
<th>Ending Nucleotide of Fragment</th>
</tr>
</thead>
<tbody>
<tr>
<td>152</td>
<td>1693358</td>
<td>1693358H1</td>
<td>41</td>
<td>125</td>
</tr>
<tr>
<td></td>
<td>249825H1</td>
<td></td>
<td>1</td>
<td>252</td>
</tr>
<tr>
<td></td>
<td>1867125F6</td>
<td>205</td>
<td>373</td>
<td>736</td>
</tr>
<tr>
<td></td>
<td>1693358T6</td>
<td>1094</td>
<td>416</td>
<td>2164</td>
</tr>
<tr>
<td></td>
<td>2248848B6</td>
<td>337</td>
<td>1103</td>
<td>2098</td>
</tr>
<tr>
<td>153</td>
<td>1707721</td>
<td>1707721H1</td>
<td>408</td>
<td>626</td>
</tr>
<tr>
<td></td>
<td>1484609T1</td>
<td>2165</td>
<td>1855</td>
<td>2820</td>
</tr>
<tr>
<td></td>
<td>1707721F6</td>
<td>408</td>
<td>987</td>
<td>1495</td>
</tr>
<tr>
<td></td>
<td>126759F1</td>
<td>1721</td>
<td>2182</td>
<td>3603</td>
</tr>
<tr>
<td></td>
<td>1484609F1</td>
<td>1855</td>
<td>2178</td>
<td>3433</td>
</tr>
<tr>
<td></td>
<td>SAA00930F1</td>
<td>544</td>
<td>1132</td>
<td>3662</td>
</tr>
<tr>
<td></td>
<td>SAA01030R1</td>
<td>1675</td>
<td>1212</td>
<td>6025</td>
</tr>
<tr>
<td></td>
<td>SAA00930R1</td>
<td>1675</td>
<td>1142</td>
<td>3510</td>
</tr>
<tr>
<td>154</td>
<td>1738735</td>
<td>1738735H1</td>
<td>7</td>
<td>236</td>
</tr>
<tr>
<td></td>
<td>SAA00944R1</td>
<td>393</td>
<td>5</td>
<td>944</td>
</tr>
<tr>
<td></td>
<td>SAA0137F1</td>
<td>913</td>
<td>685</td>
<td>409</td>
</tr>
<tr>
<td></td>
<td>SAA01626F1</td>
<td>435</td>
<td>42</td>
<td>204</td>
</tr>
<tr>
<td>155</td>
<td>1749147</td>
<td>1749147H1</td>
<td>1</td>
<td>276</td>
</tr>
<tr>
<td></td>
<td>1749147F6</td>
<td>47</td>
<td>457</td>
<td>812</td>
</tr>
<tr>
<td>156</td>
<td>1817722</td>
<td>1817722H1</td>
<td>479</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>201085H8</td>
<td>344</td>
<td>545</td>
<td>1190</td>
</tr>
<tr>
<td>157</td>
<td>1831290</td>
<td>1831290H1</td>
<td>10</td>
<td>257</td>
</tr>
<tr>
<td></td>
<td>347395H8</td>
<td>70</td>
<td>242</td>
<td>365</td>
</tr>
<tr>
<td></td>
<td>197224F6</td>
<td>163</td>
<td>617</td>
<td>236</td>
</tr>
<tr>
<td></td>
<td>130127F1</td>
<td>413</td>
<td>852</td>
<td>1265</td>
</tr>
<tr>
<td></td>
<td>1521574F1</td>
<td>1024</td>
<td>1602</td>
<td>3628</td>
</tr>
<tr>
<td></td>
<td>1561690T6</td>
<td>1729</td>
<td>1058</td>
<td>3787</td>
</tr>
<tr>
<td></td>
<td>801461R1</td>
<td>1361</td>
<td>1758</td>
<td>3119</td>
</tr>
<tr>
<td>158</td>
<td>1834177</td>
<td>1834177H1</td>
<td>59</td>
<td>337</td>
</tr>
<tr>
<td></td>
<td>158267H6</td>
<td>199</td>
<td>1690</td>
<td>3580</td>
</tr>
<tr>
<td></td>
<td>133670H1</td>
<td>1986</td>
<td>1639</td>
<td>3525</td>
</tr>
<tr>
<td></td>
<td>151901H1</td>
<td>252</td>
<td>789</td>
<td>3848</td>
</tr>
<tr>
<td></td>
<td>152204H1</td>
<td>1061</td>
<td>1318</td>
<td>3879</td>
</tr>
<tr>
<td>159</td>
<td>1841407</td>
<td>1841407H1</td>
<td>13</td>
<td>920</td>
</tr>
<tr>
<td></td>
<td>SBH1A0388F1</td>
<td>13</td>
<td>172</td>
<td>498</td>
</tr>
<tr>
<td>160</td>
<td>185239H1</td>
<td>98</td>
<td>367</td>
<td>1333</td>
</tr>
<tr>
<td></td>
<td>734410H1</td>
<td>1</td>
<td>225</td>
<td>447</td>
</tr>
<tr>
<td></td>
<td>185239F6</td>
<td>98</td>
<td>542</td>
<td>1586</td>
</tr>
<tr>
<td></td>
<td>185455H1</td>
<td>1</td>
<td>265</td>
<td>481</td>
</tr>
<tr>
<td></td>
<td>251371H1</td>
<td>37</td>
<td>50</td>
<td>935</td>
</tr>
<tr>
<td></td>
<td>782453R1</td>
<td>223</td>
<td>712</td>
<td>2438</td>
</tr>
<tr>
<td></td>
<td>185455F6</td>
<td>1</td>
<td>346</td>
<td>246</td>
</tr>
<tr>
<td>161</td>
<td>184067F5</td>
<td>1046</td>
<td>860</td>
<td>2610</td>
</tr>
<tr>
<td></td>
<td>210973H6</td>
<td>938</td>
<td>1054</td>
<td>3092</td>
</tr>
<tr>
<td>162</td>
<td>185575H5</td>
<td>17</td>
<td>224</td>
<td>346</td>
</tr>
<tr>
<td></td>
<td>304023H6</td>
<td>1</td>
<td>179</td>
<td>512</td>
</tr>
<tr>
<td></td>
<td>125207F1</td>
<td>306</td>
<td>816</td>
<td>3122</td>
</tr>
<tr>
<td></td>
<td>83576T1</td>
<td>1148</td>
<td>855</td>
<td>2003</td>
</tr>
<tr>
<td></td>
<td>192026H6</td>
<td>854</td>
<td>1161</td>
<td>3015</td>
</tr>
<tr>
<td>163</td>
<td>1861434</td>
<td>1861434H1</td>
<td>13</td>
<td>253</td>
</tr>
<tr>
<td></td>
<td>1861434T6</td>
<td>872</td>
<td>261</td>
<td>1774</td>
</tr>
<tr>
<td></td>
<td>SARA01255F1</td>
<td>426</td>
<td>808</td>
<td>2346</td>
</tr>
<tr>
<td></td>
<td>SARA02485R1</td>
<td>587</td>
<td>889</td>
<td>2373</td>
</tr>
<tr>
<td>164</td>
<td>1872344</td>
<td>1872344H1</td>
<td>1</td>
<td>229</td>
</tr>
<tr>
<td></td>
<td>187234F6</td>
<td>1</td>
<td>424</td>
<td>229</td>
</tr>
<tr>
<td></td>
<td>SBGA01368F4</td>
<td>358</td>
<td>425</td>
<td>980</td>
</tr>
<tr>
<td>165</td>
<td>1877230</td>
<td>1877230H1</td>
<td>1405</td>
<td>1677</td>
</tr>
<tr>
<td></td>
<td>251964H1</td>
<td>1</td>
<td>251</td>
<td>1345</td>
</tr>
<tr>
<td></td>
<td>1877230F6</td>
<td>1903</td>
<td>1405</td>
<td>3352</td>
</tr>
<tr>
<td></td>
<td>125469F3</td>
<td>335</td>
<td>716</td>
<td>2013</td>
</tr>
<tr>
<td></td>
<td>077029R1</td>
<td>682</td>
<td>1414</td>
<td>2196</td>
</tr>
<tr>
<td></td>
<td>123229F6</td>
<td>906</td>
<td>1507</td>
<td>2912</td>
</tr>
<tr>
<td></td>
<td>100452R5</td>
<td>1451</td>
<td>1904</td>
<td>3361</td>
</tr>
<tr>
<td></td>
<td>SARA00789F1</td>
<td>1545</td>
<td>1921</td>
<td>3930</td>
</tr>
<tr>
<td></td>
<td>SARA0264F5</td>
<td>1545</td>
<td>1923</td>
<td>3930</td>
</tr>
<tr>
<td>166</td>
<td>1877885</td>
<td>1877885H1</td>
<td>68</td>
<td>323</td>
</tr>
<tr>
<td></td>
<td>508020F1</td>
<td>499</td>
<td>51</td>
<td>1012</td>
</tr>
</tbody>
</table>

TABLE 6-continued
### TABLE 6-continued

<table>
<thead>
<tr>
<th>Nucleotide SEQ ID NO:</th>
<th>Clone ID</th>
<th>Fragment of SEQ ID NO</th>
<th>Starting Nucleotide of Fragment</th>
<th>Ending Nucleotide of Fragment</th>
</tr>
</thead>
<tbody>
<tr>
<td>1208654R1</td>
<td>1382</td>
<td>1633</td>
<td></td>
<td></td>
</tr>
<tr>
<td>880544R1</td>
<td>1450</td>
<td>1648</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2537684H1</td>
<td>434</td>
<td>682</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2005493H1</td>
<td>1</td>
<td>194</td>
<td></td>
<td></td>
</tr>
<tr>
<td>730965H1</td>
<td>307</td>
<td>547</td>
<td></td>
<td></td>
</tr>
<tr>
<td>916487H1</td>
<td>723</td>
<td>989</td>
<td></td>
<td></td>
</tr>
<tr>
<td>9961235R1</td>
<td>997</td>
<td>1598</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1920758R6</td>
<td>1306</td>
<td>1692</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1957710F6</td>
<td>1472</td>
<td>1692</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2593853</td>
<td>2593853H1</td>
<td>1</td>
<td>252</td>
<td></td>
</tr>
<tr>
<td>807497H1</td>
<td>2</td>
<td>217</td>
<td></td>
<td></td>
</tr>
<tr>
<td>914002R6</td>
<td>284</td>
<td>740</td>
<td></td>
<td></td>
</tr>
<tr>
<td>889092R1</td>
<td>416</td>
<td>729</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2622354</td>
<td>2622354H1</td>
<td>3</td>
<td>266</td>
<td></td>
</tr>
<tr>
<td>2622992H1</td>
<td>1</td>
<td>246</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1595615F6</td>
<td>81</td>
<td>358</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2641377</td>
<td>2641377H1</td>
<td>126</td>
<td>369</td>
<td></td>
</tr>
<tr>
<td>434141H2</td>
<td>10</td>
<td>345</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SBCAO07049F3</td>
<td>126</td>
<td>599</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2674857</td>
<td>196</td>
<td>393</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1972373H1</td>
<td>1</td>
<td>270</td>
<td></td>
<td></td>
</tr>
<tr>
<td>470512R6</td>
<td>1486</td>
<td>1502</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1728547H1</td>
<td>1285</td>
<td>1508</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3013651F6</td>
<td>1423</td>
<td>1987</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SBCAO0694F3</td>
<td>819</td>
<td>385</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SBCAO0694F3</td>
<td>973</td>
<td>1198</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2758485</td>
<td>2758485H1</td>
<td>20</td>
<td>267</td>
<td></td>
</tr>
<tr>
<td>3095733H1</td>
<td>1</td>
<td>158</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1579055F6</td>
<td>291</td>
<td>771</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2763296</td>
<td>2763296H1</td>
<td>63</td>
<td>301</td>
<td></td>
</tr>
<tr>
<td>3480625F6</td>
<td>1</td>
<td>130</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SBCAO0702F3</td>
<td>63</td>
<td>687</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2779436</td>
<td>2779436H1</td>
<td>1</td>
<td>233</td>
<td></td>
</tr>
<tr>
<td>SBCAO0700F3</td>
<td>1</td>
<td>608</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2808528</td>
<td>2808528H1</td>
<td>25</td>
<td>335</td>
<td></td>
</tr>
<tr>
<td>261453F6</td>
<td>2</td>
<td>489</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SBCAO0702T3</td>
<td>1058</td>
<td>443</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2809230</td>
<td>2809230H1</td>
<td>409</td>
<td>630</td>
<td></td>
</tr>
<tr>
<td>221865H1</td>
<td>1</td>
<td>133</td>
<td></td>
<td></td>
</tr>
<tr>
<td>717706B6</td>
<td>396</td>
<td>691</td>
<td></td>
<td></td>
</tr>
<tr>
<td>958323R1</td>
<td>407</td>
<td>800</td>
<td></td>
<td></td>
</tr>
<tr>
<td>O307322F1</td>
<td>1366</td>
<td>623</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2816821</td>
<td>2816821H1</td>
<td>210</td>
<td>501</td>
<td></td>
</tr>
<tr>
<td>374666H1</td>
<td>1</td>
<td>307</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2816821F6</td>
<td>210</td>
<td>682</td>
<td></td>
<td></td>
</tr>
<tr>
<td>948722T6</td>
<td>959</td>
<td>527</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 269

<210> SEQ ID NO 1

<211> LENGTH: 88

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<220> FEATURE:

<221> NAME/KEY: misc.feature

<223> OTHER INFORMATION: Incyte Clone No: 441531

<400> SEQUENCE: 1

```
Met Ser Trp Trp Leu Cys Leu Pro Leu Gly Leu Phe Gly Ser Cys Leu
 1     5     10    15

Ala Pro Ala Ala Ala Ala Ala Leu Ser Glu Phe Thr Gln Glu Gln His
```
Asp Gly Ala Gln Pro Ser Pro Lys Cys Leu Ala Gln Glu Leu Gly Asp
35  40  45

Ala Trp Thr Ile Gln Ile Glu Ala Asn Trp Tyr Arg Ala Val Asn
50  55  60

Thr Asn Gln Arg Gly Lys Leu Leu Ala Ser Glu Thr Trp Lys Gly Arg
65  70  75  80

Arg Asn Thr Phe Phe Phe Leu Pro
85

<210> SEQ ID NO 2
<211> LENGTH: 128
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 632860

<400> SEQUENCE: 2

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

Cys Ser Phe Met Gly Pro Gln Trp Ile Leu Gln Phe Cys Ser Trp Leu
Cys Ser Phe Met Gly Pro Gln Trp Ile Leu Gln Phe Cys Ser Trp Leu
20  25  30

Glu Pro Arg Gln Leu Arg Ser Trp Ser Trp Thr Glu Pro Pro Phe Thr Leu
Glu Pro Arg Gln Leu Arg Ser Trp Ser Trp Thr Glu Pro Pro Phe Thr Leu
35  40  45

Leu Asp Ser Leu Gly Leu Arg Ala Ala Gln Asp Ser Cys Ser Phe Thr
Leu Asp Ser Leu Gly Leu Arg Ala Ala Gln Asp Ser Cys Ser Phe Thr
50  55  60

Thr Leu Val Pro Leu Thr Leu Asp Ser Ser Phe Met Thr Val Asn Val
Thr Leu Val Pro Leu Thr Leu Asp Ser Ser Phe Met Thr Val Asn Val
65  70  75  80

Val Pro Phe Val Trp Thr Ser Ser Phe Arg Ala Phe Gin Tyr Pro
Val Pro Phe Val Trp Thr Ser Ser Phe Arg Ala Phe Gin Tyr Pro
85  90  95

Val Thr Ser Pro Cys Arg Thr Lys Asn Thr Pro Leu Leu Ile Asp Gly
Val Thr Ser Pro Cys Arg Thr Lys Asn Thr Pro Leu Leu Ile Asp Gly
100 105 110

Val Thr Arg Ile Gln Ala Thr Trp Pro Glu Ala Arg Ser Gin His Glu
Val Thr Arg Ile Gln Ala Thr Trp Pro Glu Ala Arg Ser Gin His Glu
115 120 125

<210> SEQ ID NO 3
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 670010

<400> SEQUENCE: 3

Met Gly Leu Leu Leu Val Leu Phe Leu Ser Leu Leu Leu Pro Val Ala
Met Gly Leu Leu Leu Val Leu Phe Leu Ser Leu Leu Leu Pro Val Ala
1  5  10  15

Tyr Thr Ile Met Ser Leu Pro Pro Ser Phe Asp Cys Gly Pro Phe Arg
Tyr Thr Ile Met Ser Leu Pro Pro Ser Phe Asp Cys Gly Pro Phe Arg
20  25  30

Cys Arg Val Ser Val Ala Arg Glu His Leu Pro Ser Arg Gly Ser Leu
Cys Arg Val Ser Val Ala Arg Glu His Leu Pro Ser Arg Gly Ser Leu
35  40  45

Leu Arg Gly Pro Arg Pro Arg Ile Pro Val Leu Val Ser Cys Gin Pro
Leu Arg Gly Pro Arg Pro Arg Ile Pro Val Leu Val Ser Cys Gin Pro
50  55  60

Val Lys Gly His Gly Thr Leu Gly Glu Ser Pro Met Pro Phe Lys Arg
Val Lys Gly His Gly Thr Leu Gly Glu Ser Pro Met Pro Phe Lys Arg
65  70  75  80

Val Phe Cys Gin Asp Gly Asn Val Arg Ser Phe Cys Val Cys Ala Val
His Phe Ser Ser His Gln Pro Pro Val Ala Val Glu Cys Leu Lys

85 90 95

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

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

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

Glu Asn Ser Ser Phe Val Val Ser Gln Arg Gly Asn Leu Ile Val Phe
35 40 45

Gly Gly Gln Lys Lys Ala Thr Phe Arg Tyr His Phe Tyr Leu Asp Arg
50 55 60

Met Pro Phe Tyr Ser Gln Ile Ser Val Tyr Phe Val Asn Gly Phe Arg
65 70 75 80

Val Asn Gly Tyr Leu Cys Asn Asn
85

<210> SEQ ID NO 7
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 962390

<400> SEQUENCE: 7

Met Gly Arg Pro Leu Leu Leu Leu Leu Leu Leu Gln Pro Pro 1 5 10 15

Ala Phe Leu Gln Pro Gly Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
20 25 30

Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
35 40 45

Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Ile Val
50 55 60

Pro Asn Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
65 70 75 80

Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
85 90 95

Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile
100 105 110

Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Asp Val Glu
115 120 125

Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly
130 135 140

Thr Lys Leu Thr Ile Thr Glu Ala Val Thr Thr Thr Thr Thr Arg
145 150 155 160

Pro Ser Ser Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys
165 170 175

Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val
180 185 190

Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
195 200 205

Leu Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro Ser
210 215 220

Ser Asp Phe
225

<210> SEQ ID NO 8
<211> LENGTH: 198
<212> TYPE: PRT
<210> SEQ ID NO: 9
<211> LENGTH: 65
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1259405

<400> SEQUENCE: 9

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

<210> SEQ ID NO: 10
<211> LENGTH: 154
<212> TYPE: PRT
Met Leu Pro Val Val Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser  
145  150  155  160

Tyr Lys Ser Pro Val Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile  
165  170  175

Ser Thr Glu Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile  
180  185  190

Glu Lys Pro Glu Ser Thr Lys His Gln Arg Val Gly Tyr Asp Ala Phe  
195  200  205

Glu Lys Asn Leu Val Leu Ile Thr Met His Arg His Phe  
210  215  220

225  230  235

<210> SEQ ID NO 12
<211> LENGTH: 225
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<222> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 1316219

<400> SEQUENCE: 12

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

Asn Val Ala Cys Pro Pro Pro Pro Val Glu Gly Gln Gln Lys Asp Leu  
20  25  30

Lys Trp Asn Leu Ala Val Ile Gln Leu Phe Ser Ala Glu Gly Met Asp  
35  40  45

Thr Phe Ile Arg Val Leu Gln Leu Asn Ser Ile Leu Thr Gln Pro  
50  55  60

Trp Arg Leu His Val Asp Met Gly Thr Thr Leu Thr His Arg Val Thr  
65  70  75  80

Ile Ser Thr Met Ala Arg Cys Thr Leu Thr Leu Leu Lys Thr Met Leu Thr  
85  90  95

Glu Leu Leu Arg Gly Gly Ser Phe Glu Phe Lys Asp Met Arg Val Pro  
100  105  110

Ser Ala Leu Val Thr Leu His Met Leu Leu Cys Ser Ile Pro Leu Ser  
115  120  125

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

Ile Leu Leu Thr Phe Thr Gln Gly Val Asn Glu Leu Thr Ile Ser  
145  150  155  160

Glu Glu Thr Leu Ala Asn Thr Trp Ser Leu Met Leu Lys Glu Val  
165  170  175

Leu Ser Ser Ile Leu Lys Val Pro Glu Gly Phe Phe Ser Gly Leu Ile  
180  185  190

Leu Leu Ser Glu Leu Leu Pro Leu Pro Leu Pro Met Gln Thr Thr Gln  
195  200  205

Val Ser Leu Pro Tyr Asn Met His Leu Ile Asn Asp Cys Ser Asn Thr  
210  215  220

Phe  
225

<210> SEQ ID NO 13
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1329031

<400> SEQUENCE: 13

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

<210> SEQ ID NO 14
<211> LENGTH: 253
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1483050

<400> SEQUENCE: 14

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

Ala Gly Ile Glu Leu Leu His Gln Lys Leu Glu Leu Pro Asp Asn Val 195 200 205

Ser Gly Glu Phe Gly Trp Ser Phe Cys Leu Ala Cys Val Ser Ala Pro 210 215 220

Leu Gln Phe Met Ala Ser Ala Leu Phe Ile Trp Ala Ala His Thr Asn 225 230 235 240

Arg Lys Glu Tyr Thr Leu Met Lys Ala Tyr Arg Val Ala 245 250

<210> SEQ ID NO 15
<211> LENGTH: 171
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1514160

<400> SEQUENCE: 15

Met Ser Leu Pro Ile Pro Trp Leu Ser Leu Pro Pro Cys Pro Ile Leu 1 5 10 15

Gly Gln Pro Ala Gly Leu Leu Leu Trp Leu Phe Arg Pro Phe Ser Gln 20 25 30

Cys Cys Gln Cys Pro Trp Glu Gly Arg Ala Ser Leu Arg His Pro Asn 35 40 45

Gly Pro Ser Gly Cys Arg Glu Ala Glu Ala Trp Pro Gln Arg Ser Leu 50 55 60

Leu Arg Gln Gln Leu Gln Gln Ala His Pro Leu Pro Thr Leu Pro Thr 65 70 75 80

Pro Glu Arg Leu Pro Gln Met Leu Phe Pro Ser Ser Ser Ser Ser Lys 85 90 95

Pro Phe Ser Leu Leu Ser Leu Thr Ile Trp Ala Arg Leu Val Gly Arg 100 105 110

Leu Thr Asn Arg Ile Cys Pro Val Pro Pro Gly Ser Val Ala Ser Ser 115 120 125

Met Ser Leu Glu Ala Gly Arg Cys Gly Asn Pro Val Val Leu Pro Gln 130 135 140

Pro Met Pro Pro Gly Leu Leu Cys Met Asn Glu Cys Ser Leu Val Pro 145 150 155 160

Gly Leu Gly Arg Gly Gln Val Asn Ser Arg Val 165 170

<210> SEQ ID NO 16
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1603403

<400> SEQUENCE: 16

Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Leu Gly Ser 1 5 10 15

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

<210> SEQ ID NO 17
<211> LENGTH: 71
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 1652303
<400> SEQUENCE: 17
Met Lys Leu Leu Ser Cys Leu Phe Leu Lys Ala Pro Leu Tyr Pro
1   5  10  15
Thr Leu Cys Ser Lys Asp Pro Arg Ala Gly His Ser Leu Ile Cys Gly
20  25  30
Gln Ala Gly Gln Ile Pro Glu Ala Gln Leu Gly Phe Ser Ser Asp Phe
35  40  45
Lys Leu Cys Trp Cys Trp Asp Gln Gln Lys Ala Asn Val Gln Pro Thr
50  55  60
His Arg Thr Val Arg Gly Leu
65  70

<210> SEQ ID NO 18
<211> LENGTH: 188
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 1693358
<400> SEQUENCE: 18
Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu Pro
1   5  10  15
Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu Tyr Phe
20  25  30
Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr Ala Thr Pro
35  40  45
Ala Lys Asp Phe Gly Ile Phe His Thr Arg Tyr Glu Gln Ile His
50  55  60
Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly Glu Leu Ser Asn Gly
65  70  75  80
Phe Phe Ile Gln Asp Gln Ile Ala Leu Val Glu Arg Gly Cys Ser
85  90
Phe Leu Ser Lys Thr Arg Val Val Glu His Gly Gly Arg Ala Val
100 105 110
Ile Ile Ser Asp Asn Ala Val Asp Ser Phe Tyr Val Glu Met
115 120 125
Ile Glu Asp Ser Thr Gln Arg Thr Ala Asp Ile Pro Ala Leu Phe Leu
130 135 140
Leu Gly Arg Asp Gly Tyr Met Ile Arg Arg Ser Leu Glu Gln His Gly
145 150 155 160
Leu Pro Trp Ala Ile Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro

1.65 170 175

Thr Phe Glu Leu Leu Gln Pro Pro Trp Thr Phe Trp

180 185

SEQ ID NO 19
LENGTH: 80
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte Clone No: 1707711

SEQ ID NO 20
LENGTH: 80
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte Clone No: 1738735

SEQ ID NO 21
LENGTH: 84
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte Clone No: 1749147

Met Ile Asp Leu Trp Leu Pro Ala Leu Phe Val Leu Val Ala Leu Glu

1 5 10 15

Ser Leu Leu Ser Pro Cys Pro Gly Thr Ser Thr Leu Thr Arg

20 25 30

Thr Phe Phe Pro Ser Leu Val Ser Cys Val Gln Val Pro Phe Ser Trp

35 40 45

Ile Pro Cys Leu Glu Cys Phe Leu Ile Tyr Phe Leu Ile Leu Ala Glu

50 55 60

Asp Val Leu Gln Leu Phe Ser Gly Asn Ala Asn Met Gln Val Asn Gln

65 70 75 80

Met Ile Asp Leu Trp Leu Pro Ala Leu Phe Val Leu Val Ala Leu Glu

1 5 10 15

Ser Leu Leu Ser Pro Cys Pro Gly Thr Ser Thr Leu Thr Arg

20 25 30

Thr Phe Phe Pro Ser Leu Val Ser Cys Val Gln Val Pro Phe Ser Trp

35 40 45

Ile Pro Cys Leu Glu Cys Phe Leu Ile Tyr Phe Leu Ile Leu Ala Glu

50 55 60

Asp Val Leu Gln Leu Phe Ser Gly Asn Ala Asn Met Gln Val Asn Gln

65 70 75 80

SEQ ID NO 21
LENGTH: 84
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte Clone No: 1749147

SEQ ID NO 21
LENGTH: 84
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte Clone No: 1749147

Met Gln Arg Pro Phe Leu Ser Val Pro Cys Leu Leu Leu Leu Pro Ala

1 5 10 15

Arg Val Val Trp Gly Cys Trp Cys Phe Leu Pro Gly Glu Asp Gly Gly

20 25 30

Gly Cys Pro Thr Pro Ser Ser Gly Arg Ile Lys Leu Leu Gln Gln Cys
Leu Leu His Pro Ser Leu Arg Ser Ile Thr Val Ser Arg Arg Ser Ala
50  55  60

Gln Leu Leu Cys Arg Leu Lys Leu Gln Asn His Ile Pro Lys Val Pro
65  70  75  80

Gly Lys Asn Val

<210> SEQ ID NO 22
<211> LENGTH: 171
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1817722

<400> SEQUENCE: 22

Met His Met Ile Leu Lys Val Leu Thr Thr Ala Leu Leu Leu Gln Ala
1  5  10  15

Ala Ser Ala Leu Ala Asn Tyr Ile His Phe Ser Ser Tyr Ser Lys Asp
20  25  30

Gly Ile Gly Val Pro Phe Met Gln Ser Leu Ala Gln Phe Phe Asp Ile
35  40  45

Ala Ser Gln Ile Gln Met Leu Tyr Leu Leu Leu Ser Leu Cys Met Gly
50  55  60

Trp Thr Ile Val Arg Met Lys Ser Ser Gln Ser Arg Pro Leu Gln Trp
65  70  75  80

Asp Ser Thr Pro Ala Ser Thr Gly Ile Ala Val Phe Ile Val Met Thr
85  90  95

Gln Ser Val Leu Leu Leu Trp Gln Phe Glu Asp Ile Ser His His
100 105 110

Ser Tyr His Ser His His Asn Leu Ala Gly Ile Leu Leu Ile Val Leu
115 120 125

Arg Ile Cys Leu Ala Leu Ser Leu Gly Cys Gly Leu Tyr Gln Ile Ile
130 135 140

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

Lys Val Trp Val Trp Lys Glu Asn Gly Leu Phe
165 170

<210> SEQ ID NO 23
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1831290

<400> SEQUENCE: 23

Met Ser Ser Gly Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val
1  5  10  15

Leu Leu Gly Val Ala Ala Ser Leu Cys Val Arg Cys Ser Arg Pro Gly
20  25  30

Ala Lys Arg Ser Glu Lys Ile Tyr Gln Gln Arg Ser Leu Arg Glu Asp
35  40  45

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

<210> SEQ ID NO 24
<211> LENGTH: 311
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 1831477
<400> SEQUENCE: 24
 Met Gly Val Pro Thr Ala Pro Ala Gly Ser Trp Arg Trp Gly Ser 1 5 10 15
 Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val Ala Ala 20 25 30
 Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gln 35 40 45
 Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His 50 55 60
 Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val 65 70 75 80
 Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Glu Aep 85 90 95
 Leu His Leu His Gly Gly His Gln Ala Ala Asn Thr Ser His Asp 100 105 110
 Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp His His Gly Asn 115 120 125
 Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Ser Gly Leu Tyr 130 135 140
 Cys Cys Leu Val Val Glu Ile Arg His His Ser Glu His Arg Val 145 150 155 160
---continued

His Gly Ala Met Glu Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser 165 170 175
Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile Thr 180 185 190
 Ala Ala Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu 195 200 205
Pro Leu Ile Leu Leu Val Leu Tyr Lys Gln Arg Gln Ala Ala Ser Asn 210 215 220
 Arg Arg Ala Gln Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile 225 230 235 240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu 245 250 255
 Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro Ser 260 265 270
Glu Ser Gly Arg His Leu Ser Gln Pro Ser Thr Pro Leu Ser Pro 275 280 285
Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro Asp 290 295 300
 Ser Pro Asn Phe Glu Val Ile 305 310

<210> SEQ ID NO 25
<211> LENGTH: 57
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1841607

<400> SEQUENCES: 25

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

<210> SEQ ID NO 26
<211> LENGTH: 82
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1852391

<400> SEQUENCES: 26

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

Lys Asn

<210> SEQ ID NO 27
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1854555

<400> SEQUENCE: 27

Met Ala Gly Thr Val Leu Gly Val Gly Ala Gly Val Phe Ile Leu Ala
1  5 10 15

Leu Leu Trp Val Ala Val Leu Leu Cys Val Leu Leu Ser Arg Ala
20 25 30

Ser Gly Ala Ala Arg Phe Ser Val Ile Phe Leu Phe Gly Ala Val
35 40 45

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

Ala Pro Glu Val Glu Val Lys Ile Val Asp Asp Phe Phe Ile Gly Arg
65 70 75 80

Tyr Val Leu Leu Ala Phe Leu Ser Ala Ile Phe Leu Gly Gly Leu Phe
85 90 95

Leu Val Leu Ile His Tyr Val Leu Glu Pro Ile Tyr Ala Lys Pro Leu
100 105 110

His Ser Tyr
115

<210> SEQ ID NO 28
<211> LENGTH: 327
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1855755

<400> SEQUENCE: 28

Met Ala Glu Leu Pro Gly Pro Phe Leu Cys Gly Ala Leu Leu Gly Phe
1  5 10 15

Leu Cys Leu Ser Gly Leu Ala Val Glu Val Lys Val Pro Thr Glu Pro
20 25 30

Leu Ser Thr Pro Leu Gly Lys Thr Ala Glu Thr Cys Thr Tyr Ser
35 40 45

Thr Ser Val Gly Asp Ser Phe Ala Leu Glu Trp Ser Phe Val Gln Pro
50 55 60

Gly Lys Pro Ile Ser Glu Ser His Pro Ile Leu Tyr Phe Thr Asn Gly
65 70 75 80

His Leu Tyr Pro Thr Gly Ser Lys Ser Lys Arg Val Ser Leu Gln
85 90 95

Asn Pro Pro Thr Val Gly Val Ala Thr Leu Lys Thr Asp Val His
100 105 110

Pro Ser Asp Thr Gly Thr Tyr Leu Cys Gln Val Asn Aen Pro Pro Asp
115 120 125
-continued

```
Phe Tyr Thr Asn Gly Leu Gly Leu Ile Asn Leu Thr Val Leu Val Pro
  130 135 140
Pro Ser Asn Pro Leu Cys Ser Ser Gln Ser Gly Gin Thr Ser Val Gly Gly
  145 150 155 160
Ser Thr Ala Leu Arg Cys Ser Ser Ser Glu Gly Ala Pro Lys Pro Val
  165 170 175
Tyr Asn Trp Val Arg Leu Gly Thr Phe Pro Thr Pro Ser Pro Gly Ser
  180 185 190
Met Val Gin Asp Glu Val Ser Gly Gin Leu Ile Leu Thr Asn Leu Ser
  195 200 205
Leu Thr Ser Ser Gly Thr Tyr Arg Cys Val Ala Thr Asn Gin Met Gly
  210 215 220
Ser Ala Ser Cys Glu Leu Thr Leu Ser Val Thr Glu Pro Ser Gin Gly
  225 230 235 240
Arg Val Ala Gly Ala Leu Ile Gly Val Leu Leu Gly Val Leu Leu Leu
  245 250 255
Ser Val Ala Ala Phe Cys Leu Val Arg Phe Gin Lys Glu Arg Gly Lys
  260 265 270
Lys Pro Lys Glu Thr Tyr Gly Gly Ser Asp Leu Arg Glu Asp Ala Ile
  275 280 285
Ala Pro Gly Ile Ser Glu His Thr Cys Met Arg Ala Asp Ser Ser Lys
  290 295 300
Gly Phe Leu Glu Arg Pro Ser Ser Ala Ser Thr Val Thr Thr Thr Lys
  305 310 315 320
Ser Lys Leu Pro Met Val Val
  325
```

```
<210> SEQ ID NO 29
<211> LENGTH: 133
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 1861434
<400> SEQUENCES: 29

Met Arg Met Ser Leu Ala Gln Arg Val Leu Leu Thr Trp Leu Phe Thr
  1    5    10   15
Leu Leu Phe Leu Ile Met Leu Val Leu Lys Leu Asp Glu Lys Ala Pro
  20   25   30
Trp Asn Trp Phe Leu Ile Phe Ile Pro Val Trp Ile Phe Asp Thr Ile
  35   40   45
Leu Leu Val Leu Leu Ile Val Lys Met Ala Gly Cys Lys Ser Gly
  50   55   60
Phe Asp Pro Arg His Gly Ser His Asn Ile Lys Lys Ala Trp Tyr
  65   70   75   80
Leu Ile Ala Met Leu Leu Lys Leu Phe Cys Leu Ala Leu Cys Ala
  85   90   95
Lys Leu Glu Gin Phe Thr Thr Met Asn Leu Ser Tyr Val Phe Ile Pro
 100  105  110
Leu Trp Ala Leu Leu Ala Gly Ala Leu Thr Glu Gly Tyr Asn Val
 115  120  125
Phe Phe Val Arg Asp
 130
```
<210> SEQ ID NO 30
<211> LENGTH: 129
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1872334
<400> SEQUENCE: 30

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

<210> SEQ ID NO 31
<211> LENGTH: 472
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1877230
<400> SEQUENCE: 31

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

Gly Ile Thr Ala Glu Val Leu Val Thr Ser Phe Asp Glu Leu Gln
145
150
155
160
Arg Arg Ala Ser Glu Ala Arg Gly Lys Ile Val Val Tyr Asn Gln Pro
ARG 165
170
175
Tyr Ile Asn Tyr Ser Arg Thr Val Gln Tyr Arg Thr Gln Gly Ala Val
180
185
190
Glu Ala Ala Lys Val Gly Ala Leu Ala Ser Leu Ile Arg Ser Val Ala
195
200
205
Ser Phe Ser Ile Tyr Ser Pro His Thr Gly Ile Gln Gly Tyr Gln Gly
210
215
220
Val Gly Pro Lys Ile Pro Thr Ala Cys Ile Thr Val Gln Gly Ala Glu
225
230
235
240
Met Met Ser Arg Met Ala Ser His Gly Ile Lys Ile Val Ile Gln Leu
245
250
255
Lys Met Gly Ala Lys Thr Tyr Pro Asp Thr Asp Ser Phe Asn Thr Val
260
265
270
Ala Glu Ile Thr Gly Ser Lys Tyr Pro Gln Gln Val Val Leu Val Ser
275
280
285
Gly His Leu Asp Ser Trp Asp Val Gly Gin Gly Ala Met Asp Asp Gly
290
295
300
Gly Gly Ala Phe Ile Ser Trp Gly Ala Leu Ser Ile Lys Asp Leu
305
310
315
320
Gly Leu Arg Pro Lys Arg Thr Leu Arg Leu Val Leu Trp Thr Ala Glu
325
330
335
Glu Glu Gly Gin Gly Val Gly Ala Phe Gin Tyr Gin Leu His Lys Val
340
345
350
Asp Ile Ser Asp Tyr Ser Leu Val Met Glu Ser Asp Ala Gly Thr Phe
355
360
365
Leu Pro Thr Gly Leu Gln Phe Thr Gly Ser Glu Ala Arg Ala Ile
370
375
380
Met Glu Glu Val Met Ser Leu Gin Pro Leu Asn Ile Thr Gin Val
385
390
395
400
Leu Ser His Gly Glu Gly Thr Asp Ile Asn Phe Trp Ile Gin Ala Gly
405
410
415
Val Pro Gly Ala Ser Leu Asp Leu Tyr Gin Leu Met Asp Phe Phe
420
425
430
His His Ser His Gly Asp Thr Met Thr Val Met Asp Pro Lys Gin Met
435
440
445
Asn Val Ala Ala Ala Val Trp Ala Val Ser Tyr Val Val Ala Asp
450
455
460
Met Glu Glu Met Leu Pro Arg Ser
465
470
<210> SEQ ID NO 32
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 1877885
<400> SEQUENCE:
Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Leu Pro Val Ala
1
5
10
15
Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
20 25 30
Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
35 40 45
Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
50 55 60
Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
65 70 75 80
Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
85 90

<210> SEQ ID NO 33
<211> LENGTH: 92
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1889269
<400> SEQUENCE: 33
Met Asn Arg Pro Ser Ala Arg Asn Ala Leu Gly Asn Val Phe Val Ser
1  5 10 15
Glu Leu Leu Glu Thr Leu Ala Gln Leu Arg Glu Arg Glu Gln Val Arg
20 25 30
Val Leu Leu Phe Arg Ser Val Gly Val Lys Gly Val Phe Cys Ala Gly Ala
35 40 45
Asp Leu Lys Glu Arg Glu Glu Met Ser Glu Ala Glu Val Gly Val Phe
50 55 60
Val Gln Arg Leu Arg Gly Leu Met Asp Ile Gly Glu Asp Leu Gly
65 70 75 80
Val Gly Trp Arg Arg Gly Phe Gly Gly Pro Cys Arg
85 90

<210> SEQ ID NO 34
<211> LENGTH: 143
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1890243
<400> SEQUENCE: 34
Met Trp Ile Lys Gly Thr Met Lys Met Arg Gly Gly Lys Thr Ser Arg
1  5 10 15
Ser Ala Val Leu Pro Val Ala Gln Leu Thr Leu Ile Ala Ser Cys Phe
20 25 30
Pro Asn Ser Gln Thr Val Leu Gly Thr Gly Thr Leu Asp Val Glu
35 40 45
Ser Ser Pro Leu Ala Leu Thr Gly Leu Trp Ala Ser Pro Glu Ser
50 55 60
Leu Ser Leu Tyr Leu Val Thr Leu Cys Val Cys Pro Ala Leu Gln
65 70 75 80
Ser Cys Glu Gly Gln Ala Asp Val Thr Leu Ala Pro Cys Glu Ile
85 90 95
Phe Ile Pro Glu Thr Leu Ala Cys Glu Pro Phe Pro Ser Glu Trp Arg
100 105 110
---continued---

```
 Ala Leu Lys Gly Ala Ser Leu Glu Ser Ser Ser Val Leu Trp Val Ala  
  115 120 125
 Pro Cys Arg Trp Pro Leu Thr Leu Arg Cys Ser Arg Val His Leu  
  130 135 140

<210> SEQ ID NO 35
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1900433

<400> SEQUENCE: 35

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

<210> SEQ ID NO 36
<211> LENGTH: 560
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1909441

<400> SEQUENCE: 36

Met Ala Lys Lys Leu Thr Glu Met Ile Pro Leu Cys Asn His Pro  
  1   5   10   15
 Ala Ser Phe Val Lys Leu Phe Val Ala Leu Gly Pro Ile Ala Gly Pro  
  20  25  30
 Glu Glu Lys Gln Leu Lys Ser Thr Met Leu Met Ser Glu Asp  
  35  40  45
 Leu Thr Gly Glu Gln Ala Leu Ala Val Leu Gly Ala Met Gly Asp Met  
  50  55  60
 Glu Ser Arg Asn Ser Cys Leu Ile Lys Arg Val Thr Ser Val Leu His  
  65  70  75  80
 Lys His Leu Aep Gly Tyr Lys Pro Leu Glu Leu Leu Lys Ile Thr Gln  
  85  90  95
 Glu Leu Thr Phe Leu His Phe Gln Arg Lys Glu Phe Phe Ala Lys Leu  
 100 105 110
 Arg Glu Leu Leu Leu Ser Tyr Leu Lys Asn Ser Phe Ile Pro Thr Glu  
115 120 125
 Val Ser Val Leu Val Arg Ala Ile Ser Leu Leu Pro Ser Pro His Leu  
130 135 140
 Asp Glu Val Gly Ile Ser Arg Asp Ile Glu Ala Val Leu Pro Glu Cys Asp  
145 150 155 160
```
Leu Asn Asn Leu Ser Ser Phe Ala Thr Ser Val Leu Arg Trp Ile Gln
165 170 175
His Asp His Met Tyr Leu Asp Asn Met Thr Ala Lys Gln Leu Lys Leu 180 185 190
Leu Gln Lys Leu Asp His Tyr Gly Arg Gin Arg Leu Gin His Ser Asn 195 200 205
Ser Leu Asp Leu Leu Arg Lys Leu Lys Ser Leu Lys Gly Asn Thr 210 215 220
Phe Pro Glu Ser Leu Leu Glu Met Ile Ala Thr Leu Gin His Phe 225 230 235 240
Met Asp Asp Ile Asn Tyr Ile Asn Val Gly Glu Ile Ala Ser Phe Ile 245 250 255
Ser Ser Thr Asp Tyr Leu Ser Thr Leu Leu Leu Leu Asp Arg Ile Ala Ser 260 265 270
Val Ala Val Gln Gin Ile Glu Lys Ile His Pro Phe Thr Ile Pro Ala 275 280 285
Ile Ile Arg Pro Phe Ser Val Leu Asn Tyr Asp Pro Pro Gin Arg Asp 290 295 300
Glu Phe Leu Gly Thr Cys Val Gln His Leu Asn Ser Tyr Leu Gly Ile 305 310 315 320
Leu Asp Pro Phe Ile Leu Val Phe Leu Gly Phe Ser Leu Ala Thr Leu 325 330 335
Glu Tyr Phe Pro Glu Asp Leu Leu Lys Ala Ile Phe Asn Ile Lys Phe 340 345 350
Leu Ala Arg Leu Asp Ser Gin Leu Glu Ile Leu Ser Pro Ser Arg Ser 355 360 365
Ala Arg Val Gin Phe His Leu Met Glu Leu Asn Arg Ser Val Cys Leu 370 375 380
Glu Cys Pro Glu Phe Gin Ile Pro Trp Phe His Asp Arg Phe Cys Gin 385 390 395 400
Gln Tyr Asn Lys Gly Ile Gly Gly Met Asp Gly Thr Gin Gin Gin Gin 405 410 415
Phe Lys Met Leu Ala Glu Val Leu Gly Gly Ile Asn Cys Val Lys Ala 420 425 430
Ser Val Leu Thr Pro Tyr Tyr His Lys Val Asp Phe Glu Cys Ile Leu 435 440 445
Asp Lys Arg Lys Pro Leu Pro Tyr Gly Ser His Asn Ile Ala Leu 450 455 460
Gly Gln Leu Pro Glu Met Pro Trp Glu Ser Asn Ile Glu Ile Val Gly 465 470 475 480
Ser Arg Leu Pro Pro Gly Ala Glu Arg Ile Ala Leu Glu Phe Leu Asp 485 490 495
Ser Lys Ala Leu Cys Arg Asn Ile Pro His Met Lys Gly Lys Ser Ala 500 505 510
Met Lys Lys Arg His Leu Glu Ile Leu Gly Tyr Arg Val Ile Gin Gin 515 520 525
Ser Gin Phe Glu Trp Asn Ser Met Ala Leu Ser Thr Lys Asp Ala Arg 530 535 540
Met Asp Tyr Leu Arg Glu Cys Ile Phe Gly Glu Val Lys Ser Cys Leu 545 550 555 560
<210> SEQ ID NO 38
<211> LENGTH: 437
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1932647

