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(71) Applicant (*for all designated States except US*): **INCYTE GENOMICS, INC.** [US/US]; 3160 Porter Drive, Palo Alto, CA 94304 (US).

(71) Applicant and

(72) Inventor: **THORNTON, Michael** [US/US]; 9 Medway Road, Woodside, CA 94062 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **YUE, Henry** [US/US]; 826 Lois Avenue, Sunnyvale, CA 94087 (US). **KHAN, Farrah, A.** [IN/US]; 3617 Central Road #102, Glenview, IL 60025 (US). **GURURAJAN, Rajagopal** [IN/US]; 5591 Dent Avenue, San Jose, CA 95118 (US). **HAFALIA, April, J., A.** [US/US]; 2227 Calle de Primavera, Santa Clara, CA 95054 (US). **WALIA, Narinder, K.** [US/US]; 890 Davis Street #205, San Leandro, CA 94577 (US). **PATTERSON, Chandra** [US/US]; 490 Sherwood Way #1, Menlo Park, CA 94025 (US). **RAMKUMAR, Jayalaxmi** [IN/US]; 34359 Maybird Circle, Fremont, CA 94555 (US). **GANDHI, Ameena, R.** [US/US]; 837 Roble Avenue, #1, Menlo Park, CA 94025 (US). **POLICKY, Jennifer, L.** [US/US]; 1511 Jarvis Court, San Jose, CA 95118 (US). **BAUGHN, Mariah, R.** [US/US]; 14244 Santiago Road, San Leandro, CA 94577 (US). **TRI-BOULEY, Catherine, M.** [US/US]; 1121 Tennessee Street, #5, San Francisco, CA 94107 (US). **BANDMAN, Olga** [US/US]; 366 Anna Avenue, MT. View, CA 94043 (US). **NGUYEN, Danniell, B.** [US/US]; 1403 Ridgewood Drive, San Jose, CA 95118 (US). **LU, Yan** [CN/US]; 3885 Corrina Way, Palo Alto, CA 94303 (US). **BURFORD, Neil** [US/US]; 105 Wildwood Circle, Durham, CT 06422(US). **LAL, Preeti** [US/US]; P.O. Box 5142, Santa Clara, CA 95056 (US). **DING, Li** [CN/US]; 3353 Alma Street #146, Palo Alto, CA 94306 (US). **YAO, Monique, G.** [US/US]; 111 Frederick Court, Mountain View, CA 94043 (US). **ELLIOTT, Vicki, S.** [US/US]; 3770 Polton Place Way, San Jose, CA 95121 (US). **RECIPON, Shirley, A.** [US/US]; 85 Fortuna Avenue, San Francisco, CA 94115 (US). **KEARNEY, Liam** [IE/US]; 50 Woodside Avenue, San Francisco, CA 94127 (US). **LU, Dyung, Aina, M.** [US/US]; 233 Coy Drive, San Jose, CA 95123 (US). **GREENWALD, Sara, R.** [US/US]; 21 Bucareli Drive, San Francisco, CA 94132 (US). **TANG, Y., Tom** [US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). **XU, Yuming** [US/US]; 1739 Walnut Drive, Mountain View, CA 94040 (US). **WALSH, Roderick, T.** [IE/GB]; 8 Boundary Court, St. Lawrence Road, Canterbury, Kent CT1 3EZ (GB). **GIETZEN, Kimberly, J.** [US/US]; 691 Los Huecos Drive, San Jose, CA 95123 (US). **YANG, Junming** [CN/US]; 7125 Bark Lane, San Jose, CA 95129 (US). **HILLMAN, Jennifer, L.** [US/US]; 230 Monroe Drive, #17, Mountain View, CA 94040 (US).(74) Agents: **HAMLET-COX, Diana** et al.; Incyte Genomics, Inc., 3160 Porter Drive, Palo Alto, CA 94304 (US).(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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(54) Title: HUMAN KINASES

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



WO 02/08399 A2

HUMAN KINASES

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of human kinases and to the use of these sequences in the diagnosis, treatment, and prevention of cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of human kinases.

BACKGROUND OF THE INVENTION

Kinases comprise the largest known enzyme superfamily and vary widely in their target molecules. Kinases catalyze the transfer of high energy phosphate groups from a phosphate donor to a phosphate acceptor. Nucleotides usually serve as the phosphate donor in these reactions, with most kinases utilizing adenosine triphosphate (ATP). The phosphate acceptor can be any of a variety of molecules, including nucleosides, nucleotides, lipids, carbohydrates, and proteins. Proteins are phosphorylated on hydroxyamino acids. Addition of a phosphate group alters the local charge on the acceptor molecule, causing internal conformational changes and potentially influencing intermolecular contacts. Reversible protein phosphorylation is the primary method for regulating protein activity in eukaryotic cells. In general, proteins are activated by phosphorylation in response to extracellular signals such as hormones, neurotransmitters, and growth and differentiation factors. The activated proteins initiate the cell's intracellular response by way of intracellular signaling pathways and second messenger molecules such as cyclic nucleotides, calcium-calmodulin, inositol, and various mitogens, that regulate protein phosphorylation.

Kinases are involved in all aspects of a cell's function, from basic metabolic processes, such as glycolysis, to cell-cycle regulation, differentiation, and communication with the extracellular environment through signal transduction cascades. Inappropriate phosphorylation of proteins in cells has been linked to changes in cell cycle progression and cell differentiation. Changes in the cell cycle have been linked to induction of apoptosis or cancer. Changes in cell differentiation have been linked to diseases and disorders of the reproductive system, immune system, and skeletal muscle.

There are two classes of protein kinases. One class, protein tyrosine kinases (PTKs), phosphorylates tyrosine residues, and the other class, protein serine/threonine kinases (STKs), phosphorylates serine and threonine residues. Some PTKs and STKs possess structural characteristics of both families and have dual specificity for both tyrosine and serine/threonine

residues. Almost all kinases contain a conserved 250-300 amino acid catalytic domain containing specific residues and sequence motifs characteristic of the kinase family. The protein kinase catalytic domain can be further divided into 11 subdomains. N-terminal subdomains I-IV fold into a two-lobed structure which binds and orients the ATP donor molecule, and subdomain V spans the two lobes. C-terminal subdomains VI-XI bind the protein substrate and transfer the gamma phosphate from ATP to the hydroxyl group of a tyrosine, serine, or threonine residue. Each of the 11 subdomains contains specific catalytic residues or amino acid motifs characteristic of that subdomain. For example, subdomain I contains an 8-amino acid glycine-rich ATP binding consensus motif, subdomain II contains a critical lysine residue required for maximal catalytic activity, and subdomains VI through IX comprise the highly conserved catalytic core. PTKs and STKs also contain distinct sequence motifs in subdomains VI and VIII which may confer hydroxyamino acid specificity.

In addition, kinases may also be classified by additional amino acid sequences, generally between 5 and 100 residues, which either flank or occur within the kinase domain. These additional amino acid sequences regulate kinase activity and determine substrate specificity. (Reviewed in Hardie, G. and S. Hanks (1995) The Protein Kinase Facts Book, Vol I, pp. 17-20 Academic Press, San Diego CA.). In particular, two protein kinase signature sequences have been identified in the kinase domain, the first containing an active site lysine residue involved in ATP binding, and the second containing an aspartate residue important for catalytic activity. If a protein analyzed includes the two protein kinase signatures, the probability of that protein being a protein kinase is close to 100% (PROSITE: PDOC00100, November 1995).

Protein Tyrosine Kinases

Protein tyrosine kinases (PTKs) may be classified as either transmembrane, receptor PTKs or nontransmembrane, nonreceptor PTK proteins. Transmembrane tyrosine kinases function as receptors for most growth factors. Growth factors bind to the receptor tyrosine kinase (RTK), which causes the receptor to phosphorylate itself (autophosphorylation) and specific intracellular second messenger proteins. Growth factors (GF) that associate with receptor PTKs include epidermal GF, platelet-derived GF, fibroblast GF, hepatocyte GF, insulin and insulin-like GFs, nerve GF, vascular endothelial GF, and macrophage colony stimulating factor.

Nontransmembrane, nonreceptor PTKs lack transmembrane regions and, instead, form signaling complexes with the cytosolic domains of plasma membrane receptors. Receptors that function through non-receptor PTKs include those for cytokines and hormones (growth hormone and prolactin), and antigen-specific receptors on T and B lymphocytes.

Many PTKs were first identified as oncogene products in cancer cells in which PTK

activation was no longer subject to normal cellular controls. In fact, about one third of the known oncogenes encode PTKs. Furthermore, cellular transformation (oncogenesis) is often accompanied by increased tyrosine phosphorylation activity (Charbonneau, H. and N.K. Tonks (1992) *Annu. Rev. Cell Biol.* 8:463-493). Regulation of PTK activity may therefore be an important strategy in controlling some types of cancer.

Substrates for tyrosine kinases can be identified using anti-phosphotyrosine antibodies to screen tyrosine-phosphorylated cDNA expression libraries. Fish, so named for tyrosine-phosphorylated in Src-transformed fibroblast, is a tyrosine kinase substrate which has been identified by such a technique. Fish has five SH3 domains and a phox homology (PX) domain. Fish is suggested to be involved in signalling by tyrosine kinases and have a role in the actin cytoskeleton (Lock, P. et al (1998) *EMBO J.* 17:4346-4357).

SHP-2, an SH2-domain-containing phosphotyrosine phosphatase, is a positive signal transducer for several receptor tyrosine kinases (RTKs) and cytokine receptors. Phosphotyrosine phosphatases are critical positive and negative regulators in the intracellular signalling pathways that result in growth-factor-specific cell responses such as mitosis, migration, differentiation, transformation, survival or death. Signal-regulatory proteins (SIRPs) comprise a new gene family of at least 15 members, consisting of two subtypes distinguished by the presence or absence of a cytoplasmic SHP-2-binding domain. The SIRP-alpha subfamily members have a cytoplasmic SHP2-binding domain and includes SIRP-alpha-1, a transmembrane protein, a substrate of activated RTKs and which binds to SH2 domains. SIRPs have a high degree of homology with immune antigen recognition molecules. The SIRP-beta subfamily lacks the cytoplasmic tail. The SIRP-beta-1 gene encodes a polypeptide of 398 amino acids. SIRP family members are generally involved in regulation of signals which define different physiological and pathological processes (Kharitonov, A. et al (1997) *Nature* 386:181-186). Two possible areas of regulation include determination of brain diversity and genetic individuality (Sano, S et al (1999) *Biochem. J.* 344 Pt 3:667-675) and recognition of self which fails in diseases such as hemolytic anemia (Oldenborg, P.-A et al (2000) *Science* 288:2051-2054).

Protein Serine/Threonine Kinases

Protein serine/threonine kinases (STKs) are nontransmembrane proteins. A subclass of STKs are known as ERKs (extracellular signal regulated kinases) or MAPs (mitogen-activated protein kinases) and are activated after cell stimulation by a variety of hormones and growth factors. Cell stimulation induces a signaling cascade leading to phosphorylation of MEK (MAP/ERK kinase) which, in turn, activates ERK via serine and threonine phosphorylation. A varied number of proteins represent the downstream effectors for the active ERK and implicate it in the control of cell

proliferation and differentiation, as well as regulation of the cytoskeleton. Activation of ERK is normally transient, and cells possess dual specificity phosphatases that are responsible for its down-regulation. Also, numerous studies have shown that elevated ERK activity is associated with some cancers. Other STKs include the second messenger dependent protein kinases such as the
5 cyclic-AMP dependent protein kinases (PKA), calcium-calmodulin (CaM) dependent protein kinases, and the mitogen-activated protein kinases (MAP); the cyclin-dependent protein kinases; checkpoint and cell cycle kinases; Numb-associated kinase (Nak); human Fused (hFu); proliferation-related kinases; 5'-AMP-activated protein kinases; and kinases involved in apoptosis.

The second messenger dependent protein kinases primarily mediate the effects of second
10 messengers such as cyclic AMP (cAMP), cyclic GMP, inositol triphosphate, phosphatidylinositol, 3,4,5-triphosphate, cyclic ADP ribose, arachidonic acid, diacylglycerol and calcium-calmodulin. The PKAs are involved in mediating hormone-induced cellular responses and are activated by cAMP produced within the cell in response to hormone stimulation. cAMP is an intracellular mediator of hormone action in all animal cells that have been studied. Hormone-induced cellular responses include
15 thyroid hormone secretion, cortisol secretion, progesterone secretion, glycogen breakdown, bone resorption, and regulation of heart rate and force of heart muscle contraction. PKA is found in all animal cells and is thought to account for the effects of cAMP in most of these cells. Altered PKA expression is implicated in a variety of disorders and diseases including cancer, thyroid disorders, diabetes, atherosclerosis, and cardiovascular disease (Isselbacher, K.J. et al. (1994) Harrison's
20 Principles of Internal Medicine, McGraw-Hill, New York NY, pp. 416-431, 1887).

The casein kinase I (CKI) gene family is another subfamily of serine/threonine protein kinases. This continuously expanding group of kinases have been implicated in the regulation of numerous cytoplasmic and nuclear processes, including cell metabolism, and DNA replication and repair. CKI enzymes are present in the membranes, nucleus, cytoplasm and cytoskeleton of
25 eukaryotic cells, and on the mitotic spindles of mammalian cells (Fish, K.J. et al. (1995) *J. Biol. Chem.* 270:14875-14883).

The CKI family members all have a short amino-terminal domain of 9-76 amino acids, a highly conserved kinase domain of 284 amino acids, and a variable carboxyl-terminal domain that ranges from 24 to over 200 amino acids in length (Cegielska, A. et al. (1998) *J. Biol. Chem.* 273:1357-1364).
30 The CKI family is comprised of highly related proteins, as seen by the identification of isoforms of casein kinase I from a variety of sources. There are at least five mammalian isoforms, α , β , γ , δ , and ϵ . Fish et al., identified CKI-epsilon from a human placenta cDNA library. It is a basic protein of 416 amino acids and is closest to CKI-delta. Through recombinant expression, it was determined to

phosphorylate known CKI substrates and was inhibited by the CKI-specific inhibitor CKI-7. The human gene for CKI-epsilon was able to rescue yeast with a slow-growth phenotype caused by deletion of the yeast CKI locus, HRR250 (Fish et al., supra).

The mammalian circadian mutation tau was found to be a semidominant autosomal allele of CKI-epsilon that markedly shortens period length of circadian rhythms in Syrian hamsters. The tau locus is encoded by casein kinase I-epsilon, which is also a homolog of the *Drosophila* circadian gene double-time. Studies of both the wildtype and tau mutant CKI-epsilon enzyme indicated that the mutant enzyme has a noticeable reduction in the maximum velocity and autophosphorylation state. Further, *in vitro*, CKI-epsilon is able to interact with mammalian PERIOD proteins, while the mutant enzyme is deficient in its ability to phosphorylate PERIOD. Lowrey et al., have proposed that CKI-epsilon plays a major role in delaying the negative feedback signal within the transcription-translation-based autoregulatory loop that composes the core of the circadian mechanism. Therefore the CKI-epsilon enzyme is an ideal target for pharmaceutical compounds influencing circadian rhythms, jet-lag and sleep, in addition to other physiologic and metabolic processes under circadian regulation (Lowrey, P.L. et al. (2000) Science 288:483-491).