<400> SEQUENCE: 38
Met Ser Ala Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro Leu 1 5 10 15
Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln His Val 20 25 30
Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys Asn Thr Ser 35 40 45
Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met Leu Ile Glu Ser 50 55 60
Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly Cys Thr Gln Ala Lys 65 70 75 80
<table>
<thead>
<tr>
<th></th>
<th>Aaa</th>
<th>Gln</th>
<th>Glu</th>
<th>Pro</th>
<th>Arg</th>
<th>Val</th>
<th>Thr</th>
<th>Glu</th>
<th>His</th>
<th>Arg</th>
<th>Met</th>
<th>Gly</th>
<th>Pro</th>
<th>Gly</th>
<th>Leu</th>
<th>Ser</th>
</tr>
</thead>
<tbody>
<tr>
<td>85</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>90</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>95</td>
</tr>
<tr>
<td>90</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>95</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>100</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>105</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>105</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>110</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>115</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>120</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>120</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>125</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>130</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>135</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>135</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>140</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>145</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>150</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>150</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>155</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>160</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>165</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>170</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>170</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>175</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>180</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>185</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>185</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>190</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>195</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>200</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>200</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>205</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>210</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>215</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>215</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>220</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>225</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>230</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>230</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>240</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>245</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>250</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>250</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>255</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>260</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>265</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>265</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>270</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>275</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>280</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>280</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>285</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>290</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>295</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>295</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>300</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>305</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>310</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>310</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>315</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>320</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>325</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>330</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>330</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>335</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>340</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>345</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>345</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>350</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>355</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>360</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>360</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>365</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>370</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>375</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>375</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>380</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>385</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>390</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>390</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>395</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>400</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>405</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>410</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>410</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>415</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>420</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>425</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>425</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>430</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>435</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<210> SEQ ID NO 39  
<211> LENGTH: 330  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2124245

<400> SEQUENCE: 39

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

<210> SEQ ID NO 40
<211> LENGTH: 148
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2132626
<400> SEQUENCE: 40

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

<210> SEQ ID NO 41
<211> LENGTH: 188
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2280639

<400> SEQUENCE: 41

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

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

<table>
<thead>
<tr>
<th>Met Gly Pro Ser Ser Cys Leu Leu Leu Ile Leu Ile Pro Leu Leu Gln</th>
<th>1 5 10 15</th>
</tr>
</thead>
<tbody>
<tr>
<td>-----------------------------------------------</td>
<td>--------</td>
</tr>
<tr>
<td>-----------------------------------------------</td>
<td>--------</td>
</tr>
<tr>
<td>-----------------------------------------------</td>
<td>--------</td>
</tr>
<tr>
<td>-----------------------------------------------</td>
<td>--------</td>
</tr>
<tr>
<td>-----------------------------------------------</td>
<td>--------</td>
</tr>
<tr>
<td>-----------------------------------------------</td>
<td>--------</td>
</tr>
<tr>
<td>-----------------------------------------------</td>
<td>--------</td>
</tr>
<tr>
<td>-----------------------------------------------</td>
<td>--------</td>
</tr>
<tr>
<td>-----------------------------------------------</td>
<td>--------</td>
</tr>
<tr>
<td>-----------------------------------------------</td>
<td>--------</td>
</tr>
<tr>
<td>Ile Ser Lys Lys Leu Ser Cys Ala Ser Val Lys Ser Gln Gly Arg Pro</td>
<td></td>
</tr>
<tr>
<td>--------------------------------------------------------------</td>
<td></td>
</tr>
<tr>
<td>50                55               60</td>
<td></td>
</tr>
<tr>
<td>Ser Ser Cys Pro Ala Gly Met Ala Val Thr Gly Cys Ala Cys Gly Tyr</td>
<td></td>
</tr>
<tr>
<td>65                70               75               80</td>
<td></td>
</tr>
<tr>
<td>Gly Cys Gly Ser Trp Asp Val Gln Leu Glu Thr Thr Cys His Cys Gln</td>
<td></td>
</tr>
<tr>
<td>85                90               95</td>
<td></td>
</tr>
<tr>
<td>Cys Ser Val Val Asp Trp Thr Thr Ala Arg Cys His Leu Thr</td>
<td></td>
</tr>
<tr>
<td>100               105              110</td>
<td></td>
</tr>
</tbody>
</table>

<210> SEQ ID NO 44
<211> LENGTH: 341
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2373227

<400> SEQUENCE: 44

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

<210> SEQ ID NO: 45
<211> LENGTH: 148
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2457682
<400> SEQUENCE: 45
Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala Ala 1 5 10 15
Leu Ala Ser Gly Ser Gin Gly Asp Arg Glu Pro Val Tyr Arg Asp Cys 20 25 30
Val Leu Gin Cys Glu Glu Gin Asn Cys Ser Gly Gly Ala Leu Asn His 35 40 45
Phe Arg Ser Arg Gin Pro Ile Tyr Met Ser Leu Ala Gly Trp Thr Cys 50 55 60
Arg Asp Cys Lys Tyr Glu Cys Met Trp Val Thr Val Gly Leu Tyr 65 70 75 80
Leu Gin Gly His Lys Val Pro Gin Phe His Gly Lys Trp Pro Phe 85 90 95
Ser Arg Phe Leu Phe Phe Gin Glu Pro Ala Ser Val Ala Ser Phe 100 105 110
Leu Asn Gly Leu Ala Ser Leu Val Met Leu Cys Arg Tyr Arg Thr Phe 115 120 125
Val Pro Ala Ser Ser Pro Met Tyr His Thr Cys Val Ala Phe Ala Trp 130 135 140
Leu Ser Gly Arg 145

<210> SEQ ID NO: 46
<211> LENGTH: 87
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2480426
<400> SEQUENCE: 46
Met Arg Pro Leu Leu Val Leu Leu Leu Leu Gly Leu Ala Ala Gly Ser 1 5 10 15
Pro Pro Leu Asp Asn Lys Ile Pro Ser Leu Cys Pro Gly Leu Pro 20 25 30
Gly Pro Arg Gly Asp Pro Gly Pro Arg Gly Glu Ala Gly Pro Ala Gly 35 40 45
Pro Thr Gly Leu Ala Gly Glu Cys Ser Val Pro Pro Arg Ser Ala Phe 50 55 60
Ser Ala Lys Arg Ser Glu Ile Arg Val Pro Pro Leu Ser Asp Ala Pro
65 70 75 80
Leu Pro Ser Thr Ala Cys Trp
85

SEQ ID NO 47
LENGTH: 383
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: misc_feature
OTHER INFORMATION: Incyte Clone No: 2503743
SEQUENCE: 47
Met Ala Gly Ile Pro Gly Leu Phe Leu Leu Phe Leu Leu Leu Cys
1 5 10 15
Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp
20 25 30
Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Aen Leu
35 40 45
Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Gln Val Ser Ser Ser
50 55 60
Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu
65 70 75 80
Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Aen Gly Ser Arg
85 90 95
Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly
100 105 110
Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg
115 120 125
Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe
130 135 140
Leu Leu Aen Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys
145 150 155 160
Thr Gly Thr Leu Val Ala Glu His Val Leu Thr Ala Ala His Cys
165 170 175
Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val
180 185 190
Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Lys Arg Gly Ala Aen Asp
195 200 205
Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val
210 215 220
Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Aen Asp
225 230 235 240
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Gln Lys Lys Pro His
245 250 255
Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
260 265 270
Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Aen Aep Arg Pro Gly
275 280 285
Aen Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Gln Thr Tyr Aep Leu
290 295 300
Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val
<table>
<thead>
<tr>
<th>305</th>
<th>310</th>
<th>315</th>
<th>320</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Gln Lys Trp Glu Arg Lys Ile 325</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro 340</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln 355</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly 370</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<210> SEQ ID NO: 48
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2537694

<400> SEQUENCE: 48

<table>
<thead>
<tr>
<th>1</th>
<th>5</th>
<th>10</th>
<th>15</th>
</tr>
</thead>
<tbody>
<tr>
<td>Met Leu Leu Pro Ala Leu Cys Ala Trp Leu Leu Trp Val Pro Trp Cys</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>20</td>
<td>25</td>
<td>30</td>
</tr>
<tr>
<td>Ser Tyr Gly Val Ser Gly Ser Gly Gly Leu Cys Cys Ser Val Cys 35</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>40</td>
<td>45</td>
<td></td>
</tr>
<tr>
<td>Arg Cys Leu Met Gly Ser Val Pro Arg Ile Phe Phe Ala Phe Tyr Pro 50</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>55</td>
<td>60</td>
<td></td>
</tr>
<tr>
<td>Ile Ala Trp Leu Pro Leu Pro Gly Ser Glu Gly Cys Trp Ser Arg Ser 65</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>70</td>
<td>75</td>
<td>80</td>
</tr>
<tr>
<td>Trp Glu Trp Pro Leu Val Glu Pro Ala Ser Cys Leu Val Cys Leu Cys 85</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>90</td>
<td>95</td>
<td></td>
</tr>
<tr>
<td>Phe Thr Phe Gly Val Leu Ser Gly Val Val Val Ala Val Lys 100</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>105</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<210> SEQ ID NO: 49
<211> LENGTH: 185
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2593853

<400> SEQUENCE: 49

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

<210> SEQ ID NO 50
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<222> OTHER INFORMATION: Incyte Clone No: 2622354

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

<210> SEQ ID NO 51
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<222> OTHER INFORMATION: Incyte Clone No: 2641377

<400> SEQUENCE: 51
Met Trp Leu Gly Ser Trp Leu Thr Ser Leu Leu Leu Ser Pro Tyr Gly
1 5 10 15
Ser Gly Trp Glu Lys Val Pro Cys Cys Val Thr Gly His Leu Arg Ser
20 25 30
Cys Ser Cys Cys Leu Leu Gly Ala Gly Val Glu Ser Asp His Phe
35 40 45
Ser Glu Gly Phe Phe Ser Glu Tyr Ser Ser Asp Val Leu Pro Trp Gly
50 55 60
Arg Arg Ser Phe Leu Pro Glu Gly Asp Ala Ser Leu Leu Ala Cys Glu
65 70 75 80
Cys Phe Leu His Leu Glu Val Val Trp Gly Glu Phe Cys Leu Leu Glu
Alanine tryptophan alanine glycine phenylalanine glutamic acid glycine serine methionine proline alanine proline serine cysteine arginine

Valine histidine tryptophan arginine valine alanine threonine cysteine alanine phenylalanine methionine serine

<210> SEQ ID NO 52
<211> LENGTH: 488
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2674857

<400> SEQUENCE: 52

Met alanine glycine lysine glycine serine glycine arginine arginine proline leucine leucine leucine leucine
1 5 10 15

Leucine valine alanine valine alanine threonine valine histidine leucine isoleucine cysteine proline tyrosine threonine lysine
20 25 30

Valine glutamic acid serine phenylalanine asparagine leucine glutamine alanine threonine histidine alanine threonine leucine
35 40 45

Tyrosine glutamic acid aspartic acid glutamine tyrosine asparagine histidine leucine glutamic acid proline glycine valine valine
50 55 60

Proline arginine tryptophan phenylalanine proline valine isoleucine alanine valine serine proline
65 70 75 80

Alanine valine tyrosine valine serine leucine glutamic acid methionine serine lysine phenylalanine serine glutamine
85 90 95

Leucine isoleucine valine arginine valine glycine valine glycine valine isoleucine phenylalanine glycine leucine tryptophan
100 105 110

Threonine leucine glutamic acid valine arginine arginine histidine phenylalanine alanine methionine valine alanine threonine
115 120 125

Methionine phenylalanine cysteine tryptophan valine methionine glutamine phenylalanine histidine methionine phenylalanine tyrosine cysteine
130 135 140

Threonine arginine tryptophan leucine proline asparagine valine leucine proline valine leucine alanine
145 150 155 160

Leucine alanine tryptophan arginine histidine glutamine tryptophan alanine arginine isoleucine tryptophan leucine serine
165 170 175

Alanine phenylalanine isoleucine valine phenylalanine arginine valine glutamine leucine phenylalanine leucine glycine
180 185 190

Leucine leucine leucine alanine glycine arginine lysine valine serine valine arginine
195 200 205

Alanine leucine arginine alanine valine alanine glycine leucine cysteine glycine leucine threonine
210 215 220

Valine alanine asparagine serine tyrosine phenylalanine arginine glutamine leucine threonine proline glycine
225 230 235 240

Lysine valine tryptophan asparagine threonine valine asparagine lysine serine asparagine tryptophan glycine
245 250 255

Threonine proline leucine tryptophan tyrosine serine alanine proline arginine glycine leucine
260 265 270

Glycine cysteine serine leucine phenylalanine isoleucine proline glycine valine aspartic acid arginine threonine
275 280 285

Histidine arginine proline threonine valine alanine glycine phenylalanine methionine alanine tyrosine serine leucine
290 295 300
LEU PRO HIS LYS GLU LEU ARG PHE ILE TYR ALA PHE PRO MET LEU 305 310 315 320
ASN ILE THR ALA ALA ARG GLY SER TYR LEU LEU ASN ASN TYR LYS 325 330 335
LYS SER TRP LEU TYR LYS ALA GLY SER LEU LEU VAL ILE GLY HIS LEU 340 345 350
VAL VAL ASN ALA ALA TYR SER ALA THR ALA LEU TYR VAL SER HIS PHE 355 360 365 370 375 380
ASN TYR PRO GLY GLY VAL MET GLN ARG LEU HIS GLN LEU VAL PRO 370 375 380
PRO GLN THR ASP VAL LEU LEU HIS ILE ASP VAL ALA ALA GLN THR 385 390 395 400
GLY VAL SER ARG PHE LEU GLN VAL ASN SER ALA TRP ARG TYR ASP LYE 405 410 415
ARG GLU ASP VAL GLN PRO GLY THR GLY MET LEU ALA TYR THR HIS ILE 420 425 430
LEU MET GLU ALA ALA PRO GLY LEU ALA LEU TYR ARG ASP THR HIS 435 440 445
ARG VAL LEU ALA SER VAL VAL GLY THR THR GLY VAL SER LEU ASN LEU 450 455 460
THR GLN LEU PRO PRO PHE ASN VAL HIS LEU GLN THR LYS LEU VAL LEU 465 470 475 480
LEU GLU ARG LEU PRO ARG PRO SER 485

<210> SEQ ID NO 53
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2758485

<400> SEQUENCE: 53

MET SER PRO ARG ARG THR LEU PRO ARG PRO LEU SER LEU CYS LEU SER 1 5 10 15
LEU CYS LEU CYS LEU CYS ALA ALA ALA LEU GLY SER ALA GLN SER 20 25 30
GLY SER CYS ARG ASP LYS ASN CYS LYS VAL PHE SER GLN GIN 35 40 45
GLU LEU ARG LYS ARG LEU THR PRO LEU GLN TYR HIS VAL THR GLN GLU 50 55 60
LYS GLY THR GLU SER ALA PHE GLU GLU TYR THR HIS LYS ASP 65 70 75 80
PRO GLY ILE TYR LYS CYS VAL CYS GLY THR PRO LEU PHE LYS SER 85 90 95
GLU THR LYS PHE ASP SER GLY SER GLY TRP PRO SER PHE HIS ASP VAL 100 105 110
ILE ASN SER GLU ALA ILE THR PHE THR ASP PHE SER TYR GLY MET 115 120 125
HIS ARG VAL GLU THR SER CYS SER GLN CYS GLY ALA HIS LEU GLY HIS 130 135 140
ILE PHE ASP ASP GLY PRO ARG PRO THR GLY ARG TYR CYS ILE ASN 145 150 155 160
Ser Ala Ala Leu Ser Phe Thr Pro Ala Asp Ser Ser Gly Thr Ala Glu
165 170 175
Gly Gly Ser Gly Val Ala Ser Pro Ala Gln Ala Asp Lys Ala Asp Ser
180 185 190
Glu Ser Asn Gly Glu
195

<210> SEQ ID NO: 54
<211> LENGTH: 84
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2763296

<400> SEQUENCE: 54

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

<210> SEQ ID NO: 55
<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2779436

<400> SEQUENCE: 55

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

<210> SEQ ID NO: 56
<211> LENGTH: 140
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
OTHER INFORMATION: Incyte Clone No: 2808528

SEQUENCE: 56

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

SEQ ID NO 57
LENGTH: 265
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: misc_feature
OTHER INFORMATION: Incyte Clone No: 2809230

SEQUENCE: 57

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

<table>
<thead>
<tr>
<th></th>
<th>195</th>
<th>200</th>
<th>205</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phe</td>
<td>Gln</td>
<td>Lys</td>
<td>Tyr</td>
</tr>
<tr>
<td>Ser</td>
<td>Gly</td>
<td>Glu</td>
<td>Thr</td>
</tr>
<tr>
<td>Val</td>
<td>Gin</td>
<td>Glu</td>
<td>Arg</td>
</tr>
<tr>
<td>Gin</td>
<td>Lys</td>
<td>Lys</td>
<td>Lys</td>
</tr>
<tr>
<td>Arg</td>
<td>Ala</td>
<td>Leu</td>
<td>His</td>
</tr>
<tr>
<td>Leu</td>
<td>Glu</td>
<td>Leu</td>
<td>Glu</td>
</tr>
<tr>
<td>Trp</td>
<td>Lys</td>
<td>Gly</td>
<td>Arg</td>
</tr>
<tr>
<td>Leu</td>
<td>225</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lys</td>
<td>230</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gin</td>
<td>235</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Leu</td>
<td>240</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lys</td>
<td>245</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>250</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Leu</td>
<td>255</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Met</td>
<td>Ala</td>
<td>Leu</td>
<td>Leu</td>
</tr>
<tr>
<td>Ala</td>
<td>Leu</td>
<td>Leu</td>
<td>Leu</td>
</tr>
<tr>
<td>Pro</td>
<td>260</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Arg</td>
<td>265</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asn</td>
<td>270</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lys</td>
<td>275</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gin</td>
<td>280</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asp</td>
<td>285</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lys</td>
<td>290</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Arg</td>
<td>300</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asp</td>
<td>305</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lys</td>
<td>310</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gin</td>
<td>315</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asp</td>
<td>320</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lys</td>
<td>325</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Arg</td>
<td>330</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asn</td>
<td>335</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lys</td>
<td>340</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gin</td>
<td>345</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asp</td>
<td>350</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lys</td>
<td>355</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thr</td>
<td>360</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Met</td>
<td>Ala</td>
<td>Leu</td>
<td>Leu</td>
</tr>
<tr>
<td>Ala</td>
<td>Ala</td>
<td>Leu</td>
<td>Ala</td>
</tr>
<tr>
<td>Ser</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Leu</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Ser</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Ser</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Gly</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Leu</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Ser</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Asn</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Arg</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Lys</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Thr</td>
<td>Asp</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
<td>Ala</td>
</tr>
<tr>
<td>Thr</td>
<td>375</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Met</td>
<td>380</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>385</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>390</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>395</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>400</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>405</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>410</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>415</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>420</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>425</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>430</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>435</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>440</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>445</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>450</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>455</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>460</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>465</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>470</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>475</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>480</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>485</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>490</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>495</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>500</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>505</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>510</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>515</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>520</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>525</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>530</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>535</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>540</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>545</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>550</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>555</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>560</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>565</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>570</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>575</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>580</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>585</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>590</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>595</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>600</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>605</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>610</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>615</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>620</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>625</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>630</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>635</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>640</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>645</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>650</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>655</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>660</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>665</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>670</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>675</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>680</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>685</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>690</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>695</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>700</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>705</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>710</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>715</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>720</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>725</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>730</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>735</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>740</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>745</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>750</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>755</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>760</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>765</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>770</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>775</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>780</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>785</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>790</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>795</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>800</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>805</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>810</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>815</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>820</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>825</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>830</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>835</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>840</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>845</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>850</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>855</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>860</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>865</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>870</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>875</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>880</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>885</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>890</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>895</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>900</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>905</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>910</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>915</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>920</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>925</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>930</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>935</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>940</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>945</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>950</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>955</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>960</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>965</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>970</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>975</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>980</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>985</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>990</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>995</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>1000</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly Leu
245 250 255
Thr Leu Ala Phe Lys Ile
260

<210> SEQ ID NO 59
<211> LENGTH: 189
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2817268

<400> SEQUENCE: 59
Met Ala Leu Leu Ser Arg Pro Ala Leu Thr Leu Leu Leu Leu Leu Met
1   5   10   15
Ala Ala Val Val Arg Cys Gln Glu Gln Ala Gln Thr Thr Asp Trp Arg
20  25  30
Ala Thr Leu Lys Thr Ile Arg Asn Gly Val His Lys Ile Asp Thr Tyr
35  40  45
Leu Asn Ala Ala Leu Asp Leu Gly Gly Glu Asp Gly Leu Cys Gln
50  55  60
Tyr Lys Cys Ser Asp Gly Ser Lys Pro Phe Pro Arg Tyr Gly Tyr Lys
65  70  75  80
Pro Ser Pro Pro Asn Gly Cys Gly Ser Pro Leu Phe Gly Val His Leu
85  90  95
Asn Ile Gly Ile Pro Ser Leu Thr Lys Cys Cys Asn Gln His Asp Arg
100 105 110
Cys Tyr Glu Thr Cys Gly Lys Ser Lys Asn Asp Cys Asp Glu Glu Phe
115 120 125
Gln Tyr Cys Leu Ser Lys Ile Cys Arg Asp Val Gln Lys Thr Leu Gly
130 135 140
Leu Thr Gln His Val Gln Ala Cys Glu Thr Thr Val Glu Leu Leu Phe
145 150 155 160
Asp Ser Val Ile His Leu Gly Cys Lys Pro Tyr Leu Asp Ser Gln Arg
165 170 175
Ala Ala Cys Arg Cys His Tyr Glu Gly Lys Thr Asp Leu
180 185

<210> SEQ ID NO 60
<211> LENGTH: 257
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2923165

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

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

<210> SEQ ID NO 61
<211> LENGTH: 82
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2992192

<400> SEQUENCE: 61

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

<210> SEQ ID NO 62
<211> LENGTH: 202
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2994822

<400> SEQUENCE: 62
Met Ala Ala Pro Trp Arg Arg Trp Pro Thr Gly Leu Leu Ala Val Leu
   1  5  10  15
Arg Pro Leu Leu Thr Cys Arg Pro Leu Gln Gly Thr Thr Leu Gln Arg
   20  25  30
Asp Val Leu Leu Phe Glu His Asp Arg Gly Arg Phe Phe Thr Ile Leu
   35  40  45
Gly Leu Phe Cys Ala Gly Gln Gly Val Phe Trp Ala Ser Met Ala Val
   50  55  60
Ala Ala Val Ser Arg Pro Pro Val Pro Val Gln Pro Leu Asp Ala Glu
   65  70  75  80
Val Pro Asn Arg Gly Pro Phe Asp Leu Arg Ser Ala Leu Trp Arg Tyr
   85  90  95
Gly Leu Ala Val Gly Cys Gly Ala Ile Gly Ala Val Leu Val Gly Ala
  100 105 110
Gly Leu Leu Phe Ser Leu Arg Ser Val Arg Ser Val Leu Arg Ala
  115 120 125
Gly Gly Gln Gln Val Thr Leu Thr Thr His Ala Pro Phe Gly Leu Gly
  130 135 140
Ala His Phe Thr Val Pro Leu Lys Gln Val Ser Cys Met Ala His Arg
  145 150 155 160
Gly Glu Val Pro Ala Met Leu Pro Leu Lys Val Lys Gly Arg Arg Phe
  165 170 175
Tyr Phe Leu Leu Asp Lys Thr Gly His Phe Pro Asn Thr Lys Leu Phe
  180 185 190
Asp Asn Thr Val Gly Ala Tyr Arg Ser Leu
  195 200

<210> SEQ ID NO: 63
<211> LENGTH: 450
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220>
<222> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2992458
<400> SEQUENCE: 63
Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser Cys
   1  5  10  15
Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly Arg Ala
   20  25  30
Cys Ser Asn Pro Ser Phe Leu Arg Phe Glu Leu Asp Phe Tyr Gln Val
   35  40  45
Tyr Phe Leu Ala Leu Ala Asp Trp Leu Gln Ala Pro Tyr Leu Tyr
   50  55  60
Lys Leu Tyr Glu His Tyr Pro Leu Gln Gly Gln Ile Ala Ile Leu
   65  70  75  80
Tyr Val Cys Gly Leu Ala Ser Thr Val Leu Phe Gly Leu Val Ala Ser
   85  90  95
Ser Leu Val Asp Trp Leu Gly Arg Lys Asn Ser Cys Val Leu Phe Ser
  100 105 110
Leu Thr Tyr Ser Leu Cys Leu Thr Lys Leu Ser Gln Asp Tyr Phe
  115 120 125
Val Leu Leu Val Gly Arg Ala Leu Gly Gly Leu Ser Thr Ala Leu Leu
<table>
<thead>
<tr>
<th>130</th>
<th>135</th>
<th>140</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phe Ser Ala Phe Glu Ala Trp Tyr Ile His Glu His Val Glu Arg His</td>
<td>145</td>
<td>150</td>
</tr>
<tr>
<td>Asp Phe Pro Ala Glu Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe</td>
<td>165</td>
<td>170</td>
</tr>
<tr>
<td>Trp Asn His Val Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val</td>
<td>180</td>
<td>185</td>
</tr>
<tr>
<td>Ala Ser Trp Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile</td>
<td>195</td>
<td>200</td>
</tr>
<tr>
<td>Pro Leu Leu Ala Leu Ala Gly Ala Leu Ala Arg Asn Trp Gly Glu</td>
<td>210</td>
<td>215</td>
</tr>
<tr>
<td>Asn Tyr Asp Arg Glu Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu</td>
<td>225</td>
<td>230</td>
</tr>
<tr>
<td>Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Gly Thr Ile Gln</td>
<td>245</td>
<td>250</td>
</tr>
<tr>
<td>Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp Thr Pro</td>
<td>260</td>
<td>265</td>
</tr>
<tr>
<td>Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe Ser Ser Phe</td>
<td>275</td>
<td>280</td>
</tr>
<tr>
<td>Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg Ile Ala Thr Ser</td>
<td>290</td>
<td>295</td>
</tr>
<tr>
<td>Lys Arg Tyr His Leu Gln Pro Met His Leu Ser Leu Ala Val Leu</td>
<td>305</td>
<td>310</td>
</tr>
<tr>
<td>Ile Val Val Phe Ser Leu Phe Met Leu Thr Phe Ser Thr Ser Pro Gly</td>
<td>325</td>
<td>330</td>
</tr>
<tr>
<td>Gln Glu Ser Pro Val Glu Ser Phe Ile Ala Phe Leu Leu Ile Glu Leu</td>
<td>340</td>
<td>345</td>
</tr>
<tr>
<td>Ala Cys Gly Leu Tyr Phe Pro Ser Met Ser Phe Leu Arg Arg Lys Val</td>
<td>355</td>
<td>360</td>
</tr>
<tr>
<td>Ile Pro Glu Thr Glu Gln Ala Gly Val Leu Asn Trp Phe Arg Val Pro</td>
<td>370</td>
<td>375</td>
</tr>
<tr>
<td>Leu His Ser Leu Ala Cys Leu Gly Leu Leu Val Leu His Asp Ser Asp</td>
<td>385</td>
<td>390</td>
</tr>
<tr>
<td>Arg Lys Thr Gly Thr Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met</td>
<td>405</td>
<td>410</td>
</tr>
<tr>
<td>Val Met Ala Leu Leu Ala Val Gly Leu Phe Thr Val Val Arg His</td>
<td>420</td>
<td>425</td>
</tr>
<tr>
<td>Asp Ala Glu Leu Arg Val Pro Ser Pro Thr Glu Gly Pro Tyr Ala Pro</td>
<td>435</td>
<td>440</td>
</tr>
</tbody>
</table>

Glu Leu
450

<210> SEQ ID NO 64
<211> LENGTH: 322
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 3044710
<400> SEQUENCE: 64

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
1  5  10  15
<table>
<thead>
<tr>
<th>Thr</th>
<th>Arg</th>
<th>Leu</th>
<th>Leu</th>
<th>Val</th>
<th>Gln</th>
<th>Gly</th>
<th>Ser</th>
<th>Leu</th>
<th>Arg</th>
<th>Ala</th>
<th>Glu</th>
<th>Glu</th>
<th>Ser</th>
<th>Ile</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gln</td>
<td>Val</td>
<td>Ser</td>
<td>Cys</td>
<td>Arg</td>
<td>Ile</td>
<td>Met</td>
<td>Gly</td>
<td>Thr</td>
<td>Leu</td>
<td>Val</td>
<td>Ser</td>
<td>Lys</td>
<td>Lys</td>
<td>Ala</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asn</td>
<td>Gln</td>
<td>Gln</td>
<td>Leu</td>
<td>Asn</td>
<td>Phe</td>
<td>Thr</td>
<td>Glu</td>
<td>Ala</td>
<td>Lys</td>
<td>Glu</td>
<td>Ala</td>
<td>Cys</td>
<td>Arg</td>
<td>Leu</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gly</td>
<td>Leu</td>
<td>Ser</td>
<td>Leu</td>
<td>Ala</td>
<td>Gly</td>
<td>Asp</td>
<td>Gln</td>
<td>Val</td>
<td>Glu</td>
<td>Thr</td>
<td>Ala</td>
<td>Leu</td>
<td>Lys</td>
<td>Ala</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ser</td>
<td>Phe</td>
<td>Glu</td>
<td>Thr</td>
<td>Cys</td>
<td>Ser</td>
<td>Tyr</td>
<td>Gly</td>
<td>Trp</td>
<td>Val</td>
<td>Gly</td>
<td>Asp</td>
<td>Gly</td>
<td>Phe</td>
<td>Val</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ile</td>
<td>Ser</td>
<td>Arg</td>
<td>Ile</td>
<td>Ser</td>
<td>Pro</td>
<td>Asn</td>
<td>Pro</td>
<td>Lys</td>
<td>Cys</td>
<td>Gly</td>
<td>Lys</td>
<td>Asn</td>
<td>Gly</td>
<td>Val</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Val</td>
<td>Leu</td>
<td>Ile</td>
<td>Trp</td>
<td>Lys</td>
<td>Val</td>
<td>Pro</td>
<td>Val</td>
<td>Ser</td>
<td>Arg</td>
<td>Gln</td>
<td>Phe</td>
<td>Ala</td>
<td>Ala</td>
<td>Tyr</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tyr</td>
<td>Asn</td>
<td>Ser</td>
<td>Ser</td>
<td>Asp</td>
<td>Thr</td>
<td>Thr</td>
<td>Asn</td>
<td>Ser</td>
<td>Cys</td>
<td>Ile</td>
<td>Pro</td>
<td>Glu</td>
<td>Ile</td>
<td>Ile</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thr</td>
<td>Thr</td>
<td>Lys</td>
<td>Asp</td>
<td>Pro</td>
<td>Ile</td>
<td>Phe</td>
<td>Asn</td>
<td>Thr</td>
<td>Gln</td>
<td>Thr</td>
<td>Ala</td>
<td>Thr</td>
<td>Gln</td>
<td>Thr</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glu</td>
<td>Phe</td>
<td>Ile</td>
<td>Val</td>
<td>Ser</td>
<td>Asp</td>
<td>Ser</td>
<td>Thr</td>
<td>Tyr</td>
<td>Ser</td>
<td>Val</td>
<td>Ala</td>
<td>Ser</td>
<td>Pro</td>
<td>Tyr</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thr</td>
<td>Ile</td>
<td>Pro</td>
<td>Ala</td>
<td>Pro</td>
<td>Thr</td>
<td>Thr</td>
<td>Pro</td>
<td>Pro</td>
<td>Ala</td>
<td>Pro</td>
<td>Ala</td>
<td>Pro</td>
<td>Ser</td>
<td>Thr</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ile</td>
<td>Pro</td>
<td>Arg</td>
<td>Arg</td>
<td>Lys</td>
<td>Leu</td>
<td>Ile</td>
<td>Cys</td>
<td>Val</td>
<td>Thr</td>
<td>Glu</td>
<td>Val</td>
<td>Phe</td>
<td>Met</td>
<td>Glu</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thr</td>
<td>Ser</td>
<td>Thr</td>
<td>Met</td>
<td>Ser</td>
<td>Thr</td>
<td>Thr</td>
<td>Glu</td>
<td>Thr</td>
<td>Glu</td>
<td>Pro</td>
<td>Phe</td>
<td>Val</td>
<td>Phe</td>
<td>Glu</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>Phe</td>
<td>Lys</td>
<td>Asn</td>
<td>Glu</td>
<td>Ala</td>
<td>Ala</td>
<td>Gly</td>
<td>Phe</td>
<td>Gly</td>
<td>Gln</td>
<td>Val</td>
<td>Pro</td>
<td>Thr</td>
<td>Ala</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Leu</td>
<td>Val</td>
<td>Leu</td>
<td>Ala</td>
<td>Leu</td>
<td>Phe</td>
<td>Phe</td>
<td>Gly</td>
<td>Ala</td>
<td>Ala</td>
<td>Gly</td>
<td>Leu</td>
<td>Gly</td>
<td>Phe</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cys</td>
<td>Tyr</td>
<td>Val</td>
<td>Lys</td>
<td>Arg</td>
<td>Tyr</td>
<td>Val</td>
<td>Lys</td>
<td>Ala</td>
<td>Phe</td>
<td>Pro</td>
<td>Phe</td>
<td>Thr</td>
<td>Asn</td>
<td>Lys</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gln</td>
<td>Gln</td>
<td>Lys</td>
<td>Glu</td>
<td>Met</td>
<td>Ile</td>
<td>Glu</td>
<td>Thr</td>
<td>Lys</td>
<td>Val</td>
<td>Val</td>
<td>Lys</td>
<td>Glu</td>
<td>Lys</td>
<td>Ala</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asn</td>
<td>Asp</td>
<td>Ser</td>
<td>Asn</td>
<td>Pro</td>
<td>Asn</td>
<td>Glu</td>
<td>Glu</td>
<td>Ser</td>
<td>Lys</td>
<td>Thr</td>
<td>Asp</td>
<td>Lys</td>
<td>Asn</td>
<td>Pro</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glu</td>
<td>Glu</td>
<td>Ser</td>
<td>Lys</td>
<td>Ser</td>
<td>Pro</td>
<td>Ser</td>
<td>Lys</td>
<td>Thr</td>
<td>Thr</td>
<td>Val</td>
<td>Arg</td>
<td>Cys</td>
<td>Leu</td>
<td>Glu</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glu</td>
<td>Val</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<210> SEQ ID NO 65
<211> LENGTH: 104
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 3120415
<400> SEQUENCE: 65

Met | Lys | Leu | Ala | Ala | Leu | Leu | Gly | Leu | Cys | Val | Ala | Ala | Ser | Cys | Ser |
| 1  | 5   | 10  | 15  |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Ala | Ala | Phe | Leu | Val | Gly | Ser | Ala | Lys | Pro | Val | Ala | Gln | Pro | 25 |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 29 |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 30 |

| Glu | Val |
|     |     |
Val Ala Ala Leu Glu Ser Ala Ala Ala Gly Ala Gly Thr Leu Ala
35  40  
Aan Pro Leu Gly Thr Leu Aan Pro Leu Lys Leu Leu Leu Ser Ser Leu
50  55  60  
Gly Ile Pro Val Aan His Leu Ile Gly Gly Ser Gln Lys Cys Val Ala
65  70  75  80  
Glu Leu Gly Pro Gln Ala Val Gly Ala Val Lys Ala Leu Lys Ala Leu
85  90  95  
Leu Gly Ala Leu Thr Val Phe Gly
100  

<210> SEQ ID NO 66
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 126758

<400> SEQUENCE: 66
Met Lys Leu Val Thr Ile Phe Leu Leu Val Thr Ile Ser Leu Cys Ser
1  5  10  15
Tyr Ser Ala Thr Ala Phe Leu Ile Aan Lys Val Pro Leu Pro Val Asp
20  25  30  
Lys Leu Ala Pro Leu Pro Leu Asp Aan Ile Leu Pro Phe Met Asp Pro
35  40  
Leu Lys Leu Leu Leu Lys Thr Leu Gly Ile Ser Val Glu His Leu Val
50  55  60  
Glu Gly Leu Arg Lys Cys Val Aan Glu Leu Gly Pro Glu Ala Ser Glu
65  70  75  80  
Ala Val Lys Lys Leu Leu Glu Ala Leu Ser His Leu Val
85  90  

<210> SEQ ID NO 67
<211> LENGTH: 71
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 674760

<400> SEQUENCE: 67
Met Thr Ala Gly Gln Phe Pro Ala Leu Val Ser Leu Ala Leu Leu Leu
1  5  10  15
Asp Gly Gly Arg Arg Ala Ser Ala Arg Arg Aan Arg Gly His Leu Trp
20  25  30  
Val Phe Cys Thr Ser Phe Leu Leu Ala Pro Trp Glu Val Glu Asp Val
35  40  
Gly Trp Lys Lys Leu Asp Leu Pro Ser Ser Ser Ser Pro Ser
50  55  60  
Pro Lys Glu Leu Ala Leu Gln
65  70  

<210> SEQ ID NO 68
<211> LENGTH: 394
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1229438
<400> SEQUENCE: 68
Met Lys Arg Gln Asn Val Arg Thr Leu Ala Leu Ile Val Cys Thr Phe 1  5  10  15
Thr Tyr Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser Glu 20  25  30
Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu Leu 35  40  45
Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gln Gln Gln Gln Gln Arg 50  55  60
Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg Phe 65  70  75  80
 Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly Tyr 85  90  95
Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met Phe 100 105 110
Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser Leu 115 120 125
Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala Lys 130 135 140
Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met Val 145 150 155 160
Leu Ile Gly Phe Phe Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala 165 170 175
 Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr 180 185 190
Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu 195 200 205
Gln Lys Asp Gln Ala Leu Glu Thr Glu Tyr Val Ala Phe Ser 210 215 220
Phe Val Tyr Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu Asn 225 230 235 240
Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg 245 250 255
Asp Ala Glu His Arg Ala Leu Thr Arg Asn Gly Gln Ala Gly Gly 260 265 270
Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser Thr 275 280 285
 Ala Ala Ala Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val Leu 290 295 300
His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu Lys 305 310 315 320
Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser 325 330 335 340
Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Arg 340 345 350
Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro Arg 355 360 365
Ser Ala Ile Ser Ser Val Ser Thr Gly Leu His Ser Leu Ser Thr Phe 370 375 380
Arg Gly Leu Met Lys Arg Arg Ser Ser Val
385 390

<210> SEQ ID NO: 69
<211> LENGTH: 72
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1236935

<400> SEQUENCE: 69
Met Cys Pro Phe Phe Pro Leu Thr Ser Leu Ile Val Phe Leu Ile Leu
1 5 10 15
Phe Phe Lys Thr Ile Ala Ser Ser Gly Ser Gly Ser Cys Leu Gly
20 25 30
Leu Pro Lys Cys Trp Asp Tyr Arg Arg His Arg Ala Arg Pro Thr
35 40 45
Ile Val Phe Ser Lys His Val Tyr Thr Tyr Ser Met Arg Met Gln Ile
50 55 60
Glu Ile Ser Thr Asn Ile Ser Gln
65 70

<210> SEQ ID NO: 70
<211> LENGTH: 71
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1359283

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

<210> SEQ ID NO: 71
<211> LENGTH: 247
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1450703

<400> SEQUENCE: 71
Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu Leu
1 5 10 15
Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu Lys Val
20 25 30
Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg Glu Val Gly
35 40 45
-continued

Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His Ala Gly Arg Glu
50  55  60
Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met Gly Ser His Thr Gly
65 70 75 80
Lys Glu Leu Asp Gly Val Gln Gly Leu Asn His Gly Met Asp Lys
85 90 95
Val Ala His Glu Ile Asn His Gly Ile Gly Gln Ala Gly Lys Glu Ala
100 105 110
Glu Lys Leu Gly His Gly Val Asn Asn Ala Gly Gln Ala Gly Lys
115 120 125
Glu Ala Asp Lys Ala Val Gln Gly Phe His Thr Gly Val His Glu Ala
130 135 140
Gly Lys Glu Ala Glu Gly Leu Gly Glu Asn His Ala Asp
145 150 155 160
Gln Ala Gly Lys Glu Val Gly Lys Leu Gly Gln Gly Ala His His Ala
165 170 175
 Ala Gly Gln Ala Gly Lys Glu Gln Ala Asn Ala His Asn Gly Val Asn
180 190
Gln Ala Ser Lys Glu Ala Asn Glu Leu Asn Gly Aen His Gln Ser
195 200 205
Gly Ser Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser
210 215 220
Gly Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
225 230 235 240
Ser Val Ala Asn Ile Met Pro
245

<210> SEQ ID NO 72
<211> LENGTH: 73
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: OTHER INFORMATION: Incyte Clone No: 1910668
<400> SEQUENCE: 72

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

<210> SEQ ID NO 73
<211> LENGTH: 70
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: OTHER INFORMATION: Incyte Clone No: 1955143
<400> SEQUENCE: 73
Met Gly Arg Leu Arg Tyr Phe Phe Ser Leu Leu Leu Leu Arg Trp Gly

1  5  10  15

Gln Leu Leu Gly Ala Asp Glu Phe Cys Cys His Lys Ser Tyr Ile Ala

20  25  30

His Leu Val Cys Thr Glu Ser Ala Ile Leu Asn Pro Gly His Ala Leu

35  40  45

Glu Leu Tyr Lys Asn Leu Gln Val Ser Ile Leu Ser Pro Tyr Pro

50  55  60

Thr Asp Pro Ile His Leu

65  70

<210> SEQ ID NO: 74
<211> LENGTH: 67
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
   <221> NAME/KEY: misc_feature
   <223> OTHER INFORMATION: Incyte Clone No: 1961637

<400> SEQUENCE: 74

Met Met Phe Thr Ser Leu Ser Leu Ala Leu Pro Phe Leu Leu Gln Thr

1  5  10  15

Met Leu Cys Leu Arg Ala Leu Leu Ile Ala Val Pro His Gly His Asp

20  25  30

Trp Aan Arg Asp Ala Thr Ser Phe Tyr Thr Ser Thr Val Ser Trp Val

35  40  45

Lys Ser Phe Phe Leu Phe Val Leu Asp Gly Val Ser Leu Leu Leu Pro

50  55  60

Arg Leu Glu

65

<210> SEQ ID NO: 75
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
   <221> NAME/KEY: misc_feature
   <223> OTHER INFORMATION: Incyte Clone No: 1990762

<400> SEQUENCE: 75

Met Trp Pro Thr Thr Thr Ala Trp Ser Trp Val Gln Thr Leu Thr Leu

1  5  10  15

Ala Leu Leu Ile Ser Cys Val Thr Leu Gly Gln Leu Ile Thr Thr Leu

20  25  30

Gln Val Ser Phe Leu Ile Cys Glu Met Asp Val Ile Ile Gly Cys Asp

35  40  45

Glu Met Ile Pro Ser Glu Ser Leu Val Leu Leu Trp Pro Pro Leu

50  55  60

Leu Leu Leu Gly Glu Phe Trp Ile Trp Asn Pro Val Ser Arg Ile Leu

65  70  75  80

Phe Trp Leu Cys His Val Pro Ala Gly Gln Leu

85  90

<210> SEQ ID NO: 76
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<212> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 1994131

<400> SEQUENCE: 76

Met Aaa Glu Trp Trp Leu Leu Leu Leu Leu His Leu His Pro Pro Arg
    1    5      10     15
Val Ile Ser Pro Phe Trp Phe Ile Val Leu Thr Ala Cys Asp
    20   25     30
Asn Arg Lys Tyr Ile Leu Leu Arg Thr Val Pro Val Phe Ser Phe Pro
    35   40     45
Glu Asn Thr Tyr Phe Asp Val Gly
    50     55

<210> SEQ ID NO 77
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 1997745

<400> SEQUENCE: 77

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

<210> SEQ ID NO 78
<211> LENGTH: 54
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 2009035

<400> SEQUENCE: 78

Met Met Leu Gln Pro Val Asp Leu Leu Gln Ser Tyr Leu Leu Leu Leu
    1     5     10    15
Tyr Cys Trp Ser Phe Ser Leu Leu Phe Thr Leu Leu Cys Asn Ala Val
    20    25    30
Arg Asn Asp Phe Phe His Leu Leu Phe Ser Ile Tyr Trp Met Tyr Asn
    35    40    45
Leu Thr His Ser Lys His
    50

<210> SEQ ID NO 79
<211> LENGTH: 57
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2009152

<400> SEQUENCE: 79
Met Lys Phe Tyr Ala Val Leu Leu Ser Ile Cys Leu Leu Leu Ser Cys
1  5  10  15
Trp Cys Ala Cys His Val Arg Asp Cys Asn Leu Ile Cys Leu Phe Ser
20  25  30
Thr Val Lys Ala Ile Thr Arg Glu Leu Leu Gln Leu Pro Ser Tyr Val
35  40  45
Lys Arg Phe Phe Phe Asn Ser Leu Arg
50  55

<210> SEQ ID NO: 80
<211> LENGTH: 52
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2061752

<400> SEQUENCE: 80
Met Gln Arg Leu Gly Ala Pro Gly Thr Trp Gln Ala Ile Ser Lys
1  5  10  15
Cys Trp Leu Leu Leu Leu Ser Leu Pro Phe Ser Gln Ser Ile Ile
20  25  30
Ile Ser Leu Arg Ala Gly Thr Met Ser Tyr Leu Pro Leu Tyr Phe Pro
35  40  45
Gln Tyr Phe Pro
50

<210> SEQ ID NO: 81
<211> LENGTH: 64
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2061933

<400> SEQUENCE: 81
Met Lys Leu Leu Leu Leu Lys Leu Asp Phe Phe Ile Leu Leu Lys Gly Ser
1  5  10  15
Glu Glu Ser Arg Cys Leu Val Asp Val Gln Tyr Val Ile Phe Phe Leu
20  25  30
Ile Glu Cys Val His Leu Lys Ser Ser Leu Thr Phe Leu Glu Arg Leu
35  40  45
Leu Ser Ile Asn Asn Gly Ile Leu Leu Glu Lys Trp Phe Phe Lys Ser
50  55  60

<210> SEQ ID NO: 82
<211> LENGTH: 65
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2081422