Homeodomain-interacting protein kinases (HIPKs) are serine/threonine kinases and novel members of the DYRK kinase subfamily (Hofmann, T.G. et al. (2000) Biochimie 82:1123-1127). HIPKs contain a conserved protein kinase domain separated from a domain that interacts with homeoproteins. HIPKs are nuclear kinases, and HIPK2 is highly expressed in neuronal tissue (Kim, Y.H. et al. (1998) J. Biol. Chem. 273:25875-25879; Wang, Y. et al. (2001) Biochim. Biophys. Acta 1518:168-172). HIPKs act as corepressors for homeodomain transcription factors. This corepressor activity is seen in posttranslational modifications such as ubiquitination and phosphorylation, each of which are important in the regulation of cellular protein function (Kim, Y.H. et al. (1999) Proc. Natl. Acad. Sci. USA 96:12350-12355).

The murine homology to *Caenorhabditis elegans* UNC51, a serine/threonine kinase, has been determined to be required to signal the program of gene expression leading to axon formation from granule cells of the cerebellar cortex (Tomoda, T. et al (1999) Neuron 24:833-346. The human homolog of UNC-51, ULK1, for UNC-51 (*C. elegans*)-like kinase 1, is composed of 1050 amino acids, has a calculated MV of 112.6 kDa and a pI of 8.80. ULK1 has 41% overall sequence similarity to UNC-51 and is highly conserved among vertebrates including mammals, birds, reptiles, amphibians, and fish. By Northern blot analysis, Kuroyanagi et al have shown ULK1 to be ubiquitously expressed in adult tissues, including skeletal muscle, heart, pancreas, brain, placenta, liver, kidney, and lung while UNC-51 has been specifically located in the nervous system of *C. elegans*. Fish and RH mapping

confirmed the localization of ULK1 to human chromosome 12q24.3. (Kuroyanagi, H. et al (1998) Genomics 51:76-85.

Calcium-Calmodulin Dependent Protein Kinases

Calcium-calmodulin dependent (CaM) kinases are involved in regulation of smooth muscle contraction, glycogen breakdown (phosphorylase kinase), and neurotransmission (CaM kinase I and CaM kinase II). CaM dependent protein kinases are activated by calmodulin, an intracellular calcium receptor, in response to the concentration of free calcium in the cell. Many CaM kinases are also activated by phosphorylation. Some CaM kinases are also activated by autophosphorylation or by other regulatory kinases. CaM kinase I phosphorylates a variety of substrates including the neurotransmitter-related proteins synapsin I and II, the gene transcription regulator, CREB, and the cystic fibrosis conductance regulator protein, CFTR (Haribabu, B. et al. (1995) EMBO J. 14:3679-3686). CaM kinase II also phosphorylates synapsin at different sites and controls the synthesis of catecholamines in the brain through phosphorylation and activation of tyrosine hydroxylase. CaM kinase II controls the synthesis of catecholamines and serotonin, through phosphorylation/activation of tyrosine hydroxylase and tryptophan hydroxylase, respectively (Fujisawa, H. (1990) BioEssays 12:27-29). The mRNA encoding a calmodulin-binding protein kinase-like protein was found to be enriched in mammalian forebrain. This protein is associated with vesicles in both axons and dendrites and accumulates largely postnatally. The amino acid sequence of this protein is similar to CaM-dependent STKs, and the protein binds calmodulin in the presence of calcium (Godbout, M. et al. (1994) J. Neurosci. 14:1-13).

Mitogen-Activated Protein Kinases

The mitogen-activated protein kinases (MAP) which mediate signal transduction from the cell surface to the nucleus via phosphorylation cascades are another STK family that regulates intracellular signaling pathways. Several subgroups have been identified, and each manifests different substrate specificities and responds to distinct extracellular stimuli (Egan, S.E. and R.A. Weinberg (1993) Nature 365:781-783). There are 3-kinase modules comprising the MAP kinase cascade: MAPK (MAP), MAPK kinase (MAP2K, MAPKK, or MKK), and MKK kinase (MAP3K, MAPKKK, OR MEKK) (Wang, X.S. et al (1998) Biochem. Biophys. Res. Commun. 253:33-37). The extracellular-regulated kinase (ERK) pathway is activated by growth factors and mitogens, for example, epidermal growth factor (EGF), ultraviolet light, hyperosmolar medium, heat shock, endotoxic lipopolysaccharide (LPS). The closely related though distinct parallel pathways, the c-Jun N-terminal kinase (JNK), or stress-activated kinase (SAPK) pathway, and the p38 kinase pathway are activated by stress stimuli and proinflammatory cytokines such as tumor necrosis factor (TNF) and interleukin-1

(IL-1). Altered MAP kinase expression is implicated in a variety of disease conditions including cancer, inflammation, immune disorders, and disorders affecting growth and development.. MAP kinase signaling pathways are present in mammalian cells as well as in yeast.

MAPKKK6 (MAP3K6) is one of numerous MAP3Ks identified. Isolated from skeletal muscle, MAP3K6 is 1,280 amino acids in length with 11 kinase subdomains and is detected in several tissues. The highest expression has been found in heart and skeletal muscle. MAP3K6 has 45% amino acid sequence identity with MAP3K5, while their catalytic domains share 82% identity. MAP3K6 interaction with MAP3K5 *in vivo* was confirmed by coimmunoprecipitation. Recombinant MAP3K6 has been shown to weakly activate the JNK but not the p38 kinase or ERK pathways (Wang,X.S. et al. *supra*)

Cyclin-Dependent Protein Kinases

The cyclin-dependent protein kinases (CDKs) are STKs that control the progression of cells through the cell cycle. The entry and exit of a cell from mitosis are regulated by the synthesis and destruction of a family of activating proteins called cyclins. Cyclins are small regulatory proteins that bind to and activate CDKs, which then phosphorylate and activate selected proteins involved in the mitotic process. CDKs are unique in that they require multiple inputs to become activated. In addition to cyclin binding, CDK activation requires the phosphorylation of a specific threonine residue and the dephosphorylation of a specific tyrosine residue on the CDK.

Another family of STKs associated with the cell cycle are the NIMA (never in mitosis)-related kinases (Neks). Both CDKs and Neks are involved in duplication, maturation, and separation of the microtubule organizing center, the centrosome, in animal cells (Fry, A.M. et al. (1998) EMBO J. 17:470-481).

Checkpoint and Cell Cycle Kinases

In the process of cell division, the order and timing of cell cycle transitions are under control of cell cycle checkpoints, which ensure that critical events such as DNA replication and chromosome segregation are carried out with precision. If DNA is damaged, e.g. by radiation, a checkpoint pathway is activated that arrests the cell cycle to provide time for repair. If the damage is extensive, apoptosis is induced. In the absence of such checkpoints, the damaged DNA is inherited by aberrant cells which may cause proliferative disorders such as cancer. Protein kinases play an important role in this process. For example, a specific kinase, checkpoint kinase 1 (Chk1), has been identified in yeast and mammals, and is activated by DNA damage in yeast. Activation of Chk1 leads to the arrest of the cell at the G2/M transition (Sanchez, Y. et al. (1997) Science 277:1497-1501). Specifically, Chk1 phosphorylates the cell division cycle phosphatase CDC25, inhibiting its normal function which is

to dephosphorylate and activate the cyclin-dependent kinase Cdc2. Cdc2 activation controls the entry of cells into mitosis (Peng, C.-Y. et al. (1997) Science 277:1501-1505). Thus, activation of Chk1 prevents the damaged cell from entering mitosis. A similar deficiency in a checkpoint kinase, such as Chk1, may also contribute to cancer by failure to arrest cells with damaged DNA at other checkpoints such as G2/M.

Proliferation-Related Kinases

Proliferation-related kinase is a serum/cytokine inducible STK that is involved in regulation of the cell cycle and cell proliferation in human megakaryocytic cells (Li, B. et al. (1996) J. Biol. Chem. 271:19402-19408). Proliferation-related kinase is related to the polo (derived from *Drosophila* polo gene) family of STKs implicated in cell division. Proliferation-related kinase is downregulated in lung tumor tissue and may be a proto-oncogene whose deregulated expression in normal tissue leads to oncogenic transformation.

5'-AMP-activated protein kinase

A ligand-activated STK protein kinase is 5'-AMP-activated protein kinase (AMPK) (Gao, G. et al. (1996) J. Biol Chem. 271:8675-8681). Mammalian AMPK is a regulator of fatty acid and sterol synthesis through phosphorylation of the enzymes acetyl-CoA carboxylase and hydroxymethylglutaryl-CoA reductase and mediates responses of these pathways to cellular stresses such as heat shock and depletion of glucose and ATP. AMPK is a heterotrimeric complex comprised of a catalytic alpha subunit and two non-catalytic beta and gamma subunits that are believed to regulate the activity of the alpha subunit. Subunits of AMPK have a much wider distribution in non-lipogenic tissues such as brain, heart, spleen, and lung than expected. This distribution suggests that its role may extend beyond regulation of lipid metabolism alone.

Kinases in Apoptosis

Apoptosis is a highly regulated signaling pathway leading to cell death that plays a crucial role in tissue development and homeostasis. Deregulation of this process is associated with the pathogenesis of a number of diseases including autoimmune disease, neurodegenerative disorders, and cancer. Various STKs play key roles in this process. ZIP kinase is an STK containing a C-terminal leucine zipper domain in addition to its N-terminal protein kinase domain. This C-terminal domain appears to mediate homodimerization and activation of the kinase as well as interactions with transcription factors such as activating transcription factor, ATF4, a member of the cyclic-AMP responsive element binding protein (ATF/CREB) family of transcriptional factors (Sanjo, H. et al. (1998) J. Biol. Chem. 273:29066-29071). DRAK1 and DRAK2 are STKs that share homology with the death-associated protein kinases (DAP kinases), known to function in interferon- γ induced

apoptosis (Sanjo et al., supra). Like ZIP kinase, DAP kinases contain a C-terminal protein-protein interaction domain, in the form of ankyrin repeats, in addition to the N-terminal kinase domain. ZIP, DAP, and DRAX kinases induce morphological changes associated with apoptosis when transfected into NIH3T3 cells (Sanjo et al., supra). However, deletion of either the N-terminal kinase catalytic domain or the C-terminal domain of these proteins abolishes apoptosis activity, indicating that in addition to the kinase activity, activity in the C-terminal domain is also necessary for apoptosis, possibly as an interacting domain with a regulator or a specific substrate.

RICK is another STK recently identified as mediating a specific apoptotic pathway involving the death receptor, CD95 (Inohara, N. et al. (1998) J. Biol. Chem. 273:12296-12300). CD95 is a member of the tumor necrosis factor receptor superfamily and plays a critical role in the regulation and homeostasis of the immune system (Nagata, S. (1997) Cell 88:355-365). The CD95 receptor signaling pathway involves recruitment of various intracellular molecules to a receptor complex following ligand binding. This process includes recruitment of the cysteine protease caspase-8 which, in turn, activates a caspase cascade leading to cell death. RICK is composed of an N-terminal kinase catalytic domain and a C-terminal "caspase-recruitment" domain that interacts with caspase-like domains, indicating that RICK plays a role in the recruitment of caspase-8. This interpretation is supported by the fact that the expression of RICK in human 293T cells promotes activation of caspase-8 and potentiates the induction of apoptosis by various proteins involved in the CD95 apoptosis pathway (Inohara et al., supra).

Mitochondrial Protein Kinases

A novel class of eukaryotic kinases, related by sequence to prokaryotic histidine protein kinases, are the mitochondrial protein kinases (MPKs) which seem to have no sequence similarity with other eukaryotic protein kinases. These protein kinases are located exclusively in the mitochondrial matrix space and may have evolved from genes originally present in respiration-dependent bacteria which were endocytosed by primitive eukaryotic cells. MPKs are responsible for phosphorylation and inactivation of the branched-chain alpha-ketoacid dehydrogenase and pyruvate dehydrogenase complexes (Harris, R.A. et al. (1995) Adv. Enzyme Regul. 34:147-162). Five MPKs have been identified. Four members correspond to pyruvate dehydrogenase kinase isozymes, regulating the activity of the pyruvate dehydrogenase complex, which is an important regulatory enzyme at the interface between glycolysis and the citric acid cycle. The fifth member corresponds to a branched-chain alpha-ketoacid dehydrogenase kinase, important in the regulation of the pathway for the disposal of branched-chain amino acids. (Harris, R.A. et al. (1997) Adv. Enzyme Regul. 37:271-293). Both starvation and the diabetic state are known to result in a great increase in the activity of the pyruvate

dehydrogenase kinase in the liver, heart and muscle of the rat. This increase contributes in both disease states to the phosphorylation and inactivation of the pyruvate dehydrogenase complex and conservation of pyruvate and lactate for gluconeogenesis (Harris (1995) supra).

5 KINASES WITH NON-PROTEIN SUBSTRATES

Lipid and Inositol kinases

Lipid kinases phosphorylate hydroxyl residues on lipid head groups. A family of kinases involved in phosphorylation of phosphatidylinositol (PI) has been described, each member
 10 phosphorylating a specific carbon on the inositol ring (Leevers, S.J. et al. (1999) Curr. Opin. Cell. Biol. 11:219-225). The phosphorylation of phosphatidylinositol is involved in activation of the protein kinase C signaling pathway. The inositol phospholipids (phosphoinositides) intracellular signaling pathway begins with binding of a signaling molecule to a G-protein linked receptor in the plasma membrane. This leads to the phosphorylation of phosphatidylinositol (PI) residues on the inner side of the plasma
 15 membrane by inositol kinases, thus converting PI residues to the biphosphate state (PIP₂). PIP₂ is then cleaved into inositol triphosphate (IP₃) and diacylglycerol. These two products act as mediators for separate signaling pathways. Cellular responses that are mediated by these pathways are glycogen breakdown in the liver in response to vasopressin, smooth muscle contraction in response to acetylcholine, and thrombin-induced platelet aggregation.

20 PI 3-kinase (PI3K), which phosphorylates the D3 position of PI and its derivatives, has a central role in growth factor signal cascades involved in cell growth, differentiation, and metabolism. PI3K is a heterodimer consisting of an adapter subunit and a catalytic subunit. The adapter subunit acts as a scaffolding protein, interacting with specific tyrosine-phosphorylated proteins, lipid moieties, and other cytosolic factors. When the adapter subunit binds tyrosine phosphorylated targets, such as
 25 the insulin responsive substrate (IRS)-1, the catalytic subunit is activated and converts PI (4,5) biphosphate (PIP₂) to PI (3,4,5) P₃ (PIP₃). PIP₃ then activates a number of other proteins, including PKA, protein kinase B (PKB), protein kinase C (PKC), glycogen synthase kinase (GSK)-3, and p70 ribosomal s6 kinase. PI3K also interacts directly with the cytoskeletal organizing proteins, Rac, rho, and cdc42 (Shepherd, P.R. et al. (1998) Biochem. J. 333:471-490). Animal models for diabetes, such
 30 as *obese* and *fat* mice, have altered PI3K adapter subunit levels. Specific mutations in the adapter subunit have also been found in an insulin-resistant Danish population, suggesting a role for PI3K in type-2 diabetes (Shepard, supra).