<400> SEQUENCE: 82
Met Lys Pro Leu Ile Pro Phe Leu Pro Pro Pro Pro Leu Leu Pro Leu
1 5 10 15
Thr Phe Phe Leu Ser Ser Leu Leu Leu Ser Leu Pro Leu Cys Arg Ala Leu
20 25 30
Gly Thr Ser Gln Ala Val Pro Pro Leu Arg Ala Leu Ser Val Thr Asp
35 40 45
 Ala His Gly Ser Leu Leu Leu Leu His Pro Lys Thr Leu Ala Cys Pro Cys
50 55 60
Leu 65

<210> SEQ ID NO: 83
<211> LENGTH: 56
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2101278

<400> SEQUENCES: 83

Met Arg Ala Asp Arg Leu Leu Pro Ile Ser Ala Leu Cys Leu Leu Tyr
1 5 10 15
Thr Pro Gly Gly Ala Leu Glu Pro Ala Gln Val Gly Tyr Thr Ile Phe
20 25 30
Leu Aaa Ser Ile Trp Leu Pro Ala Tyr Phe Phe His Leu Phe Thr Val
35 40 45
Ile Ser Gly Val Phe Leu Phe Ile
50 55

<210> SEQ ID NO: 84
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2121353

<400> SEQUENCES: 84

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

<210> SEQ ID NO: 85
<211> LENGTH: 67
<212> SEQ ID NO: 86
<211> LENGTH: 62
<212> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2271935

<400> SEQUENCE: 86

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

<210> SEQ ID NO: 87
<211> LENGTH: 75
<212> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2295344

<400> SEQUENCE: 87

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

<210> SEQ ID NO: 88
<211> LENGTH: 80
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2303994

<400> SEQUENCE: 88

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

<210> SEQ ID NO 89
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2497805

<400> SEQUENCE: 89

Met Arg Pro Ala Arg Gly Leu Gly Pro Arg Cys Ser Asp Leu Asp Phe Gly
1 5 10 15
Leu Val Leu Ser Ser Trp Leu Arg Leu Ala Arg Cys Pro Leu Glu Ser
20 25 30
Ser Phe Gly Phe Ala Phe Phe Val Cys Leu Phe Ser Pro Asn Phe Cys
35 40 45
Gln Thr
50

<210> SEQ ID NO 90
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2646362

<400> SEQUENCE: 90

Met Trp Trp Ala Leu Cys Ser Met Leu Pro Leu Leu Leu Gly Cys Ala Cys
1 5 10 15
Ser Ser Gly Cys Trp Gly Ser Gly Pro Thr Pro Leu Ala Glu Pro
20 25 30
Thr Phe Leu Cys Val Ser Ser Arg Pro His Asn Pro Leu Ser Phe Leu
35 40 45
Ser Val Leu Pro Cys Ser Arg Gly Pro Gly Pro Ser Gly Leu Gln Gly
50 55 60
Asp Gly Ala Gly Leu Pro Ala Leu Gly Pro Leu Ser Cys Ala Cys
65 70 75 80
Leu Pro Ser Leu Leu Cys Asp Leu Gly Glu Arg Cys Pro Leu Trp
85 90 95
Ala Val Arg Ser Thr Gln Cys Leu Ile Ala Gly Lys Val Leu Gln
100 105 110
Asp Lys Val Arg Gly Tyr Asp Ile Lys Leu Leu Arg Tyr Leu Ser Val 195 200 205
Lys Tyr Ile Cys Asp Leu Met Val Glu Asn Lys Val Lys Phe Gly 210 215 220
Met Asn Val Thr Ser Ser Glu Val Asp Lys Ala Gln Arg Tyr Ala 225 230 235 240
Asp Phe Thr Leu Ser Ile Pro Tyr Pro Gly Cys Glu Phe Phe Lys 245 250 255
Glu Tyr Lys Asp Arg Asp Tyr Met Ala Glu Gly Leu Ile Phe Asn Trp 260 265 270
Lys Gln Asp Tyr Val Asp Ala Pro Leu Ser Ile Pro Asp Phe Leu Thr 275 280 285
His Ser Leu Asn Ile Asp Trp Ser Glu Tyr Gln Cys Trp Asp Leu Val 290 295 300
Gln Gln Thr Gln Asn Tyr Leu Leu Leu Ser Leu Val Asn Ser 305 310 315 320
Asp Asp Ser Gly Leu Leu Val His Cys Ile Ser Gly Trp Asp Arg 325 330 335
Thr Pro Leu Phe Ile Ser Leu Arg Leu Ser Leu Trp Ala Asp Gly 340 345 350
Leu Ile His Thr Ser Leu Lys Pro Thr Glu Ile Leu Tyr Leu Thr Val 355 360 365
Ala Tyr Asp Trp Phe Leu Phe Gly His Met Leu Val Asp Arg Leu Ser 370 375 380
Lys Gly Glu Glu Ile Phe Phe Cys Phe Asn Phe Leu Lys His Ile 385 390 395 400
Thr Ser Glu Glu Phe Ser Ala Leu Lys Thr Gln Arg Arg Lys Ser Leu 405 410 415
Pro Ala Arg Asp Gly Gly Phe Thr Leu Glu Asp Ile Cys Met Leu Arg 420 425 430
Arg Lys Asp Arg Gly Ser Thr Ser Leu Gly Ser Asp Phe Ser Leu 435 440 445
Val Met Glu Ser Ser Pro Gly Ala Thr Gly Ser Phe Thr Tyr Glu Ala 450 455 460
Val Glu Leu Val Pro Ala Gly Ala Pro Thr Glu Ala Ala Ala Ala 465 470 475 480
Ala Leu Ser Asp Arg Glu Thr Arg Leu Glu Val Arg Ser Ala Phe 485 490 495
Leu Ala Tyr Ser Ser Thr Val Gly Leu Arg Ala Val Ala Pro Ser 500 505 510
Pro Ser Gly Ala Ile Gly Gly Leu Leu Glu Gln Phe Ala Arg Gly Val 515 520 525
Gly Leu Arg Ser Ile Ser Ser Asn Ala Leu 530 535

<210> SEQ ID NO 93
<211> LENGTH: 59
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2831245
<400> SEQUENCE: 93
Met Glu Met Lys Gly Ser Arg Val Trp Leu Leu Leu Leu Phe Met Trp
1  5  10  15
Lys Ala Arg Pro Thr Phe Phe Gln Ser Cys Val Val Pro Phe Ile Leu
20 25 30
Ser Pro Gln Asn Cys Val Gln Thr His Ser Leu Gly Pro Gly Val Trp
35 40 45
Leu Gly Val Phe Pro Ser Gly Ser Leu His
50 55

<210> SEQ ID NO: 94
<211> LENGTH: 119
<212> TYPE: PRO
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 3116250

<400> SEQUENCE: 94
Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met Leu
1  5  10  15
Met Ser Met Val Ser Ser Leu Leu Leu Leu Val Arg Gly His
20 25 30
Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln
35 40 46
Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe
50 55 60
Met Thr Val Ser Gly Leu Pro Lys Gln Cys Pro Cys Asp His Phe
65 70 75 80
Lys Gly Asn Val Lys Thr Arg His Gln Arg His Arg Lys Pro
85 90 95
Asn Lys His Ser Arg Ala Cys Gln Gln Phe Leu Lys Gln Cys Gln Leu
100 105 110
Arg Ser Phe Ala Leu Pro Leu
115

<210> SEQ ID NO: 95
<211> LENGTH: 120
<212> TYPE: PRO
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 3129630

<400> SEQUENCE: 95
Met Ala Tyr Ser Thr Val Gln Arg Val Ala Leu Ala Ser Gly Leu Val
1  5  10  15
Leu Ala Leu Ser Leu Leu Leu Leu Phe Leu Ser Arg Gly Lys
20 25 30
Arg Gln Glu Pro Pro Pro Pro Trp Pro Gln Val Gln Arg Arg Phe Pro
35 40 45
Pro Met Met His His Gln Ala Pro Ser Asp Gly Gln Thr Pro Gly
50 55 60
Ala Arg Phe Gln Arg Ser His Leu Ala Ala Ala Phe Ala Lys Ala Lys
65 70 75 80
Gly Ser Gly Gly Ala Gly Gly Gly Gly Gly Ser Arg Gly Leu Met
Gly Gln Ile Ile Pro Ile Tyr Gly Phe Gly Ile Phe Leu Tyr Ile Leu
100 105 110
Tyr Ile Leu Phe Lys Val Ser Arg Ile Ile Leu Ile Ile Leu His Gln
115 120 125

<210> SEQ ID NO 96
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 007832

SEQUENCE: 96
Met Tyr Lys Leu Ala Ser Cys Cys Leu Leu Phe Ile Gly Phe Leu Asn
1 5 10 15
Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser Phe Gln
20 25 30
Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu Glu Leu Glu
35 40 45
Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu Gly Ala Glu Arg
50 55 60
Gly Asp Ile Leu Arg Lys Ala Asp Ser Ser Thr Asn Ile Phe Asn Pro
65 70 75 80
Arg Gly Asn Leu Arg Lys Phe Gln Asp Phe Ser Gly Gln Asp Pro Asn
85 90 95
Ile Leu Leu Ser His Leu Leu Ala Arg Ile Trp Lys Pro Tyr Lys Lys
100 105 110
Arg Glu Thr Pro Asp Cys Phe Trp Lys Tyr Cys Val
115 120

<210> SEQ ID NO 97
<211> LENGTH: 182
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1236968

SEQUENCE: 97
Met Trp Pro Leu Ser Ser Asp Ser Ser Trp Ser Leu Trp Ile Ser Thr
1 5 10 15
Gly Met Ala Pro Ala Pro Ser Ser Thr Arg Ser Phe Ser Glu Ser
20 25 30
Leu Lys Glu Lys Leu Val Arg Val Leu Glu Glu Asn Leu Ile Leu Ser
35 40 45
Glu Lys Ile Gln Gln Leu Glu Glu Gly Ala Ala Ile Ser Ile Val Ser
50 55 60
Gly Gln Ser His Thr Tyr Asp Leu His Lys Asn Glu Gln
65 70 75 80
Leu Thr Met Gln Val Ala Cys Leu Asn Gln Glu Leu Ala Gln Leu Lys
85 90 95
Lys Leu Glu Lys Thr Val Ala Ile Leu His Glu Ser Gln Arg Ser Leu
100 105 110
Val Val Thr Asn Glu Tyr Leu Leu Gln Gln Leu Asn Lys Glu Pro Lys
Gly Tyr Ser Gly Lys Ala Leu Leu Pro Pro Glu Lys Gly His Leu
115 120 125
Gly Arg Ser Ser Pro Phe Gly Lys Ser Thr Leu Ser Ser Ser Ser Pro
130 150 155 160
Val Ala His Glu Thr Gly Gln Tyr Leu Ile Gln Ser Val Leu Asp Ala
165 170 175
Ala Pro Glu Pro Gly Leu
180

<210> SEQ ID NO: 98
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 1334153

<400> SEQUENCE: 98

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

<210> SEQ ID NO: 99
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<211> NAME/KEY: misc.feature
<222> OTHER INFORMATION: Incyte Clone No: 1396975
<400> SEQUENCE: 99

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

<210> SEQ ID NO 100
<211> LENGTH: 148
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<222> OTHER INFORMATION: Incyte Clone No: 1501749
<400> SEQUENCE: 100

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

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

<210> SEQ ID NO 103
<211> LENGTH: 142
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 1661144

<400> SEQUENCE: 103
Met Gly Cys Leu Val Trp Gly Pro Ser Trp Pro Pro Leu Ser Leu Leu
1    5   10   15
Ala Ser Leu Leu His Ser Gly Ile Ala Gly Arg Cys Leu Leu Cys Leu
20  25   30
Phe Lys Gly Leu Ala Ala Ala Ser Leu Gln Ile Arg Asp Leu Ala
35  40   45
Ser Arg Leu Thr Thr Gly Pro Arg Thr Cys Arg Val Gln Pro Pro Pro
50  55   60
His Pro Gln Ser Ser Pro Pro Pro Gly Pro Gly Pro Gly Ala Glu Thr
65  70   75   80
Cys Arg Pro Leu Ser Arg Thr Val Gly Gly Val Cys Pro Ser Asp Trp
85  90   95
Pro Val Ser Trp Leu Leu Leu Pro Leu Pro Gln Val Val Thr Cys
100 105  110
Ser Cys Pro Arg Ile Lys Ala Arg Pro Glu Arg Thr Pro Glu Leu Leu
115 120  125
Cys Ala Trp Gly Gly Arg Gly Lys His Ser Gln Leu Val Ala
130 135  140

<210> SEQ ID NO 104
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 1685409

<400> SEQUENCE: 104
Met Glu Thr Gly Arg Leu Leu Ser Leu Ser Ser Leu Pro Leu Val Leu
1    5   10   15
Leu Gly Trp Glu Tyr Ser Ser Gln Thr Leu Asn Leu Val Pro Ser Thr
20  25   30
Ser Ile Leu Ser Phe Val Pro Phe Ile Pro Leu His Leu Val Leu Phe
35  40   45
Ala Leu Trp Tyr Leu Pro Val Pro His His Leu Tyr Pro Gln Gly Leu
50  55   60
Gly Asp His Ala Ala Glu Ala Glu Lys Gly Lys Arg Glu Glu Gly Gly
65  70   75   80
Thr Gln Val Ala Leu Trp Leu Arg Val Gln Pro Ser Cys Pro Ser Pro
85  90   95
Val  Cys  Leu  Glu  Pro  Val  Pro  Pro  Arg  Ser  Arg  Phe  Leu  Leu  
       100  105  110

<210> SEQ ID NO 105
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1731419

<400> SEQUENCE: 105

Met  Ser  Arg  Ala  Gly  Met  Leu  Gly  Val  Val  Cys  Ala  Leu  Leu  Val  Trp  
      1     5     10     15

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

 Leu  Cys  Thr  His  Pro  Trp  Ser  Leu  Arg  Cys  Glu  Ser  Phe  Cys  Arg  
     35    40    45

 Ser  Arg  Val  Thr  Ala  Cys  Leu  Pro  Ala  Pro  Ala  Pro  Ala  Pro  Trp  Leu  Pro  
     50    55    60

 Phe  Leu  Cys  Pro  Met  Leu  Phe  Ser  Asp  Arg  Asn  Pro  Val  Glu  Cys  His  
     65    70    75    80

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

 His  Tyr  Phe  Trp  His  Pro  Thr  Phe  Pro  Val  Lys  Ala  Asn  Cys  Leu  
    100   105   110

 Val  Ser  Phe  Cys  Pro  Thr  Thr  Thr  Val  
    115   120

<210> SEQ ID NO 106
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2650265

<400> SEQUENCE: 106

Met  Ala  Arg  Phe  Trp  Val  Cys  Val  Ala  Gly  Ala  Gly  Phe  Phe  Leu  Ala  
      1     5     10     15

 Phe  Leu  Val  Leu  His  Ser  Arg  Phe  Cys  Gly  Ser  Pro  Val  Leu  Arg  Asn  
     20    25    30

 Phe  Thr  Phe  Ala  Val  Ser  Trp  Arg  Thr  Glu  Lys  Ile  Leu  Tyr  Arg  Leu  
     35    40    45

 Asp  Val  Gly  Trp  Pro  Lys  His  Pro  Glu  Tyr  Phe  Thr  Gly  Thr  Thr  Phe  
     50    55    60

 Cys  Val  Ala  Val  Asp  Ser  Leu  Asn  Gly  Leu  Val  Tyr  Ile  Gly  Gln  Arg  
     65    70    75    80

 Gly  Asp  Asn  Ile  Pro  Lys  Ile  Leu  Val  Phe  Thr  Glu  Asp  Gly  Tyr  Phe  
     85    90   95

 Leu  Arg  Ala  Trp  Asn  Tyr  Thr  Val  Asp  Thr  Pro  His  Gly  Ile  Phe  Ala  
    100   105   110

 Ala  Ser  Thr  Leu  Tyr  Glu  Gln  Ser  Val  Trp  Ile  Thr  Asp  Val  Gly  Ser  
    115   120   125

 Gly  Met  Tyr  Ser  Asn  Ile  Tyr  
    130   135
<table>
<thead>
<tr>
<th>Position</th>
<th>Amino Acid</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Met Leu Met Ile Ile Ile Ile Glu Pro Phe Ser Val Leu Ile Leu Phe</td>
</tr>
<tr>
<td>1</td>
<td>Lys Ser Gly Ile Leu Ala Asp Phe Ala Leu Leu Leu Leu Ile Asn</td>
</tr>
<tr>
<td>5</td>
<td>Phe Phe Leu Val Ser Phe Phe Ala Tyr Pro Leu Phe Asp Asn Gln</td>
</tr>
<tr>
<td>10</td>
<td>Ile Asn Ser Arg Ser Met Asn Glu Ile Lys Asn Leu Gln Tyr Leu Pro</td>
</tr>
<tr>
<td>15</td>
<td>Arg Thr Ser Glu Pro Arg Glu Val Leu Phe Glu Asp Arg Thr Arg Ala</td>
</tr>
<tr>
<td>20</td>
<td>His Ala Asp His Val Gly Gln Gly Phe Asp Trp Gln Ser Thr Ala Ala</td>
</tr>
<tr>
<td>25</td>
<td>Val Gly Val Leu Lys Ala Val Gln Phe Gly Glu Trp Ser Asp Glu Pro</td>
</tr>
<tr>
<td>30</td>
<td>Arg Ile Thr Lys Asp Val Ile Cys Phe His Ala Glu Asp Phe Thr Asp</td>
</tr>
<tr>
<td>35</td>
<td>Val Val Gln Arg Leu Gln Leu Asp Arg His Glu Pro Pro Val Ser Gln</td>
</tr>
<tr>
<td>40</td>
<td>Cys Val Gln Trp Val Asp Glu Ala Lys Leu Asn Gln Met Arg Arg Glu</td>
</tr>
<tr>
<td>45</td>
<td>Gly Ile Arg Tyr Ala Arg Ile Glu Leu Cys Asp Asn Asp Ile Tyr Phe</td>
</tr>
<tr>
<td>50</td>
<td>Ile Pro Arg Asn Val Ile His Gln Phe Lys Thr Val Ser Ala Val Cys</td>
</tr>
<tr>
<td>55</td>
<td>Ser Leu Ala Thr His Ile Arg Leu Lys Glu Tyr His Pro Val Val Glu</td>
</tr>
<tr>
<td>60</td>
<td>Ala Thr Gln Asn Thr Glu Ser Asn Ser Asn Met Asp Cys Gly Leu Thr</td>
</tr>
<tr>
<td>65</td>
<td>Gly Lys Arg Glu Leu Glu Val Asp Ser Gln Cys Val Arg Ile Lys Thr</td>
</tr>
<tr>
<td>70</td>
<td>Glu Ser Glu Ala Cys Thr Glu Ile Gln Leu Thr Thr Ala Ser</td>
</tr>
<tr>
<td>75</td>
<td>Ser Ser Phe Pro Pro Ala Ser Leu Asn Leu Gln Gln Asp Glu Lys</td>
</tr>
<tr>
<td>80</td>
<td>Thr Gln Pro Ile Pro Val Leu Lys Val Glu Ser Arg Leu Asp Ser Asp</td>
</tr>
<tr>
<td>85</td>
<td>Gln Glu His Asn Leu Gln Glu His Ser Thr Thr Ser Val</td>
</tr>
</tbody>
</table>

<210> SEQ ID NO 100
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 3151073
<400> SEQUENCE: 108
Met Ser Phe Val Pro Gly Leu Leu Leu Cys Phe Val Leu Leu Leu Cys
  1      5      10      15
Val Ser Pro Val Tyr Leu Pro Ser Arg Ser Pro Ser Thr Phe Pro Ile
  20     25     30
Ser Glu Pro Leu Ser Phe Ile Gly Met Ser Ala Trp Pro Gln Cys Ser
  35     40     45
Pro Ile Tyr Ser Gln Thr Pro Gly Leu Ala Tyr Glu Pro Ser Ser Phe
  50     55     60
Pro Lys Arg Arg Tyr Trp Val Cys Thr Leu His Glu Ile Lys Trp Glu
  65     70     75     80
Cys Pro Arg Ser Arg Thr Ser Asp Ala Val His Ala Asn Lys Leu
  85     90     95
Gly Leu Pro Leu Lys Ile Ile
100

<210> SEQ ID NO 109
<br> LENGTH: 95
<br> TYPE: PRT
<br> ORGANISM: Homo sapiens
<br> FEATURE:
<br> NAME/KEY: misc_feature
<br> OTHER INFORMATION: Incyte Clone No: 3170095

<400> SEQUENCE: 109
Met Lys Phe Leu Leu Leu Val Leu Ala Ala Leu Gly Phe Leu Thr Glu
  1      5      10     15
Val Ile Pro Ala Ser Ala Gly Ser Lys Ser Val Ser Asn Thr Pro
  20     25     30
Gly Tyr Cys Arg Thr Cys Cys His Trp Gly Glu Thr Ala Leu Phe Met
  35     40     45
Cys Asn Ala Ser Arg Lys Cys Ala Ser Tyr Ser Phe Leu Pro Lys
  50     55     60
Pro Asp Leu Pro Gln Leu Ile Gly Asn His Trp Glu Ser Arg Arg
  65     70     75     80
Asn Thr Glu Arg Lys Asp Lys Gln Glu Thr Thr Val Thr Ser
  85     90     95

<210> SEQ ID NO 110
<br> LENGTH: 113
<br> TYPE: PRT
<br> ORGANISM: Homo sapiens
<br> FEATURE:
<br> NAME/KEY: misc_feature
<br> OTHER INFORMATION: Incyte Clone No: 3475168

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

<210> SEQ ID NO 113
<211> LENGTH: 200
<212> TYPE: PRF
<213> ORGANISM: Homo sapiens
<220> FEATURE: name/key: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 1003916

<400> SEQUENCE: 113
Met Ala Ser Ser Leu Thr Cys Thr Gly Val Ile Trp Ala Leu Leu Ser
  1    5     10     15
Phe Leu Cys Ala Ala Thr Ser Cys Val Gly Phe Phe Met Pro Tyr Trp
  20   25     30
Leu Trp Gly Ser Gin Leu Gly Gin Leu Ser Phe Gly Thr Phe Arg
  35   40     45
Arg Cys Ser Tyr Pro Val His Asp Glu Ser Arg Gin Met Met Val Met
  50   55     60
Val Glu Gly Cys Arg Tyr Ala Ser Phe Gin Glu Ile Pro Ser Ala
  65   70     75     80
Glu Trp Arg Ile Cys Thr Ile Val Thr Gly Leu Gly Cys Gly Leu Leu
  85   90
Leu Leu Val Ala Leu Thr Ala Leu Met Gly Cys Val Ser Asp Leu
 100  105    110
Ile Ser Arg Thr Val Gly Arg Val Ala Gly Gly Ile Gin Phe Leu Gly
115  120   125
Gly Leu Leu Ile Gly Ala Gln Ser Tyr Pro Leu Gly Trp Asp
130  135   140
Ser Glu Glu Val Arg Gin Thr Cys Gly Tyr Thr Ser Gly Gin Phe Asp
145  150   155   160
Leu Gly Lys Cys Glu Ile Gly Trp Ala Tyr Tyr Cys Thr Gly Ala Gly
165  170   175
Ala Thr Ala Ala Met Leu Leu Cys Thr Trp Leu Ala Cys Phe Ser Gly
180  185   190
Lys Lys Gin Lys His Tyr Pro Tyr
195  200
<210> SEQ ID NO 114
<211> LENGTH: 225
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2093492

<400> SEQUENCE: 114

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

<210> SEQ ID NO 115
<211> LENGTH: 155
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2108709

<400> SEQUENCE: 115

Met Ser Gly Leu Leu Ile Pro Leu Pro Gly Trp Val Leu Gly Pro
1  5  10    15
Leu Met Trp Ala Cys Arg Pro Pro Gln Asp Glu Pro Ser Gly Thr Asp
20  25  30
Pro Pro Pro Pro Arg Leu Gln Pro His His Val Ser Gly Leu Gly Leu
35  40  45
<table>
<thead>
<tr>
<th>Gly</th>
<th>Gln</th>
<th>Ala</th>
<th>Trp</th>
<th>Ala</th>
<th>Gln</th>
<th>Ser</th>
<th>Trp</th>
<th>Ala</th>
<th>Pro</th>
<th>Arg</th>
<th>Gly</th>
<th>Ser</th>
<th>Pro</th>
<th>Pro</th>
<th>Leu</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>50</td>
<td>55</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thr</td>
<td>Trp</td>
<td>Leu</td>
<td>Leu</td>
<td>Pro</td>
<td>Thr</td>
<td>Leu</td>
<td>Pro</td>
<td>Leu</td>
<td>Lys</td>
<td>Asp</td>
<td>Gly</td>
<td>Pro</td>
<td>Ala</td>
<td>Ala</td>
<td>Arg</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>65</td>
<td>70</td>
<td>75</td>
<td>80</td>
<td>85</td>
<td>95</td>
<td>95</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Leu</td>
<td>Pro</td>
<td>Pro</td>
<td>Pro</td>
<td>Pro</td>
<td>His</td>
<td>Thr</td>
<td>Thr</td>
<td>Leu</td>
<td>Gly</td>
<td>Gly</td>
<td>Leu</td>
<td>Ser</td>
<td>His</td>
<td>Pro</td>
<td>Pro</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>100</td>
<td>105</td>
<td>110</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gln</td>
<td>Pro</td>
<td>Arg</td>
<td>Ser</td>
<td>Ala</td>
<td>Gln</td>
<td>Thr</td>
<td>Asp</td>
<td>Pro</td>
<td>His</td>
<td>Ser</td>
<td>Ile</td>
<td>Pro</td>
<td>Arg</td>
<td>Pro</td>
<td>Ala</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>110</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>Gln</td>
<td>Val</td>
<td>Arg</td>
<td>Gly</td>
<td>Pro</td>
<td>Val</td>
<td>Leu</td>
<td>Pro</td>
<td>Gly</td>
<td>Ala</td>
<td>Trp</td>
<td>Ala</td>
<td>Thr</td>
<td>Pro</td>
<td>Tyr</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>120</td>
<td>125</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ala</td>
<td>Ile</td>
<td>Ser</td>
<td>Ser</td>
<td>Glu</td>
<td>Gln</td>
<td>Pro</td>
<td>Gly</td>
<td>Pro</td>
<td>Thr</td>
<td>Asp</td>
<td>Pro</td>
<td>His</td>
<td>Ala</td>
<td>Leu</td>
<td>Ser</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>135</td>
<td>140</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tyr</td>
<td>Val</td>
<td>Pro</td>
<td>Phe</td>
<td>Ser</td>
<td>Pro</td>
<td>Asp</td>
<td>Phe</td>
<td>Phe</td>
<td>Cys</td>
<td>Thr</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>145</td>
<td>150</td>
<td>155</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<210> SEQ ID NO 116
<211> LENGTH: 468
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<222> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2171401

<400> SEQUENCE: 116

Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val Trp
1    5    10   15
Leu Leu Ser Ser Gly His Gly Glu Gln Pro Pro Glu Thr Ala Ala
20   25   30
Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp Cys Thr Cys
35   40   45
Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg Leu Phe Pro Arg
50   55   60
Leu Gln Lys Leu Leu Gly Ser Asp Tyr Phe Arg Tyr Lys Val Asn
65   70   75   80
Leu Lys Arg Pro Cys Pro Phe Trp Aan Asp Ile Ser Glu Cys Gly Arg
85   90   95
Arg Asp Cys Ala Val Lys Pro Cys Gln Ser Asp Glu Val Pro Asp Gly
100  105  110
Ile Lys Ser Ala Ser Tyr Lys Tyr Ser Glu Ala Asn Asn Leu Ile
115  120  125
Glu Glu Cys Glu Gln Ala Glu Arg Leu Gly Ala Val Asp Glu Ser Leu
130  135  140
Ser Glu Thr Gln Lys Ala Val Leu Gln Trp Thr Lys His Asp Asp
145  150  155  160
Ser Ser Asp Asn Phe Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala
165  170  175
Glu Tyr Val Asp Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys
180  185  190
Gly Pro Asp Ala Trp Lys Ile Trp Val Asn Val Ile Tyr Glu Asn Cys
195  200  205
Phe Lys Pro Glu Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly
210  215  220
Gln Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu
225  230  235  240
Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His Ala
245 250 255
Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu Thr Trp
260 265 270
Leu Glu Lys Trp Gly His Asn Ile Thr Glu Phe Gln Glu Arg Phe
275 280 285
Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg Leu Lys Asn Leu
290 295 300
Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu Ser Lys Val Leu Pro
305 310 315 320
Phe Phe Glu Arg Pro Asp Phe Glu Leu Phe Thr Gly Asn Lys Ile Glu
325 330 335
Asp Glu Glu Asn Lys Met Leu Leu Leu Glu Ile Leu His Glu Ile Lys
340 345 350
Ser Phe Pro Leu His Phe Asp Glu Asn Ser Phe Phe Ala Gly Asp Lys
355 360 365
Lys Glu Ala His Lys Leu Lys Glu Asp Phe Arg Leu His Phe Arg Asn
370 375 380
Ile Ser Arg Ile Met Asp Cys Val Gly Cys Phe Lys Cys Arg Leu Trp
385 390 395 400
Gly Lys Leu Gln Thr Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe
405 410 415
Ser Glu Lys Leu Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu
420 425 430
Phe His Leu Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly
435 440 445
Arg Ile Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu
450 455 460
Gln Asn Ile His
465

<210> SEQ ID NO: 117
<211> LENGTH: 403
<212> TYPE: PRO
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2212530
<400> SEQUENCE: 117
Met Ser Thr Ser Thr Ser Pro Ala Ala Met Leu Leu Arg Arg Leu Arg
1    5    10    15
Arg Leu Ser Trp Gly Ser Thr Ala Val Gln Leu Phe Ile Leu Thr Val
20   25   30
Val Thr Phe Gly Leu Ala Pro Leu Ala Cys His Arg Leu Leu His
35   40   45
Ser Tyr Phe Tyr Leu Arg His Trp His Leu Asn Gln Met Ser Glu Glu
50   55   60
Phe Leu Gln Gln Ser Leu Lys Gly Glu Ala Ala Leu His Tyr Phe
65   70   75   80
Glu Glu Leu Pro Ser Ala Asn Gly Ser Val Pro Ile Val Trp Gln Ala
85   90   95
Thr Pro Arg Pro Trp Leu Val Ile Thr Ile Thr Val Asp Arg Gln

<210> SEQ ID NO: 117
<211> LENGTH: 403
<212> TYPE: PRO
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2212530
<400> SEQUENCE: 117
Met Ser Thr Ser Thr Ser Pro Ala Ala Met Leu Leu Arg Arg Leu Arg
1    5    10    15
Arg Leu Ser Trp Gly Ser Thr Ala Val Gln Leu Phe Ile Leu Thr Val
20   25   30
Val Thr Phe Gly Leu Ala Pro Leu Ala Cys His Arg Leu Leu His
35   40   45
Ser Tyr Phe Tyr Leu Arg His Trp His Leu Asn Gln Met Ser Glu Glu
50   55   60
Phe Leu Gln Gln Ser Leu Lys Gly Glu Ala Ala Leu His Tyr Phe
65   70   75   80
Glu Glu Leu Pro Ser Ala Asn Gly Ser Val Pro Ile Val Trp Gln Ala
85   90   95
Thr Pro Arg Pro Trp Leu Val Ile Thr Ile Thr Val Asp Arg Gln
Pro Gly Phe His Tyr Val Leu Gln Val Val Ser Gln Phe His Arg Leu
115 120 125
Leu Gln Gln Cys Gly Pro Gln Cys Glu Gly His Gln Leu Phe Leu Cys
130 135 140
Asn Val Glu Arg Ser Val Ser His Phe Asp Ala Lys Leu Leu Ser Lys
145 150 155 160
Tyr Val Pro Val Ala Asn Arg Tyr Glu Gly Thr Glu Asp Asp Tyr Gly
165 170 175
Asp Asp Pro Ser Thr Asn Ser Phe Glu Lys Glu Lys Gln Asp Tyr Val
180 185 190
Tyr Cys Leu Glu Ser Ser Leu Gln Thr Tyr Asn Pro Asp Tyr Val Leu
195 200 205
Met Val Glu Asp Ala Val Pro Glu Glu Gln Ile Phe Pro Val Leu
210 215 220
Glu His Leu Leu Arg Ala Arg Phe Ser Glu Pro His Leu Arg Asp Ala
225 230 235 240
Leu Tyr Leu Lys Leu Tyr His Pro Glu Arg Leu Gln His Tyr Ile Asn
245 250 255
Pro Glu Pro Met Arg Ile Leu Glu Trp Val Gly Val Gly Met Leu Leu
260 265 270
Gly Pro Leu Leu Thr Trp Ile Tyr Met Arg Phe Ala Ser Arg Pro Gly
275 280 285 290
Phe Ser Trp Pro Val Met Leu Phe Phe Ser Leu Tyr Ser Met Gly Leu
295 300
Val Glu Leu Val Gly Arg Tyr Phe Leu Glu Leu Arg Arg Leu Ser
305 310 315 320
Pro Ser Leu Tyr Ser Val Val Pro Ala Ser Gln Cys Cys Thr Pro Ala
325 330 335
Met Leu Phe Pro Ala Pro Ala Ala Arg Arg Thr Leu Thr Tyr Leu Ser
340 345 350
Gln Val Tyr Cys His Lys Gly Phe Gly Lys Asp Met Ala Leu Tyr Ser
355 360 365
Leu Leu Arg Ala Lys Gly Glu Arg Ala Tyr Val Glu Pro Asn Leu
370 375 380
Val Lys His Ile Gly Leu Phe Ser Ser Leu Arg Tyr Asn Phe His Pro
385 390 395 400
Ser Leu Leu

<210> SEQ ID NO: 118
<211> LENGTH: 131
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: Incyte Clone No: 2253056
<223> OTHER INFORMATION: Incyte Clone No: 2253056

<400> SEQUENCE: 118

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

<210> SEQ ID NO 119
<211> LENGTH: 556
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 2280161
<400> SEQUENCE: 119

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
1  5  10  15
Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
20  25  30
Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
35  40  45
Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
50  55  60
Ile Phe Leu Lys Phe Asp Gly Lys Pro Cys Asp Leu Ser Leu Asn Ile
65  70  75  80
Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
85  90  95
Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg
100 105 110
Gly Leu Ser Gly Lys Tyr Gln Thr Ser Ser Lys Leu Phe Gln Asn Cys
115 120 125
Ser Glu Leu Phe Lys Thr Gln Thr Phe Ser Gly Asp Phe Met His Arg
130 135 140
Leu Pro Leu Leu Gly Glu Lys Glu Ala Lys Glu Asn Gly Thr Asn
145 150 155 160
Leu Thr Phe Ile Gly Asp Lys Thr Ala Met His Glu Pro Leu Glu Thr
165 170 175
Trp Gln Asp Ala Pro Tyr Ile Phe Ile Val His Ile Gly Ile Ser Ser
180 185 190
Ser Lys Glu Ser Ser Lys Glu Asn Ser Leu Ser Asn Leu Phe Thr Met
195 200 205
Thr Val Glu Val Lys Gly Pro Tyr Glu Tyr Leu Thr Leu Glu Asp Tyr
210 215 220
Pro Leu Met Ile Phe Phe Met Val Met Cys Ile Val Tyr Val Leu Phe
225 230 235 240
Gly Val Leu Trp Leu Ala Trp Ser Ala Cys Tyr Trp Arg Asp Leu Leu 245 250 255
Arg Ile Gln Phe Trp Ile Gly Ala Val Ile Phe Leu Gly Met Leu Glu 260 265 270
Lys Ala Val Phe Tyr Ala Glu Phe Gln Asn Ile Arg Tyr Lys Gly Glu 275 280 285
Ser Val Gln Gly Ala Leu Ile Leu Ala Glu Leu Ser Ala Val Lys 290 295 300
Arg Ser Leu Ala Arg Thr Leu Val Ile Ile Val Ser Leu Gly Tyr Gly 305 310 315 320
Ile Val Lys Pro Arg Leu Gly Val Thr Leu His Lys Val Val Ala 325 330 335
Gly Ala Leu Tyr Leu Leu Phe Ser Gly Met Glu Gly Val Leu Arg Val 340 345 350
Thr Gly Tyr Phe Ser Tyr Pro Leu Thr Leu Ile Val Asn Leu Ala Leu 355 360 365
Ser Ala Val Aep Ala Cys Val Ile Leu Trp Ile Phe Ile Ser Leu Thr 370 375 380
Gln Thr Met Lys Leu Leu Lys Leu Arg Arg Asn Ile Val Lys Leu Ser 385 390 395 400
Leu Tyr Arg His Phe Thr Asn Thr Leu Ile Leu Ala Val Ala Ala Ser 405 410 415
Ile Val Phe Ile Ile Trp Thr Thr Met Lys Phe Arg Ile Val Thr Cys 420 425 430
Gln Ser Asp Trp Arg Glu Leu Trp Val Asp Asp Ala Ile Trp Arg Leu 435 440 445
Leu Phe Ser Met Ile Leu Phe Val Ile Met Val Leu Trp Arg Pro Ser 450 455 460
Ala Asn Asn Gln Arg Phe Ala Phe Ser Pro Leu Ser Glu Glu Glu Glu 465 470 475 480
Glu Asp Glu Gln Lys Glu Pro Met Leu Lys Glu Ser Phe Glu Gly Met 485 490 495
Lys Met Arg Ser Thr Lys Glu Glu Pro Asn Gly Asn Ser Lys Val Asn 500 505 510
Lys Ala Gln Glu Asp Asp Leu Lys Trp Val Glu Glu Asn Val Pro Ser 515 520 525
Ser Val Thr Aep Val Ala Leu Pro Leu Leu Asp Ser Asp Glu Glu 530 535 540
Arg Met Ile Thr His Phe Glu Arg Ser Lys Met Glu 545 550 555

<210> SEQ ID NO 120
<211> LENGTH: 514
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2207405
<400> SEQUENCE: 120
Met Ser Thr Pro Arg Arg Leu Leu Arg Tyr Leu Phe Pro Ala Leu 1      5 10 15
Leu Leu His Gly Leu Gly Gly Ser Ala Leu Leu His Pro Asp Ser 20 25 30
Arg Ser His Pro Arg Ser Leu Glu Lys Ser Ala Trp Arg Ala Phe Lys
35  40  45
Glu Ser Gln Cys His His Met Leu Lys His Leu His Asn Gly Ala Arg
50  55  60
Ile Thr Val Gln Met Pro Pro Thr Ile Glu Gly His Trp Val Ser Thr
65  70  75  80
Gly Cys Glu Val Arg Ser Gly Pro Glu Phe Ile Thr Arg Ser Tyr Arg
85  90  95
Phe Tyr His Asn Thr Phe Lys Ala Tyr Glu Phe Tyr Tyr Gly Ser
100 105 110
Asn Arg Cys Thr Asn Pro Thr Tyr Thr Leu Ile Arg Gly Lys Ile
115 120 125
Arg Leu Arg Gln Ala Ser Trp Ile Ile Arg Gly Gly Thr Glu Ala Asp
130 135 140
Tyr Gln Leu His Asn Val Gln Val Ile Cys His Thr Glu Ala Val Ala
145 150 155 160
Glu Lys Leu Gly Gln Val Asn Arg Thr Cys Pro Gly Phe Leu Ala
165 170 175
Asp Gly Gly Pro Trp Val Gln Asp Val Ala Tyr Asp Leu Trp Arg Glu
180 185 190
Glu Asn Gly Cys Glu Cys Thr Lys Ala Val Asn Phe Ala Met His Glu
195 200 205
Leu Gln Leu Ile Arg Val Glu Lys Gln Tyr Leu His His Asn Leu Asp
210 215 220
His Leu Val Glu Leu Phe Leu Gly Asp Ile His Thr Asp Ala Thr
225 230 235 240
Gln Arg Met Phe Tyr Arg Pro Ser Ser Tyr Gln Pro Pro Leu Glu Asn
245 250 255
Ala Lys Asn His Asp His Ala Cys Ile Ala Cys Arg Ile Ile Tyr Arg
260 265 270
Ser Asp Glu His His Pro Pro Ile Leu Pro Pro Lys Ala Asp Leu Thr
275 280 285
Ile Gly Leu His Gly Glu Trp Val Ser Gln Arg Cys Glu Val Arg Pro
290 295 300
Glu Val Leu Phe Leu Thr Arg His Phe Ile Phe His Asp Asn Asn Asn
305 310 315 320
Thr Trp Glu Gly His Tyr Tyr His Tyr Ser Asp Pro Val Cys Lys His
325 330 335
Pro Thr Phe Ser Ile Tyr Ala Arg Gly Arg Tyr Ser Arg Gly Val Leu
340 345 350
Ser Ser Arg Val Met Gly Gly Thr Glu Phe Val Phe Lys Val Asn His
355 360 365
Met Lys Val Thr Pro Met Asp Ala Ala Thr Ala Ser Leu Leu Asn Val
370 375 380
Phe Asn Gly Asn Glu Cys Gly Ala Glu Gly Ser Trp Gln Val Gly Ile
385 390 395 400
Gln Gln Asp Val Thr His Thr Asn Gly Cys Val Ala Leu Gly Ile Lys
405 410 415
Leu Pro His Thr Glu Tyr Glu Ile Phe Lys Met Glu Gln Asp Ala Arg
420 425 430
Gly Arg Tyr Leu Leu Phe Asn Gly Gln Arg Pro Ser Asp Gly Ser Ser
435 440 445
Pro Aep Arg Pro Glu Lys Arg Ala Thr Ser Tyr Gln Met Pro Leu Val
450 455 460
Gln Cys Ala Ser Ser Ser Pro Arg Ala Glu Aep Leu Ala Glu Aep Ser
465 470 475 480
Gly Ser Ser Leu Tyr Gly Arg Ala Pro Gly Arg His Thr Trp Ser Leu
485 490 495
Leu Leu Ala Ala Ala Cys Leu Val Pro Leu Leu His Thr Asn Ile
500 505 510
Arg Arg

<210> SEQ ID NO 121
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2380344

<400> SEQUENCE: 121

Net Leu Trp Trp Leu Val Leu Leu Leu Pro Thr Leu Lys Ser Val
1  5 10 15

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

Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly Thr Arg Thr
35 40 45

Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly Thr Ala Ser Pro
50 55 60

Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro Thr Val Ser Arg Leu
65 70 75 80

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

Gly Phe Gln Gly Gly Gly Pro Cys Pro Gly Arg Arg Arg Aep
100 105

<210> SEQ ID NO 122
<211> LENGTH: 431
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2383171

<400> SEQUENCE: 122

Net Ser Trp Val Gln Ala Thr Leu Leu Ala Arg Gly Leu Cys Arg Ala
1  5 10 15

Trp Gly Gly Thr Cys Gly Ala Leu Thr Gly Thr Ser Ile Ser Gln
20 25 30

Val Pro Arg Arg Leu Pro Arg Gly Leu His Cys Ser Ala Ala Ala His
35 40 45

Ser Ser Glu Gln Ser Leu Val Pro Ser Pro Pro Glu Pro Arg Gln Arg
50 55 60

Pro Thr Lys Ala Leu Val Pro Phe Glu Asp Leu Phe Gly Gln Ala Pro
65 70 75 80

Gly Gly Glu Arg Aep Lys Ala Ser Phe Leu Gln Thr Val Gln Lys Phe
<table>
<thead>
<tr>
<th>85</th>
<th>90</th>
<th>95</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ala Glu His Ser Val Arg Lys Arg Gly His Ile Asp Phe Ile Tyr Leu</td>
<td>100</td>
<td>105</td>
</tr>
<tr>
<td>Ala Leu Arg Lys Met Arg Glu Tyr Gly Val Glu Arg Asp Leu Ala Val</td>
<td>115</td>
<td>120</td>
</tr>
<tr>
<td>Tyr Asn Gln Leu Leu Asn Ile Phe Pro Lys Glu Val Phe Arg Pro Arg</td>
<td>130</td>
<td>135</td>
</tr>
<tr>
<td>Asn Ile Ile Gin Arg Ile Phe Val His Tyr Pro Arg Gin Gin Glu Cys</td>
<td>145</td>
<td>150</td>
</tr>
<tr>
<td>Gly Ile Ala Val Leu Gin Met Glu Asn His Gly Val Met Pro Asn</td>
<td>165</td>
<td>170</td>
</tr>
<tr>
<td>Lys Glu Thr Glu Phe Leu Leu Ile Gin Ile Phe Gly Arg Lys Ser Tyr</td>
<td>180</td>
<td>185</td>
</tr>
<tr>
<td>Pro Met Leu Lys Leu Val Arg Leu Lys Leu Trp Phe Pro Arg Phe Met</td>
<td>195</td>
<td>200</td>
</tr>
<tr>
<td>Asn Val Asn Pro Phe Pro Val Pro Arg Asp Leu Pro Gin Asp Pro Val</td>
<td>210</td>
<td>215</td>
</tr>
<tr>
<td>Glu Leu Ala Met Phe Gly Leu Arg His Met Glu Pro Asp Leu Ser Ala</td>
<td>225</td>
<td>230</td>
</tr>
<tr>
<td>Arg Val Thr Ile Tyr Gin Val Pro Leu Pro Lys Asp Ser Thr Gly Ala</td>
<td>245</td>
<td>250</td>
</tr>
<tr>
<td>Ala Aap Pro Pro Gin Pro His Ile Val Gin Gin Ser Gin Pro Asp Gin</td>
<td>260</td>
<td>265</td>
</tr>
<tr>
<td>Gin Ala Ala Leu Ala Arg His Asn Pro Ala Arg Pro Val Phe Val Glu</td>
<td>275</td>
<td>280</td>
</tr>
<tr>
<td>Gly Pro Phe Ser Leu Trp Leu Arg Asn Lys Cys Val Tyr Tyr His Ile</td>
<td>290</td>
<td>295</td>
</tr>
<tr>
<td>Leu Arg Ala Asp Leu Pro Gin Glu Arg Glu Val Glu Thr</td>
<td>305</td>
<td>310</td>
</tr>
<tr>
<td>Pro Gin Glu Trp Asn Leu Tyr Tyr Pro Met Gin Leu Asp Leu Gin Thr</td>
<td>325</td>
<td>330</td>
</tr>
<tr>
<td>Val Arg Ser Gin Gin Phe Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin</td>
<td>340</td>
<td>345</td>
</tr>
<tr>
<td>Gin Gly Pro Gin Gin Leu Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin</td>
<td>355</td>
<td>360</td>
</tr>
<tr>
<td>Thr Met Ala Lys Trp Ile Gin Gly Leu Gin Gin Thr Asn Pro Thr Leu</td>
<td>370</td>
<td>375</td>
</tr>
<tr>
<td>Ala Gin Ile Pro Val Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin</td>
<td>385</td>
<td>390</td>
</tr>
<tr>
<td>Gin Thr Ser Ser Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin</td>
<td>405</td>
<td>410</td>
</tr>
<tr>
<td>Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin</td>
<td>420</td>
<td>425</td>
</tr>
</tbody>
</table>

<210> SEQ ID NO 123
<211> LENGTH: 142
<212> TYPE: PRO
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 2396046
<400> SEQUENCE: 123
---continued---

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

<210> SEQ ID NO 124
<211> LENGTH: 643
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: Incyte Clone No: 2456587
<400> SEQUENCE: 124

Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe Leu
1      5     10    15
Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu Asp Arg
20     25     30
Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys Ser Arg Thr
35     40     45
Cys Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys Leu Ser Ser Lys
50     55     60
Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr Cys Ser Asn Val Asp
65     70     75    80
Cys Pro Pro Glu Ala Gly Asp Ala Gln Gln Cys Ser Ala His
85     90     95
Asn Asp Val Lys His His Gly Glu Phe Tyr Glu Trp Leu Pro Val Ser
100    105    110
Asn Asp Pro Asp Asn Pro Cys Ser Leu Lys Cys Gln Ala Lys Gly Thr
115    120    125
Thr Leu Val Val Glu Leu Ala Pro Lys Val Leu Asp Gly Thr Arg Cys
130    135    140
Tyr Thr Glu Ser Leu Asp Met Cys Ile Ser Gly Leu Cys Glu Ile Val
145    150    155    160
Gly Cys Asp His Gln Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly
165    170    175
Val Cys Asn Gly Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr
180    185    190
Lys Ser Gln Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Ile
195    200    205
<table>
<thead>
<tr>
<th>Pro Tyr Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His</th>
<th>210 215 220</th>
</tr>
</thead>
<tbody>
<tr>
<td>Leu Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser</td>
<td>225 230 235 240</td>
</tr>
<tr>
<td>Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp Phe</td>
<td>245 250 255</td>
</tr>
<tr>
<td>Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro Leu Thr</td>
<td>260 265 270</td>
</tr>
<tr>
<td>Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala Asp Ser Thr</td>
<td>275 280 285</td>
</tr>
<tr>
<td>Val Glu Phe Ile Phe Tyr Glu Pro Ile Ile His Arg Trp Arg Glu Thr</td>
<td>290 295 300</td>
</tr>
<tr>
<td>Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly Gly Tyr Glu Leu Thr</td>
<td>305 310 315 320</td>
</tr>
<tr>
<td>Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn Arg Val Val Ala Asp Gln</td>
<td>325 330 335</td>
</tr>
<tr>
<td>Tyr Cys His Tyr Tyr Pro Glu Asn Ile Lys Pro Lys Pro Lys Leu Gln</td>
<td>340 345 350</td>
</tr>
<tr>
<td>Glu Cys Asn Leu Asp Pro Cys Pro Ala Ser Asp Gly Tyr Lys Gln Ile</td>
<td>355 360 365</td>
</tr>
<tr>
<td>Met Pro Tyr Asp Leu Tyr His Pro Leu Pro Arg Trp Glu Ala Thr Pro</td>
<td>370 375 380</td>
</tr>
<tr>
<td>Trp Thr Ala Cys Ser Ser Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala</td>
<td>385 390 395 400</td>
</tr>
<tr>
<td>Val Ser Cys Val Glu Glu Asp Ile Gln Gly His Val Thr Ser Val Glu</td>
<td>405 410 415</td>
</tr>
<tr>
<td>Glu Trp Lys Cys Met Tyr Thr Pro Lys Met Pro Ile Ala Glu Pro Cys</td>
<td>420 425 430</td>
</tr>
<tr>
<td>Asn Ile Phe Asp Cys Pro Lys Trp Leu Ala Glu Glu Trp Ser Pro Cys</td>
<td>435 440 445</td>
</tr>
<tr>
<td>Thr Val Thr Cys Gly Glu Gln Leu Arg Tyr Arg Val Val Leu Cys Ile</td>
<td>450 455 460</td>
</tr>
<tr>
<td>Asp His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro</td>
<td>465 470 475 480</td>
</tr>
<tr>
<td>His Ile Lys Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro Lys</td>
<td>485 490 495</td>
</tr>
<tr>
<td>Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Glu Ala Gln</td>
<td>500 505 510</td>
</tr>
<tr>
<td>Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser Phe Ile Pro</td>
<td>515 520 525</td>
</tr>
<tr>
<td>Glu Ala Trp Ser Ala Cys Thr Val Thr Cys Gly Val Gly Thr Gln Val</td>
<td>530 535 540</td>
</tr>
<tr>
<td>Arg Ile Val Arg Cys Glu Val Leu Leu Ser Phe Ser Ser Gln Ser Val Ala</td>
<td>545 550 555 560</td>
</tr>
<tr>
<td>Asp Leu Pro Ile Asp Glu Cys Glu Gly Pro Lys Pro Ala Ser Gln Arg</td>
<td>565 570 575</td>
</tr>
<tr>
<td>Ala Cys Tyr Ala Gly Pro Cys Ser Gly Glu Ile Pro Glu Phe Asn Pro</td>
<td>580 585 590</td>
</tr>
<tr>
<td>Asp Glu Thr Asp Gly Leu Phe Gly Glu Leu Gln Asp Phe Asp Glu Leu</td>
<td>595 600 605</td>
</tr>
</tbody>
</table>
Tyr Asp Trp Glu Tyr Glu Gly Phe Thr Lys Cys Ser Glu Ser Cys Gly
   610  615  620
Gly Gly Val Gin Glu Ala Val Val Ser Cys Leu Asn Lys Gin Thr Arg
   625  630  635  640
Glu Pro Cys

<210> SEQ ID NO 125
<211> LENGTH: 568
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 2484813

<400> SEQUENCE: 125

Met Val Leu Leu His Thr Cys Leu Leu Trp Leu Leu Phe Pro Leu Ser
    1   5   10   15
Ser Arg Thr Gin Lys Leu Pro Thr Arg Asp Gin Leu Phe Gin Met
    20  25   30
Gln Ile Arg Asp Gin Ala Phe Gin His Gin Ser Ser Val Ile Pro Asp
    35  40   45
Gly Ala Glu Ile Ser Ser Tyr Leu Phe Arg Gin Thr Pro Lys Gin Tyr
    50  55   60
Phe Phe Val Gin Gin Gin Gin Gin Gin Gin Ser Ser Gin Gin Gin Gin Gin
    65  70   75   80
Pro Cys Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
    85  90   95
Glu Gin Arg Ser Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   100 105  110
Gln Lys Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   115 120  125
Lys Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   130 135  140
Leu Tyr Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   145 150  155  160
Val Tyr Ala Thr Thr Pro Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   165 170  175
Pro Cys Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   180 185  190
Thr Leu Ala Trp Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   195 200  205
Ile Gin Tyr Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   210 215  220
Cys Ala Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   225 230  235  240
Pro Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   245 250  255
Phe Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   260 265  270
Ser Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   275 280  285
Gln Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin Gin
   290 295  300
Lys Pro Asp Thr Gln Tyr Tyr Phe Asp Val Phe Val Val Asn Ile Asn
305    310    315    320
Ser Asn Met Ser Thr Ala Tyr Val Gly Thr Phe Ala Arg Thr Lys Glu
325    330    335
Glu Ala Lys Gln Lys Thr Val Glu Leu Lys Asp Gly Lys Ile Thr Asp
340    345    350
Val Phe Val Lys Arg Lys Gly Ala Lys Phe Leu Arg Phe Ala Pro Val
355    360    365
Ser Ser His Glu Lys Val Thr Phe Phe Ile His Ser Cys Leu Asp Ala
370    375    380
Val Glu Ile Glu Val Arg Arg Gly Lys Leu Leu Leu Ser Glu Asn
385    390    395    400
Val Glu Gly Ile Glu Gln Phe Gln Leu Arg Gly Lys Pro Lys Ala Lys
405    410    415
Tyr Leu Val Arg Leu Lys Gly Ala Gly Lys Gly Ala Ser Met Leu Lys
420    425    430
Ile Leu Ala Thr Thr Arg Pro Thr Lys Gin Ser Phe Pro Ser Leu Pro
435    440    445
Glu Asp Thr Arg Ile Lys Ala Phe Asp Lys Leu Arg Thr Cys Ser Ser
450    455    460
Ala Thr Val Ala Trp Leu Gly Thr Gln Glu Arg Asn Lys Phe Cys Ile
465    470    475    480
Tyr Lys Lys Gly Val Asp Arg Asn Tyr Asn Glu Asp Gln Lys Lys Arg
485    490    495
Glu Gin Asn Gin Cys Leu Gly Pro Asp Ile Arg Lys Lys Ser Glu Lys
500    505    510
Val Leu Cys Lys Tyr Phe His Ser Gin Asn Leu Gin Lys Ala Val Thr
515    520    525
Thr Glu Thr Ile Lys Gly Leu Gin Pro Gly Lys Ser Tyr Leu Leu Asp
530    535    540
Val Tyr Val Ile Gly His Gly Gly His Ser Val Lys Tyr Gin Ser Lys
545    550    555    560
Val Val Lys Thr Arg Lys Phe Cys
565

<210> SEQ ID NO 126
<211> LENGTH: 125
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: OTHER INFORMATION: Incyte Clone No: 2493651
<400> SEQUENCE: 126
Met Trp Leu Val Gly Pro Ser Phe Leu Ser Cys Pro Leu Gly Lys Val
1     5     10    15
Pro Pro Ala Gly Leu Leu Ala Gly Ser Ser Gly Arg Gly Ala Arg
20    25    30
Arg Pro Ala Thr Pro Arg His Trp Ser Ser Thr Pro Gly Leu Arg
35    40    45
Leu Glu Ala Pro Leu Cys Gin Leu Cys Pro Leu Gly Gly Thr Arg Gin
50    55    60
Asp Cys Gin Pro Leu Ser Trp Gin Val Thr Ser Ala Phe Lys Leu Thr
65    70    75    80
-continued

Val Pro Ser Pro Phe His Ala Pro Pro Arg Ser Trp Ser Cys Leu Leu
  85   90   95
Leu Gly Ile Phe Pro Gly Glu Ala Leu Ala Leu Glu Pro Trp His Leu
 100  105  110
Phe Leu Gly Ser Met Leu Pro Arg Cys Asp Gly Glu Cys
 115  120  125

<210> SEQ ID NO 127
<211> LENGTH: 196
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2495719

<400> SEQUENCE: 127
Met Ala Ala Leu Lys Ala Leu Val Ser Gly Cys Gly Arg Leu Leu Arg
  1  5  10  15
Gly Leu Leu Ala Gly Pro Ala Ala Thr Ser Trp Ser Arg Leu Pro Ala
 20  25  30
Arg Gly Phe Arg Glu Val Val Glu Thr Gin Glu Gly Lys Thr Thr Ile
 35  40  45
Ile Glu Gly Arg Ile Thr Ala Thr Pro Lys Glu Ser Pro Asn Pro Pro
 50  55  60
Asn Pro Ser Gly Gin Cys Pro Ile Cys Arg Trp Asn Leu Lys His Lys
 65  70  75  80
Tyr Aan Tyr Asp Asp Val Leu Leu Leu Ser Glu Phe Ile Arg Pro His
 85  90  95
Gly Gly Met Leu Pro Arg Lys Ile Thr Gly Leu Cys Gin Glu Glu His
100 105 110
Arg Lys Ile Glu Glu Cys Val Lys Met Ala His Arg Ala Gly Leu Leu
115 120 125
Pro Aan His Arg Pro Arg Leu Pro Glu Val Pro Lys Ser Lys
130 135 140
Pro Gin Leu Aen Arg Tyr Leu Thr Arg Trp Ala Pro Gly Ser Val Lys
145 150 155 160
Pro Ile Tyr Lys Gin Pro Gin Trp Aen Arg Val Arg Met Pro Val
165 170 175
Gly Ser Pro Leu Leu Arg Asp Aen Val Cys Tyr Ser Arg Thr Pro Trp
180 185 190
Lys Leu Tyr His
195

<210> SEQ ID NO 128
<211> LENGTH: 214
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2614153

<400> SEQUENCE: 128
Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly Gin
  1  5  10  15
Ala Ala Leu Leu Leu Gly Asn Leu Leu Leu His Cys Val Ser Arg
 20  25  30
Ser His Ser Gln Asn Ala Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly
35  40  45
Ala Ala Gln Pro Glu Gly Pro Gly Gly Ala Ala Ser Trp Glu Tyr Gly
50  55  60
Asp Pro His Ser Pro Val Ile Leu Cys Ser Tyr Leu Pro Asp Glu Phe
65  70  75  80
Ile Glu Cys Glu Asp Pro Val Asp His Val Gly Asn Ala Thr Ala Ser
85  90  95
Gln Glu Leu Gly Tyr Gly Cys Leu Lys Phe Gly Gly Gly Ala Tyr Ser
100 105 110
Asp Val Glu His Thr Ser Val Gln Cys His Ala Leu Asp Gly Ile Glu
115 120 125
Cys Ala Ser Pro Arg Thr Phe Leu Arg Glu Asn Lys Pro Cys Ile Lys
130 135 140
Tyr Thr Gly His Tyr Phe Ile Thr Thr Leu Tyr Ser Phe Phe Leu
145 150 155 160
Gly Cys Phe Gly Val Asp Arg Phe Cys Leu Gly His Thr Gly Thr Ala
165 170 175
Val Gly Lys Leu Leu Thr Leu Gly Gly Leu Gly Ile Trp Thr Phe Val
180 185 190
Asp Leu Ile Leu Leu Ile Thr Gly Leu Met Pro Ser Asp Gly Ser
195 200 205
Asn Trp Cys Thr Val Tyr
210

<210> SEQ ID NO 129
<211> LENGTH: 86
<212> TYPE: FRN
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2655184

<400> SEQUENCE: 129
Met Ala Cys Phe Ser Phe Phe Leu Cys Phe Leu Val His Leu Leu Ile
1  5  10  15
Lys Met Asn Pro Val Thr Glu Ser Pro Ser Cys Leu Phe Ser Pro Pro
20  25  30
Ser Glu Ser Ala Leu Ala Ser Ser Ser Ala Leu Ser Ala Ser Cys Asp
35  40  45
Gln Arg Ala Pro Phe Ser Leu Ala Gly Val Val Ser His Asp Gly
50  55  60
Trp Pro Val Val Arg Leu His Arg Pro Leu Val Pro Glu His Ala Val
65  70  75  80
Phe Ser Gln Pro Ser Leu Gln Pro
85

<210> SEQ ID NO 130
<211> LENGTH: 260
<212> TYPE: FRN
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2848362

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

SEQ ID NO: 132
LENGTH: 193
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: NAME/KEY: misc_feature
OTHER INFORMATION: Incyte Clone No: 2899137

SEQUENCE: 132

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

<210> SEQ ID NO: 133
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2986229

<400> SEQUENCE: 113

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

Lys

<210> SEQ ID NO: 134
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 3222081

<400> SEQUENCE: 134

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

<210> SEQ ID NO: 135
<211> LENGTH: 865
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 443531
<240> SEQUENCE: 135

attctctaattctgactcctcttggagctcaagttggccctattgactcaccccctc

<210> SEQ ID NO: 136
<211> LENGTH: 706
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (11),(12)
<223> OTHER INFORMATION: s, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 632860
<240> SEQUENCE: 136
cggscqctggntntgttaaaaccatccctgatttttttaaggagaccaagtgccagc

acacctagagctcccaagccagagcgcgtggtgccagcgcctgctgctggtgccagc
ttttgtgg ggccactgctg gcctgcttg agcgtgcact agccccttctt gtcattattg 240
gacttctgc ggtgagag tcgccctgac tcgctgact tcaccacocct tgtccttg 300
acccctgacct ccgccacaac gtggctcctc tggctactc tttgtgcttt 360
tcggagcagt tactactact cccagcagga caacagatcaca ccatcgttgc 420
atagatgagc ttaccagatcc aacggctcaca tcgctacgag cagaccgtaa 480
cggagtggt tccagagtac gcggtggtc tagggtgttc tcgggtcgtg 540
tgatgcagt tgggggtag gcactagtact cccaggggca ttcttttcag aattcgcttt 600
tctgccatt aaccactgta cagctgctat gcgctctgtg gacatggctg taccctgttg 660
cctccagccgc tcaccaggtgg gctggccagc tggctactc ttcggtg 706

<210> SEQ ID NO: 137
<211> LENGTH: 801
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 670010

<400> SEQUENCE: 137

acccatatcgc gcctctgtgtg ttcctctcag cctcctcagc gctccctgac ggtgccctac 60
cctcagcgtc cctcctcaccct tccctgcact gcctgcctgc ggtgcctgcc gcctcctgac 120
cggagctggt gctcctctcc gcggccctct gctgcctgc ggctgcctgc gctccctgcc 180
ttctctggtt tggcctcagc gttagcgcac gttggctgcac ctggctgctgc gttggctgctgc 240
ttctctggtt tggcctcagc gttagcgcac gttggctgcac ctggctgctgc gttggctgctgc 300
ttctctggtt tggcctcagc gttagcgcac gttggctgcac ctggctgctgc gttggctgctgc 360
ttctctggtt tggcctcagc gttagcgcac gttggctgcac ctggctgctgc gttggctgctgc 420
ntctctggtt tggcctcagc gttagcgcac gttggctgcac ctggctgctgc gttggctgctgc 480
ntctctggtt tggcctcagc gttagcgcac gttggctgcac ctggctgctgc gttggctgctgc 540
tttctctggtt tggcctcagc gttagcgcac gttggctgcac ctggctgctgc gttggctgctgc 600
ntctctggtt tggcctcagc gttagcgcac gttggctgcac ctggctgctgc gttggctgctgc 660
ntctctggtt tggcctcagc gttagcgcac gttggctgcac ctggctgctgc gttggctgctgc 720
ntctctggtt tggcctcagc gttagcgcac gttggctgcac ctggctgctgc gttggctgctgc 780
ntctctggtt tggcctcagc gttagcgcac gttggctgcac ctggctgctgc gttggctgctgc 840
tacocactgag cacgctcttc gacacagaga ccacgaaccaccacgg 1020
tgctgtaa gacacccttc aggacagac ccaccacaccaccacgg 1080
tcctggtgatt tgagagcttg atggacatc gtcctccttgccctac 1140
tgctgtaa gacacagaga ccacgaaccaccacgg 1200
cctggtgatt tgagagcttg atggacatc gtcctccttgccctac 1241

tgctgtaa gacacccttc aggacagac ccaccacaccaccacgg 1400
tgctgtaa gacacccttc aggacagac ccaccacaccaccacgg 1460
tgctgtaa gacacccttc aggacagac ccaccacaccaccacgg 1520
tgctgtaa gacacccttc aggacagac ccaccacaccaccacgg 1580
tgctgtaa gacacccttc aggacagac ccaccacaccaccacgg 1640
tgctgtaa gacacccttc aggacagac ccaccacaccaccacgg 1700
tgctgtaa gacacccttc aggacagac ccaccacaccaccacgg 1760
tgctgtaa gacacccttc aggacagac ccaccacaccaccacgg 1820

tgctgtaa gacacccttc aggacagac ccaccacaccaccacgg 2000

ttcccttctta ttaccccctgg gaggtagcca tagttcccaaa cgtgagaata tctcttgagac 300
gccgcactt ccgcgaaagct ctctcttaca gcacaaagcc gcccctccatt ccacaagatt 360
agtgtgaaccg gtcctcttct cttattcag aacgtggaag gagggtagaa gacgccttcc ctcaggtctt 420
cacgccctcg gcacggagct cagctctgtg atttctgcgc agtcctgcctt gacaccccga 480
gatacggag gcagcagttct cagttccataa agggacacaa actcaacatt accgagcttg 540
tcaacaaac ccccaagtctg aagggccaga gcaaacacac ccatagcggcc ctcaggytca 600
cagggccagag aggcaacact gcgtcactgg gcttaagttc ggcacactgcag atctaggttg 660
catgtgtctgt cgtgtcgcct aaaaacccga ttttgggaact gtgtgcctcct cttctctctgt 720
gtggtgcggag aagggagagct gcacggagct cagctctgtg aattcttgac ccacattctg 780
gcgagagggct atgtgtattt gcccggggga acgtggtggt agacccgcttt ggtggtctcc 840
cacagtctgct cccctctgtg cagatacactg gcacggaccc tggagacctt ttaaaaaacc 900
agggccagac gcaagagggcc ctggtgctct gataccacgt gttggaggag cgtacccctc 960
agagcctctca tccgcacaggct cttcactgtgc accgttattg gatgggagct ctgatacacc 1020
tgaaatctc cagctgcttt tggggtgtgt ttattatag cagtcacaa gttcttttat 1080
cctcctcacaag gatgtgaaana cccactattc ttggttacc attacccctc ttttcctcgg 1140
tcataatttt ccacactctgtg ctgtggtggt tttctcttgtgc agaaggttttt gcgggataaa 1200
tagcgtgaaaaa tgcctgctgag acctaaatgct aaaaaaaa aaaaaa 1235

<210> SEQ ID NO 142
<211> LENGTH: 1034
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURES:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1259405
<400> SEQUENCE: 142
gaggagagtg gcggggggag cactccacgg gggttcacaag cttgctggcty tgcctgaccc 60
tgagctgctg ccggcggcag gcgggaggct ccgctggggc ccctgtgycct ggctgaggcc 120
tggggccccac agcccgggct gctgtggtgg ggcgtctgac agtcctgtgct 180
gctgtgctg cctgtgctgtc cttgctgcag tgcgctgac ggccgcaaga 240
attcagggt cgtcagagt gatcgtcactct cgtgcctgctaa taaagaagat ctcggtgcata 300
attaataact gacacatcct cagaaagatt cttgattggc ttcagttggt gaggccactcg 360
ctgtggtggt gcgtggtgag gcgtgctact gcgtgtgctct gcctatgagaa tcgtggtgctt 420
gaagotcgctg cacactactg gtcttcatttac ttcacatcttg cctgctcagctg 480
tcctgacact gcgtgtgact accgcagcag ctagagatgac gcactatgacag 540
atgcacatgtc gatgcgtaat gctgggtgacac cctgcacgct cccagctgtg 600
acagtgctcct cgcagtccag acgtgcctct cacaaggtta gataagctc 660
agacggcgag gcagctgcttc gcagcaggtc gcgtgccttcgc agtcctgtgctag 720
ttcacacgtg atggtgatt cggaggacag tggagacagc gcacctgggac 780
aagaactctgct aggttgtgtgct cgggttgcctc tttaatcttg tgggtttcttg accacagtgt 840
gctggagact ctcacatctgg cagcatttac tttttctctgt gttacgctag 900
<210> SEQ ID NO: 143
<211> LENGTH: 1722
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1297384

<400> SEQUENCE: 143

```
taagagaccc agccccccct cacagagctc cacagagcc ctatctctct tctttttttttttt 960
tgtcttttta taataaaaaa taagatctgg gtaaataat ctgtgttgac tttactggga 1020
acacgacctc tttttttttt tcaagtggtg tcaagtggtg tcaagtggtg tcaagtggtg 1080
tttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
```plaintext
ggcgatcttg cacagagtc gtcgaattaq tccaaatatt tcacatcagt tggagtcac 1080
ttgacctgca caacctgctc tgyggcacaac gccttccctc acggggcggcc tggccaagc 1140
cggacacgt gcacccctcc ctttcttgag gccatggcag ggaagggagaa aacagagac 1200
tgccaccttt gacacacagac aatgttttac atcagccttc gctcagggcc atagttatat 1260
gtgaaacgttt ttgcccaatca ctggctaacg ggcctgctag attttgtgaa atgctgaatt 1320
attactcaga cttaacctac ccaagttgga caacacatcgc tggctcagg atgtattttg 1380
aaactgttga ttctttgccc tttgcctctc tggattacta ttaaagcaagct atcaatttac 1440
atctaacaggt tatttttttc cctgttcttt gcacacacct tcgatagtaa ttttagaaaat 1500
aaacctctca aaccttggtg aaccttcttc ttcggggttgc gacacagccc taacgagattg 1560
gggcagcgtcc cacctgaggac aacagaagac aactccaaaaa ttttggtctg cagacagtaa 1620
acacacatc tggattttttc gcaaaatttgc ccaattttta tggagatattt ttctttggac 1680
ggtagtgta csatacaact cttctgtttttct taaaacattttaa aaaaaaa a 1722
```
aacacagaag gttggtcttt atttatat caaaccagag caaaccgact 1260
caacacaga gttgagaaac cacoatctca aaccgacact ctcacactca 1320
gggttttaat ttgatctgaa taaaggttat tctacactgtg ggagaaaaa aaaaattgta 1380
tctacaccct aacccttctg ctacactctt aaccgacact ctcacactca 1440
cacacgagtt ttgagtgccg gacccaaata atccagacttt atacaacactttg 1500
gacacgaga aaccctgctg gacacagttg ttcacaccc ttacctggat ttacacactct 1560
cctatatttt ttatcttccc atcataatgat atctctctt aaccgacact ctcacactca 1620
ccacactaat aaccctgctg caaccatgat ctctctatct ctcacacccc aaccgacact ctcacactca 1680
gccacccttt atctctatc aaccgacact ctcacactca 1740

<210> SEQ ID NO: 145
<211> LENGTH: 997
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (973)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1306026

<400> SEQUENCE: 145

ggacacacgc ttcggtggtc cacoaccgac ggtactgctg tgcacactct 60
cctttcgcc ctcagagttg gcaccagggc gggtctgctg ctgcagtgcc 120
tttactgctg gacgccgtgg gacccggtg gacaagttgc aaccgacact 180
cgtctgctgg cgggtctgctg cgtacactcc ttcacacccc ctcacactca 240
ctaatatac aaccgacact ctcacactcc ttcacacccc ctcacactca 300
agggataac caccgacact ctcacactcc ttcacacccc ctcacactca 360
agggataac caccgacact ctcacactcc ttcacacccc ctcacactca 420
ggtgaacac aaccgacact ctcacactcc ttcacacccc ctcacactca 480
agggataac caccgacact ctcacactcc ttcacacccc ctcacactca 540
agggataac caccgacact ctcacactcc ttcacacccc ctcacactca 600
agggataac caccgacact ctcacactcc ttcacacccc ctcacactca 660
cttcacactca ggcacgctg ttcggtggtc cacoaccgac ggtactgctg tgcacactct 720
cctttcgcc ctcagagttg gcaccagggc gggtctgctg ctgcagtgcc 780
cctttcgcc ctcagagttg gcaccagggc gggtctgctg ctgcagtgcc 840
cttcacactca ggcacgctg ttcggtggtc cacoaccgac ggtactgctg tgcacactct 900
cctttcgcc ctcagagttg gcaccagggc gggtctgctg ctgcagtgcc 960
cctttcgcc ctcagagttg gcaccagggc gggtctgctg ctgcagtgcc 1020

<210> SEQ ID NO: 146
<211> LENGTH: 981
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1316219
<400> SEQUENCE: 146

```
gttttaaaatt tacttaaaat atatatattt tttatatatt ttaactttttg gttttatatttt 60
toatgatttc ctttgctgct atatatcttat ttatctctgct gagttgctttgctatttt 120
tctttcttc tttatatta ctatttaactg aacactatgg gcttttttt gcttttcttcttt 180
ttacatgttt ccctagtctct ctctgatctgct tttctccttc ctttccctttttctttttttttt 240
atgcgcagag gcagagaagag ggttgctgctgcttctttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
<400> SEQUENCE: 149

gagggcgggg gagggacagg tgcgttgtgc tgcgtagagag gaggaagot gcggcagag 60
gagatgacgc tgcagacgg gagacgaccc tgcgtctcccc tgcagatccttg 120
ggcgcctgg gcagcaccgc tgcgacacgag tccttgcata gcacagtgaa tgcgtgttggt 180
ggctagcgc atcccaaccc ttcacatggc agcctcaact ggcacagact tcggtatga 240
atcagagc cccgctccag aacaaaccct cgggtataag cagggacagt ggggaa 300
cattagtct gaggcagagt aacagactta tcaagtgcga cttttctgat acaatgacac 360
gcttggttatt tgcggttatt gcagcacgcc cctgtatatt tcggcagctttc tccggcgtt 420
gacgacaag aagttgttct gtccagagt ttccagagca cctggtatatt ttcggcgtt 480
gttcttgatgc ggttggagat gcccgggtt ttttggtgctatt cttctggtttaggc 540
caggtgttatt ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt 600
atcagagc cccgctccag aacaaaccct cgggtataag cagggacagt ggggaa 660
gcttggttatt tgcggttatt gcagcacgcc cctgtatatt tcggcagctttc tccggcgtt 720
gacgacaag aagttgttct gtccagagt ttccagagca cctggtatatt ttcggcgtt 780
gttcttgatgc ggttggagat gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt 840
caggtgttatt ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt 900
atcagagc cccgctccag aacaaaccct cgggtataag cagggacagt ggggaa 960
ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt ttcggtgatt 1020
ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt ttcggtgatt 1080
gagagcgtgcccc cctgtatatt ttcggtgatt caggtgttatt ttcggtgatt caggtgttatt 1140
ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt ttcggtgatt 1200
gagagcgtgcccc cctgtatatt ttcggtgatt caggtgttatt ttcggtgatt caggtgttatt 1260
ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt ttcggtgatt 1320
gagagcgtgcccc cctgtatatt ttcggtgatt caggtgttatt ttcggtgatt caggtgttatt 1380
ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt ttcggtgatt 1440
gagagcgtgcccc cctgtatatt ttcggtgatt caggtgttatt ttcggtgatt caggtgttatt 1500
ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt ttcggtgatt 1560
gagagcgtgcccc cctgtatatt ttcggtgatt caggtgttatt ttcggtgatt caggtgttatt 1620
ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt ttcggtgatt 1680
ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt ttcggtgatt 1740
agagagcgtgcccc cctgtatatt ttcggtgatt caggtgttatt ttcggtgatt caggtgttatt 1800
ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt ttcggtgatt 1860
ttcggtgatt gcccgggtt ttttggtgctatt ttcggtgatt caggtgttatt ttcggtgatt 1920
agagagcgtgcccc cctgtatatt ttcggtgatt caggtgttatt ttcggtgatt caggtgttatt 1980
agagagcgtgcccc cctgtatatt ttcggtgatt caggtgttatt ttcggtgatt caggtgttatt 2040
agagagcgtgcccc cctgtatatt ttcggtgatt caggtgttatt ttcggtgatt caggtgttatt 2090

<210> SEQ ID NO 149
<211> LENGTH: 2403
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1514160

<400> SEQUENCE: 149

gggagacgcc acgagcag ccctctagcag acacaagggag ttgagtgtgc tcctccctccc 60
taagotcccg ggtcctgaa tcctctgaa ttcctaatgta ttgggggtggc ccgctttgcg 120
cctgtctgcc aggggggccg gaaaggtgaa acaggcttgg ggacggacag tcagatgtag 180
actcggygga gggagtctcc actcctctcct tccctctcttg agctgaagag gatygggtga 240
gctcttcagc aggcgcggag gcctagcagc gatgacgcctt agacagccgc aggctggtg 300
tctgcocogg gtcattgggc ctcattgccc gtcattgggc cgcattgacg ctagcagcgt 360
cctgtcacct cctctccccc ccctccccc cccccccccc cccccccccc ccccccccccc 420
cctggagccc ggacgccagc gcggagctgt gaaggggact tcctatccag gcagaaaaact 480
cttttacggc gggtgcctct gcgcgtgcac ccacgcaggg cagaggtctgg cctctcctct 540
agttaaccgc ggcagcagcc cctctgtctc ctctctctcc gcttctgtgc ggtccctctaa 600
actggactcc gtcctccccc ccctccccc gttctccccc ctcctccccc ccctcccccgg 660
ccagccgaccc ggcctctctg tccctctcct gcagccccttc gcgcctggct ggcagccccc 720
cctggagggg gggcctccccc tggagccacc gatgtgcgta cctctgtgca gggagccacc 780
agctttgacc gggcctccccc tcatacgccac ggcgacgccag cagagctggtg tcttctcccc 840
tgctccagcg ccagagcgcag gatgtgttcc ccatcctctc cgttaaaacc 900
attctctgtgc tgtctctctg gctctctgtgc gcgtctttct gcggctcttg ccagcagcagc 960
ctgggtcctg cgggtccttg cgggtccctct cggcagcagc cggcagcagc gcggagggggg 1020
acacccacgt gtcaggtgcc gccgggctccc ttcggtgcgt ctgtccagctc ataggtggtc 1080
acttgccggcg cgggctggccact cctgcatttt atttttatacg ggtgtggtgg gcagatccgg 1140
occaagccag gcagacgccg ggaatcattattctgcgttgcgtggactt cacgttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttacggttacttaca
<210> SEQ ID NO 150
<211> LENGTH: 451
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 1653303

<400> SEQUENCE: 150
gggcagggc gttccagctgt ctcttcagcagc agaagtgacg ccagggagagg aaggggttgct gtcagagggc 2160
agtctctgacg ggggtagcgg gaagggagagc gaggagaaac gccaggacctc 2220
cctgacttgaggc cggcagcttc toccgtctcgg gcccacacgg ccctcagcaggg 2280
ttcacattggc cctgacgcttc cggccctggtg gttccagcttt cctggcagac 2340
tttcagctacgctttaa tggttaaaaa aatcaacagc gatgaaaggt gaaaaa 2400
aaa 2403

<210> SEQ ID NO 151
<211> LENGTH: 2109
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 1652303

<400> SEQUENCE: 151
ttttacatgtg agtggctagt tttttttttttttt ttgtaaatatt gatatttttttat aataatggac 60
tttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
tccagcaga taattcatctg ggaggttttt cagagtcata cattcattctg ccctgtgtgct 840
gggcaggtg tggcacacaac gacotcttcaac gctaanagcc atctggggtct gctgttcccc 900
tttctcagcc tctggtggaag gaaactctccc tctctctctc ctgtattcaca agtgctgttg 960
aaaattcttg ccacagtggga ctctttttct ctcttctctct ctctgtctctct ctagccacatc agtcgaatag 1020
cactotcgcct attaacttct caggtcgatt cttcttctctc atcaagacato ttctgtcgcct 1080
ccttggagaa gaaagagaata cacctcaggtt gtcgagggca ctgttgttagg ccgtttttata 1140
tagctctctg ttggaatgatg actaaggctt ggcacctcatct ttttttaaaa ggcgccctaaag 1200
taatgytcgtg cagcaaccc tttgggtggga ggaacctctt ctctacgacgc caagtaagga 1260
tgcctccagc tctgattgtt gttctcagag acttatctcc tcaaatatctc tttctacacctc 1320
tttctcttct tctacacaccc ctaggtgcct cctgcatcctc ctagcgcgcc agaggggtcaai 1380
cacaagcttg catgcttctcc gggcccagaaat gacatctcg atggcagtaaat ttcttttttaaa 1440
aaaaccttgg agtcttctgtg atcttttgtg cctgttggttt ttttgcacagg catatatgaa 1500
ggcgctctct cactatttct tcgcagcgttg ggctgtgtgct ggcgcgccttc gcgcgtacac 1560
tttccagctgt ggcgctcggct gttagcgttca ttaagcagaaaa cccagctctc caactatgaa 1620
tctgctccct tgttgtggtct ctaggttttt gcgcatacat caacccaggg ttgtaatttt 1680
tccagtctat gacgacatgt ctgcaggggg ctggatcttca tttggaggttg gcagtttgga 1740
agaggggggg aagaaacttgc gcatttatct ttattatat ttttaaatgct tctacaccttc 1800
lttggcgttg atccagcctgt aatagaaacct gatagcattt aataactctcg ctctctctctc 1860
tttcgtctct ttcttttttttt ttttttttatgatgta acaaccccttttt ttcttttaaa 1920
tgatgtgctg ctctgctgt ctatacatgt taaggtctggtcg ttgtttttgtaa aggggtgattt 1980
catccctgct gcgcgcagtgg tgcgcagac gctacactgg tanagcaacca cagcagagca 2040
tctctctctg aatctcattca attaatgtct cgtaggtgttta aagatcctat ttaatttttaa 2100
aagaaaaaaa 2109

<210> SEQ ID NO 152
<211> LENGTH: 1114
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: 
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1693358
<400> SEQUENCE: 152
gggcggagcag cgtgctcaggg tgaatccttg cgacgacagc gcggcggggc gcggagagga 60
aagcogcgcgc gcggcgccgg gcggccctgg agatctgccc gcgggcgcgg gcggcgtggct 120
tgtcgtctgct cgtctccccc gcggctctgg ccggcccaag ctgctgtcata catgattatt 180
tgtcacctcg atgcgtgagt cctggagacaag ctgcttcacat cttccagacg acaactgccc 240
aggaatcttg gtgtatatctt cacaagctgt atagctcgatc tcacctctgct ccgcgtgaaac 300
cggcgcaggcct ctcgctggccttc ctcgaacacgc gttcttctcat caccgaccag attgtctcttg 360
tgtgagcgggg ggcgctcgcggct ttcgctcagc aagaatcggt gtgcgcagag cagcgcgggc 420
gggcgggtgtg cattctgctcg aacgcagcttg cacaagcagc cttctactctg gtagagtcoc 480
aggaatcagtc gcggcgcgcag gcggagctct ccgcaggcgg cctgtgtcgg gcggagaggt 540
-continued

```
gaacotcag agccaaacgc tgaagaacct cattgctcca gttccagtt gaaatgcggg  
gagaaacotg tccsattta gcgaattggga aaggaggttc ttctccagtt gtgaattgga  
gatgttcttg gtgtgctcga tgaactcacc gacgctcagg atacacagtt gagaatcct  
ctctgctc atggagactgg acgacatgg aaggaattcag tcctcagttg  
gatactcgg cccctggtga ctggttggta aggcagcacc gagtttcgaa ggaacggttg  
gagctctcgg cctcctctcgt tccctcagtt ggttggctcgt  
ggattcaga aagttgctc accctctctg ttccttcagtt gagctctcgg gctctctctg  
ccgcttag aatctaaacc aatcttacag ttcctcagtt ggttggctcgt  
ccgcttag gatctatcag ttcctcagtt ggttggctcgt  
aagttgctc aatctaatcag ggtttcagtt ggttggctcgt  
ccgcttag aatctaatcag ggtttcagtt ggttggctcgt  
ccgcttag aatctaatcag ggtttcagtt ggttggctcgt  
ccgcttag aatctaatcag ggtttcagtt ggttggctcgt  
```
cagatacagt ctctcttgcc tataatgaa ccactaggac tttatacagt tttcottaat 1440
ttgtyacat atasaatgta aatatatatt agyctttaccc tyttttgaaa tghtytgagt 1500
catctcttct actgctacct tcctggtgct ttctagaaaa cagctttcca ttccaaaata 1560
actggatcct gcctttagga cagactcacat ttttgtccct gccttctccct cccttccaga 1620
gagcattcgg tyggttccttc gtaagggca aaggttagaa ctttaaaatgg aagggagaattg 1680
tagtcogaag ccgcaagact ttttttttct tttttaatgga gttgatccat gggatatttg 1740
tgctcgaatt ctctctgaga cccttggaaa actcactcag tttgctcttt gttgcataa 1800
taaattcttt taaagcttttt ttaacatcct caaattcttc attggagtgtt gatgtygcattt 1860
taaattaact ttgctttcct tccttggacc ttcctgcttt gccaagggga gtaagagaatgg 1920
taaactttgct gggagctgta ttgcttctac ttgctggtct cttggagagg aactgctccat 1980
cagctgttaac actgcttggc ctctggagag gactctggcc ttctggctca aagtggttctca 2040
ttaaaatctct cttttaaggc ccgagggcc cttggagggc gtaggtgagga aaaaatttca 2100
aactgtctgt agctgtcgag ccaactatca atggtctgta anaatttcaata acagttaaaa 2160
taaatactt attatgtgct gtsaaatssaa aa 2192

<210> SEQ ID NO 154
<211> LENGTH: 913
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1738735

<400> SEQUENCE: 154
ctcgagcagcc tcgagagcgg ggccaaatgc ccgagacctc tctaataggt gacattcct 60
gctgattct tcgctccttc tctgttattg tctgttgcct cttggaaacc gtgcggctac 120
cocaaagcc ggaccccttc cccacccctc cccacccctc ccaccacccct tcctgtctgc 180
ttggcgaagg cctctctctcc gattccagt tttgagattt ttcttaattt aacctctcct 240
tttgggctag gatgctgcct agtgggcttc ggtggctgct aatatgcaag tgaanccagtt 300
aactgctgtt ctggcctacc agggttaata accaatcaga tttctctttt ttaaagagtt 360
taacataats caaccaagtc gggtgaagag ggcgcggcag cagaggggga aaggggaaag 420
tagcagcttc aatgygccaa aagagatgta gcaaccctag ctttccagac agttactttt 480
coccaaggg actcacttc tgaagaggc ccactaatct cgaataaacg tttggtgtttgct 540
ittaactcca ttgagagcct gaaagggcat gggagctgg tgaatgactgc gcagaggaggg 600
tccccgact tccaattcag aatattcatt agttaaagcc gaggagagga accacaagt 660
ggctgcatg taccgttgc gcgaaggaat tgaattagtt tctctctact gttgaagggat 720
tggttttttt gatgtaaat aacaaagcccc gcaacoawca actcacttc cggcggatgc 780
tggcagcag ataaatagct cactcattca gcaacagggg aacacoattc cttaaccttg 840
cctttctccca gattcactca gcagtgttca cagctgttca ccttctcctc tctctctaga 900
agacggttgca ggc 913
---continued---

<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1749147

<400> SEQUENCE: 155

cctctgttca ggcgggatt aacggttgga gcgcgtgcgc tcggccctct ttgattttat  60
attattagaga ccaacaggaa atgaagcccag ggaaacaccc ttggggaaac aaccttttct  120
tgttggacaa atgcagagcc cccctctctc tgtgctgctg tcctgctctc tacotggcgg  180
gctggtttgg gggtgtgttg gttctctccc ttgagatat gggtagatgtt gttccacaccc  240
cagctctggc agatcaagcg tgtgcagcag gttctctcct cattctcctc tacgtacat  300
cacagcgcct agagatccag ctcacatgtg ttgctgggtta aaactcaaga accacatccc  360
aaggtacact tgtctataag ttgtaaagat cttccacttc ttggaacctc agttotgcct  420
cctcggagct gcacatgatt ctaacocac ccactgcgact tgcgaacatt acacgatag  480

cgggtattt aagaaagggg acccaatgcac atgatttttaa aaggctctgt gctgctatttgg  60
cgttccacag ctcgctcagc ttgaacctt ctaaccttgc ctctcaaggc acgttacaac  120
ggtaagggg ttagcattt taggacaccc ggctgttgcgg tgcagactgc ttgcaaatct  180
cagttcataa acaacctttc attgaatgcg atgccttgga gctagcagtg acaacgatga  240
ttcgcaacag gaccctcctgcc tggaggttttt acacotgcac cctgctctgcc tggcaagatc  300
attgcgcagc cagatcagtgtt ttgctcctct tggagacttg ttgcaagata cagctcatct  360
agcaccact cccacaccac cttagcaggg cttccacaag ttgctcaag saattgctac  420
gccttcgttt ggtgcttcag acctctcaag atctccagct tggagagagc ttgcaacatt  480
agggagtctc acatacaact tcggcagata tgtgtgcggga aaggaataag ttatattota  540
ttata  545

<210> SEQ ID NO: 156
<211> LENGTH: 1746
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1831290