An example of lipid kinase phosphorylation activity is the phosphorylation of

D-erythro-sphingosine to the sphingolipid metabolite, sphingosine-1-phosphate (SPP). SPP has emerged as a novel lipid second-messenger with both extracellular and intracellular actions (Kohama, T. et al. (1998) *J. Biol. Chem.* 273:23722-23728). Extracellularly, SPP is a ligand for the G-protein coupled receptor EDG-1 (endothelial-derived, G-protein coupled receptor). Intracellularly, SPP
5 regulates cell growth, survival, motility, and cytoskeletal changes. SPP levels are regulated by sphingosine kinases that specifically phosphorylate D-erythro-sphingosine to SPP. The importance of sphingosine kinase in cell signaling is indicated by the fact that various stimuli, including platelet-derived growth factor (PDGF), nerve growth factor, and activation of protein kinase C, increase cellular levels of SPP by activation of sphingosine kinase, and the fact that competitive
10 inhibitors of the enzyme selectively inhibit cell proliferation induced by PDGF (Kohama et al., supra).

Purine Nucleotide Kinases

The purine nucleotide kinases, adenylate kinase (ATP:AMP phosphotransferase, or AdK) and guanylate kinase (ATP:GMP phosphotransferase, or GuK) play a key role in nucleotide metabolism and are crucial to the synthesis and regulation of cellular levels of ATP and GTP, respectively. These
15 two molecules are precursors in DNA and RNA synthesis in growing cells and provide the primary source of biochemical energy in cells (ATP), and signal transduction pathways (GTP). Inhibition of various steps in the synthesis of these two molecules has been the basis of many antiproliferative drugs for cancer and antiviral therapy (Pillwein, K. et al. (1990) *Cancer Res.* 50:1576-1579).

AdK is found in almost all cell types and is especially abundant in cells having high rates of
20 ATP synthesis and utilization such as skeletal muscle. In these cells AdK is physically associated with mitochondria and myofibrils, the subcellular structures that are involved in energy production and utilization, respectively. Recent studies have demonstrated a major function for AdK in transferring high energy phosphoryls from metabolic processes generating ATP to cellular components consuming ATP (Zelevnikar, R.J. et al. (1995) *J. Biol. Chem.* 270:7311-7319). Thus AdK may have a pivotal
25 role in maintaining energy production in cells, particularly those having a high rate of growth or metabolism such as cancer cells, and may provide a target for suppression of its activity to treat certain cancers. Alternatively, reduced AdK activity may be a source of various metabolic, muscle-energy disorders that can result in cardiac or respiratory failure and may be treatable by increasing AdK activity.

30 GuK, in addition to providing a key step in the synthesis of GTP for RNA and DNA synthesis, also fulfills an essential function in signal transduction pathways of cells through the regulation of GDP and GTP. Specifically, GTP binding to membrane associated G proteins mediates the activation of cell receptors, subsequent intracellular activation of adenyl cyclase, and production of the second

messenger, cyclic AMP. GDP binding to G proteins inhibits these processes. GDP and GTP levels also control the activity of certain oncogenic proteins such as p21^{ras} known to be involved in control of cell proliferation and oncogenesis (Bos, J.L. (1989) Cancer Res. 49:4682-4689). High ratios of GTP:GDP caused by suppression of GuK cause activation of p21^{ras} and promote oncogenesis.

- 5 Increasing GuK activity to increase levels of GDP and reduce the GTP:GDP ratio may provide a therapeutic strategy to reverse oncogenesis.

GuK is an important enzyme in the phosphorylation and activation of certain antiviral drugs useful in the treatment of herpes virus infections. These drugs include the guanine homologs acyclovir and bucidovir (Miller, W.H. and R.L. Miller (1980) J. Biol. Chem. 255:7204-7207; Stenberg, K. et al. 10 (1986) J. Biol. Chem. 261:2134-2139). Increasing GuK activity in infected cells may provide a therapeutic strategy for augmenting the effectiveness of these drugs and possibly for reducing the necessary dosages of the drugs.

Pyrimidine Kinases

The pyrimidine kinases are deoxycytidine kinase and thymidine kinase 1 and 2. Deoxycytidine 15 kinase is located in the nucleus, and thymidine kinase 1 and 2 are found in the cytosol (Johansson, M. et al. (1997) Proc. Natl. Acad. Sci. USA 94:11941-11945). Phosphorylation of deoxyribonucleosides by pyrimidine kinases provides an alternative pathway for de novo synthesis of DNA precursors. The role of pyrimidine kinases, like purine kinases, in phosphorylation is critical to the activation of several chemotherapeutically important nucleoside analogues (Arner E.S. and S. Eriksson (1995) Pharmacol. 20 Ther. 67:155-186).

The discovery of new human kinases, 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 cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders, and in the assessment of the effects of exogenous compounds on the expression of 25 nucleic acid and amino acid sequences of human kinases.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, human kinases, referred to collectively as "PKIN" and individually as "PKIN-1," "PKIN-2," "PKIN-3," "PKIN-4," "PKIN-5," "PKIN-6," 30 "PKIN-7," "PKIN-8," "PKIN-9," "PKIN-10," "PKIN-11," "PKIN-12," "PKIN-13," "PKIN-14," "PKIN-15," "PKIN-16," "PKIN-17," "PKIN-18," "PKIN-19," and "PKIN-20." In one aspect, the invention provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, 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:1-20, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and d) an immunogenic fragment of a polypeptide having an amino acid sequence
5 selected from the group consisting of SEQ ID NO:1-20. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-20.

The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, b) a polypeptide comprising a naturally occurring amino acid sequence
10 at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20. In one alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-20. In
15 another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:21-40.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, b) a polypeptide comprising a naturally occurring amino acid sequence at least
20 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the
25 invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, b) a polypeptide comprising a naturally occurring amino acid sequence at least
30 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is

transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, 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:1-20, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20.

The invention further provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous nucleotides.

Additionally, the invention provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

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

NO:21-40, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention further provides a composition comprising an effective amount of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, 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:1-20, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-20. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, 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:1-20, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment the composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an

amino acid sequence selected from the group consisting of SEQ ID NO:1-20, 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:1-20, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional PKIN, comprising administering to a patient in need of such treatment the composition.

The invention further provides a method of screening for a compound that specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, 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:1-20, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, 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:1-20, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test

compound is indicative of a compound that modulates the activity of the polypeptide.

The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40, iii) a polynucleotide having a sequence complementary to i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40, iii) a polynucleotide complementary to the polynucleotide of i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

BRIEF DESCRIPTION OF THE TABLES

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

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

polypeptide and its GenBank homolog is also shown.

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

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

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

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

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

DESCRIPTION OF THE INVENTION

15 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.

20 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.

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

DEFINITIONS

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

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

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

 “Altered” nucleic acid sequences encoding PKIN include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as PKIN or a polypeptide with at least one functional characteristic of PKIN. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of
20 the polynucleotide encoding PKIN, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding PKIN. 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 PKIN. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility,
25 hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of PKIN is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains
30 having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

 The terms “amino acid” and “amino acid sequence” refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic

molecules. Where “amino acid sequence” is recited to refer to a sequence of a naturally occurring protein molecule, “amino acid sequence” and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

“Amplification” relates to the production of additional copies of a nucleic acid sequence.

5 Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

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

The term “antibody” refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind PKIN polypeptides can be prepared using intact polypeptides or using fragments
15 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.

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

The term “antisense” refers to any composition capable of base-pairing with the “sense” (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified
30 sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring

nucleic acid sequence produced by the cell to form duplexes which block either transcription or translation. The designation “negative” or “minus” can refer to the antisense strand, and the designation “positive” or “plus” can refer to the sense strand of a reference DNA molecule.

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

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

A “composition comprising a given polynucleotide sequence” and a “composition comprising a given amino acid sequence” refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution.

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

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

Original Residue	Conservative Substitution
Ala	Gly, Ser
Arg	His, Lys

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

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

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

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

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

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

“Exon shuffling” refers to the recombination of different coding regions (exons). Since an exon may represent a structural or functional domain of the encoded protein, new proteins may be assembled through the novel reassortment of stable substructures, thus allowing acceleration of the

evolution of new protein functions.

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

A fragment of SEQ ID NO:21-40 comprises a region of unique polynucleotide sequence that
15 specifically identifies SEQ ID NO:21-40, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:21-40 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:21-40 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:21-40 and the region of SEQ ID NO:21-40 to which the fragment corresponds are routinely
20 determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-20 is encoded by a fragment of SEQ ID NO:21-40. A fragment of SEQ ID NO:1-20 comprises a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-20. For example, a fragment of SEQ ID NO:1-20 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-20.
25 The precise length of a fragment of SEQ ID NO:1-20 and the region of SEQ ID NO:1-20 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

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

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

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to

the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

5 Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS
10 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

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

Matrix: BLOSUM62
Reward for match: 1
Penalty for mismatch: -2
30 *Open Gap: 5 and Extension Gap: 2 penalties*
Gap x drop-off: 50
Expect: 10
Word Size: 11

Filter: on

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

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

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

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

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

Matrix: BLOSUM62
Open Gap: 11 and Extension Gap: 1 penalties
Gap x drop-off: 50
Expect: 10

Word Size: 3

Filter: on

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

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

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

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

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al. (1989)

Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. 5 Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, 10 such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acid 15 sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C₀t or R₀t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

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

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect 25 cellular and systemic defense systems.

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

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

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

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

The phrases “nucleic acid” and “nucleic acid sequence” refer to a nucleotide, oligonucleotide, 5 polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

“Operably linked” refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably 10 linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

“Peptide nucleic acid” (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of 15 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 pegylated to extend their lifespan in the cell.

“Post-translational modification” of an PKIN may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the 20 art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu of PKIN.

“Probe” refers to nucleic acid sequences encoding PKIN, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. 25 Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. “Primers” are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

30 Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers

may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

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

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence

that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have
5 been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

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

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

15 "Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

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

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

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

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

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

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

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

"Transformation" describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods
15 well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed cells" includes stably transformed cells in which the inserted DNA is capable of replication either as
20 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.

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

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

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

THE INVENTION

The invention is based on the discovery of new human human kinases (PKIN), the polynucleotides encoding PKIN, and the use of these compositions for the diagnosis, treatment, or prevention of cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders.

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the invention. Each polynucleotide and its corresponding polypeptide are correlated to a

single Incyte project identification number (Incyte Project ID). Each polypeptide sequence is denoted by both a polypeptide sequence identification number (Polypeptide SEQ ID NO:) and an Incyte polypeptide sequence number (Incyte Polypeptide ID) as shown. Each polynucleotide sequence is denoted by both a polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and an Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) as shown.

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

Table 3 shows various structural features of the polypeptides of the invention. Columns 1 and 2 show the polypeptide sequence identification number (SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for each polypeptide of the invention. Column 3 shows the number of amino acid residues in each polypeptide. Column 4 shows potential phosphorylation sites, and column 5 shows potential glycosylation sites, as determined by the MOTIFS program of the GCG sequence analysis software package (Genetics Computer Group, Madison WI). Column 6 shows amino acid residues comprising signature sequences, domains, and motifs. Column 7 shows analytical methods for protein structure/function analysis and in some cases, searchable databases to which the analytical methods were applied.

Together, Tables 2 and 3 summarize the properties of polypeptides of the invention, and these properties establish that the claimed polypeptides are human kinases. For example, SEQ ID NO:2 is 97% identical to mouse tousled-like kinase (GenBank ID g2853031) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 0.0, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:2 also contains an eukaryotic protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:2 is a tousled-like kinase. In an alternative example, SEQ ID NO:10 is 63% identical to human serine/threonine protein kinase (GenBank ID g36615) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The

BLAST probability score is $7.7e-122$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:10 also contains an eukaryotic protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:10 is a serine/threonine kinase. Note that "serine/threonine kinase" is a specific class of kinases. In an alternative example, SEQ ID NO:16 is 53% identical to human receptor protein-tyrosine kinase (GenBank ID g551608) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $4.1e-290$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:16 also contains an eukaryotic protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:16 is a receptor tyrosine kinase. In an alternative example, SEQ ID NO:19 is 93% identical to rat Calcium/calmodulin-dependent protein kinase isoform IV (GenBank ID g1836161) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $6.0e-257$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:19 also contains an eukaryotic protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:19 is a protein kinase. SEQ ID NO:1, SEQ ID NO:3-9, SEQ ID NO:11-15, SEQ ID NO:17-18, and SEQ ID NO:20 were analyzed and annotated in a similar manner. The algorithms and parameters for the analysis of SEQ ID NO:1-20 are described in Table 7.

As shown in Table 4, the full length polynucleotide sequences of the present invention were assembled using cDNA sequences or coding (exon) sequences derived from genomic DNA, or any combination of these two types of sequences. Columns 1 and 2 list the polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and the corresponding Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) for each polynucleotide of the invention. Column 3 shows the length of each polynucleotide sequence in basepairs. Column 4 lists fragments of the polynucleotide sequences which are useful, for example, in hybridization or amplification technologies that identify SEQ ID NO:21-40 or that distinguish between SEQ ID NO:21-40 and related polynucleotide sequences. Column 5 shows identification numbers corresponding to cDNA

sequences, coding sequences (exons) predicted from genomic DNA, and/or sequence assemblages comprised of both cDNA and genomic DNA. These sequences were used to assemble the full length polynucleotide sequences of the invention. Columns 6 and 7 of Table 4 show the nucleotide start (5') and stop (3') positions of the cDNA and/or genomic sequences in column 5 relative to their respective full length sequences.

The identification numbers in Column 5 of Table 4 may refer specifically, for example, to Incyte cDNAs along with their corresponding cDNA libraries. For example, 2564295H1 is the identification number of an Incyte cDNA sequence, and ADRETUT01 is the cDNA library from which it is derived. Incyte cDNAs for which cDNA libraries are not indicated were derived from pooled cDNA libraries (e.g., 71191190V1). Alternatively, the identification numbers in column 5 may refer to GenBank cDNAs or ESTs (e.g., g1164223) which contributed to the assembly of the full length polynucleotide sequences. In addition, the identification numbers in column 5 may identify sequences derived from the ENSEMBL (The Sanger Centre, Cambridge, UK) database (*i.e.*, those sequences including the designation "ENST"). Alternatively, the identification numbers in column 5 may be derived from the NCBI RefSeq Nucleotide Sequence Records Database (*i.e.*, those sequences including the designation "NM" or "NT") or the NCBI RefSeq Protein Sequence Records (*i.e.*, those sequences including the designation "NP"). Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon stitching" algorithm. For example, FL_XXXXXX_N₁_N₂_YYYYY_N₃_N₄ represents a "stitched" sequence in which XXXXXX is the identification number of the cluster of sequences to which the algorithm was applied, and YYYYY is the number of the prediction generated by the algorithm, and N_{1,2,3...}, if present, represent specific exons that may have been manually edited during analysis (See Example V). Alternatively, the identification numbers in column 5 may refer to assemblages of exons brought together by an "exon-stretching" algorithm. For example, FLXXXXXX_gAAAAA_gBBBBB_1_N is the identification number of a "stretched" sequence, with XXXXXX being the Incyte project identification number, gAAAAA being the GenBank identification number of the human genomic sequence to which the "exon-stretching" algorithm was applied, gBBBBB being the GenBank identification number or NCBI RefSeq identification number of the nearest GenBank protein homolog, and N referring to specific exons (See Example V). In instances where a RefSeq sequence was used as a protein homolog for the "exon-stretching" algorithm, a RefSeq identifier (denoted by "NM," "NP," or "NT") may be used in place of the GenBank identifier (*i.e.*, gBBBBB).

Alternatively, a prefix identifies component sequences that were hand-edited, predicted from

genomic DNA sequences, or derived from a combination of sequence analysis methods. The following Table lists examples of component sequence prefixes and corresponding sequence analysis methods associated with the prefixes (see Example IV and Example V).