<400> SEQUENCE: 157

tgggcaatacg cttgggcaagt tgtgctggtct caggt tgctttggtccg cgcgtgcgct  60
ggacgttcag ggcacaccca ggcagccacg tggagctgctgg gcctgactggct  120
cgtggtggc gggaggtcggc tgtgctgtcg tggctgggttt cagcagcgtt gctggtgcg  180
tggctcagcct caggctgaaa gaggttcagag aacactctac ccagagagaag tccgctgag  240
ggacacagca cccttcaggg gctccgccc tctctcgtgg tggcgcagcc atggctgactg  300
cccctgcag gccaggg accaagcc gcacaggttg tcgaacctta ccacacgcctg  360
gaggtcgcag cactcttcag ttccagcaga gagaagcaga cgggtcgag 420
gaggtcgcag cactcttcag ttccagcaga gagaagcaga cgggtcgag 480
cagaaagtt gattgcgacaa ttctgagcag aaggtgctca tttcgaagca gaaacacca 540
gagcaagct cccagcagg aaggcaagt gctctgtgca gaggggacct gacgctgca 600
cctgcccctg agacatggcc caatctttgt ctctgtcctt ctgctcctcc gagaagat 660
gaggaattct cggattatca gcacgtacga tctacatcag aatccgagca gttccaggaag 720
gtctggtttg ccagtcgcag aagaagcagc cctggttcctg cgggaagcagc aagccaggag 780
gaggggaaac cggatagct gatggcggcag gtgagccagc cagaagcctta ggggaagcacc 840
gaagaaaggt acgagcaaccc aagagggac gctgagcgtca tggagccgctt gotgcttccc 900
gagaccatt cccagagctg aactaactct taaacccctt gcatggttgc ttctgggagg 960
gagacagctgg cctgctggcgc gtcacgcagcg ccttcgcgcg cocggccctt gcggagcagg 1020
cacccggtcgc caggccgcctcg gcctgctgcg gttccgcgagc tttctggtt 1140
gctgtccccc agtcggccac acaaaaaacccttgccacac tgctatctgtgattctttgt 1200
gctgtatgac aagcttcctt tocattgttg gttgtcttttggttggtt 1260
gctgttgagac ctgttgcctt gaggggcag cactttacat attccgtcgttc ggtagagtac 1320
gattctcggcc gacgactatc atgttacatg atccaggcctatt cctgcaggtg 1380
tggggccctt gcgctcgcct cccttgggag gactcggcct ttcttgccgtt gtcagttcag 1440
tccaggaas ggggctgtgt gcgcatcccatt attgcgccttc agtgcagatgcttatgtct 1500
cagaaagtt gattgcgacaa ttctgagcag aaggtgctca tttcgaagca gaaacacca 1560
cctgcccctg agacatggcc caatctttgt ctctgtcctt ctgctcctcc gagaagat 1620
tggttgacg gcgtttgcag aagagttcgg gccccagagc ccccgagctt cccccatgtg 1680
cagaaagtt gattgcgacaa ttctgagcag aaggtgctca tttcgaagca gaaacacca 1740
aaaaaaa 1746
---continued---
gtggagcttg gcttcgagcc accctggcaat cttctccatt accctgcggc accctgccct 540
agtggatagc ggtcctgctt cgtggctggt gggcctggag agcacccttgg actccgagac
600
cagggccttgg ggttcctcag ggactgacag aaatggccac atctcaacctgt 660
tgggctctatt ctcttccctt cccaggttga cctgcaccatg ggttccttcc 720
ggtgcccctc atcttccaggt cctctctcct cccagtcctg ggccccctc 780
aacggaaccg gcttcgagcc gctgctgctg cggatcctgag ccagggctagg gacaccctta 940
agyatttggc aaccctggcc ttagactcc aaccctgccc cagggctgcc cggagcggc 900
agcaccctt cccctgctct atctggtgccttg gcggtgatcttg 960
gctttcgcttg cccgactggc cctgctctcc cccggtgcttg ccagagcttt cctggccct 1020
cctggactc cgtcctgagct cttccaaacttt tgggtctact tggacccagct ggggtggagct 1080
gggctctgtc ggtggtgcttg ggggctctgtc cttctctggctc cttgagttgt 1140
cctcttgcgg cttcctgctct cttcctccttt cttctggtctctt ggtgagctcagctcgt 1200
cagagccgcttcccagcctc cccctctgctt cagctcccttct ctgctcccttctc 1260
cctgctgactc ggggtgcctt ggggtgctcct tggagcctgaactt ccacctgctgcct 1320
aacggtggcg aaccctggcc ttagactcag tggactccag cagccatgtc cggagctggg 1380
tagttccttgcc agatatgcctt ggtggtcttg cctcgcacact gggacaagtg agacatcggg
1440
ccacgctcgg cggagcggc cagccgcttcag cccctgctct cttctctggtct 1500
tgggtgccttg ggtgagctgct cctgctctcc cttcctctgtg cttctgctctg 1560
ggtgagctgc cggagcgccttg cccctgctct cttctctgctt tggaggtcctct 1620
cagctgctg ctgctcccttct tcctcgtgcc cccctgctct cttcctgtctgc 1680
ctctgtccctg cccctgctct cttgctcct gccttctctctgt cttgctcctc 1740
cctgctgtgc cggagcggctctg ggtggtcttg gagggccttcag cccctgctct 1800
tggagccttggt ggtggtcttg cccccctgctct cttgctcctctgtc cttgctcctctctgt 1860
cctgctctgcc cccctgctct cccccctgctct cttgctcctctgtc cggagcggctctg 1920
cccctgctct cttgctcctctgtc cttgctcctctgtc ggtggtcttg cttgctcctctgtc 1980
actctggtgg gsaacctgcc gsaacctgc gsaacctgcc gsaacctgc gsaacctgcc 2040

<210> SEQ ID NO: 159
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (440)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1841607
<400> SEQUENCE: 159
ccccgctgcg cggaaaaaga cggaaaaaga aatgggcttc atcttcttcc ctgctgactt 540
cccctgctct cgtggctgctt gggcgctttg cttctcttgctt cggagcggctctg 600
tgcctgctt ccacgcttcag cccagcttcag cctcctctctgg cagccatgctgcctc 660
cctccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 720
ggtgagctgc cggagcgccttg cccctgctct cttgctcctctgtc cttgctcctctgtc 780
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 840
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 900
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 960
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1020
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1080
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1140
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1200
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1260
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1320
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1380
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1440
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1500
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1560
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1620
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1680
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1740
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1800
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1860
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1920
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 1980
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 2040
cccctgctct cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc cttgctcctctgtc 2100

---continued---
-continued

```
atattatccat  tattgaggctg  cagttggtcttg  cnaaagggcag  gcactcacaat  ttgaaaggctt  900
atatttaatgt  gatasatttyg  agaacatcatc  cagagtgtgyg  tcattgaacaa  cttcgycatc  960
atattttctgg  gaagcctctgt  ggaagccagt  agtgcacact  ccccctggtct  taataagca  1020
atatataataa  gcattagggg  tgccttctcc  ttgaaamaaa  maamaa  1068
<210> SEQ ID NO: 162
<211> LENGTH: 1173
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> OTHER INFORMATION: Incyte Clone No: 1855755
<400> SEQUENCE: 162

gttcgcttcc  tggccagccc  gggyggtctg  cttggggggt  tcttctctct  goocagacaac  60
cagacccggc  tggccggccc  acctggcaggy  agacggaagc  gagcgccgga  cgcgyccatg  120
gccygcctgcc  ggggcttccc  tcttgggggctg  goocctgtcyg  tcttgatggyg  180
cygcgctgct  agtyggaggt  aaccccaacag  cccctggagca  gcgcctgggg  gaaacgaccc  240
gagctgaccc  gcocatggtg  cagctgcttg  ggaagacagct  cggcctggyg  gtyggtggctt  300
gtgcgcyggg  ggaacaccaatc  cttcgcttcc  ctccttacttcc  tctttcttacatc  caagcyccatc  360
tctgtatccct  cttgcttctatc  gttccagccccg  gcggcgctgg  ttcgagctgg  tccgagatgg  420
ggcgcgtccag  ccctgagcact  gaagccggtc  cccctctcag  acgctgacact  ctccttctctc  480
cagcttacac  ccccccagcag  cttttgctctttc  ggtcagcta  cctttacttac  ctttactctac  540
tgtgccctcc  cctaacatcc  cttattcagct  cagcttgggc  aacccctgctg  gggaggcttct  600
acctggcctga  gtcagtggctg  ttcggagcgg  gcctctactc  gcgtgagcyctgc  660
tgtgccttctt  tgtcccagccc  tctcttctctct  gcagcggtcct  aaggygggtgt  gttgcggccag  720
tctttcttca  cccctccttc  cccctcttct  cttggccctgg  acgctgatcct  gcgccttgggc  780
cgcctgctgc  ctggtcggygtc  tggccgcttg  cccctctcctt  gctggcgcag  cgggctgccag  840
gccgctgcgg  gttcttcggtg  gtcgtctcagct  gcggctggctc  gcggcgtgcct  tggcctggct  900
tggcctgctca  ggtcggacaa  agagaggcgcag  aagaggccca  aggaggacata  tgggggtgctg  960
gcgcctgctgg  agagctgctgc  cggcctttgg  atcttctgcag  accctcttct  ggggygggtcag  1020
ttttgcagaag  gtggctctgg  aagccctgctg  tggccagctg  cccctcttcag  cccctcttttg  1080
agctcccttc  tgttcgcttg  atccctctct  atctctctgtct  gcggctggggg  ggaatctccac  1140
taatagcttg  tgtgggtact  ccccccaccc  cccaaaga  1173
```

<210> SEQ ID NO: 163
<211> LENGTH: 890
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> OTHER INFORMATION: Incyte Clone No: 1861434
<400> SEQUENCE: 163

cgcgacgcgg  agagctcttc  taccgcacgtc  gttggaggag  gogcctcagta  agtcttctctct  60
taatatatct  gtcggcgttct  ctgttcttct  tgggggctaaa  aggccggcag  aggacaaaa  120
tcccaagctg  cgaattttcgt  ctttccttcc  ootcctcggc  gcgccgctgg  180
ccagggtaata ttcctttttt tcctgatcctg caacagcctc ttttaactgt tttaatgaga 240
atgtcttgg ctctagagag tctactcacc tggccattccc caactacttt cttgctaatg 300
ttggttgtaa aatctgagta gaaacagcct ttggaaattt ctgcattatt cttacaggc 360
ttggatatgg atctactctct tcttgctcttg cttggattca aaactgcttg gggctgaag 420
tttggcttgg acctagagac tggagcacaac aaataaaaga aaaaaagccctg tgaatcaatt 480
gaaatgtac attaaatgc cttcttgcttc gcacattgtg ataaactgga aagttttact 540
acctaaactc tatctgtctg atctctcatt cttctgctctt ttgctggctg tggctttaaca 600
gactctggtg atatgctttt ttcttgagga gctgctactc ttgatcactt atctctcttc 660	tttgcgttc gaaccaagta acataaaggt gttctgataat tcacagggg cagagatc 720
agcagaaagcg gggagataac ctaattaagtt tttaataactc ttgataaaaaa cagaggtggt 780
gaacagcag cttctgacag ctacatagct tttaatttca gcagttgtgt attagactct 840
cattactctc atgagttaa ataatgtttgt tttgacccca aaaaaaaaaa 890

<210> SEQ ID NO: 164
<211> LENGTH: 906
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<222> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 18772330
<400> SEQUENCE: 164
tggacatgag cccagagcag gacatttttcg ttcctttttt tcctgatcctg caacagcctc ttttaactgt tttaatgaga 60
cctgctcttg ctgcctagctc tggccctacta agggccgacg aatgctggg gatctacaag tttctttcttg gaaacagcct ttggaaattt ctgcattatt cttacaggc 120
ggtctcttgg gacccagagc gacatagctt ctgcaccttg tcctcctatttcgacagcctt ttgctggctg tggctttaaca 180
tttgcgttc gaaccaagta acataaaggt gttctgataat tcacagggg cagagatc 240
tttggtttgg gcactctactc cttctgacag cttctgacag cttctgacag cttctgacag cttctgacag cttctgacag 300
gggatcaaga caggtgataa tttactattg gctgagacac gatctgataa tttctttcttg gaaacagcct ttggaaattt ctgcattatt cttacaggc 360
cattactctc atgagttaa ataatgtttgt tttgacccca aaaaaaaaaa 420
cacatgag gtaaagtcag cccagagcag gacatttttcg ttcctttttt tcctgatcctg caacagcctc ttttaactgt tttaatgaga 480
tttctttcttg gaaacagcct ttggaaattt ctgcattatt cttacaggc 540
gactctggtg atatgctttt ttcttgagga gctgctactc ttgatcactt atctctcttc 600
tttgcgttc gaaccaagta acataaaggt gttctgataat tcacagggg cagagatc 660
tttggtttgg gcactctactc cttctgacag cttctgacag cttctgacag cttctgacag cttctgacag cttctgacag 720
gggatcaaga caggtgataa tttactattg gctgagacac gatctgataa tttctttcttg gaaacagcct ttggaaattt ctgcattatt cttacaggc 780
tttctttcttg gaaacagcct ttggaaattt ctgcattatt cttacaggc 840
tgctggcccc gcacaagttaa ggcacagcgg ccagcacttg ctctgggcgc gcactctctg 120
cgcgcgcg acggccggcg ttcggagctt ccctcttgcg ctcagtactg aaacttagtg 180
gaaattcttt ttttctgctt gttctgcctt tcctctcttg actuactctg gctctggga 240
eactagtg aagactgtc tctcctctgc gcgctactg gcacactgtt gaaactttgt 300
cagtctgtcg acagctgctg gctcttcttg tccttttcttg gttgctcttg aagacagtgg 360
cagcactct taactccgct gactctcttg ggcgtactct ttcactcttg ggcgccgctc 420
cagaccttc gcacacgcgg ctacatgctg gctttctcttg ggcgcctttg agttttgctc 480
gacgttccgg ccgctgctc ggctctgggc gcagccgctg gcctcgctcg gcctccttcg 540
gagctgagc ctactcttgc tggcctgtg cctcctccgc gcggctgctc gcgctccttcg 600
gacctccgct gacggccgct gacggcttctt ccttctctctc gtcctcttgc gcctccttgc 660
gaagctcagtg gcacgcgctc gcgctccttt gttgctcttg gcgctccttg gcgctccttt 720
gggagctcgc agcggcgcgg cggctgcttg gcgctccttg gcgctccttt gcgctccttt 780
gctctctct ccctgcgctc gcctctctct ccctctctct ccctctctct gcctctctct 840
gacgctgtg caactggctc gcagctgctc gcgctccttg gcgctccttt gcgctccttt 900
gacgttccgg cggctccttg gcgctccttt gcgctccttt gcgctccttt gcgctccttt 960
gccctcgcg ccctctgctt ccctcgcgctc gcgctccttt gcgctccttt gcgctccttt 1020
gcgcgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1080
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1140
gccctcgcg ccctctgctt ccctcgcgctc gcgctccttt gcgctccttt gcgctccttt 1200
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1260
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1320
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1380
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1440
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1500
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1560
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1620
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1680
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1740
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1800
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1860
gacgctgctc gcgctccttt gcgctccttt gcgctccttt gcgctccttt gcgctccttt 1920
aaa
1923
ttgacacccg caggggtgacg tacgctatyt ctaaccttcgct gctgcccccag actgctcttg
60
gagttctagt gacacagcct ctgctgcccgg ccctgcccag cacoaagagc cocatagtgc
120
atctgggtac ccctcctctcct cctgtttaca tccccagtcg tggagctcag cagacocctcag
180
ggagagacag atacccctcctt gctttacaacct gccctcttct gctcttgacct
240
gctccctctcct cctgcctctccct ccctggctccct ccttgctcggct gcgtcgcgctg gcgtcgtcgcgt
300
tcacacgct ggcgcgtgctgc cttgcccctccc gctggtgcgcg gccgtgcgtgc ctgcacgccg ctgcacgccg
360
goaacacgtta goaacacgtta cctgggaggt gctgcctctcct cctgcctctccct gccggtgcgtgc ctgcacgccg
420
tctgcacccct ctcctctctcct cctggtgctgc gccggccggag cacoacccag acctgctcttg
480
gacgcaacctg aacacacaccc aacacaccc
518

<|endoftext|>
-continued-

gctggaacag ggtatcTcga gcccatcctc ccaccttcct ttcctggtct gttctgtgac 1500
ttcctaaaa gggaaattg ggtctgaga taacctgacct ggagggascc gagggttgcc 1560
tgagcagaga tttgctgcatc gaaatccag cttggccaaac acaagcgacag ccatacctcaaa 1620
\n\n\n\n<210> SEQUENCE: DNA
\n\n\n<210> SEQ ID NO 169
<211> LENGTH: 1548
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<222> OTHER INFORMATION: Incyte Clone No: 1890243
<223> QUALITY:
<225> QUALITY: 168
\n\n\n\n<240> SEQUENCE: 168
\n\n\n<210> SEQ ID NO 169
<211> LENGTH: 616
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 1900433
<400> SEQUENCE: 169

gccagctctg tgcagccctc gcgaagaagta gctgagcggta ccaggtggaa ggcagaggtga 60

<210> SEQ ID NO 170
<211> LENGTH: 1981
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 1909441
<400> SEQUENCE: 170

cgacagtctct tttgcacgcc ategaggcccc ctggagcttaa cgtgtgaaaa cgcagataac 60

<210> SEQ ID NO 173
<211> LENGTH: 169
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 1900433
<400> SEQUENCE: 169

gccagctctg tgcagccctc gcgaagaagta gctgagcggta ccaggtggaa ggcagaggtga 60

<210> SEQ ID NO 170
<211> LENGTH: 1981
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 1909441
<400> SEQUENCE: 170

cgacagtctct tttgcacgcc ategaggcccc ctggagcttaa cgtgtgaaaa cgcagataac 60
ttatctgctcc ataaggagta cttgaactgtg atccaactcga aagggaaagaa tttttgggca
ccggtgctga acatccattta totaaacttga gatattgagaa cctcttttata ttaggtgttc
ctgattttct ctgcaagcaga cttgaaatttt ttccacaaaaa gctgctaaag gccttttttta
atcataaaat cttgcotaga cttgacggct acactggtaga attatctcota ctgacgagctg
caagagctca gttacatcct atggagtttaa atagactcagt ctgctttggga tggccctgtg
atcgatcag ctgttttcgcc gacggttctct gccacactata taatataggtt atctgtggca
ctggtggca aacaagagag atttttttta ttggagcata ggtcactagga ggaacaattgt
ctggaaagc ctcgggttgc agcctttttt acaacagag caattggag ttgatctttg
atccaaaaag aacatctctt cggtaagtc gcacataaat acgatggtgga caacagcagc
aatagctcttg gcacaaatgt atggaataaag tttgacagca gttggaacagc cagggctgaa
gggatttct gggaaatttg gatcttaaa gagaatct ccaatcat ggaaggaaga
caacactcgc tattaaagaa cagttgcagct gttacaagttg ccagcaagttg
ctggggctcag cctgggaactgc atggcattgc atggagtttaa atagactcagta gttgtatgg
ctgatcag ctgttttcgcc gacggttctct gccacactata taatataggtt atctgtggca
g

<210> SEQ ID NO: 171
<211> LENGTH: 1492
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1932226
<400> SEQUENCE: 171

cctccccctggcgaggaagagatcgtgctgaaatacgacagccagacaagctggccattcctgggtggcgccctggagttgatcgcagctggccattcctgggtggc

-continued

gggcggaggt cagcacaacc ccaagtcaccgg gccttgccccc cctggaaggtta gctgactccaa 1080
gccttcacag cacaatacta gacatcaggag cccatatct cccacactc aagtaagttt 1140
ctcagtctcc tagtctccct ttctcaccocoa cctcttccag gttgctcatc taccocaggc 1200
ccagcccttc ggcctcctag ccaggcggcc tccctcagac tggactccag cagtocacctt 1260
gtgggttcct ggcctcctc cotaagtctta ttgtctgctg gggctgtcttg gtgtocctcc 1320
taccocctat tgaactccag ctggggccag ggtgggtgag gggctggaag aagtaatgtaa 1380
tttttctct cttttatgtt cttttttcgtct ctttcocctca cccctgcccc ccccoccccac 1440
caaaaaaga aaaaaaacaa acacaataaa atatotgcag ggaaaaaaaa aa 1492

<210> SEQ ID NO 172
<211> LENGTH: 1613
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 1932647
<400> SEQUENCE: 172

cctggaatcc ggtctgagac gggctcagag cgcggtttta cttgctggccct tccctggttt 60
cagcccttcca ctcgacagag tcagggcgtct gcttgcgccgc tttggaacag tcaccagcttg 120
gtggaggctt tccagactac ccagggactg ccaccctaag acaccagcct gcacacggggg 180
cctgaggttgc caggacaagct gtagttgctag ttatgagcgt cccctgggag ccgccgtttc 240
cctcaggggt tccagggggc ccagggccct gcacaccagc gcacactgag acggagttgg 300
cccggttccct cttccgcctc ctacactctc cttgctgcggc caggagacct tctgcaacaaa 360
cctcgtaacc ctcctccgctc tccctggccc caccctccga gcgcagcccaag gatccttggag 420
gtcgcggacg tgtgctctaa tggagggctg tttggagggg aacacgaga agatctgcgcg 480
cagggggac ccactcttctg gttatgacgt cttcagcccct agggagggg gacacccttc 540
catctctag cttcagggtg gctggtccca gcaggtgggc aacggtgctt ctggggacaac 600
ggagggggc cccggtgtta tgaactgaaga cttgcacagag aagatgttttct gcacgcyctga 660
tccggggac accatatagc cacaaccgaa attttgttctt gttggccaaa 720
atcgaatcc gcagagtctcg ggtggtggga cggctgtcag gacacgcgtgc ttccctagag 780
ttgatgacct ctcacacccgc tttgtgacggc aaaaagctgg aacgtcttgg ggtgccaaa 840
tccgagacgg cacactccac acacggccct tccccggtctg tttggtgactt cccattcggca 900
ccttctgctc tctgagctgt gcaatttgct gcacagcagt gcagttctgc tgaactctctc 960
cctcctcacc cttggctctc cttgctcagac gcttgggctgt ctaccctctc gcaagcccgct 1020
ttttctggtg taccagctga cccocccgat gcocgcgcccc aagggccgca cttcatgtaa 1080
tgatgggctt atctatctct ccaggggcttg ggtctgcccc aaaaagctgc ctctggggtcg 1140
cctgtgacct cttctctgctg cccctgcca aacagtcagc tcttctctgc tctctctgctg 1200
ctgtagagac agtcttgactgc cctccactgc gacgggtggc ccccagccct gcacagcagt gcacagtc 1260
tccgggtcct ctcctctggg ggtggggttg ggaactgcgc ccacgctgctg ggtggggttg 1320
ggtttgctc ctctgtaacc tctattccct ccacgattct cccgtgtgcgc ctcacccaca 1380
cctcacaacc ccttccgacc ttcctaatca atggctggag cccacacgtt cttcccaatt 1440
ctgctccatga atcactttcgg ccacacaa ctccttcctt ctttttcctt aacagcacaa 1500
cacggtcag cctggaacat cggagcagc gcctggtttag gcgctgatg 1560
cctggttag ctgatataag agacacctgc ctttcttccaa aaaaaaaa aaa 1613

<210> SEQ ID NO: 173
<211> LENGTH: 1622
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2124245
<400> SEQUENCE: 173
tgtggtagct ggacgccgact agtgatctgg agggtagagcc 100

ggctggttag cctggttagc ctgactggcc ctcctcctct cgggtctttg 120
gctggcttct cctggtggta ctgtaattcg aggctgtgcc ctgctggact 180
gctggtttg gccagggtta ctgcctggct gctggccgct ggactgactg 240
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 300
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 360
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 420
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 480
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 540
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 600
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 660
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 720
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 780
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 840
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 900
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 960
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 1020
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 1080
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 1140
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 1200
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 1260
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 1320
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 1380
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 1440
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 1500
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 1560
ggctggttag cctggtggta ctgtaattcg aggctgtgcc ctgctggact 1620
tg 1622

<210> SEQ ID NO: 174
<211> LENGTH: 1320

gctgaccca gcctgagcgc gcacagcctg gagaagagag cgtagcgctgc ccagcactc 60
cctccctgc gcctagctgt ccgctcctgg ccgcccaag gaggcgctgc ccaacgac 120
ggccttgag agagagctgc cctgtgctgg aagagttcct cagacatgt gggcagagtc 180
gacgctctga agctgctgcc aggctcgccag tctacgtgtct ctatagagag tttgcaacc 240
tgaccggaga tggagccgca tgtacgtggc tcgtactgcct ccagccgccc ggcgcggc 300
ctctaccgcc gcctccagac gcctgctttcc tccaactgcga ccgctgcaac ggtgcaacc 360
ggaagcctcc cacgagagtt tctcactccgc ctgatcgttat aaccag receptive tctgaactgc 420
gccctggctgc gcgtgctgtct ggcygcgcgc acacagcctgc acacgctctgc tgcgaggtc 480
cggagagag tggagaggtc caccgctgcc gcggcagggag ggtagggaga 540
gcggtggtgc gcctcgcctgc tcacgctact gcggcctcc acaccagcttc ctagccgc 600
ccccctctgc ctgctgctgc ctgctgctgc ctagccgcag cttgagacctgc cggcaggtc 660
agagctacgc ccacacgcct tgctgctgc tggagcgcgcc gcagagagaat gtgagacgctc 720
cagagctttg ctgctgctgc gccagccgcct tggagagagct ctagcagtcgt ctagccgc 780
cgggagcctac gcggcagccct tttctctgcgc cagagcgcct gcagagaagtct 840
gggagcctac agctgccagt tggagactaga tctgctctgc gcaccagatt ctagccgc 900
cctgcgctgc gcggagcctgc ctagccgcag cttgagagctgc ctagccgctg 960
cctggagctgc ctgcgagctgc cttgagagctgc ctagccgctgc 1020
agagctgagag gcggagcgag gcggagagag gcggagagag gcggagagag gcggagagag 1080
cacccotcct gagcgcgctac ggcggcagag gcgggagagag gcggagagag gcggagagag 1140
gcggaggtcct gacgctgccgt cggagagag gcgggagagag gcggagagag gcggagagag 1200
ccgagggcctc tcaggtgcggt gggagggccgt ctcggaggtgc ctcttcgctgtc cctcgtgtc 1260
ctggagagag gggagggccgt ctcggaggtgc ctcttcgctgtc cctcgtgtc 1320
agcctgggct gcccacggtg cgtgagggg ggcggagggg aagcagaggg aagaagagcg
atgtatcaac tgtagacgct ttcgaagggc tgcacacctc gagccagctc cggttagag
agagcttgcc cggagagggt cgtgcaaggg ccctgctctg cgcctggctc tcggtgctg
cgagcccttt gaccagagcc gacactttca gggcccgggg gcgccttccc acacagctcc
gagcctggga tgtgagggcc tgtgagggcc ttcagagagct ctctgggctc ccctgggct
ctttcgctcc ctctgctggc ctgctgggcc cagcgatccag cagggcttcg cagggcttcg
gagctggggag cagcctttgg cctgagggcc aagcctttgg ggcggccgg cagcctttgg
gcgcagctg ttcgagggcc cccgagccag ttcgagggcc cccgagccag ttcgagggcc
gctcctggtg cctcgggtgc cccgagccag ttcgagggcc cccgagccag ttcgagggcc
gggtgggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg gggttggtgg
<210> SEQ ID NO 177
<211> LENGTH: 1477
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 2292356
<400> SEQUENCE: 176
ctcgctcggt ctgctctggg cctgggggct tgccttgctt ttcgccccat ctcctccctg cgtccttggt 60
gctcttgcc gcctcctggt ccctccctct ccctccctcct ggcgtctgtcc ccctccctct 120
gttgcctcccc ccctccctct gtgcctccct cgggctcttg gcgcctccct gcgcctccct 180
ggcctccct ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 240
gggtccctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 300
cgcctgctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 360
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 420
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 480
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 540
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 600
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 660
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 720
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 780
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 840
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 900
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 960
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 1020
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 1080
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 1140
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 1200
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 1260
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 1320
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 1380
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 1440
ggcctcctcc ccctccctct ccctccctcc ccctccctcc ccctccctcc ccctccctcc 1500
<211> LENGTH: 662
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2349310

<400> SEQUENCE: 177

ttgggtgaaga attaattctct tccagacccc tacattgctt ttcaaaactgc 60
ttaaaagac acaataatcg tgcacctggt tttcttatctt tcctccccgg aaactaca 120
cggttcttc tttctctttc cacaccacccag gacgctag gattacagt gttccctct 180
tttccctgc cccacagcac cttgatcttc gcaggtctgg ggcgtcctct tttccctct 240
ttaaactaatt cccattotctt cagctgtatc aacggtggaag taacatgtgt ttoattaact 300
cggttattga taagagacag aagatgcttc ttcacagtgt aagtacagct cctctotcta 360
ttaaagacacgattctgcag taagtcttaa aagccacagc agaagcttccg accttgcttcg 420
cgtggtttgct tcgttgctgc cgggttgggt gctgtggcttg ggtgtggcttg gattgtgctg 480
tggtatcagc cccctggctgc tgggtggcttg gcacgcttccg ccctgtgctgc 540
acgagccct gcggagaggg ggctgagacag ctggtttggt gaaactagaca gtaaagacac 600
caggggcaac ccagacata ctaacccaaa cggccccactt atttgcttcttttattgatt 660
cctggtatt aagccacacac tt 682

<210> SEQ ID NO: 178
<211> LENGTH: 1508
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (11)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (139)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2373227

<400> SEQUENCE: 178

gctggctgccc tttacgccgtt ataagcagtt ttcagctgcc tgtattacc 60
cggcgacycg gcggcagcag gcggcagcag acaattggtctgc aaggggctgccc 120
tggcccccct ccacgctgcag gtaagaagctt aagctgcttg cctc 180
ttgctgtgtgt gcggctgcttgc cttgactacgt cgcagcagcgc gttgtgcttg gccgcttgcct 240
cagcagcagcctt gcggctgcttc gttgactacgt cgcagcagcgc gttgtgcttg gccgcttgcct 300
gcgggaagctt gggcagcagcctt gcggctgcttc gttgactacgt cgcagcagcgc gttgtgcttg gccgcttgcct 360
gcgggaagctt gggcagcagcctt gcggctgcttc gttgactacgt cgcagcagcgc gttgtgcttg gccgcttgcct 420
gcgggaagctt gggcagcagcctt gcggctgcttc gttgactacgt cgcagcagcgc gttgtgcttg gccgcttgcct 480
ttgctgtgtgt gcggctgcttgc cttgactacgt cgcagcagcgc gttgtgcttg gccgcttgcct 540
cagcagcagcctt gcggctgcttc gttgactacgt cgcagcagcgc gttgtgcttg gccgcttgcct 600
gcgggaagctt gggcagcagcctt gcggctgcttc gttgactacgt cgcagcagcgc gttgtgcttg gccgcttgcct 660
gcgggaagctt gggcagcagcctt gcggctgcttc gttgactacgt cgcagcagcgc gttgtgcttg gccgcttgcct 720
-continued

acacacagag agcttccag tgcgaacctc aatacagcgg ggaagttcag cacgaggtttt 780
ataagcaata tgcagaccgc tgaatacaggg tctacttcaac gctgtgcgcgg ctoccccggg 840
aggtctactg aggaacctgc aggtctccag gcacaacctgga gccaagtgtcc caacaccccg 900
tctacccgcg ggcagctgag gtcacccctaa ccacacagcag tggacatccc tggagatctg 960
cggctgtggc tcagcgcgctt ggccgctggg caactcgcact gcacagtggg caacatgacg 1020
cggagcgcgtct tcgagaaacct gcacgacgtt tcgggggaccc tcggagtttg gcggctgcagc 1080
cagctgccgc gggagcaccag gcttgcaccc ttcaccaact gtcctgcgaac cgcacctcgg 1140
gagacgacgcc cccctgacag gactttcgttg actgacaccc actgctgcctc tccagacacc 1200
accaccaacaga gggcgccaac tccggcccttc cccacacacc acectcaagag cagctccagc 1260
cctgcaacccgg cccagcctgct cccgacgctg gctttttgga aacgggatcg gattggtcttg 1320
gagatttcc ggaatagcgt cttctcagtg ttcacagaga tgccacacta agacagaaac 1380
cagagatct gcggctcttc tcccagctag gcgaggtccag tatctcaacc tctcttgccc 1440
ttcacatctt agacacagag atatatattt attacagaaaa aacaaaaacty gaaaaaaca 1500
aaaaaaa 1508

<210> SEQ ID NO 179
<211> LENGTH: 558
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2457682

<400> SEQUENCE: 179

ggagagagag ggccccgctc ggccgacgct ttgctcgtg tagctgaggg aaggggcctg 60
gcgagcgctc gcgcacggag ctgcgtgcgg gcgtgacgctg actgagtcgt gcagttcggaa 120

gagacaagct gggcygaggg ccgtccagat catttcctgg cccagcagcc aacctacagt 180
agctccgact gcggcagctc tgggacagc tggatagatg aggatggctg gttacggtct 240
ggcttcoccc ttcagagggc tcaacacagt cccagctccct gcggagatgt cccctggccc 300

cgctcctctt cccttggagg gcaggcagctg gcgtgagcct ccgttttttca cgcgttcgctc 360

agctctcgca gttctgaccg ctacccgacc ccgctgggag accgccaccg ccctctccctc 420
acgagtcggct ccgtctcgcgtt tcgggttgg aacagagagc cgcctacgct gcagagagtcg 480
agagcagcag ttccagctgt actgagaccc atggagccag gttctcccaaa gttgggcata 540
cctccgggct gccgctgctg 558

<210> SEQ ID NO 180
<211> LENGTH: 502
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2480426

<400> SEQUENCE: 180

cctggagcgtt ggagagagag aaggggcagc gcggagagag gcggagagag cggagagag 60
ggagagagag gggccagctg ccgcagcagc aaggggcagc gcggagagag cggagagag 120
ggagagagag tggagagagag ccggagagag cggagagagag gcggagagag cggagagag 180
<210> SEQ ID NO 181
<211> LENGTH: 1659
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<222> FEATURE:
<223> OTHER INFORMATION: Incyte Clone No: 2503743
<224> SEQUENCE: 181

gtctgtgcgc gggccagggc tgggagcgcg gcgcctcctc ccggcgcgcg cacctgtctg  
gagcggcgcg gaggccgccg ccgcgccggc cgcgcctgcg ccaggctgcc  
agggcaaca ccggtcctct ttctctctctttcctgtctg ggcgaatgg  
ccctcctggt gcctcgccga aacccaatcg gctgcctcgg gtcgtctgtc  
cgctctgccg tgtgggcggt gcggcagcgc gggcgcacgc gcaggccggt  
ggaggccgca aggtcgacga ctatcgagag ggtggccccc cgggtgcctc  
gggctcctgt ctcctcctgc ttgtcttcct atatccacgt ttattcggcg gtgccgcggg  
cagtctggtc gcggagagcg attgctctcc gcgtgcgccc tgggagtttc  
cggccagggc gcgcctcgc cgggtcgacg ctcaggtgcgg gaaacagctcgattg  
cggccagggc gcgcctcgc cgggtcgacg ctcaggtgcgg gaaacagctcgattg  
cggccagggc gcgcctcgc cgggtcgacg ctcaggtgcgg gaaacagctcgattg  
cggccagggc gcgcctcgc cgggtcgacg ctcaggtgcgg gaaacagctcgattg  
cggccagggc gcgcctcgc cgggtcgacg ctcaggtgcgg gaaacagctcgattg  
cggccagggc gcgcctcgc cgggtcgacg ctcaggtgcgg gaaacagctcgattg  
cggccagggc gcgcctcgc cgggtcgacg ctcaggtgcgg gaaacagctcgattg  
cggccagggc gcgcctcgc cgggtcgacg ctcaggtgcgg gaaacagctcgattg  
cggccagggc gcgcctcgc cgggtcgacg ctcaggtgcgg gaaacagctcgattg  
cggccagggc gcgcctcgc cgggtcgacg ctcaggtgcgg gaaacagctcgattg  
"
<210> SEQ ID NO: 182
<211> LENGTH: 2059
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 2537604

<400> SEQUENCE: 182

aaagcaacag gcaoagtctc acacgaccag gtagggcctg cctgggtggc

ccgacgctc ggttggtaga ggccctacc tgcctgtaag ttatggttgc cggaaacgag

5'atacgccaa cgaagagagt attgctggcg agagacggcc tggcaagtgc ctcttgttg

3'gttataaaatc ggagagatg ggcttaacctt ttccttctctat ccagggaggt ggcaattcata aaggtagatc

<400> SEQUENCE: 360

ttcgcatg agcagacatg agtagtgccg ggtcggagcg ccaggttgttg cggagtgttg

<400> SEQUENCE: 480
tctgtaga atgcaatatgt cctggtatata cagaatatata gtagacaacct ccttctctat

<400> SEQUENCE: 540
cagagagcg ctcgtggctc tgctatgatg cctggtggtgt gcggcaggag gcgtgacggtg

<400> SEQUENCE: 600
tggtggtcgt tcctctgattg tgcgtggca gcctggtggc ccggaggtgg ggtcttgctg

<400> SEQUENCE: 660
tgcgtgtcgt ggttctcttg cctttgtcctt cattggctct tctgggtgctt gcggggtgct

<400> SEQUENCE: 720
tggggcttg gggagttcgt cgtcggctgt cggaggagcg ggccgagggag agttgctggtg

<400> SEQUENCE: 780
tcgtgtgct gcctgcgttg gcctctctgc ggccttctgc ctggaggtggt gcgggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
gcggggtgtg
ggggacccct cacccctcttg tggagtttttc cacccctctcag aagttctcttc tttcgcgag
caagacoac gacatasaata aacctatg

<210> SEQ ID NO: 185
<211> LENGTH: 1248
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2641377
<400> SEQUENCE: 1248

cggctcgag gtttcccacag ttctgacca a cctctctgcc tttcgcgatc cttctctccatt
60
ggctcagatt ctttctccgc agttgtgccg ttccatccct ccagttctgg ccacgccgctg cttccagctgag
120
aatcctgttg ggtgctctgg cccagtaact ccacaccaacct atttgttacc ttttgggtcg
180
gttcatctct caagccacag gccaagccct gcagttgtgg cagatacagtt ccaagtttcc
240
cctgaagcctt ttcattcctcg ggtggctctgg cggccgctggt cttctctctgg ccacgccctgag
300
cctctccagg aagttcttttg ggtgttcttg cccagtttcc cttctctctgg cggccgctggt
360
catgttacct tgcaggtttgc ggtcagtctga ttaagagttc agttttttttt tggcggctgtgg
420
ttcgtgctat ttcacgctag ttcacgctag ctttcccact ctttcccact ctttcccact ctttcccact
480
tgctctccag ttcaggtttc ctttcccact ttcaggtttc ctttcccact ctttcccact ctttcccact
540
tctctctcctg aagctctcag aagctctcag aagctctcag aagctctcag aagctctcag aagctctcag
600
cactcttcctg aatcctgttg cccagtttcc cttctctctgg cggccgctggt cttctctctgg cggccgctggt
648

<210> SEQ ID NO: 186
<211> LENGTH: 1210
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (1932)
<223> OTHER INFORMATION: a, c, g, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2674657
<400> SEQUENCE: 1210

cggcgcgcct ctttactctag gggacacaggg ttcttcgagc cgcaagctggg cggggctgcg
60
ttagccagtt tgcctttgag caagttctgg agtccctgctg gccgtcggctg cgggtcggctg
120
tctctctcgg cagctgctgg ggaattctgg gcgtgctggg cgggtcggctg cgggtcggctg
180
ggcacatgtt ggacgcgcgtg tgcctttttc ctcctctctgg cgggtcggctg cgggtcggctg
240
ggtctggttga ggtcgtggttga ggtcgtggttga ggtcgtggttga ggtcgtggttga ggtcgtggttga
300
tctgggttgct gtgggttgct gtgggttgct gtgggttgct gtgggttgct gtgggttgct
360
ggggggggttgc ggggggggttgc ggggggggttgc ggggggggttgc ggggggggttgc ggggggggttgc
420
cgtgcgcgct gcggcgcgct gcggcgcgct gcggcgcgct gcggcgcgct gcggcgcgct
480
tgtagctgcg tagctgcgct tagctgcgct tagctgcgct tagctgcgct tagctgcgct
540
tctctctctcag tgcctgggtt gcgggtggtct gccgggtggtct gcgggtggtct gcgggtggtct
600
ttcacattgc aagttgtgttgc gcgggtggtct gcgggtggtct gcgggtggtct gcgggtggtct
660
cgggagtgc cggggcctcact gtcgtggttgc ctcctctctgg gcgggtggtct gcgggtggtct
720
ttcggtgctc ttgctctctta cacotcggca tagcagtgcg acocgcccag ggaccagcgtg 600
gtgctgcag cggcgcagc cagacacac gcgtctgagc agtaattgag aytgatggaa 660
acaaagtgtta ctttaactga acgattttaa aaatgcctaa aatgttactc taatagata 720
atatctttc aanactaag gcacgttttg tgcatttgta atttctctct ctt 773
<210> SEQ ID NO 180
<211> LENGTH: 714
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 2763296
<400> SEQUENCE: 180

gggagcctcc caagctcctcc agtcactcg gcagggccgc gggaccaggg ctggcaggtt 60
agaactctgg ggttgctgcc tgaagatggg ttcagctgcc tgggacctcc 120
caagttgcag caggcttggc ctttcaagag tgaactcagt gcagggaaaat gacocccagc 180
tgtgctctgc agaagactct gttcctgtgc agttcttcat ttcctgtccaa agttgcccac 240
gggaggggcc acaggaagaa ctttgcctgc tcagcccgcc gcacacccagc acacaggagc 300
agcctcactcg actacgctgc atcgtggcag cagccggcgg gttgcccttc cctctgtaag 360
agcactcctg agaagccggc ggtccttcct cggccttgcg caaagagcat gcaggtggga 420
ttgcttcct gccctctctgc ccaagctagt gcggctcgtct gcagacactcg 480
tcttgcctcc gcggcctcctc cggcgcctct gcagcatgtt ctggacggcc ctttctgtaag 540
agcactctgg cagcctccgc ctggcttggc tgcagctctc tcagcgttgc agccttgcct 600
ctttgcttc cgggtctccg gcctcactcg agtcactcgc gcagtcagtt gcagctggcc 660
atgctgctcatt agtactgtcc cccacattgc ttcacacacc gcctgagggc tcgt 714

<210> SEQ ID NO 189
<211> LENGTH: 609
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 2779436
<400> SEQUENCE: 189
cgccgcaggg gcgccagcgc cggcatccac aggagacatt gcagctcgcg acttgggtccc 60
tcttgctgcc cctctctgcg tctgcaagct tctgagacgc aagcataatgg tgtcaacagt 120
cagaggtgct gcagaggtgc ctcctactct ctggagcttc gcagggctcc aaccacttgtg 180
tctctcggct ccacgggctc ttcagatagc cccagctctg gcagggactcc aaccacttgtg 240
goacatagt gcggccgctg attccaccccg ttggcctgct gcccttcgta tcctttcgttt 300
gctgcacgc cagcagcttg gcacactgcc aacactgact gcggctggcc ccctgccgacct 360
tcagggccccc cagcccccag cagcttggcgc ccagggctcc cgcgcggccccc tcctcgagca 420
tctgcacgc cagcctcccag gcggctggcc gcagctggcc aagcagaccttt gtcctaggg 480
agctcttggt ggaggcttcg ctcctactcg tgcagctcagc gcctgggcgc cccttgctcc 540
gccgccccct cagctccgca ctcocccaca ataaaaatgt gcctgtccgt gcagtcggca 600
aaaaaaac 609
<210> SEQ ID NO: 190
<211> LENGTH: 1088
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: 
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2808528

<400> SEQUENCE: 190

tgtagaagac agggcctttg ccattggcgcc gctctctggag caggtgttgt ctctgtgtct 60
gttggtgctg cttgtggtggt gcacgcacgc gctgtgaaag cgggctcctg cgggctcctg 120
ggaggttact cggcccacgc gggccacgca gttgctccag ggcgcttggag ccctctctct 180
gaactctgcg taacctgctc cttttctcct ccacacgtgtg ggtgctctcc tctattaacct 240
cacacctgca taagagatctc tcagcctgga tcgcatccttg tgcacactgctgatcctat 300
cctcactgct atggtgcaaca aggccatcgg ataggattttg cgggtaggtg tgggtgaagcg 360
tggccatgctgc ctcgtctttc taggaatttc aacctgccaga cgacgctcaag tgggtgcatcc 420
cacgagagcg caagcattacg ttgagaggg ccgaacccac ttcagcctct gctgcctcca 480
gggagcctgg gggcattgga gttggtgcaag tgagccccag gcaagcgatc ttcgcccctc 540
tggtcttact tctctctctc tcttgggga taacacgctac ctcagtggatc acaataagagc 600
aacagatgca aagagttttt gtagccctaa gttgctgctt ggcggtgag ggattgcaaa 660
ggactctga cgtgctccct cagcagcctt cctggccugg cagctctctc cctgtcaaca 720
ttcagacgcc caagccagcct cccatctaacct cgggctgatt gatgctgtaca tttggggtg 780
tttcagcgct ccagctgcaag cagagcctgc cagctgccag cttgagccagc 840
aacagctgcg ccagagcctgc cagagcctgc cagctgccag cttgagccagc 900
acggagggag cagcctgctg ccagcctgctg ccagcctgctg 960
gcctgccca ccagctgctg ccagcctgctg ccagcctgctg 1020
aacatgtgaa ggcagccgcc cccccagctc cagcagcctt ggcgagttcg atgtgcacta 1080
aacagttat 1088

<210> SEQ ID NO: 191
<211> LENGTH: 1377
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: 
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2809230