Prefix	Type of analysis and/or examples of programs
GNN, GFG, ENST	Exon prediction from genomic sequences using, for example, GENSCAN (Stanford University, CA, USA) or FGENES (Computer Genomics Group, The Sanger Centre, Cambridge, UK).
GBI	Hand-edited analysis of genomic sequences.
FL	Stitched or stretched genomic sequences (see Example V).
INCY	Full length transcript and exon prediction from mapping of EST sequences to the genome. Genomic location and EST composition data are combined to predict the exons and resulting transcript.

In some cases, Incyte cDNA coverage redundant with the sequence coverage shown in column 5 was obtained to confirm the final consensus polynucleotide sequence, but the relevant Incyte cDNA identification numbers are not shown.

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

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

The invention also encompasses polynucleotides which encode PKIN. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:21-40, which encodes PKIN. The polynucleotide sequences of SEQ ID NO:21-40, as presented in the Sequence Listing, embrace the equivalent RNA sequences, wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses a variant of a polynucleotide sequence encoding PKIN. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least

about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding PKIN. 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:21-40 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:21-40. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of PKIN.

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 PKIN, 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 PKIN, and all such variations are to be considered as being specifically disclosed.

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

The invention also encompasses production of DNA sequences which encode PKIN and PKIN 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 PKIN or any fragment thereof.

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:21-40 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-

511.) Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied Biosystems), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding PKIN may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National

Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full length cDNAs, it is preferable to use libraries that have been
5 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.

Capillary electrophoresis systems which are commercially available may be used to analyze
10 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, Applied Biosystems), and the entire
15 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.

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

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter PKIN-encoding sequences for a variety of purposes including, but
25 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.

30 The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Cramer, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve

the biological properties of PKIN, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding PKIN may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) *Nucleic Acids Symp. Ser. 7*:215-223; and Horn, T. et al. (1980) *Nucleic Acids Symp. Ser. 7*:225-232.) Alternatively, PKIN itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) *Proteins, Structures and Molecular Properties*, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) *Science* 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems). Additionally, the amino acid sequence of PKIN, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

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

In order to express a biologically active PKIN, the nucleotide sequences encoding PKIN 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 PKIN. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding PKIN. Such signals

include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding PKIN 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,

5 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.)

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

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

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding PKIN. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding PKIN can be achieved using a multifunctional *E. coli* vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPO11 plasmid (Life Technologies). Ligation of sequences encoding PKIN into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for *in vitro* transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of PKIN are needed, e.g. for the production of antibodies, vectors which direct high level expression of PKIN may be used. For example, vectors containing the strong, inducible SP6 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of PKIN. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast *Saccharomyces cerevisiae* or *Pichia pastoris*. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, *supra*; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; and Scorer, C.A. et al. (1994) Bio/Technology 12:181-184.)

Plant systems may also be used for expression of PKIN. Transcription of sequences encoding PKIN may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Bröglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., *The McGraw Hill Yearbook of Science and Technology* (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding PKIN may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses PKIN in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc.

Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

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

For long term production of recombinant proteins in mammalian systems, stable expression of
10 PKIN in cell lines is preferred. For example, sequences encoding PKIN 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
15 selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine
20 phosphoribosyltransferase genes, for use in *tk* and *ap^r* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g.,
25 Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate
30 luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest

is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding PKIN is inserted within a marker gene sequence, transformed cells containing sequences encoding PKIN can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding PKIN 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.

In general, host cells that contain the nucleic acid sequence encoding PKIN and that express PKIN 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.

Immunological methods for detecting and measuring the expression of PKIN using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on PKIN is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

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 PKIN include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding PKIN, 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 WI), 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.

Host cells transformed with nucleotide sequences encoding PKIN 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 PKIN may be designed to contain signal sequences which direct secretion of PKIN through a prokaryotic or eukaryotic cell membrane.

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

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding PKIN 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 PKIN protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of PKIN 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 PKIN encoding sequence and the heterologous protein sequence, so that PKIN may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled PKIN may be achieved in

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

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

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

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

PKIN of the present invention or fragments thereof may be used to screen for compounds that modulate the activity of PKIN. Such compounds may include agonists, antagonists, or partial or inverse agonists. In one embodiment, an assay is performed under conditions permissive for PKIN
30 activity, wherein PKIN is combined with at least one test compound, and the activity of PKIN in the presence of a test compound is compared with the activity of PKIN in the absence of the test compound. A change in the activity of PKIN in the presence of the test compound is indicative of a compound that modulates the activity of PKIN. Alternatively, a test compound is combined with an in

vitro or cell-free system comprising PKIN under conditions suitable for PKIN activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of PKIN may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

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

Polynucleotides encoding PKIN may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al.
25 (1998) Science 282:1145-1147).

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

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of PKIN and human kinases. In addition, the expression of PKIN is closely associated with bladder cancer, prostatic, ovarian, brain, colon, ileum, penis, skin, adrenal tumor, digestive, and cancerous tissues. Therefore, PKIN appears to play a role in cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders. In the treatment of disorders associated with increased PKIN expression or activity, it is desirable to decrease the expression or activity of PKIN. In the treatment of disorders associated with decreased PKIN expression or activity, it is desirable to increase the expression or activity of PKIN.

Therefore, in one embodiment, PKIN 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 PKIN. Examples of such disorders include, but are not limited to, a cancer, such as 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, leukemias such as multiple myeloma and lymphomas such as Hodgkin's disease; an immune disorder, such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a growth and developmental disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in

particular, 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, renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy,

5 gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and

10 sensorineural hearing loss; a cardiovascular disease, such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery, congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease,

15 degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, congenital lung

20 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

25 pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-

30 induced lung disease, and complications of lung transplantation; and a lipid disorder such as fatty liver, cholestasis, primary biliary cirrhosis, carnitine deficiency, carnitine palmitoyltransferase deficiency, myoadenylate deaminase deficiency, hypertriglyceridemia, lipid storage disorders such as Fabry's disease, Gaucher's disease, Niemann-Pick's disease, metachromatic leukodystrophy,

adrenoleukodystrophy, GM₂ gangliosidosis, and ceroid lipofuscinosis, abetalipoproteinemia, Tangier disease, hyperlipoproteinemia, diabetes mellitus, lipodystrophy, lipomatosis, acute panniculitis, disseminated fat necrosis, adiposis dolorosa, lipoid adrenal hyperplasia, minimal change disease, lipomas, atherosclerosis, hypercholesterolemia, hypercholesterolemia with hypertriglyceridemia, primary hypoalphalipoproteinemia, hypothyroidism, renal disease, liver disease, lecithin:cholesterol acyltransferase deficiency, cerebrotendinous xanthomatosis, sitosterolemia, hypocholesterolemia, Tay-Sachs disease, Sandhoff's disease, hyperlipidemia, hyperlipemia, lipid myopathies, and obesity.

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

In a further embodiment, a composition comprising a substantially purified PKIN 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 PKIN including, but not limited to, those provided above.

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

In a further embodiment, an antagonist of PKIN may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PKIN. Examples of such disorders include, but are not limited to, those cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders described above. In one aspect, an antibody which specifically binds PKIN may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express PKIN.

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

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic

efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

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

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

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

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

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate
30 antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. USA 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce PKIN-specific single

chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton, D.R. (1991) Proc. Natl. Acad. Sci. USA 88:10134-10137.)

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

Antibody fragments which contain specific binding sites for PKIN may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

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

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for PKIN. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of PKIN-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 PKIN epitopes, represents the average affinity, or avidity, of the antibodies for PKIN. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular PKIN epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the PKIN-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 PKIN, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell,

J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of PKIN-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 PKIN, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding PKIN. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding PKIN. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ.)

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

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

(Blaese, R.M. et al. (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) Cell 75:207-216; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:643-666; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and N. Somia (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in PKIN expression or regulation causes disease, the expression of PKIN from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

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

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

and Blau, H.M. supra)), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding PKIN from a normal individual.

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

10 In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to PKIN expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding PKIN under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences
15 required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al.
20 (1987) *J. Virol.* 61:1647-1650; Bender, M.A. et al. (1987) *J. Virol.* 61:1639-1646; Adam, M.A. and A.D. Miller (1988) *J. Virol.* 62:3802-3806; Dull, T. et al. (1998) *J. Virol.* 72:8463-8471; Zufferey, R. et al. (1998) *J. Virol.* 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference.

25 Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) *J. Virol.* 71:7020-7029; Bauer, G. et al. (1997) *Blood* 89:2259-2267; Bonyhadi, M.L. (1997) *J. Virol.* 71:4707-4716; Ranga, U. et al. (1998) *Proc. Natl. Acad. Sci. USA* 95:1201-1206; Su, L. (1997) *Blood* 89:2283-2290).

30 In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding PKIN to cells which have one or more genetic abnormalities with respect to the expression of PKIN. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to

be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544 and Verma, I.M. and N. Somia (1997) Nature 389:239-242, both incorporated by reference herein.

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

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding PKIN to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and K.-J. Li (1998) Curr. Opin. Biotechnol. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting the coding sequence for PKIN into the alphavirus

genome in place of the capsid-coding region results in the production of a large number of PKIN-coding RNAs and the synthesis of high levels of PKIN in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of PKIN into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

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

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

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 PKIN. 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
5 that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

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

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

At least one, and up to a plurality, of test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in altering polynucleotide expression; selection from an existing, commercially-available or proprietary
30 library of naturally-occurring or non-natural chemical compounds; rational design of a compound based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding PKIN is exposed to at least one test compound thus obtained. The sample

may comprise, for example, an intact or permeabilized cell, or an in vitro cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding PKIN are assayed by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding PKIN. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a Schizosaccharomyces pombe gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruce, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruce, T.W. et al. (2000) U.S. Patent No. 6,022,691).

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

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

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

The compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal,

intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Compositions for pulmonary administration may be prepared in liquid or dry powder form. These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration without needle injection, and obviates the need for potentially toxic penetration enhancers.

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

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

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

A therapeutically effective dose refers to that amount of active ingredient, for example PKIN or fragments thereof, antibodies of PKIN, and agonists, antagonists or inhibitors of PKIN, 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, which can be expressed as the LD₅₀/ED₅₀ ratio. Compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are

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.

5 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 or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response
10 to therapy. Long-acting 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.

Normal dosage amounts may vary from about 0.1 μ g to 100,000 μ g, 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.

15 Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

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

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

between standard and subject values establishes the parameters for diagnosing disease.

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

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

15 Probes may also be used for the detection of related sequences, and may have at least 50% sequence identity to any of the PKIN 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:21-40 or from genomic sequences including promoters, enhancers, and introns of the PKIN gene.

Means for producing specific hybridization probes for DNAs encoding PKIN include the
20 cloning of polynucleotide sequences encoding PKIN or PKIN 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 appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ³²P or ³⁵S, or by enzymatic labels,
25 such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding PKIN may be used for the diagnosis of disorders associated with expression of PKIN. Examples of such disorders include, but are not limited to, a cancer, such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain,
30 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, leukemias such as multiple myeloma and lymphomas such as Hodgkin's disease; an immune disorder, such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress

syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins,

5 erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis,

10 thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a growth and developmental disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and

15 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, renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker

20 muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly,

25 craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss; a cardiovascular disease, such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery, congestive heart failure, ischemic heart disease, angina pectoris,

30 myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy,

myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, congenital lung anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; and a lipid disorder such as fatty liver, cholestasis, primary biliary cirrhosis, carnitine deficiency, carnitine palmitoyltransferase deficiency, myoadenylate deaminase deficiency, hypertriglyceridemia, lipid storage disorders such as Fabry's disease, Gaucher's disease, Niemann-Pick's disease, metachromatic leukodystrophy, adrenoleukodystrophy, GM₂ gangliosidosis, and ceroid lipofuscinosis, abetalipoproteinemia, Tangier disease, hyperlipoproteinemia, diabetes mellitus, lipodystrophy, lipomatosis, acute panniculitis, disseminated fat necrosis, adiposis dolorosa, lipid adrenal hyperplasia, minimal change disease, lipomas, atherosclerosis, hypercholesterolemia, hypercholesterolemia with hypertriglyceridemia, primary hypoalphalipoproteinemia, hypothyroidism, renal disease, liver disease, lecithin:cholesterol acyltransferase deficiency, cerebrotendinous xanthomatosis, sitosterolemia, hypocholesterolemia, Tay-Sachs disease, Sandhoff's disease, hyperlipidemia, hyperlipemia, lipid myopathies, and obesity. The polynucleotide sequences encoding PKIN 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 PKIN expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding PKIN may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding PKIN may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding PKIN 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.

In order to provide a basis for the diagnosis of a disorder associated with expression of PKIN, 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 PKIN, 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.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

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

Additional diagnostic uses for oligonucleotides designed from the sequences encoding PKIN 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 PKIN, or a fragment of a polynucleotide complementary to the polynucleotide encoding PKIN, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding PKIN may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease

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

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

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

profile.

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

5 A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number
10 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The
15 resultant transcript image would provide a profile of gene activity.

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

Transcript images which profile the expression of the polynucleotides of the present invention
20 may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000)
25 Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested
30 compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not

necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed
5 gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be
10 quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of the polypeptide sequences of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global
15 pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is
20 achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, *supra*). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot
25 is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass
30 spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

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

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

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

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

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) *Proc. Natl. Acad. Sci. USA*

94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

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

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

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

inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, PKIN, 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 PKIN and the agent being tested may be measured.

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

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

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

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, including U.S. Ser. No. 60/220,038, U.S. Ser. No. 60/222,112, U.S. Ser. No. 60/222,831, and U.S. Ser. No. 60/224,729 are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

Incyte cDNAs were derived from cDNA libraries described in the LIFESEQ GOLD

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

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

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the
15 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-
20 1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSPORT1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), or pINCY (Incyte Genomics, Palo Alto
25 CA), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids obtained as described in Example I were recovered from host cells by in vivo
30 excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP

96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

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

III. Sequencing and Analysis

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

The polynucleotide sequences derived from Incyte cDNAs were validated by removing
25 vector, linker, and poly(A) sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The Incyte cDNA sequences or translations thereof were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and hidden Markov model (HMM)-based protein family
30 databases such as PFAM. (HMM is a probabilistic approach which analyzes consensus primary structures of gene families. See, for example, Eddy, S.R. (1996) Curr. Opin. Struct. Biol. 6:361-365.) The queries were performed using programs based on BLAST, FASTA, BLIMPS, and HMMER. The Incyte cDNA sequences were assembled to produce full length polynucleotide sequences.

Alternatively, GenBank cDNAs, GenBank ESTs, stitched sequences, stretched sequences, or Genscan-predicted coding sequences (see Examples IV and V) were used to extend Incyte cDNA assemblages to full length. Assembly was performed using programs based on Phred, Phrap, and Consed, and cDNA assemblages were screened for open reading frames using programs based on

5 GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length polypeptide sequences. Alternatively, a polypeptide of the invention may begin at any of the methionine residues of the full length translated polypeptide. Full length polypeptide sequences were subsequently analyzed by querying against databases such as the GenBank protein databases (genpept), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and hidden

10 Markov model (HMM)-based protein family databases such as PFAM. Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also

15 calculates the percent identity between aligned sequences.

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

20 which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score or the lower the probability value, the greater the identity between two sequences).