<400> SEQUENCE: 191

gggaggacctt ccagctgcctg tttcccaaggc ctcacaagcg cagggcgagatgtgcatcc 60
gggtgctgct cctctctctg caggggctaag cgggctaaaa gctacccctcc cttgctctct 120
gacagatag ctcctccgcttc ggcggtgtaag tgggtgctgtgc ctcacagtgg 180
tctctgactc cagagccttg cagcgcagag gdcgcctcct ttcctctctgt 240
agagcctggt gcagcttcac caggcaggtcg gtcgctgctg ctcagctgcctgc 300
gtccctggag gaggctgcaag cgggctctcc tacgctgctg ccagctgctgctg 360
ggatggcagc gcagcctgctg ctcgctgctg cagagccttg cgcgaagaggc ttcctgaggg 420
cctgctctct cctgactgctg cagagccttg ctcgctgctg ctcagctgcctgc 480
ataccagctttatatcatgc taacacaaca acaacactgc aactattgac gtagcggagg agaatttat
540
cataaacgct tgtattctgt gcaactgca caactgtctg cccacagagg tttaattctgt
600
tatgggtggtc gctggggttc ggaactgtca ggtttgtcta cttatatccaa cacagtgac
660
actagctctga atgytatctgaa atatattattact gacttttattg gctcagggct
720
gtaacggaggt gttttttttag gataaaccga ggctcggctgt gctgtgggctag ttgcttcag
780
atattgcagct tgtgggccga tccgtttgag ggctctgctga ttgcttttcct caatagtccct
820
attactgcctg tcgaagcaca tccgcacgat agaacttgc aacttatgta ctgagcactgtg
880
attcagcagct atacaacgtg aatggtcgtg aagaaattgc aagcactgtg aaccatctct
920
gagacacott cagtaatact acaacagac gaacgtgagga agtgcgtctga aacgtgtggt
960
cactgtgagc tggaggtacct cgtcaagstgc cgtggtgcga cagacacaggt gcaagctttt
1020
gggctgctgg ctgctgctgg ctttgtggctg ttttcctctct ggcacccactc tttgcttggt
1200
atccacccct atatactctgt ttgcattgtg ttctcatat atctcactat agaatttttg
1260
acccacacgc gccttacttc aacctaaact aacttataactttcttacttact ttttactscttaa
1320
<210> SEQ ID NO: 192
<211> LENGTH: 905
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: <221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2816821
<400> SEQUENCE: 192
ggcggccccgc ggtctcgcaga cctgctccag ggtctcgcgta cctgtgaccc tttgctctgc 60
tccggccgctc gccttggtgc acggcttgcc cccgtctccct gcggccgctg 120
cggccgctgct ggcctggcag ccgggctcgct tctgctctgct cttttgggg 180
ggcggccgctc ccctggccgag agaaggtgc gcggctcgct gttctcccctt gggggagu 240
gcgctgctgg gcctgctgctg ttggtgtgcct gcggggcccc cggggtgcag gggggcttgct 300
gggctgctgg gcctgctgctg gcggggcccc cggggtgcag gggggcttgct gggggcttgct 360
tttggccaca ccttgccgctc tctcagccag ccagaagggct gcggacgctg gcggcccctg 420
cggcctcctgc gcggccccctgcttcggcc gcggcccccc gcggcccccc ggtgtgaccc 480
gcgccggcgg ccggccccctgcttcggcc gcggcccccc gcggcccccc ggtgtgaccc 540
gagccagaat gcgccttggct gcggccggcc cctgggacgcc gcggcccccc ggtgtgaccc 600
cggccggcgg ccggccccctgcttcggcc gcggcccccc gcggcccccc ggtgtgaccc 660
ccttcgctgc gcggctctgc gcggctttggct gcggcccccc gcggcccccc ggtgtgaccc 720
tctcggctgc gcggctctgc gcggctttggct gcggcccccc gcggcccccc ggtgtgaccc 780
gagacccacgc ggacgctgcg gcggcccccc gcggcccccc ggtgtgaccc 840
gcgccggcgg ccggccccctgcttcggcc gcggcccccc gcggcccccc ggtgtgaccc 900
gagccggcgg ccggccccctgcttcggcc gcggcccccc gcggcccccc ggtgtgaccc 960
gtcggccggc gcggcccccc gcggcccccc gcggcccccc ggtgtgaccc 1020
cocaacagctg cggcttaacg taacagacgc gagaactctctg gggcagagcgc gagaagagcg 60
gtggatättg agtcgagctgc tcggcagctc gggcagagcgc cggctcctctg cggctcctctg 120
gggaccttg gggcagagcgc cccggcgccgc ggcctgggag gggcagagcgc cggctcctctg 180
gcgctaggg cgtctctctc gggcagagcgc cccggcgccgc ggcctgggag gggcagagcgc 240
tgtggggtcg cggcttaacg taacagacgc gagaactctctg gggcagagcgc cccggcgccgc 300
gagcagcttg ctaacactctg cgaagcgcgc gcgggacgctgc cggcttaacg taacagacgc 360
gggctgcctctg cggcttaacg taacagacgc gagaactctctg cggcttaacg taacagacgc 420
tagcctctctc cccggcgccgc ggtgctctctctgttcctctctctg cggcttaacg taacagacgc 480
tgtggggtcg cggcttaacg taacagacgc gagaactctctg cggcttaacg taacagacgc 540
gggcagagcgc agaggatgc gggcagagcgc cggcttaacg taacagacgc gagaactctctg 600
cagctgtctgg acaacatggtg gcggcagctg cggcttaacg taacagacgc gagaactctctg 660
gggcagagcgc cggcttaacg taacagacgc gagaactctctg cggcttaacg taacagacgc 720
cggcttaacg taacagacgc gagaactctctg cggcttaacg taacagacgc gagaactctctg 780
tagcctctctc cccggcgccgc ggtgctctctctgttcctctctctg cggcttaacg taacagacgc 840
tgtggggtcg cggcttaacg taacagacgc gagaactctctg cggcttaacg taacagacgc 900
tagcctctctc cccggcgccgc ggtgctctctctgttcctctctctg cggcttaacg taacagacgc 960
tgtggggtcg cggcttaacg taacagacgc gagaactctctg cggcttaacg taacagacgc 1020
ggtggcgtgtg agggcagat gcggcagctg cggcttaacg taacagacgc gagaactctctg 1080
gggcagagcgc cggcttaacg taacagacgc gagaactctctg cggcttaacg taacagacgc 1140
gggcagagcgc cggcttaacg taacagacgc gagaactctctg cggcttaacg taacagacgc 1200
tgtggggtcg cggcttaacg taacagacgc gagaactctctg cggcttaacg taacagacgc 1260
tagcctctctc cccggcgccgc ggtgctctctctgttcctctctctg cggcttaacg taacagacgc 1310
<table>
<thead>
<tr>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>gtgaaggttt gagagttta aacccaggtg agacagccac cttctatgca cttgctggct 360</td>
</tr>
<tr>
<td>atgtttotgg tctggggttt gtaactagta gttgagtatt ttccttttggt aataacttat 420</td>
</tr>
<tr>
<td>ctgacctcct ggctccaggg aacatggtgca ttcctgggaa tttctctcctaa tttctctctctt 480</td>
</tr>
<tr>
<td>atgccagtt catcgagctg tctatattct ttcggtcagtt attotggggc attgtatttt 540</td>
</tr>
<tr>
<td>tggatgtgct tgtgaagaaaa aagttgaggcc tttctctcttat cttgctctctg aaccacgtcgc 600</td>
</tr>
<tr>
<td>tgtgctcagc ccacagctcct ataagttctt atatatggaat acacccgggct ccagccttta 660</td>
</tr>
<tr>
<td>taactcgtgt gctctagggc aacctggcatt tttctatttc gggaggcgcgg tgcogaagggc 720</td>
</tr>
<tr>
<td>tgaactacgc cttgcctcgc caagacagaactttctct ttacacccag cgcctcagct 780</td>
</tr>
<tr>
<td>aacccctagg aacccgacact tccacacccag cgaactcct cttttaggga agcacaacagt 840</td>
</tr>
<tr>
<td>tgtccttttct tcacattctt ttttttcctgt ggaaatgaga aagaaataaaa actatcgaag 900</td>
</tr>
<tr>
<td>tatgaanaaaa aaaa 914</td>
</tr>
</tbody>
</table>

<210> SEQ ID NO 195
<211> LENGTH: 606
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2949622

<400> SEQUENCE: 195

<table>
<thead>
<tr>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>ttttttaata atgcctttta gtggatgtt aatattacctg gttttttcatgt gttgatattac 60</td>
</tr>
<tr>
<td>agtcctgtat caaatatgga aacocctgct tttcttcttc aattttttatt cttctttctto 120</td>
</tr>
<tr>
<td>tctctttca atatagctca gatgtctcata gcatttagctg atgtggtggttcg 180</td>
</tr>
<tr>
<td>ctttttttattttctgacagc ttaaaagaaaa taacacaaaaa gtttctctaat tatacagtt 240</td>
</tr>
<tr>
<td>gtgtgctata ggcgtcaggtag atgtagctct cacaaggtta gaaasgtttcctttttctta 300</td>
</tr>
<tr>
<td>gtttctagggc tttaaagttct ttaattgaaat gccaaactttac caaaatgctct 360</td>
</tr>
<tr>
<td>tgtttgctgc tgtctgtgata atctatattc ttcctattcat atacacctct tcctgtgc 420</td>
</tr>
<tr>
<td>atgtgaatata gttggctgat attatattcct tttctattctt tttctattctttatttcg 480</td>
</tr>
<tr>
<td>tacctctcct gttttttttc tctcaacactct gttggtgccg tgcctagctca tttctttctttttctct 540</td>
</tr>
<tr>
<td>agtggattctctctactgtgt gttcgtaga aatggtgctgt tttcttctctttttttcttttttg 600</td>
</tr>
<tr>
<td>tttctgaa 606</td>
</tr>
</tbody>
</table>

<210> SEQ ID NO 196
<211> LENGTH: 893
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2992192

<400> SEQUENCE: 196

<table>
<thead>
<tr>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>caacccaggg gacctggttgg gcacacccggc gcctttggagg ctgagcggccca cggggtgctct 60</td>
</tr>
<tr>
<td>agccgtgttg cggccgccct gcctactgcgc gcctctctcg ccagacgagc tggacacggga 120</td>
</tr>
<tr>
<td>tgggtcctcg tttctagcttt cttgcgggccc attctctaccc atctccgaggc tgggttctgc 180</td>
</tr>
<tr>
<td>ggcccaaggg gtttttttgg cttcttgctg tgctccagtct gttgcacgagc ccccggttcc 240</td>
</tr>
<tr>
<td>ggtgcaagcgct cttgtgtgct gtagcttccaa tcttgccccc tctgacccct gcctgctgct 300</td>
</tr>
</tbody>
</table>
-continued

cggcctgcc ctggcagcgg gccagcgcg ctggatgccc cggccagcgc ctggctggcc 360
tttttttt cttctccctg ctgacctggt cttgctggtg cttgagcgtg 420
gacatctcc acctacgccc ctttggcttc cttaagcgct cccttgagcc 480
gatgcctgg gatggcctg ccgctccgct ctgcgtgtgc ccgccggttg 540
cgagatccg tatttctctcg ttgacaaacc tggagccctg ctcataaacaa cacctttgga 600
cataacttg gcgtgctgcc gaggctttgg aagaaatacg ctcgattcgc ctcacctcgc 660
dggggtgga ttaaaactga acctttgggag gcagagcctg ttagttcaca cctctttgaa 720
tccagacttt ctgagggatt gcgcagagcg ctcgctgcag gcgcagcttg gcgcacattg 780
cgagagatt ctctttttc cccaaatb cccaaatg cccaaccagtt ttagttgagg 840
gtctacaaagtg ggtgtacac gcgtctattaa ccaacattaa caacattaa agg 893

<210> SEQ ID NO: 197
<211> LENGTH: 1730
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2992458
<400> SEQUENCE: 197

ggccccagcc tgtccggcac cggcgcggcg gctgtctcgg gacggtcggcc ctggctgaccc 60
gagcgctgag cggagacgc agcggggacg ctggtctgcgc ggcagctggg cgggcgtgttc 120
ggggggtcc cgcagagcgc gcggcttggc tctgccggtgc ggccacattg cctggagcttg 180
cctccctgtg ctctgcttcc ctcgcttgggg gctgtgacgt ctcagcatgg 240
gggtctggtc gctctggcgt gcgtctggcc ctttagat gcctggct 300
tctctctcgt ctctctcttg gcgtctggc cgtctctgctc ctggtctggc ctggtctggc 360
dcatcattc ctcctttgctt ctgtctctgt ctcgctggctct ggctgtctggtg 420
tggtctgtac gcgttctggtc ctgtctctgt ctgtctctgt ctggtctggtc ctgggtgtgg 480
gagatcttttg tctgccagtt tctgctctgt tctgccagtt tctgccagtt tctgccagtt 540
ggagtccgtc ggcgctttgg cctgcgctggt cgtggctgcct ggtctctgtt 600
tggtctggtc gcgggcccttg ctttagttgc ggttgttcgg cttggtctgttct 660
gtggtggtctc ggtgcaggtgt cctgcgctgtt ggttcgctgtt ggttcgctgtt 720
csacgctgg cagataggttt gccgttgtctt ccccgtctttt ccccccccccc 780
tggtggtcgc gcgtctggtc ggctgccctcttt ccctctctct ccctctctct 840
agctgccgct ccgctgtcct ctgcttccgg cccgctgtcct cctgcgctgtt 900
cgtggtctggt cggcccgttc gccgctgtcc cctgcgctgtt tgggtggtgt 960
tctggcttt cgctctgcgg cccgctgtcc cctgcgctgtt cccgctgtcc cccgctgtcc 1020
tggtggtctt ccgctgcgct gggtctctgc ccgctgcgct gggtctctgc ccgctgcgct 1080
agaagggctc cggcgctgct acgatgcttgc tgcgtgtctc gccgtgtctc cctgcgctgtt 1140
tggtgtctcgc gccgctgttgc gcggctgtcc cgggttgtggt tgcgtgtctc cctgcgctgtt 1200
tggtggtctt ccgctgttgc gcggctgtcc cgggttgtggt tgcgtgtctc cctgcgctgtt 1260
gggaaggttc gcgtctggtc cccgctgtcc cgggttgtggt tgcgtgtctc cctgcgctgtt 1320
tggtggtctt ccgctgttgc gcggctgtcc cgggttgtggt tgcgtgtctc cctgcgctgtt 1380
cggcagctca gaccctttct tcaagctctga aagaagacca cgtatccacc tgtacgtgca
cttctgagc0 cggtaagac0 aaaaagattg cagaaaaattg tagcccctga aagcctatga
ctttcctata actttgacc0 taacctcttg aataagcttaa aataagaaa taataaagc0
ggttatagc cagttacagg0 tcaagctggga ctagaaccac agaaggaggta aagtttgttt
cttgcacgcc0 attgctttg0 aatctcgttt tgaacccac acacttacct tttttgtgct
ctcctcgc0 tctatccttc tcaaggaatt atccttttacc atctccaaa aataaaaaact
ttttatattttt tctgagttac aagatgtgtt actagaagag atacactagt
aatttgtttta aataagtaaa aatcttccaa accattttaa aaaaaaaa

<210> SEQ ID NO 199
<211> LENGTH: 543
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 3120415

<400> SEQUENCE: 199

cggcagctca gaccctttct tcaagctctga aagaagacca cgtatccacc tgtacgtgca 60
cggttttccc cggccctcag cggccccccct cccctgacag ctccttcgct cggccctccct 120
gggctgaggt gtcgctgctg tccgtgcgtg atctttttagt gggctgacggc aagaagctgg 180
cggccctctg ctcgctgtcg ggtgcgcgcgg cgggcgaccc cggccctccc cggccctccc 240
cggccctg0 ctcggccctc ctcgagcttc tcagagccag cttgggcttg agcttcctgcgc 300
cgtgctgcctg cggccctccc cggccctccc cggccctccc cggccctccc cggccctccc 360
tggtgagctg gggggggtg tgcagttg ttggtgagctg gagaagctgg 420
cgtgctgcctg cggccctccc cggccctccc cggccctccc cggccctccc cggccctccc 480
gggcagctcc atcctctcttc cggccctccc ctcgacccg tgggttaaga gtaaaaaaaa 540
aaa 543

<210> SEQ ID NO 200
<211> LENGTH: 531
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 126750

<400> SEQUENCE: 200
gcagctggaa ccttctgctt ggtggatattt tgtagatttt ttctgatttta aaactctctga 60
aagatgtgtt actagagctt gcagaatctc ttctgctctg gccgaagctg 120
ttcttgtggt acctctctct ctgcgccttc ttcacccaaag ctgcctctctcc tggg aggctg 180
ttgccacctt ccacctctgg cccctttttg atccttatgata gctccctctg 240
aagactctcg gatctctctg tgcgaagctt ggtggagggg taaaaggagt ttaaatagtg 300
cggccctccag atctcctctg cagcttctctg aactctctgtg aggccctatc acacttggcg 360
tgcagcttctg taaagagccgg gggtggtgg tggggagacc atgactgtctc atctctctctc 420
gccagctaa gttctctact cttatatcag aaatccctctg aacttgctgtg acccctctct 480
gagccatcag aacgcaagatctctactta ctgcagcatt cgaatggaaaa a 531
<210> SEQ ID NO: 201
<211> LENGTH: 491
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 674760

<400> SEQUENCE: 201

ccttcoccat gacgtgctgg cagtttcttg cacttttttc tactgcttta ttgctgga cg 60
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 120
ttcctctcgc aacgtggggg acggtggggg acggggagctg gcacgccctc ctcacccc 180
ttcctctctct cctctctctg gacagagctg gctggctgtc gtaagccgctg accttctcct 240
cctctctctct cctctctctg gacagagctg gctggctgtc gtaagccgctg accttctcct 300
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 360
cgagggacgg cgctgactgg ccctcctcct gtaagccgctg accttctcct 420
cgagggacgg cgctgactgg ccctcctcct gtaagccgctg accttctcct 480

caaaaaaaaa 491

<210> SEQ ID NO: 202
<211> LENGTH: 1551
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1229438

<400> SEQUENCE: 202

cgagggacgg cgctgactgg ccctcctcct gtaagccgctg accttctcct 60
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 120
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 180
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 240
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 300
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 360
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 420
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 480
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 540
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 600
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 660
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 720
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 780
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 840
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 900
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 960
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 1020
gggtggaggg gcagctggag caagggctag ggaggtcct gttggttttc ttgctccttt 1080
-continued

tagcactcacc gacgatctcc caccacaccc acacacccac ccaccatctcc ggccttttccg gcccagactt 240
tccttccctgc ccacagccag gcacgttact thectctcct gatcagttgc gatctctctct gcctctctct 300
atcctggccc ggcagagac gacagagact gacagagact gacagagact gacagagact gacagagact 360
ggcagagatg gacagagatg gacagagatg gacagagatg gacagagatg gacagagatg gacagagatg 420
ttaaatggatt ag 432

<210> SEQ ID NO: 205
<211> LENGTH: 971
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1450703

<400> SEQUENCE: 205

gggaggaggg gagaatagca gctggtctcc cccgctctcc cctcctctcc cctcctctcc cctcctctcc 60
tccgccctct acagctctgt ccagcctcttc ccttcctctc ccttcctctc ccttcctctc ccttcctctc 120
ggcctctct gcacgcttct ccacgcttct ccacgcttct ccacgcttct ccacgcttct ccacgcttct 180
ccgccctct cccggtgag gcagcctct cccggtgag gcagcctct cccggtgag gcagcctct 240
aagcctcctgc ggcaggtttc acacgctttc ccagcctttc ccagcctttc ccagcctttc ccagcctttc 300
ccgagcgcgc cagcctgtgc acacgctttc ccagcctttc ccagcctttc ccagcctttc ccagcctttc 360
tgcacgccc tccagcttct gccctttgca gcaagctttc gagacagag gacagacag 420
tggagttctcc ggcaggtttc acacgctttc ccagcctttc ccagcctttc ccagcctttc ccagcctttc 480
cagcctttc cccagctttc ggcaggtttc acacgctttc ccagcctttc ccagcctttc ccagcctttc 540
tgcacgccc cagcctttc ggcaggtttc acacgctttc ccagcctttc ccagcctttc ccagcctttc 600
tgcacgccc cagcctttc ggcaggtttc acacgctttc ccagcctttc ccagcctttc ccagcctttc 660
ggcagccttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc 720
cacacacacgc cagcctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc 780
tgcacgccc cagcctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc 840
tacatgcctgc gtcacgccc cagcctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc 900
tttcctgcct gcagcctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc 960


<210> SEQ ID NO: 206
<211> LENGTH: 1832
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1910668

<400> SEQUENCE: 206

cgcagttta cctgctctcg agacgagc ggcagccctct cctttctctct ttgtttcaagt 60
tcaagggac tcaagggac cctttctctct cctttctctct ttgtttcaagt 120
ggcagggac cctttctctct ttgtttcaagt 180
tctttcctcc ccacacacacgc cagcctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc 240
ttcacacacgc cagcctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc gcacgctttc 300
-continued

tgcoccccag tgcgtgtgct tgtttctgct accctgaccc cacatgatgc caggtgcat 360
tccctctact gcttcttcgg aagagctggg acatgtgqgg cagttgtcag atgtaaaga 420
acagctggag cagagggcgt gtcagtaatg attgctccct ggggaangtc tggttgtgtc 480
cagcagcagc aggcaatttg gatctcttcg ggtacgagtt gattctcggg acaagtagct 540
gttctgttgg agctgctttag gacagggcct agagggctag gccagagggg aagtcgcaag 600
ggaagggcg gcaggggcca gtgagagggg agactgcttt ccoccaacct gcgctgctct 660
tgctcaacag gcggtttctgg gcacaattgc tcagggccga aagcaagacu caggcocag 720
cctgtgygca aagccaatag ctctgaatgg attcagatg aagcagagtt gcaggggaag 780
tctcttgct tgttcctgttg ttgctttttc aactataagc aactggtctc ctcttgctcct 840
cagcgctcgct cttggtgctg toctcaacoc gcggacaacu ccctaccctt tgcaggtgat 900
gtgtttagcc cgcggtggtc gtctgcttgc aacagagttg agaanctggc tggctagggc 960
tctagcgtyg tgcggggtct gcaggggagt ggtcctgcgc ccaagagggc tctgcccctt 1020
toccacctc occcctccca ccaagaggtc gctagaggtc tttggaacaa aatccaaacc 1080
ccctctgttg acctgctgct gcttcagctg tggaaacccaa taccctagct tacgagccat 1140
cctgagccag ggccgtctgg aasitctctt ctctgtggtc ctttaggttt gggoaacaaas 1200
tataattgcg tcccctctct cccatcttttc cctctgggag caatgtgcac agtcgccgtg 1260
aactggaaag gtacctagcgt ctgagccccc tttccccttc cttctctctc ccaccctcgg 1320
aagctgtgctg cccctctcctc ttcctctctc gttagccgct gcggcctcgt gatccagctc 1380
cctgctacgg atccgtaccg tyttggatgt tacctccatt gatctctcctg ytctacgctc 1440
cctcttggtg tgtgcaata tggccatgct cttgctctac cttggtggag cctgtacgctg 1500
gttgtgytg ccagcgtgggg gcgctttggc aatgctgtctg tggagccaaa ttcggctttt 1560
cccgggaggg gacgctgact gagaaggggg gcaggggccac acctctatct tgttaggaag 1620
gtggcttgtc ggctggtggg aagagggcc cgcgctttct cttgctgcct atggacgctg 1680
tttgcctttt cttctgttgc gctgtgctgg cttctgtttg ggtcgttgag ttcctccgct 1740
ggcagttgg cgctgggcgc ccagttgtctg gctttggtga actgtgtgaa cctatataaa 1800
gggaaactt tgtgcctgtgg aaaaaaaaaa aa 1832

<210> SEQ ID NO 207
<211> LENGTH: 567
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1955143
<400> SEQUENCE: 207

cataagatcacc taatccatactatctgctgg ccaaaaacagtattaatggg gtggagaatgg 60

gcagatgagata tggctccctc tcctccttctc gtctaggtgag gggcaacctt tcgctgca 120
tctagtctcg tgcagggccaggtataatgc gctgctttc ggccgtctgg aacagtcttct 180
cacatcttgg tgtccttcgatatct gcaagtgctg aaatctatctt ccagtcacctcctacagtcc 240
cacagcagctt gcacacgtgctt atccatgata aagccacaagc atggatatgta caattcatg 300

eattttgctt tatacagcgcggatgggtgtgca gacatagctctgcagcttctctttatctctct 360
tggagataaa ggaatgctgg ctgagatggagacccatccatggctacaattttatatgct 420
acocctgacct tggaactact tattagctgt tgcacoccttg gcacagtttaa taccacctctg 180
caggtcagtt cccctccctg tggagctggt gtaaactaag ygtgtgatga gatgacccct 240
agtgag AGTG gttggttgtc tgggoccaca caacttgggt taoctgggaga gtttggtatt 300
tgaa acctcgct tctttt cgtggctcct tggcaagctgg gcagcgttag 360
gaaaccttt cctctctgag cccctccctt caagcttctta aaccttgggcct cacaactgtc 420
gcaacctgt ttgggggtgg atcttttgta agaagggcaca gcggagaagat ggcgtacagt 480
aatagttgtg gatgtgtgag cctggtactcc ctggtgacct ggttcctgga tgggctcact 540
gttggtgcc ctgggtctggg accttccggg atcttctgaac ttggggctcct taagggccagc 600
cccggccagg gatgccccct gttgggtgttta ccaagttgcct tggggtccag gcggctccagc 660
catcctggtg ctgggtgcttg gctttttcttc acgtggtttc ttgcaaggtct gtgtggccc 720
agttgtaagg gatggtggtc tcggagaggtc aagccagtgag gatgtgtggcg cctggacgtca 780
cacatcctg ggccagaccct ctcgaagtagg ttgggtctag ggtagaagcc ctcggtggg 840
tcctgttttt ccttccccag aacctgggata atataactagc ccacccctcgag ggacagggg 900
atgaaaaag ctgaccatag aatccocctcg gccacatcgc tggggtcggc atgtgcgtaac 960
ccggggccct cctacagtgt gcggagcctgg gcggccaggg gaggggcggg cctggccagc 1020
tccatccttg tggggtctgg gaggaggggct tgggtattta tccgagaggca tggggtccat 1080
ggggggtgacc cccttggtcgg gcgggtgtcgg gcgggtgtcgg gcgggtgtcgg gcgggtgtcgg 1140
gccggtgtgg ggtttgggtta cgggtgcggt cagccgtctg tcatggtgctt ggtggtccagc 1200
tcgggtgttg cccctcctctg tgggttttcttc gcggtgttctg tggagccacttc cctggacgct 1260
gggtgctag ggccagacct tccctgactg tggagatggt gcccagactt cggcaactgtc 1320
ccttttttttt tcgtgaagcc tggcagacgc aenac 1355

<210> SEQ ID NO 210
<211> LENGTH: 776
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1994131
<400> SEQUENCE: 210
gttcacaaggt ggaaagtaaa aagttcctgt atattgtagg aagtaaggtg 60
tgtaatagg aagttggctc cgtattatag ctcacctctc accctccaaag agtaaatctcc 120
ccatctgggg tattatgttc tgtgacctct gttgtggtgta atgattgtgg attaggttg 180
agagaagctcg ccgttgctttct ttcggctgaa aacaaaaact tggagttggt cggcaatagt 240
tcacaacaag ggctccaccc acagcatccc cgaattcaggg gggagcttgg 300
tggtttttg tcgcaacagag ccttttttttt cttttttttt tttttttttt tttttttttt 360
cacaacggga acaacacgccc ccggctaagaa caacactgca ggtacatctgc 420
ggttctggga accacagcgc gcgggtgtctc atcagctggcat gttggtggtc 480
taattttcg tcccctcactc acgatagagc ttgggttttc aaggtgttctg tgtgggagc 540
atcacttct cttttggtgt tttctggtctt cgoatctttg gtatttttctt tccacaaatv 600
tttttttttt cccacgctg cccctctctct cggcccagcg cctggggtcag tcgcttttttt 660
gtggagtccc cctgattttg tgggtgtgtg tctggtttta agaagctctt cggttgttat 720
agttttttat agtttttttt acaattaaatt gaaagtagct gctctccgga aagcag 776

<210> SEQ ID NO: 211
<211> LENGTH: 817
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1997745

<400> SEQUENCE: 211

ggaggctgta gaggagctgc cttgggagcc tcagggagtc cctttgccag tgggtttttc 60
cctggcactgc cagggcaagtctggggcc ccaagatcgg tggctgtatg agggttat 120
catcagggaca aagaccccaca gcattgtgct accctgccccgc ccattttttc tggccaccac 180
tatatctgca atatcgtcag ccatccctcc tttttttttt cttctcttacat 240

ttttctatg accttttcct gatgacatcc atctttcttt tgggctttct cagacaggg 300
catttgctg agagccctctt ccggaggtc tcgtggtgctg tccctctgca gcactgtgctg 360
ttcctcaggg ggtcatctcag aagacccccct ctcgcttccct tggggcctct caggggaca 420
ttcatgtgctt agtctcaagt ctccaaacaacttctgccg agggc aaagactgtgcg 480
ttggtctctg gttctctatgc tgggctttttc cctgctgcccc gcactgtgctg 540
gcatgttttc ctctgttctg gcactgtgctg cccctttttc cctgctgcccc gcactgtgctg 600
cagggcagct cggcactgtgc cccggtttttc gctgtgctgg cttgttttctt caggggaca 660

taggttgatt ggttggaggg cggcagagct cgcccagcag gctcttcgcc gcctgcctcc gctgtgggtgc 720
tggggttgggg gttttggagg ggtatgctct tgggtttttc tgggtttttc aataataatg 780
cacctatttt tgtttttttt tttgcaaaaaa anaanaa 817

<210> SEQ ID NO: 212
<211> LENGTH: 484
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2009035

<400> SEQUENCE: 212

tttttttttta taatgagactg ttactotaca aacataggtg ttgattttttt 60
acttttttttc tccatatttt gttgagcatc tctccaggttt tttttttttta ccccttttttc 120
ttaatagatg ccttggagct ccaagtgagtt ttattcgctt tttctttatg tgggtctct 180
gtttgtctgt taggttggct ttcctctccc tattgaagct gcttttttttt 240

ttataactt tttcctatttt tgaggatattt attaattcata ttctacagatt aatcttttttt 300
acagacatatt cagataaaaa cccaggtatttt cttattttt ttaattctggcc 360
acagtggctgt tccacgatttt tgggggagccc cccattttttct cctttttctttta 420
gagccctagg gtctcagagttt aagctgggaa cttggtgtata cccatactaaa 480
aanaa 484

<210> SEQ ID NO: 213
<211> LENGTH: 509
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2009152

<400> SEQUENCE: 214

ccccgtttt cacacagtta cccctccttt ttgtccattc attttacactc aatgtaataa
60
tataaattt tatatttattt attattattt aaataatattt taatatatat
120
tataaaaa gtttaataaa ataccaaaaa taatttttaaa atgtgaaaaa attaatattaa
180
atgaaatcct atggttctct cttcgcaatt ccgtttttgt tatttctgtg gtctgtgtga
240
catgtgaggg actgcaactt gattgcaata ttttcaacag tccaaagcat tacaagagaa
300
tgcttaaact taacccgatta tgcgcagaga tttttttttta attaaactag gtgacgataaa
360
ggaagatgta ttaaatagat atattttatatatattgta ccgaggtggg ggggtacttg
420
tttttgaata aatgagtgag tttttgca tgaacaaaaa aaaaagagt acgaatcc
480
catggaatt taagttccct ctaaccttt
509

<210> SEQ ID NO 214
<211> LENGTH: 1130
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2061752

<400> SEQUENCE: 214

ggatttatca cattctgct tgaatcatag ggaacagcat gtgtaggtgga atgaacacag
60
gcctctggat ccaagatagc atgtagaacttc ccaagctttgg agggggttaac ttataaggttc
120
atggtcatccttc tcttttcttc ctaatatat gatgtattctaa atatcaatct cagagcagta
180
tggtggatca tacatgcaag gattgggtaa agacagtggc acatgcaag cgattgcaaac
240
atgctgtta ccatttcctt tttctttcct cttttcccag ttatactataa cttctgtgag
300
tagcagtccc acgtctttat taacccctgta ttttcccagac tctttccctc agtgagttac
360
cctaaaggtaa tcatcctgaa atttcacaatta ccctgtaatgct tsnasayctg
420
ggatttataattgatatag tgaattcagaa atacccaaat gctatgtatg gatgatagtgg
480
aatcacaataa tgaattctgaa atacccaaat gctatgtatg gatgatagtgg
540
tctgacattg tctactatag gtagacactg gagarough tattgtgcaat aagccagaca
600
gaaagaggata aactacagtta cattccccct cattgaagatcta cattagatgtgt atactaatgaa
660
agaaaagaca atgtacagtt gctaccccaaa atctgasayct gaaagdctgc caaaccagyca
720
aacctttctaa atgcggcaac gatgtcctaa gaacgtcgtat attggagtac ctagatcctg
780
ggattttttag atttggttag ctcacattggc aatgtagaacttc ctatttccac tgcacaaaaa
840
ttagtgatatt aaccactactt ttgctcctag gcgtttggtat acaggctactgt ctagtgcaga
900
cattgcagtt gtagttgttgc gagtaggtagc gagatattgct ttagatactgct ttagatactgct
960
aatgcacgatc agacacgcaat cattgctaccttatgactgtgcctacttc tagctcttacatc
1020
ccagggatgtctcagttctgttacacct tttctctcaac ctattagga ctaagagttgcag
1080
atatttttgta tgcctctaaac ccataaaaga agtttttttaa aaaaaaaaa
1130

<210> SEQ ID NO 215
<211> LENGTH: 1273
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2061933

<400> SEQUENCE: 215

atattctccc tcagaagc actaaatag gagttggtgct gatattttta agatatagtg
  60
agatotgtga gtgtatgaa ggtatatatt aaaaacctgg attctatcc agtggaggtt
  120
ttggttta attctccttg gtggagggaa ggctttgagc agggctacgt gcctcaacgtc
  180
ttccttatta atgtctcctg cagcggatag tgctgtcagtga agggggaggg gggcgggcg
  240
cgtaagccg ccgggccacg ggtgtgagaa gatgtataa ggaggctcg gaagggggcg
  300
gggggggtc ggtgggtgtgt cggtgggtgt gtgggggggt gacccggccg ggttttctcct
  360
ggagagagc atccggtcag gtcttttaat gccttgczat gacttagaat cacaagcggt
  420
ggtatttag agatgctcct cagcggatag cgtgggttta ttgatgtcag ctaatgcgtg
  480
ggggtgggg gaggtggggcag gttggggggcag gttggggggt cttgtgggtc ccttttttttt
  540
gagttgggg ggtttggggcag ggtgtgccag cgttttacttta cttttttttta ttaat.taaca
  600
tatgtgatat ttaattatttt ttaattatttt tataattatttt ttaattatttt ttaattatttt
  660
"aaaattatag atggggcatt tccgggggtt gtttttttctt gttggggtttt gttggggtttt
  720
cacccggcag cttggggtttt gtttttttctt gttggggtttt gttggggtttt gttggggtttt
  780
agggggcctg gttggggtttt gtttttttctt gttggggtttt gttggggtttt gttggggtttt
  840
ttcctttttg cttggggtttt gtttttttctt gttggggtttt gttggggtttt gttggggtttt
  900
tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt
  960
aatattatttt ggttttttttt gtttttttttt gtttttttttt gtttttttttt gtttttttttt
 1020
"aaaattatag atggggcatt tccgggggtt gtttttttctt gttggggtttt gttggggtttt
 1080
gatgggtcag cttggggtttt gtttttttctt gttggggtttt gttggggtttt gttggggtttt
 1140
tggggggtttt gtttttttctt gttggggtttt gttggggtttt gttggggtttt gttggggtttt
 1200
tctttttttt gttttttttt gtttttttttt gtttttttttt gtttttttttt gtttttttttt
 1260
"gaagaagggaaa
 1273

<210> SEQ ID NO: 216
<211> LENGTH: 1279
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2081422

<400> SEQUENCE: 216

cctttttttt gttttttttt gtttttttttt gtttttttttt gtttttttttt gtttttttttt
 60
ttcctttttt gttttttttt gtttttttttt gtttttttttt gtttttttttt gtttttttttt
 120
cacccggcag cttggggtttt gtttttttctt gttggggtttt gttggggtttt gttggggtttt
 180
ttcctttttt gttttttttt gtttttttttt gtttttttttt gtttttttttt gtttttttttt
 240
cctttttttt gttttttttt gtttttttttt gtttttttttt gtttttttttt gtttttttttt
 300
cctttttttt gttttttttt gtttttttttt gtttttttttt gtttttttttt gtttttttttt
 360
-continued

tggttttctc tttaactctt ttctcacaac tgtataatta tggccatagg tgtcaagtct 420
aaaagtttta ttaacaaacc agtaggtggc aagaattact tatcataaat ccagcaagtt 480
tgagaagaac caaagttggg gagaacaccg gtagaatcoc accgtgaacc tggattggg 540
ggocaaacttc ttaaagaaag cagatatta ctgctgtatg tagctcctgt tatcpeateda 600
cagctatat agaatgcttt gacatcacaac atttgctcct taaaagatag tagctggttc 660
gctcctcag ttgcaaccag gcttttggtc ttcttcttaag tgtctgtggt tagtctcgtt 720
attataaag ctttaaaccg gcccctatgg ataagttcctc ttggcaactct tgtatctcct 780
ttcatctag cttgtagcct cctacactag ttgttagaacc gggaaaaacc ctgtagttgc 840
tgtaatagc atatatattc tctagatttt cttgtttcct cgttagagag cccctgtgtc 900
cctcaactag ctggcctctt ctcgcccctg acagctgtgc ttagcggcaca ttctctatag 960
getgottctc ctaagcctcc cctggcttctt ctoctcccttc tctactttcttcttacctc 1020
ccttcctcc tttcccttcct tcctctttgc tctctcctcct ctctccacat cctctttccc 1080
ccttttgcct cttgtaactgc tggaaagtt ttagaatatt tagaatatgt ctggagagt 1140
cctgacgaga gttctttcgt tagcctaatct aagsgaatgt ggttgatgtt tataatgcc 1200
atcataaac tttcataact amggctctaa ggttagaaa ctotaaatgt ttatatatat 1260
actataagat gggggggg 1279

<210> SEQ ID NO: 217
<211> LENGTH: 899
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME: KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2101278
<400> SEQUENCE: 217

tggttttctc tttaactctt ttctcacaac tgtataatta tggccatagg tgtcaagtct 60
cocacagac gcaccgcctt caggtggtgg ggaagatcag tggctttgtc acggttgac 120
tgggtactt ttggtctttc ggctgcaccc caagcatcctc gatttttggc ggttatctag 180
acatcttctt ggtctgggtc tttggtactc gggctctttc ggaagatgtt ccagctttcc 240
cacacaccctt acacagtctt ggtctgcaga tcagagccag gcttgctttc cccatcactg 300
cattggctc gttgtagact cctgtggtgg cccgagctat ggtatagact tttcctttct 360
tccctttttc tttcctatgg ttggcgcctt atttttcttc cttggcctta ttgctatctg 420
gcgctttttt ttttttactt atggcggggt ggtataggtt gtttataaa 480
atactacggt cattcctgg gctgtcacttg gacccctttt cttctttttc gagaataatac 540
ttgatgttc cttcctcttc ttctcttatt ggctttttct ttttttcccc gctttttgca 600
tctctttttc ttttacacgc atctctctct ctcctccttc cttctgtgtc 660
taagctggac aactactacag tttcttactt tcaagggagt ttggtgtgct 720
gatggcttctt tttaaaaaag tggacagcct tcctttttctc ttttttttttttcttc 780
tggttttctc tttaactctt ttctcacaac tgtataatta tggccatagg tgtcaagtct 840
ggtctgaggg ttttctttcct cattttatata acggtatgta aaggggtcctt cctctttggg 899

<210> SEQ ID NO: 218
<211> LENGTH: 645
<213> ORGANISM: Homo sapiens

<220> FEATURE: misc_feature

<223> OTHER INFORMATION: Incyte Clone No: 2121353

<400> SEQUENCE: 219

```
caacgagtcg gacactcaact cggcaacagcc cggcaacagcc cggcaacagcc cggcaacagcc cggcaacagcc cggcaacagcc cggcaacagcc
60
agggaaagta agcagccaga gasketta accactccag cggcaacagcc cggcaacagcc cggcaacagcc cggcaacagcc cggcaacagcc
120
cccggttct cggccgctg cggccgctg cggccgctg cggccgctg cggccgctg cggccgctg cggccgctg cggccgctg
180
tctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt
240
tctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt
300
gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt
360
tctaaacac gaagaagaa tctaaacac gaagaagaa tctaaacac gaagaagaa tctaaacac gaagaagaa tctaaacac
420	gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt
480
tctaaacac gaagaagaa tctaaacac gaagaagaa tctaaacac gaagaagaa tctaaacac gaagaagaa tctaaacac
540
gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt gctggctgt
600
tctaaacac gaagaagaa tctaaacac gaagaagaa tctaaacac gaagaagaa tctaaacac gaagaagaa tctaaacac
665```

<210> SEQ ID NO 219

<211> LENGTH: 536

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<220> FEATURE: misc_feature

<223> OTHER INFORMATION: Incyte Clone No: 2271935

<400> SEQUENCE: 220

```
cacac gccgcggttc gcttgtatcga aaaaattgaataaaggttacta aaaaattgaataaaggttacta 60
agagattt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt
120
aatagttc tatttcag cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt
180
tcttgttct cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt
240
tcttgttct cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt
300
tcttgttct cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt
360
tcttgttct cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt
420
tcttgttct cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt
480
tcttgttct cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt
540
tcttgttct cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt
600
tcttgttct cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt cccccggt ggtcggtt
665```
-continued

tttcctctc aatcagatgt ctcgacggga aatcggctag gtggagtgtt gctgctggtg 60
aatgaacgct cctcctcact tctctctcgt tctctcatt aatcctactt gcccttcttc 120
tgccgtaat cggcctcttt gttgatgaa aatgagcagt tcacagcaga 180
atctactaccc tcgggaggtgg ggacgaatac cactgttgggt gggttggcgc 240
gaggtgcttg tcggcctatt tcctccgaag ggacaggggttg gggtctgtgac tcctggcctt 300
tgaagctcag ccacagcgtc taactcactc tcactgtgcat gtcaccaaat ttgacaaac 360
tggagatctg ttttccctt gttgctcaggg gcacagcttg ttagacacgtc 420
agacgcttt gctcgcggag gcacacaccc aacctgcctct ctagctcaga ggcaagacat 480
gcggcagtct ttcacctcag tcgcggctca cgtgctgtgg tgtgataatt agatg 536

<210> SEQ ID NO: 221
<211> LENGTH: 790
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2295344

<400> SEQUENCE: 221

tcgtcctcggc gccttggtat ttctctctct tttcagggcc atatgtgggtat gtttttggttt 60
ttggagcttt ctatatagtg gtttttttct ataaatttta aatattgctg aatgctttttct 120
ttttaacatt gcctctcttt ttcctctctt atctgtggtctc agctctgtgc ttctccccct 180
tcttaataat ctgcctcatt ttggtgttgc tctctctctt atctgtggtctc agctctgtgc 240
tgagttgttc gatctcctct ttcgagtggga gttgctttaag ctcggtgggtt 300
agacatcag cacagatgct cgtcctttag cggcggttgct cggcggcact ctggcc 360
tctcgagatc ttttttgttct ctcggtgggtt tcagctttgctc tctctctctt ttcctctcttcctg 420
tttcggcgag gggagcgtcc ttcctctctct gtcgtgctct gggagcgtcc 480
aacaccagc caagatcgtcg ttcctctctct gtcgtgctct gtcgtgctct gcgtgggctg 540
caggtggtgc atacatcactc ggcgtgcttc ttgcggttggat cgcgtgggctg 600
tttggtgtgc cctaccgcct ggttgctgct ctgcggtggtgc ctgcggtggtgc ctgcggtggtgc 660
gcggggtggc cggtggtggc cttcggcact gcggggtggc gcggggtggc gcgtgggctg 720
cttcggcagc cgggtggtggc gcggggtggc gcgtgggctg gcgtgggctg gcgtgggctg 780

<210> SEQ ID NO: 222
<211> LENGTH: 1045
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2303994

<400> SEQUENCE: 222

ggcaaggtgua gggtgcaggtg aactatggtt ttccacactcg atcccagctt ggccacacag 60
atgaggtctc gcgtcctctct cccccccct cccccccct cccccccct cccccccct cccccccct cccccccct 120
tttggaaggg cgcagctggt ctggccctct ctggccctct ctggccctct ctggccctct ctggccctct ctggccctct 180
tttgaagtgg gcagctggt ctggccctct ctggccctct ctggccctct ctggccctct ctggccctct ctggccctct 240
-continued

ttgcttttta ggtggttctca gattgaggcg aggttatattc gatctaaatg aacgacctt 300

   ttcttttag cctctctggg cacoctctggg atctctctctt atgggcaag cacattgagaa 360
tgatatanac ctcgtagacat ggcatttgggc aaaaactcaca tgcaatctttaa ctagctctttttt 420
tactagcag cttccacagca gaaaattact tcccttgaa aaaaactggg cctgtacct 480

   ttccccctgt agctttaagc agagacatca agcgttggca ttcacatag taaatttttttt 540

tatatatatat ataataaaaa agatatcattt atcattcttt tataaggctc 660

   aggtagatct atcataaggg ttcacacatc ccacacatgaa agaatatttt atatgatatc 720

   aataaggtta agttagatcg gttatctatg tagagatggg aagagactaa 780

tgccccttaca tataataacgt gccggtgcpa ccggtggcag cattggtctc cacaatcc 840

cataagaga cgggtttagc ggtttgcttt ctaaaacctg cccatcctaaag aaaaaaaaaa 900
gacccgcgttg tattgccttc cgcgtgtcgc tataatccag cccatcctaaag ttaaaaaaac 960

   cttggttaac ccctgagcatt cactctcttt ccctgtggccc tataatccaa attaaaaatt 1020

gttccacttc tgggaaaaaa aaaaa 1045

<210> SEQ ID NO: 223
<211> LENGTH: 553
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2497805

<400> SEQUENCE: 223

cctggcaagac cggacgggac ggaacgggtg tctcactgta gacacacttc tctctggcct 60
ttcttggca ctcctccgca cccacctgcgg ctgctctcttc tctcttttgra accttgacat 120
ccagggcag cggagtgttga ctccttttct ggaacggtgt ccacacacgg ccggtgctttg 180
cctgtcttt ccacctggac cctggtgcct ccggtgcttt gcgtgtcgcag acaggttgc 240
ggggtgtgct gcggaggtct ccctgctgta ggagggacgg gcggaggggg ggggtggg 300

eaggcctggc ccggcggcag cgggtgtgcag cccggtggtgg cggtggcagaa ggtgtggttg 360
tctgggttgg ggtggttgcct ctcctggctc ctctcctcc gttggtttggct 420
tatatgttt ggtggttttt tggggttttc ttcctggctgtt ccctggtatc 480

   aagttttgct ccattttgttc ctatggtgag actactttta ttctctgagg aatatttt 540
gcctgtgat cca 553

<210> SEQ ID NO: 224
<211> LENGTH: 706
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2643562

<400> SEQUENCE: 224

cgcgaccccc ccgccacagt ggcgctggaa ggcgctgtca tctgacagt ggggcctgtc 60
ggcgaccca ccacactgcca gaatacgggg tgtggcgcct gtaacacccca ggcgacccg 120
agacagcagg cctctgtgcc ctcggagagg ttgggaggg agctcggggg cacccttgt 180
-continued

gtgggctctg tcggacagt gtctcttgct ttgctgtgcc tcggagctcaag ggctgtggggg 240
tcggaaacc acocccctgg tgtgaggaac aaccttcttc tgtgtgtcaca gaaggcocca 300
cacccctcct cctttccttt caggcttctcc atggacgcca ggcocgggacc ctctgagact 360
ccaaggaag ggtcggaggg tgtggccgccc ttcagctccga ttcgtgtcctcc 420
ttcattgtcg tgtgacccgg ggcgaagcga gtcgctcttc ttcggcagctg gatcaccaca 480
gttctaaa gacgaggaaga agttacttca aagacctctc cctctgaggtc aagagaggtat 540
gggcctttcc aactttatat attatatata aasttagtagt gatagttacc aaaaagctta 600
ttgggtggttt tgtgctgtgct tgtgcccat atttgaggtat ttagagaggg aagtgagatg 660
ttgtgaggg gcagcggtgtt gtggagagtct tcagtgatata ttcgag 706

<210> SEQ ID NO 225
<211> LENGTH: 509
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (492)
<223> OTHER INFORMATION: a, c, q, t, unknown, or other
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2657146

<400> SEQUENCE: 225

aaatattagt gtatactctt tygctttctct gttatagtgc agcataaagtt tgcctttgtt 60
acaatctagt tgggttgata atggtgtatcc aagggaaaga aagcatatgt ttactacgca 120
tgtactgca agttattaagg cttgggtgg agitaggtgcag tggctataa tggctttttcc 180
tgcagagtct aacctgcctt cttactcag caagtttctc aagtgcccatg gcagctcatc 240
gtaagcaca aaggggtact ttccaggtat ggcaggtttg tgcgtatgcgt tgttgaggaag 300
agtcaacctg ttcctctctg tgaacaagtc ctcctccctc aaggaacctgtg ctgaggccac 360
tatctctggt tggccagata tgtgattct ctagcacttg cactctctctg tagccattggg 420
atgtgtagat aaggggctgt tgaagagggg aagagatgaa aagcacttggt tgtggatttt 480
cctcagcga gcacctccgca cagccgaca 509

<210> SEQ ID NO 226
<211> LENGTH: 2153
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2755796

<400> SEQUENCE: 226

gaagggctgt gcggaggccc ttcgaggagt tctagtgtgc gcggaggtgt ctgggaggtgg 60
ccagggccc gcggagggca cactgagggg aggcccgggcc cggcgcctgg cggcgcctgg 120
gcggcgcgg ccggcgcctc gcggaggtgt ctgcgcctctt cggcaggc ggcggctcag 180
gagcggggggt ttgggcggag tgcggaggag tcgcctgaggc ggcggcctgg 240
ggcggcggg ccgggctgttc tttggtttgg ggcgtttcag cgcgtttcag acggagctg 300
ggcggagact tacttgctcg cgctgatgc aaaaagaaatg ggtgatttgc ttcggggat 360
cggcggcaca tcgcggcatt ggcgtgtttg aggagatgg cagccgagtt cagcgggctg 420
gtgcacgcc acctcttgg ccccaggttg tgtgctgggt tgtttcccctc tgtgaagtctt 300
cactagacct cctgagttga ctggcaggaag acacttttaaa acactttca aagcagtttt 360
cctctccttc tataggccct aactctctac aatctgaggt gcattgtcct 420
gggagcagc acatctcttgct cttgcctca gcctctgcac gcctgcagga aatattattgt 480
ataagacaa aaggggttc ggcagagtga aacgctgtga atacctgcaat tttgggagggc 540
tcagactcgt ggcagacagct gccagcaaccc tgtgaacacaa gctatgcgc aatgcgcaaa 600
cctctctct acataactca ccaattgttc gtaagctgat gcgtggtgcg gttaacccca 660
gtcatctgga ggctgagcgc gaaactctgt gcactcgaggg gcagagagtt gcattaaggg 720
tacagacttg cattctctggt cagggtaaacc cgtgctcgg gcattttcgg gcatttcgg 780
catcctcacc a 791

<210> SEQ ID NO 228
<211> LENGTH: 764
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 3129630

<400> SEQUENCE: 229

gcacctcagc cccctctgcc cctctctggc gtcccacccac gcctcagagc ctgccttgcc 60
tgttcgggt tgtctctggc tgtctctggt gcctcagacag gcctcctggc 120
```
ggpgcaggag cgccgccgca cactggaaggg aaaaatggag gcgatttcaca ctatgatgcag 180
tcaacacag gcocctcag atgyccagact ctctggyggt tcttcccaga ggtctacatt 240
tgccgagcag ttgtgcaagg ccaaagatacg agtggaggtgt gtgagggagag gaggtaggttgg 300
aagaggctcgg atgggagca tttttttttt ctactggtttttty gcgctttttttt gtttattttttt 360
gtcattctga tttatttcttg ttagattcat ccctaactca ttcçattcat gaaaaatttt 420
tataggtagata aaatctatgg tagattcgata aacttttatttatttatttt attttatttttttt 480
atctattcat tttttttttt ctctgcttttct ccaatggattt ttatggaata gctcttgttttt 540
catttggaca ttagtatttatttatttatttt ttagttggattt tggcttatttattttatttttttattttattttttttt 600
acatattttta ccctccggagaa aattttggtaga aagctgccttttattttttattttttattttttttttttattttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
-continued

tgattaaaaa aaaaaaa

<210> SEQ_ID NO 232
<211> LENGTH: 1010
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 1334153

<400> SEQUENCE: 232

gggaaaccac ttatgtagga cacagtccac ggcagatcca gcaggttga ggccotgtgg
  60
tcccaatctt tggagaaag tcaagcgc acacatgaa gcatccotgt tgcgtcatac
  120
actgcaagtc tggctgacg tgtgaaatct cggagtctcg tcgctgtaaa ttccatggga
  180
aactgtcrg tcacagcag tgccttggaa tgcctctcag atccccaact cagctgtatc
  240
agctccotcc tccagtcgac ccagtgacac ctattctgct tcagtctctc gttgtctcg
  300
tcagcgcgact gcagctgag gggagcacac attacagcct tcaacttcca ctggtcctgt
  360
ggacaatct ttcattcttt actagagctgg agcagctgac agacacacag caccacccag
  420
gacgcaagcc tcttcggagc gttcttgcct tggaggttg TAGCCTAGTC
  480
ggacaggtta gccatatc ccagggggcg gttctttgct tttggtcgct
gggacagcagt tggagtctgg ggctgctgct gctgctgct gctgctgct
  540
caacagcctt tggacagcag gccacctttc gacagtggcc gttctttgct
gttctttgct tggaggttg TAGCCTAGTC
  600
ggacagcagt tggagtctgg ggctgctgct gctgctgct gctgctgct
  660
ggacagcagt tggagtctgg ggctgctgct gctgctgct gctgctgct
  720
ggacagcagt tggagtctgg ggctgctgct gctgctgct gctgctgct
  780
ttggactttc ggtcaggtct cagctgctgct gctgctgct gctgctgct
  840
ttggactttc ggtcaggtct cagctgctgct gctgctgct gctgctgct
  900
ggacagcagt tggagtctgg ggctgctgct gctgctgct gctgctgct
  960
ttggactttc ggtcaggtct cagctgctgct gctgctgct gctgctgct
 1010

<210> SEQ_ID NO 233
<211> LENGTH: 1981
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc.feature
<223> OTHER INFORMATION: Incyte Clone No: 1396975

<400> SEQUENCE: 233

cagctctttt cggagctgtgt ttcgaacctc tggatcagg tgttccaacct ggcctcagctt
gtcaggtct cagctgctgct gctgctgct gctgctgct 60
tcacaaggtgg ggtgtcagcc ttcgcttcac tgtatctgcc cagctgctgct
tcaggtcttgc ggttctcagc cagctgctgct gctgctgct 120

cagcgagtg gaatcttttg tacattaaggc cagggcaca cagtcnaagag gtcnaaggtgt 180
gaggcoctga ggctggaccc tagctgtcag gcasaggtttt cccactccgc cgcgcttgcc 240
acctctctcc caaggccaggt tggggaacct ggaggagtc cggcagaaat aatcagcaaa 300
gacacttccc acacacaccc cagcccccag cctcgttggt tccacagcacs gtcctccagt 360
agtgtgtcag agccagatag ccgctgcccc ccacccactc caacgccaca cacaggcato 420
cataaacccc agaagacctt ccaaattgagg ccaagctcac ggtcagcyyg aatgagtctt 480
tgccccctga aggctctggt ggaaaggggc acacataatgg aggtctgaaac ggcagcccaaa 540
acctgctgtc attgcccctcc agccctgtgct tcctctctct ctttctccag tggctccctg 600
tgagccaca gcaacccggca ggcagaccc ttcctcccccc ttcagccctt ctacgtgcct 660
ttcacacgt gttcttgctct ttttatcact ccctctctga ggcaccaaat ctgtggttcc 720
gcctctgcag tggccccaaag gtcacattaa cttgaggggg aagggctgtg tggatcacaag 780
atgatttctc ttgtagctgc cattttgcac gttgcccccct ttcctatcctg atgtgtctctg 840
tccctctagt ctttccctta ctctgctgctact gctacccatt caagggctatt 900
tgatatcagg ctctgggtgtg gcttggagcttg gggagactctg ggaggaatctt cctctgcttg 960
ggagagtgg ccagggggag gcgcaggtgt gcgtgctctct gcgaatcgctt tcacacataag 1020
ccagctgtc agttggtgcc tggagggccc ccctacttcg cccagttactt gcgggtgctcg 1080
gcctctctgc cttttcccttt gctgcaacgg gccagccaca gcgttatgcct cctttctccag 1140
cctctctctt tcaagccacg cccagcagcc gcaagactgc ccaagggcagc acatgtggcg 1200
acccctccgg gtttagctgc cacaacccgga ggcgccggcg ccgctttttt ggcgaggag 1260
gcctctctctt tcaagccacg cccagcagcc gcaagactgc ccaagggcagc acatgtggcg 1320
gtctctctgg ccgctttttt ggcgaggag gcctctctctt tcaagccacg cccagcagcc 1380
agctgctgcc cttctctctg ccgctttttt ggcgaggag gcctctctctt tcaagccacg cccagcagcc 1440
ctctctctgc tcaagccacg cccagcagcc gcaagactgc ccaagggcagc acatgtggcg 1500
gcctctctctt tcaagccacg cccagcagcc gcaagactgc ccaagggcagc acatgtggcg 1560
ctctctctgc tcaagccacg cccagcagcc gcaagactgc ccaagggcagc acatgtggcg 1620
tgagatggt cgctgctggcc tggggttagc tctctgtatt cccacctccgg cccacacaco 1680
cactctctgc cactacccggt gtgtctgctg ctacgctgcc cagccgtgctg ctcctctggtt 1740
tccacccaaa tgccccaggg cagggcagag caggtgtgct ccaaggtggt gttttctctgc 1800
ggcagaaag ggcagagttga tgaagggggt tgggccccag cccacccggg ttcctctctc 1860
gcgatgtct ccacccaccc ccagccagctg ccccagcttg cccctccagc ccgctgggagc 1920
ggctcctgc cactcttggg ggcctctctg agggcagctt ttaagcccaaa taacacattt 1980
a

<210> SEQ ID NO 234
<211> LENGTH: 744
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1501749
<400> SEQUENCE: 234
ggcgcggggt gtcctctgca gcacctgaa gtcgacctc gtcgctcct gtcgctcc 60
ggcgtcagtg ctgcctccgc ggggcgggtg gctgcctcag cctgagcttg gctgcctcct 120
cctctgctcc tggctgctgg gcacaggtgcc atagcttgga aataaactca gctgatgctt 180
caaaacagag aagacgtgtg tcaactaag aatcagatg gctgatgctg gagaagac 240
aaagaatcct tgccgagcct gaagggcagc agcagggcag ctcggtgccag gccggtgccc 300
ggcgtgagc gctcgtaacc gcaagttcct ctacaggtgct tggccgaagc gaaatttgaa 360
ggcgctacca ctcttcgtggg taacagagat cggaaatggac atggaata ctgctgttatc 420
tcaacattgct agacgattca acagcctgca atggtctgcc gggcctcccg cggctttggg 480
cagttgagcc ggtcgacact ccttggtgctgtgctccgc tggccacagc tggtaaaga 540
agcggacag ctctcgtctt atgtgatatc ttggcgctct tattctctt ggcggtgtct 600
ggtctatcct ccattccttc tggctgtgct cccaaatgaa gagccttaaac caaactgatc 660
agcggatcct caatgctccc ggtgatgcct ctcatatcctt ggtcgctttc aattctagtaa 720
agcggatcct ctttcatcttt gaaaaaacacg cgggtgtctcc ccttctttg gtaaattaat 770

&lt;210&gt; SEQ ID NO 235
&lt;211&gt; LENGTH: 979
&lt;212&gt; TYPE: DNA
&lt;213&gt; ORGANISM: Homo sapiens
&lt;220&gt; FEATURES:
&lt;221&gt; NAME/KEY: misc_feature
&lt;223&gt; OTHER INFORMATION: Incyte Clone No: 1575240

&lt;400&gt; SEQUENCE: 235

ccccccggtgct cgacgagttg cggaggcg cttgatgcttg ggtggtgcgg aaacaagggc 60
ggtggtggtg cggaggcccc ccacctgcgt atggcaactc tggcagacac gcacaacagtg 120
ccccccggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 180
tggctgctcc tggccgcttc tattctcgcag ggcggtgtcc cgggtgtcctcc 240
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 300
tggctgctcc tggccgcttc tattctcgcag ggcggtgtcc cgggtgtcctcc 360
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 420
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 480
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 540
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 600
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 660
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 720
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 780
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 840
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 900
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 960
ggcggtgct ccacccggtgct ccacccggtgct ccacccggtgct ccacccggtgct 979
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<223> OTHER INFORMATION: Incyte Clone No: 1647884

<400> SEQUENCE: 236

cocagcttg ggcgcgcgtt gccggtggtt cccggggcga caggggcccc gcgggtgggg 60
caggggctgt ggcgcgcgtt ttcctgcgtc gttctctgccc gttccccaggg atgcgcccgg 120
gttctgtggtg ccgcctggct tacccggctc agctccccctg cctggtaaag gctcccaag 180
cctctgctc agatggagaa aactgagcccg gggagaggsaa agccacacct cacatgccc 240
cagagacacc tccacagcct cagcggagaac ccctcagcccg ggcgcggtgg gtccttccc 300
cctctgctc tagttgcaag gcgcacaggg ggcacaagtgt tcaacattttct catttgacag 360
atgagaaacc tgggctgtgg aagggtaagc tcgctctgct gagaattgag gcgcacaggg 420
gtgcaggtaa tggggactgt ggggcacggc ctgagtcgca tgcgcctcag tgggctccttgc 480
tgatcttgg cgaactcgc ggtgacattg tggcttgcct gacgtaacctc cctctctggtt 540
tgccttggcg gtaaaaccag gtaatctccc gcggatctctt ccaatgggt acggggacaag 600
ttcgctgccc ttgcacagtgc gtaactagc tgggctcagc cggccgctgtg cctctctggg 660
aatccacca ctggcaggtg cgcaggcaag accactgtgaa ggcggcaggt gggcgcctgg 720
cgggcaggt gcgcacaggc aatcctggaa ggcgcaggt gcgcacaggg 760

cocagcttg ggcgcgcgtt gccggtggtt cccggggcga caggggcccc gcgggtgggg 60
caggggctgt ggcgcgcgtt ttcctgcgtc gttctctgccc gttccccaggg atgcgcccgg 120
gttctgtggtg ccgcctggct tacccggctc agctccccctg cctggtaaag gctcccaag 180
cctctgctc agatggagaa aactgagcccg gggagaggsaa agccacacct cacatgccc 240
cagagacacc tccacagcct cagcggagaac ccctcagcccg ggcgcggtgg gtccttccc 300
cctctgctc tagttgcaag gcgcacaggg ggcacaagtgt tcaacattttct catttgacag 360
atgagaaacc tgggctgtgg aagggtaagc tcgctctgct gagaattgag gcgcacaggg 420
gtgcaggtaa tggggactgt ggggcacggc ctgagtcgca tgcgcctcag tgggctccttgc 480
tgatcttgg cgaactcgc ggtgacattg tggcttgcct gacgtaacctc cctctctggtt 540
tgccttggcg gtaaaaccag gtaatctccc gcggatctctt ccaatgggt acggggacaag 600
ttcgctgccc ttgcacagtgc gtaactagc tgggctcagc cggccgctgtg cctctctggg 660
aatccacca ctggcaggtg cgcaggcaag accactgtgaa ggcggcaggt gggcgcctgg 720
cgggcaggt gcgcacaggc aatcctggaa ggcgcaggt gcgcacaggg 760

<210> SEQ ID NO: 237
<211> LENGTH: 1080
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:  
<221> NAME/KEY: misc_feature  
<223> OTHER INFORMATION: Incyte Clone No: 1661144

<400> SEQUENCE: 237

tttttgtat ttttaggca gataaggctca aactagtgtg ctaggtggtg ctagaactcc 60
tgatcotaag ctagctccct gcccataacat cccaaagttg tcggagttgca gcttgagccc 120
aacgggaccc gggcacctt cttgaaactc agtatcactg tgccacagt ggggctgc 180
caggaggccg ggccagcttg gttcactcttg cctgccgtct cttccctctg ggcggtgcttg 240
cgggaccccg ggatgagagc agaactgtt caagttagcc ggaaccttgg ggggtgcttg 300
tttgggaccc atcctgcaggc ccccttcagc tttgaggctcct ctctgctgagct aatggggctg 360
cgggctggctt cttctcagtg cttcactggt ctgcctcactgc ctggactgcactg ctaggtggtg 420
ggcagctgggt tgcctgtgtg ccgaactcgc cagggcaggg gcgggctgcct cttctctggt 480
aatccaccc tccacacccc ttggctgcagct ctagagctgc aaggtactca cggggcctgtt 540
caggagcttg gggggagagc tcgagtgctgt ggcggtgctgc ctctctctct caggggtgtg 600
catcccagc ggtggtagcc cggcagctgc cgacaggctc aatctggcaca aatggggctg 660
cgggcaggt gcgcacaggc aatcctggaa ggcgcaggt gcgcacaggg 720
ggatctcgtg gtagctccag ggcggcactgg ggcgcacaggg cgggccagtg 780
gagattctt gttggctctt ccggactcgc cattggagagc ggggatctcg ggcggtattc 840
ggcctcagc ggggactcctt ggggctcaggt ggcggcagtg gcgggtgtcc 900
ggggctcct gcggaccagc ggggctgagag ggggccagtg gcgggactcctt 960
ggggtggcttg gtagctcgtg gtagctcgtg gtagctcgtg gtagctcgtg gtagctcgtg 1020
gaacotggga ggccagacct acaacacgaccc gaaattgcac caactgcactgc cagcaggt 1080

<210> SEQ ID NO: 238
<211> LENGTH: 1129
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1685409

<400> SEQUENCE: 238
caacotgacg cccacacggg gcagactacc gggcaagtgt ggagccacct gcctgctgat 60

gaccgcgttc atggcgccgg agctcgccgg ccagaaagct atggacaggc agagacatc 120

gtttaaggg aagccgcatg atgcaggtat tctgtccgcc gcgcccaacc ggcagtagg 180

caggagaggg gagggtggag aactgggttg gagcaaggtt tatagaagga 240

cagagagctct gcctcaggtct gaaagtgtgag ctcagctgctg ggcagcagct gctatttgtc 300
ttcaggtgt ttcttctctc cccacocctcc cactgtaggg ctcaagacct tccaggaag 360
ggagggggcg gcgcttgccg ctcaggctgta tttctgacag ccctctggtggt gcacottaag 420
gggagggaca gggaggtcct catttcaaat ccctggttgg ttaccggcagcc caagctaccttt 480
tgctccctct tcogtctcgg ctctctcctct cccctaccac ctcctcactag ttggtgctgg 540
tggtctcctc cattcagacg ttagacgtct ggggtctgctg ttcagacacgct tctgccctctctt 600
tgagcggacag cccattggag atgctgcctct ctggctgccg ccgctgcttcc tctctcttct 660
tctagagcgt gcggatccag gcagcaacagc gtaacctaggt ccacatcact cctacacactt 720
cctttgcctc ccctaccocct ctcagacgtttc ttctttttct ccctgtctag ctcagagctc 780
ccttccttc ctcccaccgc gggcttgagac atcagcagctgg agacgcaacc gaaagaac 840
gagcaagag gcagggcacc atgcgttctgt ggcttcgttg ccaccctctct ttgctccctgc 900
cgtgtctctgc gtcagccgtcc caacacacgt cagttctcct ctgtctgtg gtcacaggtc 960
cagcagctg gcagctccct ttcggcttgg gtcctggcag gttccccttct ttcgccctctgc 1020
coccagcgta gccttcctcct ccctgagggcc ctcctggggt gcaggtgtgtt accccttc 1080
agttttttaatatcctgggt ggcctacccct aaatgtatgca aagtagctt 1129

<210> SEQ ID NO: 239
<211> LENGTH: 2370
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: modified_base
<223> OTHER INFORMATION: a, c, g, t, unknown, or other

<400> SEQUENCE: 239
agaacacttg ccacagttgg tcagctgcc ggtgatgaaa gaaactcagtg ttttcccaagtt 60
gctgctagct gcgagaggtgc tcgtgctgggt gggttcaagt ctgctgctttgg ggcagctgac 120
angnqggtg gcggagcgtct gtcacattct ctcctgggt tttacacaac gcaggagctc 180
cccctcgggt gcagtaaagt ggacccaccc agctcccccg tgtttcacgc tggggtcgcc 240
cctgcgtctgc tctgcaccc gcgaacccgg gcggcctgg ggccccgtgc gctgggtttt 300
cctgcgtcaggt aagttggagg tacaatgtgc ttatggggtt gttttggagg tttatgac 360
tgggtgcgtctgc ggtggagagg cctgctgcct cccgagggag gacccgagtt gttttttta 420
tttgacaaactg tgggacacta tatccacactc ctgtgtgcgc cccccctctg 480
ggttcattgg cagacaacag gattcctttgc cattctctcc cagctcacoac cttggtgctgg 540
cctgctgcttg ctgsgctcact cattggtgggc tgaagaggtct cggccgacag atggacgagc 600
cctgcggagag aggctttcttg ccagcagcag tttgttctgt gcgttttgc gttgttggg 660
gtctggcccgct cttcggagc cttcgtgggc gctctccgt gcgtcagcgg caaaaaaggg gattctccctt 720
ggacgccgct cctctttttc tccacctgcgc cccagcagcag ccctcgtgag cacccagaga 780
gatgtagtgag gcagacacag cacagctttcgc cggccgcttg ccttcctccgt 840
gagacccctcg cccccctctcg cttcagcctc acggtgctac cctgctccc ccagacgctcg 900
gtctggcccgct cttggtctcc cggccgcttg ccctcgcccc gcgttggagtc tggggtcctgt 960
gccgtggcccg gcagcggatt gagccttctc cttcgtctgg gcggtgatcc ggtgatgtgtc 1020
cctgcctcaac ccctcctctc gagctgtggc cgtgtgtgag atgtgttggc gatgtgtgtgc 1080
gtctggcccgct cttggtctcc cggccgcttg ccctcgcccc gcgttggagtc tggggtcctgt 1140
tctgccgttt gcagcccttc gcctcctgttt ggtgatgtgtc tccgctccgtgc 1200
cctggctgctg gggctgaggg ggtgtggaat tgtggatgtc aagatagtct ggggtgaatt 1260
tggagctgagc gggcaggtgg cagctagtcc cctctcggag cccctcctgg gggtgtgatt 1320
gttcsacgag tccgtgcgtgt gggctgaggg ggggtgaatt cagccccgtc cgggtgtgatt 1380
gctccgcgac gcggcacaca gcggtttcgc gttgtctgtgc gcgtgctgctg tccgctccgtgc 1440
tctgcgtgtct gcagctgtctgc ggggtgaggg ggggtgaatt cagccccgtc cgggtgtgatt 1500
tctgcgtgtct gcagctgtctgc ggggtgaggg ggggtgaatt cagccccgtc cgggtgtgatt 1560
gctgggggag gcggctggtct ggcggcaatt ggagagctgc aggggttcgc ggggggtgag 1620
tctgcgtgtct gcagctgtctgc ggggtgaggg ggggtgaatt cagccccgtc cgggtgtgatt 1680
tctgcgtgtct gcagctgtctgc ggggtgaggg ggggtgaatt cagccccgtc cgggtgtgatt 1740
cgagcgtccat gcggtgttgc cgggtgttgat ccctctcgcc gcggaggtgc acagctgtctgc 1800
tccgctgccttg gcggaggtgc acagctgtctgc 1860
atctgctgag caggctgccttg gcggaggtgc acagctgtctgc 1920
tccgctgccttg gcggaggtgc acagctgtctgc 1980
tctgcgtgctgc cagccccgtc cgggtgttgc cgggtgttgat ccctctcgcc gcggaggtgc 2040
atctgctgag caggctgccttg gcggaggtgc acagctgtctgc 2100
ctgcgtgctgc cagccccgtc cgggtgttgc cgggtgttgat ccctctcgcc gcggaggtgc 2160
tccgctgccttg gcggaggtgc acagctgtctgc 2220
tccgctgccttg gcggaggtgc acagctgtctgc 2280
ctgcgtgctgc cagccccgtc cgggtgttgc cgggtgttgat ccctctcgcc gcggaggtgc 2340
ctgcgtgctgc cagccccgtc cgggtgttgc cgggtgttgat ccctctcgcc gcggaggtgc 2370
cggactgcgg tcgggacgg aaggtgtgt ctactgtgca gcccagaag cctgacagtga 60
ggcggggac cccgaaatgc acacgaagtg cggagctggt tctcttgat ttcatttcgc 120
cctgctctct gtctcttc acgcaaacag ctcgcaca tcgggggag ggaaagcgaga 180
taggctcttc ggcccccggg cagccctctct tggccggtgc aagcccttgac gcgtgagcgc 240
tgatcggtcgg tccccggccg acctggygag cccccccc cccggttccc gtcgctctat 300
gggagatgc tgggtctggc tagccggtgc tgggtcttctt cttgtcatctt tgggtttgca 360
ttgcgcggtt tggggctctc cagttttgag gacccactct tttgcatttt cctgagggcac 420
tggagaatt tttttcgggt tgggtctggc tgggtctttct caccagatgt ccgacgagc 480
acacactctt tgggctgag tggactccc ctacggaggt gtttcctctg gtcgaagagg 540
ggataacat cacccgagat taggtgcttg acggaggtga acttctttac gggcctggaa 600
ttacactgt gaacacacct atgtgattat ttcgaacggt acctctagtt aacacgctctg 660
tggactgacg gatgaggg gttggatgta tagaataacct tagaaaacc tagaactggg 720
aatcactct tggactctg cccctttggt attttaggaa acagagctgg ctgaactctga 780
ttgaatttc tttaacgatt cagacacca cccatattta ttggtattt cttgctttctc 840
tttggtgact tttttttttttttttttttttaaccactgcttttctggc 900
ctttggggac cggagggcgg ggtgttacgag gcggaggg cctggagcgg ctggagcgaac 960
agctgtaac ccgctgctcc a 981

aggagagaga ggttaatttc ttaagcatta taataattag tcgtaatagc ttaatgtcat 60
aatcactgga ccctctctcag tctctcctctt atgtattatc agataattgct ctacctctctctt 120
tgatctactg ctatattaatttttttc gcgtctccc ttcctgtgct accctttgg 180
bialcacaata atttttttttttgg caacacacta gattagagag agatgctagt ctgaactggt 240
gagcagttgaa cccccggccg cttctctttgga agatagaggact agatgctagt ctgaactggt 300
cggctgagg gttgctgtgc agaggtgaac gcgttgttaga gttttgcaag gcgtactaat 360
tgggtgaat ggttgacaaa ctgcaatcctg ctaaattgag atttattttttt ttcggaggg 420
acctagtaatt tttggaaatagc ttaataattag gcgtcagttgcc taagagacagc 480
ctgactagtg tttgactagc ctaataattag ctaatattag gggagagagas tgggttttg 540
ttagaattcg ccgctgacttata cctccctctc taaaatttt tagaattcttg 600
ccagagatt tggccggttg gcaagacttg gttgcctggc aagtttaagc aagtttaagc 660
-continued

tgttgtggaac gcagacaaac acacacaaag caaatctaac atggacctgg gtttaaccttg 720
aagcgagaa ttgaagtttg acttccaaat tctgtgcgcc aaaaatcaag tctgaaaga 780
atgcaacag atcagctgt taataaatcg ttcgagcttc ttccagctgc cattaacaacc 840
taatctcag cacagcagaa aacgcagacc ttcgcctgt tttaaagttg aagctagct 900
gacctcggc cagcacacaa actgagaaga acattccaccc acttctgtct gtagtgacaa 960
tatctcaac caattttaaa cttttttaaa ttgctgatt gagaatag cttataacatg 1020
gcttaaaga agtttaagg gagaatctt ggcctattt cttssaaagaa aatgtgacct 1080
cacaaattgc agcatcttttt ttaacacaga tttcaagttt aagcttgttc ttataagttg 1140
taatctctta taagtcctgc gggcataatt ctccttctt ctaaatcttg cctcctcttct 1200
cgag 1204

<210> SEQ ID NO 242
<211> LENGTH: 784
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 3151073

<400> SEQUENCE: 242

cacaagacaa cgcgtcaacag ctggttctgg atgctctttg ttccggtctc gcctttcttg 60
	tcttcctctc tcctgctttt tgctctctgc ttcgcttcacc ctcgctgttt 120
	cacaagacaa agcgcgtgat cttctaggg atgctctttg ggcctcaagyy tagctcttt 180
taagccgaca ctgctgttgct tcgcctacag ccatctctct cttccaaagaa ggtctgtg 240
gtctgtttg cgtctgttca aatgctgtaaa tgcgcctgaa cggctcctgg aatgtgtcg 300
gtcacgccca ataaatggct ctccttccaa aatcacactg caaaatgctt cagcctgctg 360
	aggacgttaa gacgttaaa gttttctcts aatacaagtc cccacacaac taagctttt 420
	taagctgtt cccagaggtt agatagccca aagctgttta ctttccaga cttagagttc 480
tgctgtgtgg ctggtttctct gcctgtgtct gggcggcc ctggccggtt cttccaga cttagagttc 540
gcgctgtttg ctggtttctct gtcctgtttg cttccaga ctttccaga ctttccaga cttagagttc 600
attgccgtg atgttcggat cttgctggat ttcgactct tttttttataa aagctgtgcct 660
	taagctgttt ctcgctttcttc ggcctctctc cccacacaac taagctttt 720
taacatatgc ttcgctgtttt ctcgctttcttc cccacacaac taagctttt 780

<210> SEQ ID NO 243
<211> LENGTH: 426
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 3170095

<400> SEQUENCE: 243

tctcctttaaa cccccacgac ctcctttaaa ccccctccta gcatgagtt ttcgctcttt 60

ggggctctc gcccctgctt tcgctgac caaagccttt ctcgcctgctcgtctgctc 120

tagtggagt aacacagcag gatactgcag gcacgtttgg cactgggaggcagcagcatt 180
gtcctagtgc aacgcttcca gaaaaatgtg catcagctac tcotctctgc cgaagctctg  
ctcagcag ctctcgtga aacccagcga atacgaga aagaacacac aaggaagaag  
caagaagca caacagaccg taacacata ataaaccctg ctatgcotc cacaoactca  
gagaaatac atttccacag ttttacttcg ttcctacttg tctaggacta gccaaggtgc  
ctttt  

cggagaca gcaagtcctc ggtctcagag gcacaagtc aacgctctcc tcagaggtaga  
agttccaccg cgocacttg tggagttttg tcgtttttgt tcactctgctg aacocagoc  
cccagcagc cggctgctcc gcacaagtc gcagataacc cttgggaagc aagacagcg  
tcccagcag agtctcagca aacagaccc gcacagcaat cttctcctct gcacactctg  
ccacagctg tgcctacttc tcgagccagc aagatttcct cctctgtttc ccagaaactcc  
cctctactc ctcacccagag ggaagctatt aaactcggcc gcacacccac atctagtcc  
aggaatgctgctc tctctcaggg atcctctgtg tggagaagc aaaccctcggg attctctcct  
tgtttccttg ccctgactocg tcctgcctcc ctgctctctc ctccactcgcct ctccctctcc  
taccctcagc gcccactgct ccctctctct tcctctctct gcacactctg cggagctctg  
occcgggctcg ctcagctgcg tccctctcct gcctgagccg ctctctctct gcacactcag  
gggctctcc ccaacactctc tcggttgcac acataagccg cagacccctc caacocccc  
gacctctcct tcgacgagct acggctcttc taacctgcgct ccagggccgg gatttttttc  
tgttgctgctcg cccactgcga tccactgctg ttgcaagtgtg taagttgcct  
acoaccctg gtgtagtgcg tgaatgaacc ctcctcctaag aagatgctgg gcagagctg  
tggcatttt gcctgacccca aggacccac gcctgtttgt gattagcgcc  
ggagagcg cgggtgtctg ccacatcctgg agtgggtctg tggaaatctc cttggaggag  
atccactaga tcggagtcag gcctcacta ctggataccg gigactctcc gcctgcaagc  
ccctcagctg cagcctttcg ccctctccag ctgcattgcgt ggctctattcct  
gggctgaccc aggtctgcag acctctctct ttgagctcttc tagctctgcag gactgtgtgtg  
tccagctccg ccagcgcgggc cagaggtgta gctgctcacc ctatctgtggc  
cagcagaccg agatctccag gccttaaccg tgggtgcctg tggaggtgcct ggctgacacc  
tccacagtcttcgctatgcctgc tcocctctccg gocctgtgac tcggatctga tcggccactc  
tccagctcag tttatatcct ctggggccat atttggctc tcggctcagc cctttccagc
-continued

ttgtgtact gggccaggtc actctcatctc tactgtctca gctctctcatc tggcagaggg 1440
acaaataagag tacccctcttc ggcccatgtg ttggctactca tggctattac ccagaagcctt 1500
tggcagaagc acocggagaga atctgcttga gacaggaggtg tggagtcggc cctggygcaac 1560
atagttagac ccctttctct caaaataattt aaaaaattt cccaggttct tgggctggtt 1620
cctgtstact cacgctttctt aggctgtagc nccgcnaggtat tggctgagcc cagccagtgg 1680
agctgctaggcg gactgtgtagc ttagccctgt agcggccttc acaccccaca aaaaaaaaaa 1732

<210> SEQ ID NO: 245
<211> LENGTH: 918
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 3836893

<400> SEQUENCE: 245

agcctctacgt cttcctgtgt gctttttgtc ttcctgctctg gactcctggagc gccctcgca gcaagttgag 60
cctgtgtcga cggagagttg ggcgcagcag gctcttgaggct gttcgaggatgc gcgtctctgt 120
cctgacaaa cggcagcagg ctaaaattaac tgggaatag tggaaactga aagagggca 180
gacagtctgt gttgaattttg acacccctgc aagagagttt gcacagcagc agaaagctgt 240
gccagataaa agggcaggg gacgctcgac ggtcagcagc gtctctgttttt 300
gatccttcct ccccagcagctg cttttcattc cgtatttttt tgtgcttggcag 360
agctgcctgtt gcaagttcattg gaacatctta ggaagctgatc aagttgtgat 420
cctctcaagc cccccagcagc ctcaagcactg ctcctctgcttg cgtgctctgag 480
ggttcccccg gggccggctgc ggtctcctgc gcaaaatgc tgaatcattt cagacacac 540
taattcctg cttgcctcct cttttcctgg gcaagctcagc tggcagctc 600
tccacccgaa ttcacagcttg atgcctgttc ggctcactttt cggcctcagc ttcaccactgc 660
gcagatattt atcaggtatg cgtgtgcctgaa ccttctgtttt ccgtcctctgc agttgttcc 720
ggagatcagc tggagtttctct gcagctgcttgg ctgagttctt ggtctcttt 780
ggccccgagac ccagtcctgg gcctctttc ctttcgagcgc ctttcttggcttgcagc 840
cagagggag cggagaggtt aaaaagcgag ggtattccaa caatttattt atctgtattct 900
accgctcaca aaaaaaaaaa 918

<210> SEQ ID NO: 246
<211> LENGTH: 676
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 4072159

<400> SEQUENCE: 246

gttcctacag cttccggccac ggtccagccgc ctcctctcttc cttctgttcg cgtctctgcttgcg 60
gttctccct cttcctctctcctctgcttgg gcaccccagggctctccatgg 120
gctgtctcc caaaaacccca aagcaagcgt ggaagcagc agcaacttccac gaggasattg 180
gagatgacg tctcccttcgg gggcctctgg gcacaccacgc acagctgacg tggccccagc 240
tgagagttg tggagccgcag aagctgtgac gtcacccgag ctccttgagg gcagggggcc 300
<210> SEQ ID NO: 247
<211> LENGTH: 2255
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 1003916

<400> SEQUENCE: 247

gcggctggcgg tcctgctcttg tctccccgggg cgcggccgaa gggactgga 60
ggagggggag gcggccggcc ggaggcggag gcggccggcc ggcggccggc 120
ggagggggag gcggccggcc ggaggcggag gcggccggcc ggcggccggc 180
ggagggggag gcggccggcc ggaggcggag gcggccggcc ggcggccggc 240
ggagggggag gcggccggcc ggaggcggag gcggccggcc ggcggccggc 300
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 360
ggagggggag gcggccggcc ggaggcggag gcggccggcc ggcggccggc 480
ggagggggag gcggccggcc ggaggcggag gcggccggcc ggcggccggc 540
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 600
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 660
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 720
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 780
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 840
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 900
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 960
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 1020
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 1080
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 1140
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 1200
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 1260
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 1320
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 1380
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 1440
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 1500
tagggcacga ggcggcagac cgggtgttcc gctgggttgc tggcggcag 1560
gttttagttt ttttttttta aaggtaggag acagacaatt tggctgttaa ctaagaacat 1620
gttatgttg agggtcaggtt aacccoaag agttccttg tgaattcgag ccttcccaaa 1660
agcacaacaac cacatacaca catactgcaoc cocaacacag octatgcaca aagttgtgatt 1740
atgtgacaca cttggagagt gttggttgca tttctctct gttgggggtt ttatactcat 1800
tttaaatacata tattatcata ctttataaaac ataatttaaag octatasaat ggacccasaas 1860
gcacaactat cagatattttg tatacctgga aataactcata atttagttcct ctaactattt 1920
tactagtgtt tactgacgata ttagtgatgta ctctcagtttt tttctcacaat 1980
tgactatattt ctctgagagt ctctctgctat gatattctta mgaagaagaag gggaacccttt 2040
tgctcactttaagagagaaactacgcagaaatgagaaacaatttccacagagagagagagagaaaga 2100
tataagatat gggtgtttct tttcttcattt gttatactggt gtctagaccaca ttttatattttttt 2160
ttatttttt gttaaaaaat taaaaggtgc attttgttgg tattggaaaa ttcctgtgaa 2220
tattttctct cttgtgatcaag tagoaaaaaa aaaaaa 2255

<210> SEQ ID NO: 248
<211> LENGTH: 1223
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2093492

<400> SEQUENCE: 248

gagccacacc cagctccctg gctgctgctgaa gctctcttccct cctctctgga 60

ggaacgtcaca cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

gagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60

cagccacacc cagccacacc cagctcctgcc cctctcttccct cctctctgga 60
ttascttggy gassssssssssss

<210> SEQ ID NO 249
<211> LENGTH: 1388
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2108789

<400> SEQUENCE: 249

gccctctcca ggcgtcccag aacacggtag ggagccatga tggygctcctt ggagccaggt 60
cgcagggcag aagtcagcttt taggcacca cttgtccac agcgcctgtc gctgtgcccc 120
gtttgaaac atgtggtgtg aacgagggcg tgacgcaag gtcgaacgcgt tgcgtgccc 180
tttttttttttttt gacgatatgg tcttctccat tgtgcctcag ctttgccagct ccttgccgag 240
cctggtcctc ccgcacaaag aagaccccat ctcacgata ggcggcagcc gggctggcaaa 300
tctgcccctc cgcggcctaa cagacgtggg atgggcgttg aagtggtgcc tggagagccc 360
tgccccacct cagacgagga gctgggctcct cccttcacgt tggtaactcc cgcgcttacc 420
agactgagc aacccctgcct cgcctgcagtc cttgcagcag ttcaagccga cagacaagca 480
agagacatac atggagctgtt agaagttaa aaaaaagaca ctcagtcgca tgcagagatc 540
gagacacacc gtcgacagt gacgagggag aacctgatgt ttgccttttca atctctctct 600
tgcgaggctgtg gttgctggga cctttatgtg ggccagcctg tccacccacag aacagccatat 660
cagggacaca ccggccaccc ccaaggtgcc acaagacacca tttctcaagg ttggggtggy 720
ggcgctgcgt gttgacccct tggccacccc ggccagcccc aacccctacc tggctctcct 780
cacgctgcc cttgagaggt ggccgctgtg cagcttccct tctcaccacc cttcacaacc 840
tgggggctct gccacctttt cttgcgctca gacgacccct cactctctcc 900
ccagacatgc agcacaagtg gcggcgcctg cttcccaagg ggccggtccgg accctataat 960
catcaagtag cagcagagcgg ggcgccacag aacccatagc atcctctatc ttcgtgcatct 1020
cacagaccct tttttgact tatttataa agatcaaaaa ctaaatattgc tggaaaaag 1080
agagacactt tatttacttttttcaat ttaataactt acagcttttt tccaaagacat 1140
tgttatgagc tttgtataaa cttgagatgc aagtcaaaaa aaaaaaa 1188

<210> SEQ ID NO 250
<211> LENGTH: 1792
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2171401

<400> SEQUENCE: 250

cggcgcctggg ggcgagcccc acgggtcatct cttgagggccg aagggcggccgc acggagcttg 60
cggacctgc ccccacggtt ggggccacaa gttgccggag cttgaattgg cgcgcctgtg 120
ggtattctttg ttggctccct ggcgcgcttg tgtgctttca gttgagcgccta cgcagaggg 180
cgcccgcggag cgacagcgcgc cagaggttcg tgttgcaggg tgtgtcttt tttggtgtat 240
tttgagctgag atgtgtaaac cttggtagaa tttaaaacc cagcttttcc cccagacact 300
caaaactct ctggaaaagt caacctttgg ttttaccag taaaacctgaa gaggagcttg 360
cttttctgga atgacactca ccagcttgga aagaagcact gtcgctgca ecacgtcga
420
tctgatgga tgtctgatg aataaatcct ggcgtcatac agatgtttca aagaaccaat
480
aatctctatg aagatgtgga aacaagctgaa cgaactggag cagttgatga atctctgagt
540
gaggaacac agaagctgct ttcagctgga aacaagctgat agatctttca agataacctc
600
tgtgaagctg atgacactca gtcocotgca gctgatagag tagatgtctc tttaatccct
660
gagacctaca cttgatttca aacggcatga gacgcttgaat ttagaatgtc atatcctgaa
720
gacactgtt ttaacccaca gacactttaa agaccttaaa atcttttgcc ttctgctca
780
gggacacagc aaaaagacat cttttacagt tggctcagag gtctccttgat agaanaaaca
840
gacctctca gtcctatttc tgcgctacat gcaagccctg atgtgccctt gaggcacaag
900
tttctttaca aacaggccttg gataaacaag aatgtgggac acaacattac aagatccaca
960
cagccatttg atgggaatgt gcagtcagga gaagctccaa gaagttttaa gaaacttctg
1020	tacctctact taaatagcact aggcttctta tccacattgt taccatctctt cggagcgcctca
1080
gatatttacac tttttaagtg gatatttaat cggatgaggg aaaaaggaacct gtaactctcgt
1140
gaaatctca atgacactca gtcocotcct ttcagcttctt atggaacttctt tttttgttct
1200
gggataaaa aagagacga caacactttaa ggaacatctc tccgctttaat tgaatctttggt
1260
tcaagacta tgtgatggtg tgtcttttttt aatcgcctgc tgcctgggaaa gtcgaccact
1320
cagtttttgc gcagctgctt gaaactttta tttcttgcaga aatgtgacgc aatactgcac
1380
gaaagtggac cttgctagta aatccatac aagacacaggt aatctgacta atattcacaac
1440
gactttgga aatagcttgaag aataagagaa actttcggga ctctttcagc
1500
aatattcat aaaaaacactg aagttaatag tgcccgttttc tggcaaatg ggggaaagaaga
1560
gtggacttt acataactca aatattggca aagctcctgcg ggggacacac catcttattata
1620
agttctttt gcacggata attatatctc ttttaagtaaa cacatctttta aaaaatttctg
1680	tacgctctatg tataactca cttgctgatg aagtaatact tttaataagtt ggtccccaaatt
1740
ttataagattataa aagagaggac ttcacatttc aaaaaaaaaa aaaa
1792

<210> SEQ ID NO: 251
<211> LENGTH: 205
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2212530

<400> SEQUENCE: 251

gagagaggag aggagctgag ggcggcgccg ccaccccccac ccagcctgagc ccgctctccc
60
cgggcccggg agatgggccc cctacccgga tggctgcacc ggctggggca atacccgagg
120
gggcctggag gcggctggag ggcggagctgg gcggctggccca aacaggttgg aatccgtgtgg
180
acccgcttgt cgcggccagc atggttttttttt cttgggacca gacagtcacc aaaaagttgcc
240
tcgctgatcc ccgtgtgac ccagctctcc gcgcgtctcgg ggcgtctggg ccgactctctct
300
ggggtgagcg tgcagctgcgc cttccttctc ctcgtcctct gacgctgctg caatacttggg
cggtctggcc
360
ccggcccttg ccgctggttt ctacaactct ttactctctc tggcctgggg cagcttggaac
420
aagctgctgg aagctgctgg ccagctgcct gcagctgggag ctccttctct
480
tggagacagct tgcggctcag ctcgctggg caaagtggag ctcgctggg ctcgctggg
540
ctggtgctgt gatcaccatc atcaactgtgg aagggcagcc tggctttccac tcacgtcttg  600
eaagtgctgto ccaagtccac cggcttcctc acaaatgtgg ccoccaaggc gggggcacc  660
aacotcctc gtgcaagtgg gaggagtcttg tgcocacatt tgacgcaag tgtcctctca  720
agatagtcgcc tgtggccatc cggcttgagg gcacgctggg actgatattg gatgacccctt  780
cgacccacto gtttgagaaa gagaagcagg acatagtcctt tgtgctggag tcacgctgctg  840
agacotaac ccoccaacacc gtcctgtacgg tgaagaacgta tcgctgacca gcagacgaa  900
tttccagtt cttgccgcggg ctctgtcctc tcgacccacat ctcagagagtt  960
ccctttacct cagctgtcat cacccgacag ggctccacgc ctcacattcc ccacagaccc  1020
tcgccctcct ggaatgggttt gtgtgagcuca gttgctgggg gcoccaactota acotggaatt  1080
aatagacggttgtc ggcacagccg ccagggctta ggtggcctctg atagctcttc ttctcctgctg  1140
atggcccttg gtctggtgcgt gctgctgctgc ctcaggttgg ccacccagccg atacgtcctcc  1200
gtctcctcgt gacacagttg tggcctgctc ctccagctggcc ccaacccagc atccgctccc  1260
cgacccagcg gcggccggcg acoccaacct acctgcacctc aaagtgactgc gcacagggctc  1320
tgggaaaaa tgccccacgt tactctggct tgaggccaaaa ggagagaggg gctatgtag  1380
tggccaggg ccctgccagac ccagccggcc ctcgctccag tcctggctgc acgtcctggcc  1440
caggttcctc ctgggtgcgc aagagatgccc ttggcagcctt ttcgagatct  1500
aatatattct cttctttatt acaaatgggt ggctccggag gatctacagtg ttactgctgt  1560
tagatata ggaacgtgggg ccagctgtgac aacataaatat gtaaagacgg ttgggtttgg  1620
tagtcccctc gcggagagag cagttgccca cggctgccga ccctttccctc ccaacccgga  1680
cactgcccgt gccatgtcgg ccocccagtg gagggtgcct tgacacatcc atatatattct  1740
ccattggttc ccgctcctgc cttggtgcta gcaccggta ctgcacaaaat tttggtgcc  1800
agtgattga atgtggcttg atccataagg gatctgggatt gacccagctg  1860
aatagtgtt cttctctcctt ggtatagagtt ttagatataat atgacccaggc  1920
agcagagcgg atgtggataat atccattttg tttccctcgg atctgtagat taaaacacag  1980
aaagggctgt cagttgcccgg cctct  2005

&lt;210&gt; SEQ ID NO: 252
&lt;211&gt; LENGTH: 471
&lt;212&gt; TYPE: DNA
&lt;213&gt; ORGANISM: Homo sapiens
&lt;220&gt; FEATURE: &lt;221&gt; NAME/KEY: misc_feature
&lt;223&gt; OTHER INFORMATION: Incyte Clone No: 2253036
&lt;400&gt; SEQUENCE: 252
tggtgatgtgc ccgctccccat cggcttcttg ttcacactatgt cccttgcttg  60
ttcacagagt tcagcccccct ccctggactg gctgctggcc ccctctcctca ctgtagcaca  120
tgctggccca ctgcttctcg cagctggatgt gcaacgccg gctgtggcc ccctggtca  180
tctggaggttc cggctcctgt gctgtgttct ggggacccc tccaacacta tcgtgcatgt  240
tgcgctaccg ctgcttgaga acacagtgg gtggaggcac taaacctagt tgagagagtgt  300
cagccgccga atccagacgt tgttggtctgg ccgccgctc agcacaacctg ccaaggtaat  360
gcaccgtaa gatgctgacg ccgctagact acagaaaaa ccacacactc gggccgccc  420
<table>
<thead>
<tr>
<th>position</th>
<th>sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>210</td>
<td>tggttgaac astcataac aastaaatg gttaatttt taaaaaaaa a</td>
</tr>
<tr>
<td>211</td>
<td>471</td>
</tr>
<tr>
<td>212</td>
<td>&lt;210&gt; SEQ ID NO 253</td>
</tr>
<tr>
<td>213</td>
<td>&lt;211&gt; LENGTH: 3775</td>
</tr>
<tr>
<td>214</td>
<td>&lt;212&gt; TYPE: DNA</td>
</tr>
<tr>
<td>215</td>
<td>&lt;213&gt; ORGANISM: Homo sapiens</td>
</tr>
<tr>
<td>216</td>
<td>&lt;214&gt; FEATURE: misc_feature</td>
</tr>
<tr>
<td>217</td>
<td>&lt;215&gt; OTHER INFORMATION: Incyte Clone No: 2280161</td>
</tr>
<tr>
<td>218</td>
<td>&lt;400&gt; SEQUENCE: 253</td>
</tr>
<tr>
<td>219</td>
<td>tcotctgag ggtctcact atgctctct ctcatttatc ttacagcgg ttagtttga</td>
</tr>
<tr>
<td>220</td>
<td>60</td>
</tr>
<tr>
<td>221</td>
<td>aagatctctg agtgctcctaa agttataatt gcctcaggga cttcagctac ttcctacttc</td>
</tr>
<tr>
<td>222</td>
<td>120</td>
</tr>
<tr>
<td>223</td>
<td>ttttctattct cgcctaat cattctcct gtcctgcagagt cattctctcag cttcattcag</td>
</tr>
<tr>
<td>224</td>
<td>180</td>
</tr>
<tr>
<td>225</td>
<td>gttttggttc cttttcagga ctcctcagac ttcttactct gttttttagac gttttttactc</td>
</tr>
<tr>
<td>226</td>
<td>240</td>
</tr>
<tr>
<td>227</td>
<td>gttataattc agctcataaa ttctctcttt tactattcattatatagc gagcagcag</td>
</tr>
<tr>
<td>228</td>
<td>300</td>
</tr>
<tr>
<td>229</td>
<td>ctcattcactt tcctctcttt ttctcagcca ggtgctgttt ccttctcttt ctctcactt</td>
</tr>
<tr>
<td>230</td>
<td>360</td>
</tr>
<tr>
<td>231</td>
<td>caactaagc cggcctgttg acctctctta gaagcgcctt ttcctgcagct tcctttactc</td>
</tr>
<tr>
<td>232</td>
<td>420</td>
</tr>
<tr>
<td>233</td>
<td>gattcctatg cgtctcctgt aataattttt atcctactcag ctcctctcttc cactttata</td>
</tr>
<tr>
<td>234</td>
<td>480</td>
</tr>
<tr>
<td>235</td>
<td>ccttttactt gtcctctctc grentctcag cccctctctc gtcctctcag ctcctctcag</td>
</tr>
<tr>
<td>236</td>
<td>540</td>
</tr>
<tr>
<td>237</td>
<td>caagggctt cgggctcttt tataataagc gatgtgtggt tctttttaaa attataaacc</td>
</tr>
<tr>
<td>238</td>
<td>600</td>
</tr>
<tr>
<td>239</td>
<td>gtactcact tgcagacttt ttcggtggttt ctcctctctt gtcctctctc ctcctctctc</td>
</tr>
<tr>
<td>240</td>
<td>660</td>
</tr>
<tr>
<td>241</td>
<td>ttcgctcttt tgccttggtc cttttctctg cctggttgtt cttttctctc cttttctctc</td>
</tr>
<tr>
<td>242</td>
<td>720</td>
</tr>
<tr>
<td>243</td>
<td>tgccaaattt tgcagattg cttgcgggtgt atggcagcag tggcgttgggg aggagcctg</td>
</tr>
<tr>
<td>244</td>
<td>780</td>
</tr>
<tr>
<td>245</td>
<td>aatgctggc cgcctgcctg cctcagagcag ctcctctct tggccttcag ctcctctctt</td>
</tr>
<tr>
<td>246</td>
<td>840</td>
</tr>
<tr>
<td>247</td>
<td>aggcctcct tgcctggtgt cggggctttc ggtctgggtg ctcctctctc ctcctctctc</td>
</tr>
<tr>
<td>248</td>
<td>900</td>
</tr>
<tr>
<td>249</td>
<td>cttcttatttc tgcctctctt gtcctctctc ctcctctctc ctcctctctc ctcctctctc</td>
</tr>
<tr>
<td>250</td>
<td>960</td>
</tr>
<tr>
<td>251</td>
<td>ggccactcct ctctctctct cttctctctt gtcctctctc ctcctctctc ctcctctctc</td>
</tr>
<tr>
<td>252</td>
<td>1020</td>
</tr>
<tr>
<td>253</td>
<td>gtagcgtgc cgcagcctc ccaatgcagtt gcggagccag aaatatatat tggccttcag</td>
</tr>
<tr>
<td>254</td>
<td>1080</td>
</tr>
<tr>
<td>255</td>
<td>agtggctgca aatactctct tgcagctgca ctcctctctt gtcctctctc ctcctctctc</td>
</tr>
<tr>
<td>256</td>
<td>1140</td>
</tr>
<tr>
<td>257</td>
<td>ttagcatc tcctctctct cttcctctct cttcctctct cttcctctct cttcctctct</td>
</tr>
<tr>
<td>258</td>
<td>1200</td>
</tr>
<tr>
<td>259</td>
<td>tatactacag cgtcctctct gcggcctcct cttcctctct cttcctctct cttcctctct</td>
</tr>
<tr>
<td>260</td>
<td>1260</td>
</tr>
<tr>
<td>261</td>
<td>ttgctctctc atctataaga ctttattacct cttcctctct cttcctctct cttcctctct</td>
</tr>
<tr>
<td>262</td>
<td>1320</td>
</tr>
<tr>
<td>263</td>
<td>acacagcttc ttcctcgac acgtctacg aatactctct cttcctctct cttcctctct</td>
</tr>
<tr>
<td>264</td>
<td>1380</td>
</tr>
<tr>
<td>265</td>
<td>ggcttcgag tggccttcttc cttcctctct cttcctctct cttcctctct cttcctctct</td>
</tr>
<tr>
<td>266</td>
<td>1440</td>
</tr>
<tr>
<td>267</td>
<td>tggcaaatg gtcgccagtc ctatttatct cttctctct cttcctctct cttcctctct</td>
</tr>
<tr>
<td>268</td>
<td>1500</td>
</tr>
<tr>
<td>269</td>
<td>aagctcattt ctaaagatat ttcctctctt ctattatatc ttcctctctt ttcctctctt</td>
</tr>
<tr>
<td>270</td>
<td>1560</td>
</tr>
<tr>
<td>271</td>
<td>gtagtgcgctt cttctttttt ctattatatc ttcctctctt ttcctctctt ttcctctctt</td>
</tr>
<tr>
<td>272</td>
<td>1620</td>
</tr>
<tr>
<td>273</td>
<td>tgaattatttc gtagtgcgctt cttctctctt ttcctctctt ttcctctctt ttcctctctt</td>
</tr>
<tr>
<td>274</td>
<td>1680</td>
</tr>
<tr>
<td>275</td>
<td>gtagtgcgctt cttctctctt ttcctctctt ttcctctctt ttcctctctt ttcctctctt</td>
</tr>
<tr>
<td>276</td>
<td>1740</td>
</tr>
<tr>
<td>277</td>
<td>tggcttcgac acgtctctct cttcctctct cttcctctct cttcctctct cttcctctct</td>
</tr>
<tr>
<td>278</td>
<td>1800</td>
</tr>
<tr>
<td>279</td>
<td>atagtcctcct tggagtagtc ctcctctctt ttcctctctt ttcctctctt ttcctctctt</td>
</tr>
<tr>
<td>280</td>
<td>1860</td>
</tr>
<tr>
<td>281</td>
<td>atagtcctcct tggagtagtc ctcctctctt ttcctctctt ttcctctctt ttcctctctt</td>
</tr>
<tr>
<td>282</td>
<td>1920</td>
</tr>
</tbody>
</table>
gttagctcgc gacocctcta tccttgcctc tgctggcagtgg aaggggtctt cagagttact
1980
gggtagtat cttatcctt gacotctgta tgaacctgg ccccttgcacg aqtgatgagc
2040
tgtagttttt tattgagatt ttattagctg actaaccaccaga tgaagctatt taaacaacctg
2100
eagccacatg taaacctctc ttggtgcctg cctttcacc caacgcccttat ttggcgcgctg
2160
gcgaacttca ttgcttttat ctcatggaac acaatgagat tcaagatagt gacatgttacg
2220
tggcactggg gggagctgttg ggtgacagat gcaatcggcc gotgctgtgt ctctcagatc
2280
cctttgcttc tctttgtcctc ttggcgcacaa tctgcmaaca accagaggtt tgtcttttca
2340
cagcatgctg aggaagtggaa aggattgaa caaagagcc acatgtcggaa agaagcatggt
2400
gagagaaaga aatagagaa taccaacaa caacccagatg gaaataatgta aagttaacaa
2460
gcacccagag atagtttgtaa gttggttagag gaaagatgctttccttaggt gacagtgta
2520
gacttcaag ccttcgtgta ttccagtggc gaaacgcgcta acaaacccct tgaagctgcc
2580
caaatgtggc aagagaaggg aagattaagca gttaaagatg goatacatac ggaagagat
2640
cgcactcgtg gtcgctgtcc tgcctggttc ctggyctgta aaggaagcaca tgaacctctg
2700
cctgtgccct tgcctgtccgt gggattgtgg cgctggagagg tgctcagaca acaagaca!t
2760
cctactgaaa acacgtctat aagatgagaa aatocctcaag gttctttttat tcaacacagt
2820
cctgcocctt ctgccctcaag ctgcacgatg gatgtttcag caaccttgaat ggtgttgccc
2880
tgaactctgt gtaaatggact atcccccaaa tggccacaaac taaaaggtttt aacctctttt
2940
aaaaaggact tagaacaacc ataatactga atgacacagga gcaactgcct gtaattaattta
3000
ttattttagg gattgcatata ggttaggggg gaattgttag actactttttt attttctttg
3060
gagatcaaggt tccatcttgg cagaggtttg tttgagaaaa aagggcctgt ctaggtaaag
3120
gagcctagtg tctatctccat atccaaagaga anaaaaaaa aagagaacac gtaacagat
3180
gatcagatc ataaaaaa gaacaatccaa gtcgaaattt gtttacaatat ggtgtatatc
3240
aaaaaattttt atcctaaag tagaacaactaat gatgctttaa cttttgcataatc
3300
tctgtactgtg gacacatcct ctgggtggca attggtggcc caacocagaa cttttacctta
3360
tctttttttg aggctcacag gttggtcattt cgggctcttt aggcaatggg tgttttgtcct
3420
tttagacag aggctgctgaa ggtggtctgtt gtagagacag atcyaattgc	acg
3480
ttagagaatt ttgcaatctt caaagggacac agtgtctgtgc ggttattttt aacaggttat
3540
tagctgaggt acgttggagg cccctggactg ctgtctgtcttt tttgagatg aqtgatgctg
3600
tctctgttag tggctgacgt actgtaataa aggacatca caaggtctag ggtcttcatc
3660
gagacactct atccccctaggtttttaa atccacatgt gtttcctcaaa gatggttgctg
3720
tacatctgaaa gtttattatat ataaaaaaaat taacaaaaaa aaaaa!
3775
<210> SEQ ID NO: 254
<211> LENGTH: 1856
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2207485
<400> SEQUENCE: 254

cggcgcaccc ggcggcggg gggagccaga ggcggcgccc ggttggcggg gcacaaacac
-continued

ggcggcgccc gcggcggcgc ggccaggcgc ggactgggag agacctgagct cggcgcgcctc 120
cgccctgcct gcggcgccgc gcggcgcccc ggcggcgccc ggcggcgcccc cggcgcgcctc 180
cgccctgcct gcggcgccgc gcggcgcccc ggcggcgccc ggcggcgcccc cggcgcgcctc 240

ggggagggc tcggcgcgccc ggcggcgcccc ggcggcgccc ggcggcgcccc cggcgcgcctc 300
cgccctgcct gcggcgccgc gcggcgcccc ggcggcgccc ggcggcgcccc cggcgcgcctc 360
cgccctgcct gcggcgccgc gcggcgcccc ggcggcgccc ggcggcgcccc cggcgcgcctc 420

tttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt...
acactacatta aamtrtggtt ttgtgttctct tgsaacttgc ctttaaccttc cttaaccacgt 240
ggatctgccct ctggctgctct gggcccaacc tggccctgcc ttgggaaagct gaaccagaggt 300
ttccacccac octctccctctt cagacgcggcg cagacgtcct caactgtgctg gcctctctgttg 360
agcagttgcct ccccaaaatct cctcagctgtg cggagccctct acctggccagt tggcagtctcat 420
tgcggcttatt ggtgtgctgct gttctgctgctc tgggctgctg gctgctgctgta gaagtgctggt 480
acaacgcgcct agatctcaaat ggcagatgcgt ccacactgcctg aggccatctgc ctgtgtgctg 540
tgactcagct gcctgggtgct cagacggggt ccgtgcagct gttctgctgctct gcctctctctct 600
acatccagct gcggccgctcat ctaacctctct ctggcctgctg cctaatctctc atctctctctct 660
taatctggaaa cctggcctgcc cttaaccacgcc gttgagctgct gcctctctgctc agacgagggaa 720
gttctgctgct tggacactct cggctttgctg ctgcagccct dcgctctgctg gttccttgagctgctctggctgctc 780
gaacgcgcct gggagcgtccg tggccctgcc tggagctgctg gcctctctctct gcctctctctct 840
agaactgggt cggctttgctg cttcagcactgc cctgctctct ctgctcttgctg gctgctgctgctc 900
ggagggctgc gcctgggtgct cagacggggt ctttgggtgctg ctttgggtgctg ctttgggtgctg 960
cctgtcggcg ccctggctgcc cttaaccacgcc gttctgctgctct gcctctctctct gcctctctctct 1020
tgctgagccc gcctggctgcc cttaaccacgcc gttctgctgctct gcctctctctct gcctctctctct 1080
catggccttgctc ccttgggtgctg ctttgggctgct gcctctctctct gcctctctctct gcctctctctct 1140
catggccttgctc ccttgggtgctg ctttgggctgct gcctctctctct gcctctctctct gcctctctctct 1200
tgctgagccc gcctggctgcc cttaaccacgcc gttctgctgctct gcctctctctct gcctctctctct 1260
tccttggtcggc cttaaccacgcc gttctgctgctct gcctctctctct gcctctctctct gcctctctctct 1320
tgctgagccc gcctggctgcc cttaaccacgcc gttctgctgctct gcctctctctct gcctctctctct 1380
tgctgagccc gcctggctgcc cttaaccacgcc gttctgctgctct gcctctctctct gcctctctctct 1440
tgctgagccc gcctggctgcc cttaaccacgcc gttctgctgctct gcctctctctct gcctctctctct 1500
agagggctgc gcctggctgcc cttaaccacgcc gttctgctgctct gcctctctctct gcctctctctct 1545

<210> SEQ ID NO: 256
<211> LENGTH: 1671
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2303171
<400> SEQUENCE: 256

gaaacctgcc gctctggctgc cccatatggtc aggcgcagcc accacagcag aagtggtgctg 60
gagctccgct cttgctggtgct cggagtggcacttgctgcc ctgtcgtgtgctg ccgcctgtctgtg 120
cctggccacctctg cagacgcggcg cagacgtcctc tcggaccctgcct gcgggacgcgctgc 180
ccttacccag ccactctgtcct cctcgccgctgc cctccgggaccctgcctgcctgcctgcctgcctgc 240
cgcagcggctc ctcagctgctc attcagctgtctc gccctgctgcc cccagagctgtcgtgctgc 300
gcccccagcc gctctggtgctc cctttggtgctgc ccggaccctgcct gcgggacgcgctgc 360
ggacagcggcg gctctggctgc cccatatggtc aggcgcagcc accacagcag aagtggtgctg 420
ggagggctgc gcctggctgcc cttaaccacgcc gttctgctgctct gcctctctctct gcctctctctct 480
ggccttgcct gctctttggctgc cccatatggtc aggcgcagcc accacagcag aagtggtgctg 540
caacactato cagcgcactct tctgccaact actctgggcag caggagcttg ggatttgtct 600
cctgagagct atggaaaccc aagttgtgtat gcccacaaag gagaaggtct tcttgtgtat 660
tcagatctttt ggacgaaaaa gttaccacac gttcagatgtg gttgagcactg agctgcttgt 720
cootcatctt atgacatca atcccttcccg cagcgcggcc gaccgtcgtt 780
ggagctggcc atgttgtgccc tgcggcactc ggagctgtac cttagtgccaa ggctcaccat 840
cttacaggtt cttctggccaa aagcttcaacg agttctgcaac gttcccccct cagcccacat 900
cgtgagactg cagcgcctcg atctggcagcg cgcctgcccg cgcacaactc cagcgcggcc 960	tgctttggtt gggccgctct tctcctgtgt gttcggccac aagttgtgtat atcaccacat 1020
cctcagagct gactttggtgc ccccgagggc gcacggaggt ggcagagctg cgggaggtct 1080
gaacotctac taccctgtgtc agcttggagcc ggtatgttgtc aggtatgtgtc ggccacacca 1140
cagatttggac atcaacaagcg tggagagggc cctcgctttt gcatactgtcag tggcccgtgc 1200
tcttgccactg gcagagttttg tcaacttgtat ccagggcctgt cagggacaac acccccctcct 1260
ggocagact cccgtggtgc ctgctgctgct ggggctccag cgggagctcgc agatcctctct 1320
tgaggtccct gggccagcgc cccctgcccag ccgacccactg gtaggaggag cttaacctgca 1380
gggagagagct cagcgcctcg gctgtctgta gcggcgcggc ggccagggcct gtggggccct 1440
gggagctggtc gactttggtgc atcagagctgc tcttgagtttt gcaccaacac aatgcttttcc 1500	tgcttttggc tctctctcct ctcctttagc agttggtgac ccocctccag ggtccgctggc 1560
tgtgagaggaa cgacacaggag cagacccctc agatcctctgc ggcgctctcg ttctcgcacc 1620
ttttaaaaaggggagcgcgcttggttgctgg gtttgccgca aaaaaaaaaa a 1671

<210> SEQ ID NO: 257
<211> LENGTH: 792
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2396046

<400> SEQUENCE: 257
sattttaggg agatgtgggg gggttggtgg gttaccttccc atttaccaca tattttgttt 60
ttcagatctttt cccacaataac agtattcaat acatacttac aaaaaaagaga tggggagag 120
gggagagac acaccttacag agcttttctgt gggttctgtct gtctctctaag tgaagctttc 180
tggtaactac cttgagagct gattgagcc ggttctctctgt gcgtctgact ggcacgggcc 240
tgtgagcgcc gttctcttgagttc ctcttctttc ttaacgatgc ggggcttttct cccacgagaa 300
ttctggtcct gggagagatc agttcttcaaa atgcctttctg atgcctttctg ggcctctctg 360
ccttacaggg ccacacttaca ctcctactcc cccacactaca aacaacttccc cccagggctc 420
cagatctttt cccacaataac agtattcaat acatacttac aaaaaaagaga tggggagag 480
caatatgttct cattttctctc atcactac ggtgagagct gttaccttccc atttaccaca tattttgttt 540
ttcagatctttt cccacaataac agtattcaat acatacttac aaaaaaagaga tggggagag 600
ttctggtcct gggagagatc agttcttcaaa atgcctttctg atgcctttctg ggcctctctg 660
ttcagatctttt cccacaataac agtattcaat acatacttac aaaaaaagaga tggggagag 720
ttcagatctttt cccacaataac agtattcaat acatacttac aaaaaaagaga tggggagag 780
atggtgtgtat ca 792
<210> SEQ ID NO 258
<211> LENGTH: 3045
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2456587

<400> SEQUENCE: 259

tgagaggg ctgatggaga cgaggagca gacgaggtg tgttagcaca gaactggagt 60
tgacagacgc agacgagca ctttcagct tttcagttg cctcttcgac 120
gatcagcgc tggagagctg cctgagggca acgtctggca caactgctct cttctggct 180
tggagcttg cggagcagag gaccgcagac tgaggggaggc aaggagggcg cctcaggtg 240
gcggccgtc cgagggctga atggcagcgc aagcgggggg gaggaggcct ctacgtctctg 300
agcgctgcg tgcgcagcgc gggcggaggg gggcggagcg ccgtagtgag ccgctctctctcag 360
aatgctggtc ggcggcgagc agcagggatt tgttgaacg agcagagcctag 420
gatgctcagc acacagtgcgc gttttatgaa tgtgtctcttg tgtttatcg gctgctctctcag 480
cacgtctgc ggagcgaagc gcacggcggg gcacagcgcag ttttgtatgg tttgagctctg 540
gctgagatg cggagctgac aacatcagaa cttgttgagag ttttctcttg gtttcatcag 600
cattgttgg tctggcagaa cgagagcggag aacatcagaa cttgttgagag 660
tgcgccgaag gttgctccag cttgaggggc tttgagctccg cttgacgccg ccggtctctcag 720
gcagccacat gggagatcgc cctgccgctgg gggagcggag gggagcggag 780
ggcagacgt gcctgctcag ttttatcttg gtaacctaaa ccttcccaggg gacatagttt 840
gcaggcggc ctcagccagc aagagatcgc cttgaggggc aagagatcgc cttgaggggc 900
aagagaggt ggtcagccagc aagagatcgc cttgaggggc aagagatcgc cttgaggggc 960
acacagtgcgc ggcagcgaac gttcgaggag cttcagctag cgattcagtt ccgagttgctgc 1020
atccagcagcg ggcagcgaac gttcgaggag cttcagctag cgattcagtt ccgagttgctgc 1080
ccgagttgctgc gtcgggttgct gcgggagcgg ccgagttgctgc gtcgggttgct gcgggagcgg 1140
tgtgagcatt ccagcggaggt cccaggagtt cccaggagtt cccaggagtt cccaggagtt 1200
cctggtgcag cccaggagtt cccaggagtt cccaggagtt cccaggagtt cccaggagtt 1260
cctcaggcgg ggcagcgaac gttcgaggag cttcagctag cgattcagtt ccgagttgctgc 1320
acacagtgcgc ggcagcgaac gttcgaggag cttcagctag cgattcagtt ccgagttgctgc 1380
tggagacgc gcgagcggag cttcagctag cgattcagtt ccgagttgctgc 1440
cctacaatag ccggagcggag cttgaggggc aagagatcgc cttgaggggc aagagatcgc 1500
tgcggtcag cccaggagtt cccaggagtt cccaggagtt cccaggagtt cccaggagtt 1560
acacagtgcgc ggcagcgaac gttcgaggag cttcagctag cgattcagtt ccgagttgctgc 1620
aagagaggt ggtcagccagc aagagatcgc cttgaggggc aagagatcgc cttgaggggc 1680
agcgggggcc gttcagctag cgattcagtt ccgagttgctgc 1740
tgcggtcag cccaggagtt cccaggagtt cccaggagtt cccaggagtt cccaggagtt 1800
tgcggtcag cccaggagtt cccaggagtt cccaggagtt cccaggagtt cccaggagtt 1860
tgcggtcag cccaggagtt cccaggagtt cccaggagtt cccaggagtt cccaggagtt 1920
agccctttg aggcatgcca ctttggtatc cttcttgata attcagtgta aagaagcagt 900
ttcacagcag acgccctcc aaaaagggg cytcactgct actcagcaac ccaaggtagt 960
attcagaaaa ttctgcatag aaaaanaagc acctccagct ttcctgatct gaaacccgac 1020
acgcagact actcctggct attggtgctc accatccaca gcaacatggc ccccttttat 1080
gtgaagctct tttgcaagac caaggaagaa gcacaacaag agacagtga gctaaaaagat 1140
ggagagataaa caagtttatt tggtaaaaaag aagagggcaoa aggcttctacy gttgcttca 1200
gtccttcct cccaccacacg cacccctctt attcacctctt gttctgatgc tggtaaactc 1260
cacgatgtaa gggatggggaa acctcctctgt ttctgcaatt gggggctgct ttcacagttt 1320
cagggtaaq gaaacactaa acgtaatcgt tccggacag cgaagggaaaa ccaaaaggag 1380
gctcttgt tgtaaacttt cagctccaa ccggctcaca gagcatcata acaagctccct tcctcttctt 1440
cotcaaaaa ccgaaaaaaa acgctctcgc ggattcatttt accggcaagg cggccagtgc 1500
gttcagagc gcaacaggag aagagagaa ttttgcacat ccccacaaaa angagagtat 1560
aatcacaat ccaagggcag gggagggcag caaaccacc ggtctgacc agatataag 1620
aagaagcgc aaaaagttct ctgtaaatatt ttccagacgt aacaacctga gaagacagt 1680
accccaaaa cantaaggg tctccagcct ggaacactt taccggctag ttgttttgtgccc 1740
atagacagtt ggggcaactc tgtaaagtag caggtggaag ttgtggaaac tagaaaaagcc 1800
ttgttgctct ttctccattag aagatataata tgtgaaagtct cagggggcgct attaacttcc 1860
tttaagttata aactggatct acocaccaag gagaaggttt ggtggactga ttgtgtagt 1920
ggaagagg atacgcctgt tggttatagag attgttatag aagtaactct tgaagggtgaa 1980
tttgcgagc gtcgcccatac gtaacttggt tggctgtcgt gcgggtggtt tcgaaagata 2040
gaggctctct tggagacact gtcgcttctct gctttgccacct atcgtcatatag attttatattc 2100
attatatatat aacaatattaa taatacttttg gcacaacacc accaatgcac 2160
atatttttc ttttttttt acaatattta tataaaattt tttataaat cttgtttttattt 2220
atgcagagtt tttctgattg gaaactatttt aatatttttt ctttaaatag tccaagctta 2280
attcagatg tttataagtt agtcctctct atcgcaggtat aagctctatt ctaacttctctg 2340
tttggtttagc aaaaagttta aataacttat gttctcatttg tcaaaaatttt aacatactta 2400
tttcagatr ctttcatatta aagagaatag attatatag tttca 2445
---continued

tggcagctt gcccctttggg ggcacaccag cggacatgcc agcgctctc ctggcaggtg 360
aacatgacct tcaagctcctg tgtgccttca ccaattctag atcctccaaag gtcctgctca 420
tgtctttcttg tgttacctct cgagcagcac gcagctgcac tggagactgg gcacattgtt 480
tctggcttca tgcctccag gttgtgactg ggcggttctg actggtgtta 540
agacctgcaaa tgttctgctg tgtggtggtg ttgctcagag agatcccat 600
tgatgctact gggctgaggg agccagacc acctcaaccc caggtgggca ccacccaatc 660
ggctgcaag cc 672

<210> SEQ ID NO 261
<211> LENGTH: 1183
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2495719

<400> SEQUENCE: 261

gagagaaagt atgtgacgag agcaagcgaag ccacaacccc gccccgcgt cccgtcccca 60
ccacctgcgc ggcgcgggct aagttcctag agggasatg gcagagaggt caggytagt 120
ttttgaagt gggcggcctc aaggtcttgg ttgagctcctgtcctcctg 180
ctactgggg ccgagggagcg accagctgtg ctgctgctctg acgctgggct caggtgggga 240
tgtggyagcc ccaagaggg acacacacta ctcctggaga gcgctcaca ccagcagcaca 300
agagagctcc aacactcctct acccctctctg caggtgcctc ccactcgcctt gagaactga 360
agaacaatgt tacatctgtc cacggtgcctc gacgatatcg ccgctcgggct 420
gcaggtgcc cgcagaggtc acagagatct gccagggagc acacagcagcg atccggagt 480
gcgttaggt gggcggcctc acagtgcttc ctcaccagc cctcctcggg cctcctgga 540
agagctctt ccagagcaga cccacacttac accagtttcct gcaggtgctt gctcgtggt 600
cctcagcgg ccctcacaac agacgccccg gtcggaacag ggctgtgcacg ccggtgctgg 660
ccacccctct gaggcactt gtcggtgact ccagaaccag tggagacttg tctacgtcac 720
agagagcgt gctccctgag tccctcctgc accttgctgtg gggagtgaggc gcggctccaa 780
caagccttg cccacacttacactccttg cccacccacc acagattggct gctccctcag 840
acatgcattc acagggcaga ggtggacctt cttcctgagg cttgcggcctc acctgtgcac 900
tgctggggac tagagccagg cagggagttt ggtgcctctag ccagtgactgt gggtctttg 960
gcagctgcca gctggcggga caggtgatggt cgcacacgca tggcataaa cttggtctcat 1020
ggagtaccc cttggtgttc gcctcacttc ttgctcagag aggctttggc tgtgctcacc 1080
gcagcgctgg tgtgcagctgt acctctggt catgggtccttt ggcagggcaca tgtgcaat 1140
caatctcct ggccaaacagct ccatactcc ttcwaaaaa aaaa 1183

<210> SEQ ID NO 262
<211> LENGTH: 1266
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2614153

<400> SEQUENCE: 262
```
---continued