The programs described above for the assembly and analysis of full length polynucleotide and

25 polypeptide sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:21-40. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies are described in Table 4, column 4.

IV. Identification and Editing of Coding Sequences from Genomic DNA

Putative human kinases were initially identified by running the Genscan gene identification

30 program against public genomic sequence databases (e.g., gbpri and gbhtg). Genscan is a general-purpose gene identification program which analyzes genomic DNA sequences from a variety of organisms (See Burge, C. and S. Karlin (1997) J. Mol. Biol. 268:78-94, and Burge, C. and S. Karlin (1998) Curr. Opin. Struct. Biol. 8:346-354). The program concatenates predicted exons to form an

assembled cDNA sequence extending from a methionine to a stop codon. The output of Genscan is a FASTA database of polynucleotide and polypeptide sequences. The maximum range of sequence for Genscan to analyze at once was set to 30 kb. To determine which of these Genscan predicted cDNA sequences encode human kinases, the encoded polypeptides were analyzed by querying against PFAM models for human kinases. Potential human kinases were also identified by homology to Incyte cDNA sequences that had been annotated as human kinases. These selected Genscan-predicted sequences were then compared by BLAST analysis to the genpept and gbpi public databases. Where necessary, the Genscan-predicted sequences were then edited by comparison to the top BLAST hit from genpept to correct errors in the sequence predicted by Genscan, such as extra or omitted exons. BLAST analysis was also used to find any Incyte cDNA or public cDNA coverage of the Genscan-predicted sequences, thus providing evidence for transcription. When Incyte cDNA coverage was available, this information was used to correct or confirm the Genscan predicted sequence. Full length polynucleotide sequences were obtained by assembling Genscan-predicted coding sequences with Incyte cDNA sequences and/or public cDNA sequences using the assembly process described in Example III. Alternatively, full length polynucleotide sequences were derived entirely from edited or unedited Genscan-predicted coding sequences.

V. Assembly of Genomic Sequence Data with cDNA Sequence Data

“Stitched” Sequences

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

type (cDNA to genomic sequence). The resultant stitched sequences were translated and compared by BLAST analysis to the genpept and gbpr public databases. Incorrect exons predicted by Genscan were corrected by comparison to the top BLAST hit from genpept. Sequences were further extended with additional cDNA sequences, or by inspection of genomic DNA, when necessary.

5 **“Stretched” Sequences**

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

VI. Chromosomal Mapping of PKIN Encoding Polynucleotides

The sequences which were used to assemble SEQ ID NO:21-40 were compared with
20 sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:21-40 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for
25 Genome Research (WIGR), and Généthon were used to determine if any of the clustered sequences had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO., to that map location.

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

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

5 VII. Analysis of Polynucleotide Expression

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

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

15

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

The product score takes into account both the degree of similarity between two sequences and the
 20 length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by
 25 gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced, either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the
 30 other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

Alternatively, polynucleotide sequences encoding PKIN are analyzed with respect to the tissue sources from which they were derived. For example, some full length sequences are

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

VIII. Extension of PKIN Encoding Polynucleotides

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

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

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

repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

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

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

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

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

IX. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:21-40 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 OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [5 γ -³²P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase
10 I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

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

X. Microarrays

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, supra.), mechanical
20 microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned technologies should be uniform and solid with a non-porous surface (Schna (1999), supra). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may
25 be produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements: (See, e.g., Schna, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645; Marshall, A. and J. Hodgson (1998) Nat. Biotechnol. 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may
30 comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection.

After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

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

Microarray Preparation

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

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C

oven.

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

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

Hybridization

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

Detection

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

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

although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

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

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

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

XI. Complementary Polynucleotides

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

XII. Expression of PKIN

Expression and purification of PKIN is achieved using bacterial or virus-based expression systems. For expression of PKIN 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 PKIN upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of PKIN 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 PKIN by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, PKIN 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 PKIN at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch. 10 and 16). Purified PKIN obtained by these methods can be used directly in the assays shown in Examples XVI, XVII, XVIII, and XIX where applicable.

XIII. Functional Assays

PKIN function is assessed by expressing the sequences encoding PKIN at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include PCMV SPORT (Life Technologies) and PCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a

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

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

XIV. Production of PKIN Specific Antibodies

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

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

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using Fmoc chemistry and coupled to KLH (Sigma-

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

XV. Purification of Naturally Occurring PKIN Using Specific Antibodies

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

Media containing PKIN are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PKIN (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/PKIN 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 PKIN is collected.

XVI. Identification of Molecules Which Interact with PKIN

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

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

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

XVII. Demonstration of PKIN Activity

Generally, protein kinase activity is measured by quantifying the phosphorylation of a protein

substrate by PKIN in the presence of [γ - ^{32}P]ATP. PKIN is incubated with the protein substrate, ^{32}P -ATP, and an appropriate kinase buffer. The ^{32}P incorporated into the substrate is separated from free ^{32}P -ATP by electrophoresis and the incorporated ^{32}P is counted using a radioisotope counter. The amount of incorporated ^{32}P is proportional to the activity of PKIN. A determination of the
5 specific amino acid residue phosphorylated is made by phosphoamino acid analysis of the hydrolyzed protein.

In one alternative, protein kinase activity is measured by quantifying the transfer of gamma phosphate from adenosine triphosphate (ATP) to a serine, threonine or tyrosine residue in a protein substrate. The reaction occurs between a protein kinase sample with a biotinylated peptide substrate
10 and gamma ^{32}P -ATP. Following the reaction, free avidin in solution is added for binding to the biotinylated ^{32}P -peptide product. The binding sample then undergoes a centrifugal ultrafiltration process with a membrane which will retain the product-avidin complex and allow passage of free gamma ^{32}P -ATP. The reservoir of the centrifuged unit containing the ^{32}P -peptide product as retentate is then counted in a scintillation counter. This procedure allows assay of any type of protein kinase
15 sample, depending on the peptide substrate and kinase reaction buffer selected. This assay is provided in kit form (ASUA, Affinity Ultrafiltration Separation Assay, Transbio Corporation, Baltimore MD, U.S. Patent No. 5,869,275). Suggested substrates and their respective enzymes include but are not limited to: Histone H1 (Sigma) and p34^{cdc2}kinase, Annexin I, Angiotensin (Sigma) and EGF receptor kinase, Annexin II and *src* kinase, ERK1 & ERK2 substrates and MEK, and myelin basic protein and
20 ERK (Pearson, J.D. et al. (1991) Methods Enzymol. 200:62-81).

In another alternative, protein kinase activity of PKIN is demonstrated in an assay containing PKIN, 50 μl of kinase buffer, 1 μg substrate, such as myelin basic protein (MBP) or synthetic peptide substrates, 1 mM DTT, 10 μg ATP, and 0.5 μCi [γ - ^{32}P]ATP. The reaction is incubated at 30°C for 30 minutes and stopped by pipetting onto P81 paper. The unincorporated [γ - ^{32}P]ATP is removed by
25 washing and the incorporated radioactivity is measured using a scintillation counter. Alternatively, the reaction is stopped by heating to 100°C in the presence of SDS loading buffer and resolved on a 12% SDS polyacrylamide gel followed by autoradiography. The amount of incorporated ^{32}P is proportional to the activity of PKIN.

In yet another alternative, adenylate kinase or guanylate kinase activity may be measured by
30 the incorporation of ^{32}P from [γ - ^{32}P]ATP into ADP or GDP using a gamma radioisotope counter. The enzyme, in a kinase buffer, is incubated together with the appropriate nucleotide mono-phosphate substrate (AMP or GMP) and ^{32}P -labeled ATP as the phosphate donor. The reaction is incubated at 37°C and terminated by addition of trichloroacetic acid. The acid extract is neutralized and subjected

to gel electrophoresis to separate the mono-, di-, and triphosphonucleotide fractions. The diphosphonucleotide fraction is excised and counted. The radioactivity recovered is proportional to the enzyme activity.

In yet another alternative, other assays for PKIN include scintillation proximity assays (SPA),
5 scintillation plate technology and filter binding assays. Useful substrates include recombinant proteins tagged with glutathione transferase, or synthetic peptide substrates tagged with biotin. Inhibitors of PKIN activity, such as small organic molecules, proteins or peptides, may be identified by such assays.

XVIII. Enhancement/Inhibition of Protein Kinase Activity

Agonists or antagonists of PKIN activation or inhibition may be tested using assays described
10 in section XVII. Agonists cause an increase in PKIN activity and antagonists cause a decrease in PKIN activity.

XIX. Kinase Binding Assay

Binding of PKIN to a FLAG-CD44 cyt fusion protein can be determined by incubating PKIN
to anti-PKIN-conjugated immunoaffinity beads followed by incubating portions of the beads (having
15 10-20 ng of protein) with 0.5 ml of a binding buffer (20 mM Tris-HCL (pH 7.4), 150 mM NaCl, 0.1% bovine serum albumin, and 0.05% Triton X-100) in the presence of ¹²⁵I-labeled FLAG-CD44cyt fusion protein (5,000 cpm/ng protein) at 4 °C for 5 hours. Following binding, beads were washed thoroughly in the binding buffer and the bead-bound radioactivity measured in a scintillation counter (Bourguignon, L.Y.W. et al. (2001) J. Biol. Chem. 276:7327-7336). The amount of incorporated ³²P is proportional
20 to the amount of bound PKIN.

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

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID
2564295	1	2564295CD1	21	2564295CB1
2837050	2	2837050CD1	22	2837050CB1
7474590	3	7474590CD1	23	7474590CB1
7474594	4	7474594CD1	24	7474594CB1
7477585	5	7477585CD1	25	7477585CB1
7477587	6	7477587CD1	26	7477587CB1
7594537	7	7594537CD1	27	7594537CB1
70467491	8	70467491CD1	28	70467491CB1
7478559	9	7478559CD1	29	7478559CB1
1698381	10	1698381CD1	30	1698381CB1
7474637	11	7474637CD1	31	7474637CB1
7170260	12	7170260CD1	32	7170260CB1
1797506	13	1797506CD1	33	1797506CB1
1851973	14	1851973CD1	34	1851973CB1
7474604	15	7474604CD1	35	7474604CB1
7474721	16	7474721CD1	36	7474721CB1
7478815	17	7478815CD1	37	7478815CB1
7477141	18	7477141CD1	38	7477141CB1
2190612	19	2190612CD1	39	2190612CB1
7477549	20	7477549CD1	40	7477549CB1

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
1	2564295CD1	g186555	0.0	Insulin receptor-related receptor [Homo sapiens]
2	2837050CD1	g2853031	0.0	Tousled-like kinase [Mus musculus]
3	7474590CD1	g6453611	5.1e-86	Protein kinase (mutant form) [Mus musculus]
4	7474594CD1	g3879221	5.6e-99	Predicted using Genefinder similar to casein kinase I [Caenorhabditis elegans]
5	7477585CD1	g348245	3.5e-62	Protein serine/threonine kinase [Homo sapiens]
6	7477587CD1	g312998	7.4e-73	Protein kinase [Homo sapiens]
7	7594537CD1	g485398	0.0	90kDa-diacylglycerol kinase [Rattus norvegicus]
8	70467491CD1	g3089349	0.0	Cdc25C associated protein kinase C- TAK1 [Homo sapiens]
9	7478559CD1	g7960111 g9998952	4.2e-114 1.00E-123	Ethanolamine kinase [Homo sapiens] [Homo sapiens] ethanolamine kinase Lykidis, A. et al. Overexpression of a mammalian ethanolamine-specific kinase accelerates the CDP-ethanolamine pathway J. Biol. Chem. 276, 2174-2179 (2001)
10	1698381CD1	g36615	7.7e-122	[Homo sapiens] serine/threonine protein kinase Meyerson, M. et al. (1992) EMBO J. 11:2909-2917
11	7474637CD1	g1181079	0.0	[Homo sapiens] diacylglycerol kinase delta Sakane, F. et al. (1996) J. Biol. Chem. 271:8394-8401
		g1401232	0	[Cricetinae gen. sp.] diacylglycerol kinase eta Klauck, T.M. et al. Cloning and characterization of a glucocorticoid-induced diacylglycerol kinase J. Biol. Chem. 271, 19781-19788 (1996)

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
12	7170260CD1	g8101585	3.5e-126	[Mus musculus] testis specific serine kinase-3 Zuercher, G. et al (2000) Mech. Dev. 93:175-177
13	1797506CD1	g3300094	4.5e-227	[Homo sapiens] protein kinase/endoribonuclease Tirasophon, W. et al. (1998) Genes Dev. 12:1812-1824
		g12407081	0	[Homo sapiens] protein kinase/ribonuclease IRE1 beta Iwawaki, T. et al. Translational control by the ER transmembrane kinase/ribonuclease IRE1 under ER stress Nat. Cell Biol. 3, 158-164 (2001)
14	1851973CD1	g1853976	1.3e-37	[Schizosaccharomyces pombe] protein kinase Samejima, I., and Yanagida, M. (1994) Mol Cell Biol. 14:6361-71
		g9294489	5.00E-47	[Arabidopsis thaliana] IRE homolog; protein kinase-like protein Sato, S., Nakamura, Y., Kaneko, T., Kato, T. et al. Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones DNA Res. 7, 131-135 (2000)
15	7474604CD1	g1171250	2.0e-218	[Mus musculus] protein kinase related to Raf protein kinases Therrien, M. et al. (1995) Cell 83:879-888
16	7474721CD1	g551608	4.1e-290	[Homo sapiens] receptor protein-tyrosine kinase Fox, G.M. et al. (1995) Oncogene 10:897-905
17	7478815CD1	g2873349	0.0	[Homo sapiens] Hexokinase I Ruzzo, A. et al. (1998) Biochem. J. 331(Pt 2):607-613

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
18	7477141CD1	g7239696	1.6e-87	[Homo sapiens] myosin light chain kinase Garcia, J.G. et al. (1997) Am. J. Respir. Cell Mol. Biol. 16:489-494 Garcia, J.G.N. et al. (1996) Biochem. Biophys. Res. Commun. 1:1-1
		g11385416	0	[Mus musculus] striated muscle-specific serine/threonine protein kinase Hsieh, C.M. et al. Striated Muscle Preferentially Expressed Genes alpha and beta Are Two Serine/Threonine Protein Kinases Derived from the Same Gene as the Aortic Preferentially Expressed Gene-1 J. Biol. Chem. 275 (47), 36966-36973 (2000)
19	2190612CD1	g1836161	6.0e-257	[Rattus sp.] Ca2+/calmodulin-dependent protein kinase IV kinase Okuno, S., Kitani, T. and Fujisawa, H. (1996) J. Biochem. 119:1176-1181
20	7477549CD1	g5006445	3.6e-179	[Homo sapiens] CDC42-binding protein kinase beta Moncrieff, C.L. et al. (1999) Genomics 57:297-300
		g2736151	0	[Rattus norvegicus] myotonic dystrophy kinase-related Cdc42-binding kinase Leung, T. et al. Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector in promoting cytoskeletal reorganization Mol. Cell. Biol. 18, 130-140 (1998)

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
20		g2217968	1.40E-161	[Homo sapiens] myotonic dystrophy protein kinase Kedra, D. et al. The germinal center kinase gene and a novel CDC25-like gene are located in the vicinity of the PYGM gene on 11q13 Hum. Genet. 100, 611-619 (1997)

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
1	2564295CD1	1297	S151 S238 S271 S49 S564 S666 S741 S758 S827 S887 S900 S93 S962 T223 T348 T475 T486 T494 T581 T582 T629 T64 Y454 Y652 T1014 T1020 T1063 S1163 T1171 T1187 S1245 T1275 T1284 S1073 T1128 S1253 T1145	N311 N411 N47 N492 N528 N616 N634 N756 N885 N898 N949	PROTEIN KINASE DOMAIN DM00004 P14617 980-1238: S980-F1239 RECEPTOR PRECURSOR SIGNAL TRANSFERASE TYROSINEPROTEIN KINASE TRANSMEMBRANE GLYCOPROTEIN ATPBINDING PHOSPHORYLATION PD006834: A603-R745, F760-I818 RECEPTOR PRECURSOR SIGNAL TRANSFERASE TYROSINEPROTEIN KINASE TRANSMEMBRANE GLYCOPROTEIN ATPBINDING PHOSPHORYLATION PD005347: Q466-P602 PUTATIVE INSULINLIKE PEPTIDE RECEPTOR PRECURSOR EC 2.7.1.112 TRANSFERASE TYROSINEPROTEIN KINASE TRANSMEMBRANE GLYCOPROTEIN ATPBINDING PHOSPHORYLATION SIGNAL PD146134: L344-E495, V773-G899, D513-C799, E825-R855 PRECURSOR SIGNAL INSULINLIKE RECEPTOR TRANSFERASE TYROSINEPROTEIN KINASE TRANSMEMBRANE GLYCOPROTEIN ATPBINDING PD004354: V330-G410 Receptor tyrosine kinase BL00239: G464-P473, E1030-E1077, M1092-R1114, A1117-E1142, D1144-Y1193, N1198-I1242 Receptor tyrosine kinase BL00240F: T1143-E1190 Receptor tyrosine kinase BL00790H: S831-L856 Tyrosine kinase catalytic domain PR00109: M1059-R1072, Y1105-V1123, L1154-L1164, S1173-G1195, C1217-F1239 Protein kinases signatures and profile protein_kinase_tyr.prf: E1091-T1143 Receptor tyrosine kinase class II signature receptor_tyr_kin_ii.prf: R1119-G1167 Signal peptide: M1-D25 Transmembrane domain: V922-Y944, Furin-like cysteine rich region: G173-K329 Receptor L domain: N47-N170, G346-N472 Eukaryotic protein kinase domain pkinase: I979-E1248 Protein Kinase Atp L985-K1013	BLAST-DOMO BLAST-PRODUM BLAST-PRODUM BLAST-PRODUM BLAST-PRODUM BLAST-PRODUM BLIMPS-BLOCKS BLIMPS-BLOCKS BLIMPS-BLOCKS BLIMPS-PRINTS PROFILESSCAN PROFILESSCAN HMMER HMMER HMMER-PFAM HMMER-PFAM HMMER-PFAM MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
2	2837050CD1	718	S165 S186 S194 S238 S246 S257 S275 S298 S44 S46 S509 S605 S632 T176 T269 T344 T403 T488 T558 T78 Y571 Y97	N340 N36 N548 N630 N713 N714	PROTEIN KINASE DOMAIN DM00004 P34314 736-1002; L409-D677 TOUSLEDLIKE KINASE PD102959: M2-E183 KINASE PROTEIN TOUSLEDLIKE PD013350: M237-D400, Q287-L409 TOUSLEDLIKE KINASE KIAA0137 PROTEIN PD035377: K184-T236 TOUSLEDLIKE KINASE MULTIPLE TESTIS TRANSCRIPT PD026280: A682-N718 Tyrosine kinase catalytic domain PR00109: L490-K503, V608-N630 Protein kinases signatures and profile protein_kinase_tyr.prf: E512-S570 Eukaryotic protein kinase domain pkinase: Y408-L687 Protein Kinase Atp: L414-K437 Protein Kinase St: I534-L546 PROTEIN KINASE DOMAIN DM00004 P27448 58-297: V30-T265 Tyrosine kinase catalytic domain PR00109: Y136-V154, V202-S224, L244-A266 Protein kinases signatures and profile protein_kinase_tyr.prf: Q94-G174 Eukaryotic protein kinase domain pkinase: Y28-L275 Protein Kinase St: V142-V154 PROTEIN KINASE DOMAIN DM00004 P48730 11-265: K144-Y392 SIMILAR TO CASEIN KINASES PD115501: F332-D422, L130-T233 Eukaryotic protein kinase domain pkinase: W140-F374 Protein Kinase Atp: I146-K169 Signal cleavage: M1-L19	BLAST-DOMO BLAST-PRODOM BLAST-PRODOM BLAST-PRODOM BLAST-PRODOM BLIMPS-PRINTS PROFILES SCAN HMMER-PFAM MOTIFS MOTIFS BLAST-DOMO BLIMPS-PRINTS PROFILES SCAN HMMER-PFAM MOTIFS BLAST-DOMO BLAST-PRODOM HMMER-PFAM MOTIFS SPSCAN
3	7474590CD1	497	S17 S286 S291 S3 S314 S356 S372 S375 S381 S382 S409 S440 S447 S5 S70 T225 T265 T427 T445 T461	N243		
4	7474594CD1	741	S397 S402 S471 S592 S641 S652 S656 S737 T237 T274 T292 T308 T388 T587	N119 N291		

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
5	7477585CD1	645	S251 S273 S277 S372 S414 S454 S47 S490 S522 S600 S64 S84 S97 T211 T302 T329 T340 T538 T547 Y368	N598 N71	PROTEIN KINASE DOMAIN DM00004 P51957 8-251: L35-S277 Tyrosine kinase catalytic domain PR00109: T108-Q121, Y148-L166, Y256-A278 Protein kinases signatures and profile protein_kinase_tyr.prf: Q134-S185 Eukaryotic protein kinase domain pkinase: Y29-L287 Protein_Kinase_St: I154-L166 PROTEIN KINASE DOMAIN DM00004 P53350 55-295: R99-A267, S253-L310 Tyrosine kinase catalytic domain PR00109: Y212-L230 Protein kinases signatures and profile protein_kinase_tyr.prf: E198-G250 Transmembrane domain transmem_domain: L555-S575 Eukaryotic protein kinase domain pkinase: Y97-A267, S268-F319 Protein_Kinase_Atp: I103-K126 Protein_Kinase_St: I218-L230	BLAST-DOMO BLIMPS-PRINTS PROFILES-SCAN HMMER-PFAM MOTIFS BLAST-DOMO BLIMPS-PRINTS PROFILES-SCAN HMMER HMMER-PFAM MOTIFS MOTIFS
6	7477587CD1	623	S32 S393 S439 S54 S61 S67 S80 S93 T195 T367 T454 T463 T584		PHORBOL-ESTER AND DAG BINDING DOMAIN DM01331 P49621 326-792: V321-K789 KINASE DIACYLGLYCEROL PHORBOLESTER BINDING TRANSFERASE DIGLYCERIDE DAG MULTIGENE FAMILY DGK PD002939: I575-P755 PROBABLE DIACYLGLYCEROL KINASE EC 2.7.1.107 DIGLYCERIDE DGK DAG HYPOTHETICAL PROTEIN TRANSFERASE CALCIUMBINDING PHORBOLESTER BINDING PD078865: A118-G236, L10-D85, T50-S81 KINASE DIACYLGLYCEROL PHORBOLESTER BINDING PROTEIN TRANSFERASE DIGLYCERIDE DAG MULTIGENE FAMILY PD002780: P431-W555	BLAST-DOMO BLAST-PRODROM BLAST-PRODROM
7	7594537CD1	797	S11 S136 S165 S208 S25 S294 S380 S670 S675 S684 S81 T2 T26 T274 T298 T312 T320 T388 T518 T62 T625 T689 T743 T762 T766 Y449	N546 N646 N793		BLAST-DOMO BLAST-PRODROM BLAST-PRODROM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					DIACYLGLYCEROL KINASE, BETA EC 2.7.1.107 DIGLYCERIDE KINASE DGK DAG 90 KD TRANSFERASE CALCIUMBINDING PHORBOLESTER BINDING MULTIGENE FAMILY PD119174: D352-H430	BLAST-PRODOM
					Diacylglycerol kinase catalytic domain PF00781: H331-Q336 P431-Y462 R483-L497 P509-Y532 K539-V559 N577-Y613 L655-G668 L747-Q758	BLIMPS-PFAM
					Diacylglycerol kinase catalytic domain DAGKc: P431-W555	HMMER-PFAM
					Diacylglycerol kinase accessory domain DAGKa: I575-P755	HMMER-PFAM
					Phorbol esters/diacylglycerol binding domain d DAG_PE-gind: H238-C287, H303-C351 EF hand efhand: K146-M174, I191-T219	HMMER-PFAM
					Phorbol esters/diacylglycerol binding domain BL00479: Q264-C279, L514-L526, H238-G260	BLIMPS-BLOCKS
					Phorbol esters/diacylglycerol binding domain dag_pe binding domain.prf: Y250-G378	PROFILES CAN
					Dag_Pe_Binding_Domain: H238-C287	MOTIFS
					EF_Hand: D155-L167, D200-W212	MOTIFS
8	70467491CD1	749	S141 S2 S24 S346 S374 S417 S424 S444 S456 S457 S461 S49 S494 S495 S516 S634 S653 S659 S664 S730 T118 T283 T302 T33 T36 T508 T512 T519 T535 T614 T618 T623 T82 T9 Y113	N386 N399 N400 N479 N533 N637	PROTEIN KINASE DOMAIN DM00004 P27448 58-297: L62-L303 KINASE SERINE/THREONINEPROTEIN PROTEIN TRANSFERASE ATPBINDING SERINE/THREONINE PUTATIVE KIN1 EMK PAR1 PD004300: G633-L749 KINASE SERINE/THREONINEPROTEIN SERINE/THREONINE PUTATIVE TRANSFERASE ATPBINDING PROTEIN EMK P78 CDC25C PD008571: S413-E632 KINASE SERINE/THREONINEPROTEIN PUTATIVE SERINE/THREONINE TRANSFERASE ATPBINDING PROTEIN PAR1 KP78 EMK PD005838: I312-R412 SERINE/THREONINE KINASE PD119193: S551-P622	BLAST-DOMO BLAST-PRODOM BLAST-PRODOM BLAST-PRODOM BLAST-PRODOM BLAST-PRODOM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
9	7478559CD1	386	S237 S259 S355 S38 T20 T322 T85 T93 Y271	N188	Tyrosine kinase catalytic domain PR00109: Y173-L191, V239-Q261	BLIMPS-PRINTS
					Protein kinases signatures and profile protein_kinase_tyr.prf: K122-G212	PROFILES CAN
					Eukaryotic protein kinase domain pkinase: Y60-E85	HMMER-PFAM
					Eukaryotic protein kinase domain pkinase: F137-I312	HMMER-PFAM
					Protein_Kinase_St: I179-L191	MOTIFS
10	1698381CD1	342	S180 S205 S238 S284 S288 S38 T247 Y15 Y211	N23	do CHOLINE; KINASE; YDR147W; B0285.10; DM01931 P35790 128-455: D258-K376, F131-P300	BLAST-DOMO
					do CHOLINE; KINASE; YDR147W; B0285.10; DM01931 P46560 1-305: E125-A289	BLAST-DOMO
					KINASE CHOLINE TRANSFERASE PROTEIN MULTIGENE FAMILY PUTATIVE LIKE CHROMOSOME III PD003547: V222-L382, V109-E240	BLAST-PROD OM
					KINASE TRANSFERASE CHOLINE PD02952: V243-I256, H263-N292	BLIMPS-PROD OM
					Choline/ethanolamine kinase Choline_kinase: T85-T356	HMMER-PFAM
10	1698381CD1	342	S180 S205 S238 S284 S288 S38 T247 Y15 Y211	N23	Eukaryotic protein kinase domain pkinase: Y4-F286,	HMMER-PFAM
					Protein kinases signatures and profile protein_kinase_tyrosine: E90-G154	PROFILES CAN
					PROTEIN KINASE DOMAIN DM00004 Q00532 7-278: K6-C277	BLAST-DOMO
					PROTEIN KINASE DOMAIN DM00004 Q00526 6-286: K6-F286	BLAST-DOMO
					PROTEIN KINASE DOMAIN DM00004 P23437 6-286: K6-G218	BLAST-DOMO
10	1698381CD1	342	S180 S205 S238 S284 S288 S38 T247 Y15 Y211	N23	PROTEIN KINASE DOMAIN DM00004 P51958 6-277: K6-G218	BLAST-DOMO
					KINASE TRANSFERASE PROTEIN SERINE/THREONINE PROTEIN ATP-BINDING II PHOSPHORYLATION	BLAST-PROD OM
					CASEIN ALPHA CHAIN PD002608: V161-F286	BLAST-PROD OM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Tyrosine kinase catalytic domain signature PR00109: F116-I134 Serine/Threonine protein kinases active-site signature C122-I134	BLIMPS_PRINTS MOTIFS
11	7474637CD1	1164	S114 S119 S152 S258 S39 S399 S41 S432 S450 S511 S56 S586 S587 S591 S608 S623 S654 S66 S664 S695 S766 S820 S873 S958 S967 S1075 T316 T419 T486 T514 T518 T659 T678 T863 T908 T955 T1046 T1118	N124 N314 N651 N1059 N1122	Phorbol esters/ diacylglycerol binding domain: F188-A259 signal_cleavage:M1-A32 Phorbol esters/diacylglycerol binding domain (C1 domain): H176-C225, H248-C298 PH domain: S66-T158 DAG kinase catalytic domain: P332-W457 DAG kinase accessory domain: V770-A927 PHORBOL-ESTER AND DAG BINDING DOMAIN DM01331 P49621 326-792: P332-H505, V770-E865, F869-L946, C279-L313, G198-C225 PHORBOL-ESTER AND DAG BINDING DOMAIN DM01331 Q09103 683-1148: V330-I459, T752-R948, C279-P310, A2-I61 PHORBOL-ESTER AND DAG BINDING DOMAIN DM01331 P23743 308-734: P332-L500, V770-F869, P872-L946 PHORBOL-ESTER AND DAG BINDING DOMAIN DM01331 I59282 352-782: C279-H505, V770-L946 KINASE DIACYLGLYCEROL ETA DIGLYCERIDE DAG TRANSFERASE PHORBOLESTER BINDING REPEAT MULTIGENE PD040467: S458-C769 DIACYLGLYCEROL PHORBOLESTER BINDING KINASE ETA DIGLYCERIDE DAG TRANSFERASE REPEAT MULTIGENE PD038733: A927-V1130 KINASE DIACYLGLYCEROL PHORBOLESTER BINDING TRANSFERASE DIGLYCERIDE DAG MULTIGENE FAMILY DKG PD002939: V770-E926 KINASE DIACYLGLYCEROL PHORBOLESTER BINDING PROTEIN TRANSFERASE DIGLYCERIDE DAG MULTIGENE FAMILY PD002780: V330-W457	PROFILES SCAN SPSCAN HMMER_PPFAM HMMER_PPFAM HMMER_PPFAM BLAST_DOMO BLAST_DOMO BLAST_DOMO BLAST_DOMO BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM

Table 3 (cont.)