gctgaccacc gcgctttcct ggctcgtgct cgcctgccgg ggttctgtgg tgggccggt 60
tgcgtcctc ctgctcgccg agatgtgctg actgttgctg ccgtgatgtt ccactcctc 120
gtgcggcgcg gcgctttcct gcgcgtcgcc gttctgctgc ttcacgctt gcggctgcct 180
coaatacga aaattctgag ctgagtcgta gcacacatcc ccggggggga 240
ggaggccggc gcggccagca gcggcggata tgccgacccc caactcttag gcctcctctg 300
ccttcatcct ccctgagat ttttatagtg ttagagccca gttgtcctag ttggaaatgc 360
aacagcatcc caggaacctg gttatggttg ttcacgtcc gcggcggcag cctacacggc 420
cgctgcacc a acttcgacgc a ggtgcgagct cctgagtcga a tggcgggtc gggcgtcctg 480
gaccccttca cggagaaaaa accctttgct aaccctagtc cgcacactc ctataaacc 540
ttacatcct taactctctct tcgcagtttt cggacagaat cgtcgtctct cggagacac 600
tgcgactgca tgagggaag tcggagcgct tggagggact ggatttggtg ggtttgtgca 660
cctacttttgt cttaaccttg gcggctgtat gcagccgtag cggcgggtct gcggccgct 720
ttcataaaga aagctgcatc catggcggcc gcggcggcgg gcagatccgg cgccttctct 780
tcctctctct ctctctcttt atacacagcc tgggtttatat tcctccttct ctctctcttt 840
tgcggggttt tggttgcggg aagaagcttt ctttgccact tggaaacttc aaccagatctt 900

tacottgac gcgggagtt aacccttac ctggagagct tggaaatcct aaccagatctt 960

tccgagcaca aaataaaag atagtcggag cttactacgc gcggcttctct ttgacacaggct 1020
ttccctctct ctactcgtcct atgcgtccct gtcctcttcgg caaagcacc taaatcagtt 1080

gcggccaa taatgtcgtt gcactgccat cttgcacgtt gcggccggc aaccagatctt 1140

ttcgaactg caacactaad atcttcagca gaaatcagaa tggcgtccta ttgtaataca 1200
catggcttt cttccctct cttcttcctct taattcagat ttttcgaccc ttggaaatgc 1260

aaaaaa 1266
```

<210> SEQ ID NO 263
<211> LENGTH: 1093
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE: misc_feature
<223> OTHER INFORMATION: Inocyte Clone No: 2655184
<400> SEQUENCE: 263

```
gatggtcttg ttttccttcttt ttttgctcttt tttgctctct caatttaaat gaaaatttcct 60
cggcacgtg ccggttgctg accttcttt accttctaag ctgtttgctg 120
acactgccttc taagcgcactgt cgcgctggcc gccttgctctt aacctgcggtt ccactcctc 180
acataccggc cgcgttcgct tgcgccgtgt ggcccttactt gcctgtcctg tcggtgcctg 240
ttcctcttg cttctctctc ccacactcag ccactttacct ctgctgtctgt gcggcggcgt 300
acacccctgt cgcctgcttt cgcctgcttt cggccagcag ccgctgcttt gcggcggcgt 360
ggcgcgttc ccacgctgtg cgcacactgc cgtttgtggt gcggcgggtt gcggcggcgt 420
tctacacgact ccactctctct ctgcgtcctg ccgctgcctg gcggcggcgt 480
gcggggttt tcgggttctg ccctgtcctt ggctggtgtg ccgctgcctg gcggcggcgt 540
gcgttctct cgcctctctct ccgtgtcttt ccgctgcctg gcggcggcgt 600
ttcgagtg gagaagagag ccgctctct ctgcgtctgt gcggcggcgt 660
```
-continued

tcataatgaaa ggaataagaa gacagtttgc aagagaagct ggtacacgg aatattcctca 720
ttgacagga gtatgtaacg aaaaaatcaag ttttgtttaa gacctcataa gctgggtgca 780
ttttttattag tttttattagtt tttaatcttg ttatctttt ctttaaagctga cacaaggtg 840
taatatctca tggtgaaagcg ggtgctgta atacacagaa attggtcctt 900
aacggttcc ctaaagccta attgaatttg ctttgacctt ttatctttagc acagagcatg 960
ataaaacct ttaaactctc gcagggaaagt gttttttttt ttaattttaa tatacacaac 1020
tctgaaaaaa ttggaactag attattcttt tttttcatag ctgggatata gggggtgcc 1080
tctgaggtcg ac 1093

<210> SEQ ID NO 264
<211> LENGTH: 1183
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2849906

<400> SEQUENCE: 265

ggaggtcag cgggggtcgc acaaaagacct tcctggtctcg cccacagcac agctgaggac 60
cctggccccg ggcctgggce ctgcgttcca caggatgagg cgcgtcagtgct cctgcccccc 120
tgcgcctct tgtgctcgag ggtgcgtgcgc ctgctgcctc tcggctggg ggcctgcac 180
agctgcgcgg agccggcaag aagctctgac cccaggaaga agggcggcga ggcagcgggc 240
ggctggcgag gcggcagcgg ccgggcggca aagctgctcc ttgcggcggc ccacccgctg 300
cctgctggcg acagtaagc caagagtcga gcagctgcgc acgggccccg ggcagcgcag 360
ggcctggcg ccgctcgacag tggatcttct gcggcccacac tcggctgagag cttccagggg 420
catcagccc cggccaggca ccccctcatgc cttccacac caggagctgc ccgggctctc 480
ggctggcagct cacgcaccccg cagggcggtcg gccctgcgcag gccacacttc cccagctggg 540
gctgggccgcc ggcgcgtacgcc ccagggtgcg ccgcacccgc gcggcgcagg ggcagcgcag 600
cctgctgcagac gctccaggg acccacgcac gcgcacccgc gccagcagcgc gcggcgcagg 660
ggctgacgcc gcggcagctgc acctcagctgc ccgcacccgc gcggcgcagg gcggcgcagg 720
ggacccagca cccacgcacag ccgggtctgc gcggcgcagg gcggcgcagg gcggcgcagg 780
ggctggcagct ctcggctgac gcggcgcagg gcggcgcagg gcggcgcagg gcggcgcagg 840
cctgctgccg cctccgctcc gcagcgcgcgc gcggcgcagg gcggcgcagg gcggcgcagg 900
gtggcgctcg ggcggtccgc cttgcgtccgc cttccgctcc gcagcgcgcgc gcggcgcagg 960
cctgctgccg cctccgctcc gcagcgcgcgc gcggcgcagg gcggcgcagg gcggcgcagg 1020
cctgctgccg cctccgctcc gcagcgcgcgc gcggcgcagg gcggcgcagg gcggcgcagg 1080
cctgctgccg cctccgctcc gcagcgcgcgc gcggcgcagg gcggcgcagg gcggcgcagg 1140
tagagaagcc gcggcgcctcc ataaagccgc acgcagctgc gcggcgcagg gcggcgcagg 1163

<210> SEQ ID NO: 266
<211> LENGTH: 840
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> OTHER INFORMATION: Incyte Clone No: 2899137
<400> SEQUENCE: 266
goatgtcgag gcgcgtccag tcggccgggg aggggtgtacg gcgaaggttt ctgcgagggc 60
tgcggagcag acctggttgg acacagctcg ggctgggggg ggctgggtgcgc 120
gtcggtttgg ccagaaggttc tcggctggga gcggctgggg gcggctggag gcggctgaga 180
ggctggcccgg ccggctgggc cgccgtgcctc ggcgtctggt gcggctgggc 240
ggcctgcggcag gcggctgggc gcgcagccgc gcggctgcggc gcggctgcggc gcggctgcggc 300
ggctgggcag gcggctgcggc gcgcagccgc gcggctgcggc gcggctgcggc gcggctgcggc 360
ggcctgcggcag gcggctgcggc gcgcagccgc gcggctgcggc gcggctgcggc gcggctgcggc 420
cctgctgctgc agacgctgcgc gcggctgcggc gcggctgcggc gcggctgcggc gcggctgcggc 480
ggcctgcggcag gcggctgcggc gcgcagccgc gcggctgcggc gcggctgcggc gcggctgcggc 540
tgcgcctgcag ccacacccgc gcgcagcgcgc gcggctgcggc gcggctgcggc gcggctgcggc 600
cctgctgcggcag gcggctgcggc gcgcagccgc gcggctgcggc gcggctgcggc gcggctgcggc 660
ggcctgcggcag gcggctgcggc gcgcagccgc gcggctgcggc gcggctgcggc gcggctgcggc 720
tgcggggccg acacccggcc tcagttggtg gcggctggcc gcggctgggg gcggctgggg 780
tgagtagggc tggaccctga tggagctgc aatataatcg aaaaacagga aaahaaaaa aaaaaaaa

<210> SEQ ID NO 267
<211> LENGTH: 606
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 2986229

<400> SEQUENCE: 267

aataattgtg gacagagaa agagcattgg ctatgatta gtaatattca tagttatgg 60
atatatatta aasagcatatt gcctttccac taaacatgta agggagaag gcctgagagt 120
tatatagtt aatagttaaat atagcataga cggggtataa aatgttttgt ataggtgca 180
tactttggga taattaagag tcccatctaa ttctctgtca cttaagaga gaacaatgg 240
caatattttatt gactttgagg aagagcagac agttcttattt tcaacattta cctgattact 300
cctttttttt ccctttgcag ctaagacact agattgttct tggagtcattct gctctcccac 360
tgagaac(aa) aactggagtc ttcgacaccc tttgagtcgg tccgctttctttttgtttttg 420
cggttttcgc tgaacctotccc aaggggccc acctgttgtgg aattttatattc 480
tgtgatagatt ttagggttag ttcgtaaatt atcatttac acagagggcc tctattgtgc 540
tgtattaccc agttttagag ttgtagttt ttctctggtga aatatattttaa 600

aataaa

606

<210> SEQ ID NO 268
<211> LENGTH: 1025
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Incyte Clone No: 3222081

<400> SEQUENCE: 268
gtctttgtag ctactcctgc tggccgccc gttttctcgc tactctgaac ctttaggttt 60
gtctgycocc atttgagac caggagtttg atcaactccc aggcggctga gagacggtgag 120
cggaattggg aactgagcc ggggtggtct agcggagaag cggcggcgcgt gcttgagctgtg 180
cctctgtagg cgtgagcgc cgtcctactgc cttcctgccct cttggtgagcc ggacgcctgc 240
cggcagccccc gagtaattgga agggagagcc ctgaggtttat tgtattttct tgaacaactcc 300
cgggaggcc aaagccccaca tatttttaaa ggcttgagagc tagctctttg aagttgttgt 360
gaatccagc agataatgag aagatagatatta ctggttactc gccaacagtcgtagttttt 420
cotctcctgt ctttgcagc ccctattggc cttggctgac cagtaaact ctgctcagtcatt 480
cttgaacatt ggatcatttgc cagataactt actttagagc gaacacactt cagaagaaaaa 540
gacacataa agcagataaa tgcacagag cggagctgccc gctcattgagc aaccccacac 600
tacgggggac ttgaggtaca gttgtgtctt gcaggtgtct gtagctgatt ttaagggcga 660
cgccctgct caagcttttttatgatctttg tatactagctt tactagctga gacactctgatt 720
tttatctact atgtttttgg aacccagttgagctctct ccatct tgtttataag 780
ctttatcctt atcagacgct cattttttagg cagatttttttt ccaagccgaca 840
taattcata aggtatttct cttctgaccc baseatatac actctcagga aggagttttaatttcttttc 900
1. 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:1-134,
   b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-134,
   c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, and
   d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-134.
2. An isolated polypeptide of claim 1 comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-134.
3-8. (canceled)
9. A method of 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. A method of claim 9, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-134.
11. An isolated antibody which specifically binds to a polypeptide of claim 1.
12-16. (canceled)
17. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.
18. A composition of claim 17, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-134.
19. (canceled)
20. A method of screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:
   a) contacting a sample comprising a polypeptide of claim 1 with a compound, and
   b) detecting agonist activity in the sample.
21-22. (canceled)
23. A method of screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:
   a) contacting a sample comprising a polypeptide of claim 1 with a compound, and
   b) detecting antagonist activity in the sample.
24-25. (canceled)
26. A method of screening for a compound that specifically binds to the polypeptide of claim 1, the method comprising:
   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.
27. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, the 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,
   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 compound that modulates the activity of the polypeptide of claim 1.
28-29. (canceled)
30. A method for a diagnostic test for a condition or disease associated with the expression of HSPP in a biological sample, the method comprising:

a) combining the biological sample with an antibody of claim 11, 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.

31. The antibody of claim 11, wherein the antibody is:

a) a chimeric antibody,

b) a single chain antibody,

c) a Fab fragment,

d) a F(ab')2 fragment, or

e) a humanized antibody.

32. A composition comprising an antibody of claim 11 and an acceptable excipient.

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

34. A composition of claim 32, further comprising a label.

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

36. A method of preparing a polyclonal antibody with the specificity of the antibody of claim 11, the method comprising:

a) immunizing an animal with a polypeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, or an immunogenic fragment thereof, under conditions to elicit an antibody response,

b) isolating antibodies from the animal, and

c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-134.


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

39. A method of making a monoclonal antibody with the specificity of the antibody of claim 11, the method comprising:

a) immunizing an animal with a polypeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NO:1-134, or an immunogenic fragment thereof, under conditions to elicit an antibody response,

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

e) isolating from the culture monoclonal antibody which specifically binds to a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-134.

40-55. (canceled)