SEQ ID NO: ID	Incyte Polypeptide	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
11					Phorbol esters/diacylglycerol binding domain proteins BL00479: H176-G198, H202-C217, L415-L427 Diacylglycerol kinase catalytic domain (presumed) PF00781: K278-K283, P332-F363, R384-L398, C410-Y433, Q441-T461, N772-Y808, L848-G861, V919-Q930 Diacylglycerol/phorbol-ester binding signature PR00008: H202-A213, H214-K226 KINASE PROTEIN DOMAIN PD00584: K74-K84, L386-G395, L466-L473 Phorbol esters/diacylglycerol binding domain: H176-C225	BLIMPS_BLOCKS BLIMPS_PFAM BLIMPS_PRINTS BLIMPS_PRODOM MOTIFS
12	7170260CD1	268	S161 S188 S255 S29 T15 Y124 Y21		Eukaryotic protein kinase domain pkinase: Y10-L265 Protein kinases signatures and profile protein_kinase_tyrosine: G82-H162 PROTEIN KINASE DOMAIN DM00004 P27448 58-297: K14-I256 PROTEIN KINASE DOMAIN DM00004 I48609 55-294: K14-S255 PROTEIN KINASE DOMAIN DM00004 Q05512 55-294: K14-S255 PROTEIN KINASE DOMAIN DM00004 JC1446 20-261: Q11-I256 Tyrosine kinase catalytic domain signature PR00109: Y124-L142 Protein kinases ATP-binding region signature: I16-K39	HMMER_PFAM PROFILESCAN BLAST_DOMO BLAST_DOMO BLAST_DOMO BLIMPS_PRINTS MOTIFS
13	1797506CD1	965	S234 S326 S527 S530 S607 S636 S741 S841 S879 S884 S92 T111 T143 T155 T174 T202 T215 T229 T29 T372 T619 T685 T82 T922 T932 T963 Y173	N227	Eukaryotic protein kinase domain pkinase: F559-F820, Protein kinases signatures and profile protein_kinase_tyr.prf: E652-G709 PROTEIN KINASE DOMAIN DM00004 Q09499 536-784: P561-A811 PROTEIN KINASE DOMAIN DM00004 P32361 676-970: V564-Q732, T740-A811 KINASE; THREONINE; ATP; SERINE; DM06305 Q09499 786-924: V814-Y949	HMMER_PFAM PROFILESCAN BLAST_DOMO BLAST_DOMO BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					KINASE; THREONINE; ATP; SERINE; DM06305 P32361 972-1114: Q813-L946 PROTEIN KINASE/ENDORIBONULCEASE PUTATIVE SERINE/THREONINE PROTEIN KINASE C41C4.4 CHROMOSOME II PRECURSOR TRANSFERASE PD152704: T197-L422, L88-E190 SERINE/THREONINE PROTEIN KINASE PRECURSOR TRANSMEMBRANE SIGNAL TRANSFERASE ATP-BINDING PROTEIN IRE1 GLYCOPROTEIN PD032590: W821-Y949 Tyrosine kinase catalytic domain signature PR00109: H666-I684, G721-L731, V743-D765 Serine/Threonine protein kinases active-site signature: I672-I684 Phosphorylase kinase family signature PR01049: P812-R823	BLAST_DOMO BLAST_PRODUM BLAST_PRODUM BLIMPS_PRINTS MOTIFS BLIMPS_PRINTS
14	1851973CD1	329	S264 S270 S293 S31 S311 S320 S7	N73	Eukaryotic protein kinase domain pkinase: F35-V180 Protein kinases signatures and profile protein_kinase_tyrosine: M132-R184 PROTEIN KINASE DOMAIN DM00004 P43565 796-1240: I37-R184 PROTEIN KINASE DOMAIN DM00004 A56155 714-1002: V38-L177 PROTEIN KINASE DOMAIN DM00004 P38679 238-527: V38-S178 PROTEIN KINASE DOMAIN DM00004 P53894 353-658: V38-S178 Tyrosine kinase catalytic domain signature PR00109: M110-H123, Y146-I164 Serine/Threonine protein kinases active-site signature: I152-I164	HMMER_PPFAM PROFILESSCAN BLAST_DOMO BLAST_DOMO BLAST_DOMO BLAST_DOMO BLIMPS_PRINTS MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
15	7474604CD1	945	S110 S157 S193 S246 S289 S290 S31 S329 S356 S359 S405 S411 S611 S623 S636 S645 S67 S934 T170 T2 T217 T322 T42 T47 T496 T712 T839	N140 N155 N382 N631 N756 N888	Eukaryotic protein kinase domain pkinase: L661-M920 Protein kinases signatures and profile protein_kinase_tyrosine: K757-L801 PROTEIN KINASE DOMAIN DM00004 P27966 85-332: I663-F916 PROTEIN KINASE DOMAIN DM00004 P15056 458-705: I663-F916, PROTEIN KINASE DOMAIN DM00004 P10398 312-559: I667-F916 PROTEIN KINASE DOMAIN DM00004 B26126 305-552: I667-F916 KINASE SUPPRESSOR OF RAS1 KSR1 HB PROTEIN PD103125: V390-P557, K501-L661 L222-P323 KINASE SUPPRESSOR OF RAS KSR PHORBOLESTER BINDING RAS1 KSR1 HB PD017776: L21-E344 S485-T519 Tyrosine kinase catalytic domain signature PR00109: Y771-Y789, W867-I877, M894-F916 Serine/Threonine protein kinases active-site signature: I777-Y789	HMMER_FFAM PROFILES SCAN BLAST_DOMO BLAST_DOMO BLAST_DOMO BLAST_DOMO BLAST_PROD OM BLAST_PROD OM BLIMPS_PRINTS MOTIFS
16	7474721CD1	1009	S184 S203 S244 S293 S325 S44 S473 S62 S625 S682 S686 S805 S825 S851 S980 T108 T121 T133 T162 T214 T224 T232 T32 T423 T488 T551 T616 T619 Y504 Y766 Y801	N311 N486	Eukaryotic protein kinase domain pkinase: V645-H897 Ephrin receptor ligand binding domain EPH_lbd: E35-C211 Protein kinases signatures and profile protein_kinase_tyrosine: Q746-A799 RECEPTOR TYROSINE KINASE CLASS V DM00501 S51741 33-382: V36-G394 RECEPTOR TYROSINE KINASE CLASS V DM00501 P54759 33-382: V36-G394 RECEPTOR TYROSINE KINASE CLASS V DM00501 I48611 34-382: I37-G394 RECEPTOR TYROSINE KINASE CLASS V DM00501 I48612 34-382: I37-G394 KINASE RECEPTOR PRECURSOR TYROSINE PROTEIN EPHRIN TRANSFERASE ATP-BINDING PHOSPHORYLATION TRANSMEMBRANE GLYCOPROTEIN PD001495: E35-C211	HMMER_FFAM HMMER_FFAM PROFILES SCAN BLAST_DOMO BLAST_DOMO BLAST_DOMO BLAST_DOMO BLAST_PROD OM

Table 3 (cont.)

SEQ ID NO: ID	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					KINASE RECEPTOR PRECURSOR TYROSINE PROTEIN EPHRIN TRANSFERASE ATP-BINDING PHOSPHORYLATION TRANSMEMBRANE GLYCOPROTEIN PD149648: A213-A284 EPH FAMILY PROTEIN PD002683: P339-T451 KINASE RECEPTOR PRECURSOR TYROSINE PROTEIN EPHRIN TRANSFERASE ATP-BINDING PHOSPHORYLATION TRANSMEMBRANE SIGNAL PD001551: C285-R336 Receptor tyrosine kinase BL00239: E694-Q741, L747-R769, A772-S797, E798-Y847, G852-I896 Receptor tyrosine kinase BL00790: L751-A772, S805-W837, E838-G862, F863-K911, A955-R998, E35-N56, D65-P116, K172-A225, P252-Q276, C282-P329, R351-L377, C390-S433 signal peptide: M1-A33 transmembrane domain: V568-W589 signal_cleavage: M1-A33 Hexokinase hexokinase: E16-V463 Q464-L910 Hexokinases signature hexokinases: I577-R642, V130-R195 HEXOKINASES DM00597 P27881 465-915: Q466-A913, D17-Q464 HEXOKINASES DM00597 P52789 465-915: Q466-A913, D17-Q464 HEXOKINASES DM00597 S48809 465-915: Q466-A913, D17-Q464 HEXOKINASES DM00597 P27595 465-915: Q466-Q911, D17-Q466 HEXOKINASE TRANSFERASE KINASE GLYCOLYSIS ATP-BINDING TYPE ALLOSTERIC ENZYME HK DUPLICATION PD001109: Q466-D886, E699-A907, E16-D439, D251-R462 Hexokinases proteins. BL00378: V22-K49, V509-I545, V207-G250, M255-D266, Y724-G769, S892-V906 Hexokinase family signature PR00475: L529-I545, L597-F622, I650-Y666, V226-E240, Q291-M313, V818-I840, M890-V906 Hexokinases L597-F622	BLAST_PRODUM BLAST_PRODUM BLAST_PRODUM BLIMPS_BLOCKS BLIMPS_BLOCKS HMMER HMMER SPSCAN HMMER_PFBM PROFILESAN BLAST_DOMO BLAST_DOMO BLAST_DOMO BLAST_DOMO BLAST_PRODUM BLIMPS_BLOCKS BLIMPS_PRINTS MOTIFS
16	74777421CD1	1009				
17	7478815CD1	917	S243 S364 S379 S449 S503 S547 S551 S772 S787 S791 S810 S826 S896 T114 T161 T172 T275 T35 T508 T523 T569 T625 T722 T726 T811 T877 Y27 Y497	N122 N208 N655		

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
18	7477141CD1	2380	S143 S166 S241 S277 S278 S285 S299 S343 S480 S537 S553 S568 S602 S711 S736 S996 S1033 S1035 S1037 S1062 S1127 S1523 S1571 S1245 S1435 S1468 S1506 S1586 S1609 S1679 S1691 S1747 S1117 S1527 S1557 S1578 S1594 S1613 S1736 S1747 S1876 S1947 S2137 S2171 S2253 S2321 S2058 S2062 S2165 S2269 S680 S754 S986 T108 T153 T158 T170 T350 T408 T476 T498 T578 T614 T692 T803 T862 T957 T1068 T1082 T1311 T1493 T1802 T1981 T2080 T1301 T1856 T1901 T2069 T2101 T2144 T2348 T1608 T2343 Y632 Y772 Y822	N37 N1675 N1847 N1874 N2099 N2299	Eukaryotic protein kinase domain pkinase: Y714-F967, Y2079-L2331 5396: D715-D952, E2083-L2322 PROTEIN KINASE DOMAIN DM000004 P53355 15- 257: Q718-D952, E2083-L2322 PROTEIN KINASE DOMAIN DM000004 JN0583 727- 969: I716-D952, L2082-L2312 PROTEIN KINASE DOMAIN DM000004 P07313 298- 541: Q718-R953, G2088-S2321 Tyrosine kinase catalytic domain signature PR00109: Y822-V840 signal peptide: M52-A70 Eukaryotic protein kinase domain pkinase: Y2079-L2331 Protein kinases ATP-binding region signature: I720-K743 Serine/Threonine protein kinases active- site signature: V828-V840, V2194-L2206	HMMER_PFBM BLAST_DOMO BLAST_DOMO BLAST_DOMO BLAST_DOMO BLIMPS_PRINTS HMMER HMMER_PFBM MOTIFS MOTIFS
19	2190612CD1	505	S100 S117 S160 S330 S419 S425 S437 S458 S69 S74 S82 T108 T26 T430 T58	N147	Eukaryotic protein kinase domain: Y128-V409 Protein kinases signatures and profile protein_kinase_tyrosine: Q251-N303 PROTEIN KINASE DOMAIN DM000004 A57156 130-399: L130-V400 PROTEIN KINASE DOMAIN DM000004 P50526 136-399: E133-I398 PROTEIN KINASE DOMAIN DM000004 P38990 135-438: E133-E320, N303-V400 PROTEIN KINASE DOMAIN DM000004 P43637 52-334: I134-I378	HMMER_PFBM PROFILES SCAN BLAST_DOMO BLAST_DOMO BLAST_DOMO BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
20	7477549CD1	1572	S161 S280 S307 S363 S407 S430 S471 S545 S625 S629 S646 S675 S711 S730 S737 S807 S811 S815 S841 S1058 S1294 S1162 S1500 S1405 S1414 S1556 T455 T590 T673 T888 T956 T1088 T1378		KINASE PROTEIN BETA CA2+/CALMODULIN DEPENDENT CA+/CALMODULIN DEPENDENT CAM KINASE IV ISOFORM PHOSPHORYLASE B PD031900: M1-Q127 KINASE PROTEIN BETA CA2+/CALMODULIN DEPENDENT CA+/CALMODULIN DEPENDENT CAM KINASE IV ISOFORM PHOSPHORYLASE B PD019141: V409-F463 KINASE PROTEIN CA2+/CALMODULIN DEPENDENT IV ISOFORM PHOSPHORYLASE B GLYCOGEN SYNTHASE A PD027014: E464-S505 Tyrosine kinase catalytic domain signature PR00109: Y265-L283, G312-I322 ATP/GTP-binding site motif A (P-loop) G485-S492 Protein kinases ATP-binding region signature: I134-K157 Serine/Threonine protein kinases active-site signature: I271-L283 Phorbol esters diacylglycerol binding domain: C900-S963 Eukaryotic protein kinase domain pkinase: F71-F337 PROTEIN KINASE DOMAIN DM00004 Q09013 83-336: I73-R325 PROTEIN KINASE DOMAIN DM00004 S42867 75-498: I73-H252, V232-Y398 PROTEIN KINASE DOMAIN DM00004 I38133 90-369: E72-L220, V232-G324 PROTEIN KINASE DOMAIN DM00004 P53894 353-658: L74-G215, V232-R325 PHORBOL ESTER BINDING KINASE DYSTROPHY KINASE RELATED CDC42 BINDING SIMILAR SERINE/THREONINE PROTEIN GENGHIS KHAN PD150840: W1355-G1462 PHORBOL ESTER BINDING KINASE DYSTROPHY KINASE RELATED CDC42 BINDING SIMILAR SERINE/THREONINE PROTEIN GENGHIS KHAN PD151400: T1039-R1140	BLAST_PRODROM
						BLAST_PRODROM
						BLAST_PRODROM
						BLAST_PRODROM
						BLIMPS_PRINTS
						MOTIFS
						MOTIFS
						MOTIFS
						PROFILESSCAN
						HMMER_PFAM
						BLAST_DOMO
						BLAST_DOMO
						BLAST_DOMO
						BLAST_PRODROM
						BLAST_PRODROM
						BLAST_PRODROM
						BLAST_PRODROM
						BLAST_PRODROM
						BLAST_PRODROM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					KINASE RHO ASSOCIATED COILED COIL PROTEIN FORMING PHORBOL ESTER BINDING DYSTROPHY KINASE RELATED CDC42 BINDING PD006715: T944- V1038, H433-L456	BLAST_PRODUM
					PHORBOL ESTER BINDING DYSTROPHY KINASE RELATED CDC42 BINDING KINASE GENGHIS KHAN MYOTONIC MYOTONIC PD011252:S694-S815	BLAST_PRODUM
					Tyrosine kinase catalytic domain signature PR00109: C257-E279, M148-S161, S185-L203	BLIMPS_PRINTS
					Phorbol esters/diacylglycerol binding dom DAG_PE-bind: H887-C935	HMMER_PFAM
					Phorbol esters/diacylglycerol binding domain: H887-C935,	MOTIFS
					Protein kinases ATP-binding region signature I77-K100	MOTIFS
					Serine/Threonine protein kinases active-site signature: Y191-L203	MOTIFS
					CNH domain: L1100-K1380	HMMER_PFAM
					Protein kinase C terminal domain: P351-D366	HMMER_PFAM
					PH domain PH: T956-R1074	HMMER_PFAM
					signal_cleavage: M1-S37	SPSCAN

Table 4

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment (s)	Sequence Fragments	5' Position	3' Position
21	2564295CB1	4298	701-1736, 3536-3629, 1- 356, 2349- 2589, 3956- 4298, 2841- 3428	FL2564295_g7160581_000014_g 387060_1_15-16 FL2564295_g7160581_000014_g 387060_1_16-17 FL2564295_g7160581_000014_g 387060_1_7-8 55078393J1 FL2564295_g7160581_000014_g 387060_1_8-9 55078386J1 FL2564295_g7160581_000014_g 387060_1_18-19 2564295H1 (ADRETUT01) g186554_CD FL2564295_g7160581_000014_g 387060_1_9-10 3599581H1 (DRGTNOT01) FL2564295_g7160581_000014_g 387060_1_1-2 FL2564295_g7160581_000014_g 387060_1_10-11 FL2564295_g7160581_000014_g 387060_1_20-21 FL2564295_g7160581_000014_g 387060_1_11-12 FL2564295_g7160581_000014_g 387060_1_2-3 FL2564295_g7160581_000014_g 387060_1_12-13 FL2564295_g7160581_000014_g 387060_1_3-4 FL2564295_g7160581_000014_g 387060_1_4-5	3200 3253 1938 37 2167 1 3594 4048 442 2335 3453 441 2531 3884 2573 994 2794 1298 1441	3482 3593 2334 717 2530 709 3883 4298 4250 2572 3756 1297 2793 4250 2930 1440 3093 1585 1800

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
21				FL2564295_g7160581_000014_g 387060_1_14-15	3094	3252
22	2837050CB1	2863	1-430, 2346- 2863	FL2564295_g7160581_000014_g 387060_1_19-20 6854541H1 (BRAIFEN08) g1164223 71191190V1 7728560H1 (UTRCDIE01) 71972220V1 71972389V1 6881340H1 (BRAHTDR03) 7401101H1 (SINIDME01)	782 1 1439 79 2227 2180 1555 598	1467 496 2085 681 2863 2857 2209 1293
23	7474590CB1	1494	1-1494	GBI.g8103343_000001.edit FL7474590_g7630344_000002_g 6779549_1_1	1 1	1494 1116
24	7474594CB1	2341	682-792, 1- 262, 1522- 2341, 1254- 1373, 339-361	55053685J1 6949237H1 (BRAITDR02) 8016740J1 (BMARTXE01) GNN.g8247875_000031_002 7278940H1 (BMARTXE01) GNN.g6689704_000006_002	1512 858 340 1 1281 1180	2341 1544 959 426 1779 1590
25	7477585CB1	2552	1-465, 1075- 1150	71975408V1 55030002H1 55030074J1 1406660F6 (LATRTUT02) 6329987H1 (BRANDIN01) 71987367V1 6704049H1 (DRGCNOT02) 55030089H1	1988 612 1241 1 1384 2019 1849 679	2534 1305 1900 686 1930 2552 2517 1390
26	7477587CB1	2176	1276-1873, 1- 286	g8671962_edit 5823464F7 (PROSTUS23)	1 1662	1980 2164

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
27	7594537CB1	4277	2383-2614, 1- 611-1170, 1- 518, 2763- 2834, 1714- 1859, 3119- 4277	7594537H1 (LIVRNO07)	130	766
				7328693H1 (UTRCDIE01)	1	351
28	70467491CB1	2616	1717-2616, 1- 425	2395018F6 (THP1AZT01)	2015	2520
29	7478559CB1	1253	1215-1253, 1- 53	FL70467491_g7708222_g759580 0	1	2250
				g3770955	1	321
30	1698381CB1	1790	1-146, 892- 1313, 1659- 1790, 186-237	7661715J1 (OVARNOE02)	655	1253
				g5769093	314	804
				1698381F6 (BLADTUT05)	523	1019
				55068293J1	1	786
				71870273V1	1186	1790
31	7474637CB1	4132	3420-3535, 1- 377, 4035- 4132, 1301- 2486	1698381T6 (BLADTUT05)	774	1363
				4129796F6 (CARGDIT01)	3639	4132
				55076747H1	2871	3468
				55075847H1	1379	1783
				55075848H1	1623	1987
				55077477H1	1045	1472
				GBL.g8247425_000008_000011. edit	504	1126
				55076756J1	3148	3745
				GNN.g6648263_002.edit5p	2805	3026
				6286993H2 (EPIPUNA01)	1041	1168
				7721743H2 (THYRDIE01)	35	503
				6766106H1 (BRAUNOR01)	1893	2356
				55061367H1	2149	2841
32	7170260CB1	1137	877-1137	6766106J1 (BRAUNOR01)	368	909
				1752420H1 (LIVRTUT01)	1	157
				55046242J2	694	1137
				3152909F6 (TLYMTXT02)	1	145

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
32				7659273J1 (OVARNOE02)	416	971
				55046250H1	692	1108
				3343082F7 (SPLNNOT09)	144	555
33	1797506CB1	3365	1-1032, 3340- 3365, 1532- 1735	1513994T6 (PANCYTUT01)	2793	3365
				FL1797506_g7458755_000012_g	1	2898
				3766209		
34	1851973CB1	2049	1-125, 1836- 2049, 806-915	7667239H1 (URETTUC01)	1289	1800
				55075655J1	547	1222
				55077257J1	378	1221
				55067487H1	1	532
				1454205F1 (PENITUT01)	1179	1617
				1454205T6 (PENITUT01)	1436	2049
35	7474604CB1	2962	1-1526, 1757- 2114, 2481- 2962	55075789J1	1760	2440
				8104459J1 (MIXDDIE02)	1	746
				55056946J2	1734	2433
				6884701F6 (BRAHTDR03)	2255	2962
				55067076J1	1214	1763
				55075383J1	651	1335
				6802884F6 (COLENOT03)	2055	2826
				71976507V1	1564	2315
36	7474721CB1	3112	2395-3112, 1353-1459, 2014-2280	55057353J1	314	980
				GBI:g6996165_000001.raw	1910	3112
				GBI:g6996165.raw	140	1735
				55062828H1	1	712
				71980671V1	1418	2051
				55076655H1	1	658
37	7478815CB1	3650	862-1366, 1826-1999, 1- 787, 3623- 3650	6934749H1 (SINTTMR02)	1710	2388
				238539R6 (SINTNOT02)	3159	3647
				614864T6 (COLINTUT02)	3004	3614
				70845065V1	1862	2441
				70842842V1	2420	3073

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment (s)	Sequence Fragments	5' Position	3' Position
37				72026676V1 55075416J1 g657793 70863076V1 2605255F6 (LJUNGTFUT07)	966 358 919 2471 3378	1742 926 1011 3154 3650
38	7477141CB1	7789	1-699, 6785- 6880, 7767- 7789, 7184- 7214, 1237- 6218	7355120H1 (HEARNON03) GBI:g8014664 g7242948_CD 3012344H1 (MUSCNOT07) 71179707V1 7642405J1 (SEMVTDE01)	7201 1 63 7488 6783 6728	7767 260 6763 7772 7436 7294
39	2190612CB1	1937	727-1188, 1- 643, 1731- 1761	70775995V1 55024095J1 (PKINDNV04) 6854667H1 (BRAIFEN08) 7188730H2 (BRATDIC01) 70780513V1 70780809V1	1 914 1441 1353 500 384	498 1558 1937 1820 981 919
40	7477549CB1	5373	4983-5373, 1- 1612, 2046- 2470, 4414- 4442, 2596- 2647, 2814- 3056	55121415H1 55121423J1 7992167H1 (UTRSDIC01) 71999521V1 6822270H1 (SINTNOR01) GNN.g4755212_010.edit 6594083H1 (LJNGFER02) 7164493R8 (PLACNOR01) 71583419V1 7402224H1 (SINIDME01) 7694930H1 (LNODTUE01) 7978995H1 (LSUBDMC01)	4574 4413 3402 1448 857 1 2835 3204 713 289 1082 1478	5373 5274 4043 1590 1407 4567 3147 3711 1385 795 1448 2186

Table 5

Polynucleotide SEQ ID NO:	IncYTE Project ID	Representative Library
21	2564295CB1	ADRETUT01
22	2837050CB1	THYRN0T03
24	7474594CB1	BMARTXE01
25	7477585CB1	BALNON02
26	7477587CB1	PROSTUS23
27	7594537CB1	LIVRNOC07
28	70467491CB1	PROSN0T18
29	7478559CB1	OVARNOE02
30	1698381CB1	BLADTUT05
31	7474637CB1	EP1PUNA01
32	7170260CB1	OVARNOE02
33	1797506CB1	COLENOR03
34	1851973CB1	PENITUT01
35	7474604CB1	BRAHTDR03
36	7474721CB1	COLENOR03
37	7478815CB1	SINITUT03
38	7477141CB1	SKIRNOR01
39	2190612CB1	ADRETUT07
40	7477549CB1	SINTNOR01

Table 6

Library	Vector	Library Description
ADRETUT01	PSPORT	Library was constructed using RNA isolated from right adrenal tumor tissue removed from a 50-year-old Turkish male during a unilateral adrenalectomy. Pathology indicated a metastatic renal cell carcinoma that formed a circumscribed, spongy, hemorrhagic nodule situated in the region of the medulla. The patient presented with corticoadrenal insufficiency, incisional hernia, and non-alcoholic steato hepatitis. Patient history included renal cell carcinoma. Family history included liver cancer.
ADRETUT07	pINCY	Library was constructed using RNA isolated from adrenal tumor tissue removed from a 43-year-old Caucasian female during a unilateral adrenalectomy. Pathology indicated pheochromocytoma.
BLADTUT05	pINCY	Library was constructed using RNA isolated from bladder tumor tissue removed from a 66-year-old Caucasian male during a radical prostatectomy, radical cystectomy, and urinary diversion. Pathology indicated grade 3 transitional cell carcinoma on the anterior wall of the bladder. Patient history included lung neoplasm and tobacco abuse in remission. Family history included malignant breast neoplasm, tuberculosis, cerebrovascular disease, atherosclerotic coronary artery disease, and lung cancer.
BMARTXE01	pINCY	This 5' biased random primed library was constructed using RNA isolated from treated SH-SY5Y cells derived from a metastatic bone marrow neuroblastoma, removed from a 4-year-old Caucasian female (Scherer AG). The medium was MEM/HAM'S F12 with 10% fetal calf serum. After reaching about 80% confluency cells were treated with 6-Hydroxydopamine (6-OHDA) at 100 microM for 8 hours.
BRAHTDR03	PCDNA2.1	This random primed library was constructed using RNA isolated from archaectox, anterior hippocampus tissue removed from a 55-year-old Caucasian female who died from cholangiocarcinoma. Pathology indicated mild meningeal fibrosis predominately over the convexities, scattered axonal spheroids in the white matter of the cingulate cortex and the thalamus, and a few scattered neurofibrillary tangles in the entorhinal cortex and the periaqueductal gray region. Pathology for the associated tumor tissue indicated well-differentiated cholangiocarcinoma of the liver with residual or relapsed tumor. Patient history included cholangiocarcinoma, post-operative Budd-Chiari syndrome, biliary ascites, hydrothorax, dehydration, malnutrition, oliguria and acute renal failure. Previous surgeries included cholecystectomy and resection of 85% of the liver.
BRALENON02	pINCY	This thalamus tissue library was constructed from 4.24 million independent clones from a thalamus tissue library. Starting RNA was made from thalamus tissue removed from a 35-year-old Caucasian male who died from cardiac failure. Pathology indicated moderate leptomeningeal fibrosis and multiple microinfarctions of the cerebral neocortex. Microscopically, the cerebral hemisphere revealed moderate fibrosis of the leptomeninges with focal calcifications. There was evidence of shrunken and slightly eosinophilic pyramidal neurons throughout the cerebral hemispheres. Scattered throughout the cerebral cortex, there were multiple small microscopic areas of cavitation with surrounding

Table 6 (cont.)

Library	Vector	Library Description
		gliosis. Patient history included dilated cardiomyopathy, congestive heart failure, cardiomegaly and an enlarged spleen and liver. The library was normalized in two rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228-9232 and Bonaldo et al., Genome Research (1996) 6:791, except that a significantly longer (48 hours/round) reannealing hybridization was used.
COLENOR03	PCDNA2.1	Library was constructed using RNA isolated from colon epithelium tissue removed from a 13-year-old Caucasian female who died from a motor vehicle accident.
EPIFUNA01	PSPORT	Library was constructed using RNA isolated from untreated prostatic epithelial cell tissue removed from a 17-year-old Hispanic male. Serologies were negative.
LIVRNOC07	pINCY	Library was constructed using pooled cDNA from two different donors. cDNA was generated using RNA isolated from liver tissue removed from a 20-week-old Caucasian male fetus who died from Patau's Syndrome (donor A) and a 16-week-old Caucasian female fetus who died from anencephaly (donor B). Family history included mitral valve prolapse in the mother of donor B.
OVARNOE02	PCDNA2.1	This 5' biased random primed library was constructed using RNA isolated from right ovary tissue removed from a 47-year-old Caucasian female during total abdominal hysterectomy, bilateral salpingo-oophorectomy, incisional hernia repair, and panniculectomy. The patient presented with premenopausal menorrhagia. Patient history included osteoarthritis, tubal pregnancy, and polio osteopathy of the left leg. Previous surgeries included gastroenterostomy, plastic repair of the palate, adenotonsillectomy, dilation and curettage, cholecystectomy, and bladder reconstruction. Patient medications included vitamins, iron, and zinc. Family history included benign hypertension and type II diabetes in the father; and type II diabetes in the sibling(s).
PENITUT01	pINCY	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, atherosclerotic coronary artery disease, angina pectoris, gout, and obesity. Family history included malignant pharyngeal neoplasm, chronic lymphocytic leukemia, and chronic liver disease.

Table 6 (cont.)

Library	Vector	Library Description
PROSNOT18	pINCY	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.
PROSTUS23	pINCY	This subtracted prostate tumor library was constructed using 10 million clones from a pooled prostate tumor library that was subjected to 2 rounds of subtractive hybridization with 10 million clones from a pooled prostate tissue library. The starting library for subtraction was constructed by pooling equal numbers of clones from 4 prostate tumor libraries using mRNA isolated from prostate tumor removed from Caucasian males at ages 58 (A), 61 (B), 66 (C), and 68 (D) during prostatectomy with lymph node excision. Pathology indicated adenocarcinoma in all donors. History included elevated PSA, induration and tobacco abuse in donor A; elevated PSA, induration, prostate hyperplasia, renal failure, osteoarthritis, renal artery stenosis, benign HTN, thrombocytopenia, hyperlipidemia, tobacco/alcohol abuse and hepatitis C (carrier) in donor B; elevated PSA, induration, and tobacco abuse in donor C; and elevated PSA, induration, hypercholesterolemia, and kidney calculus in donor D. The hybridization probe for subtraction was constructed by pooling equal numbers of cDNA clones from 3 prostate tissue libraries derived from prostate tissue, prostate epithelial cells, and fibroblasts from prostate stroma from 3 different donors. Subtractive hybridization conditions were based on the methodologies of Swaroop et al., NAR 19 (1991):1954 and Bonaldo, et al. Genome Research 6 (1996):791.
SKIRNOR01	PCDNA2.1	Random-primed library was constructed using RNA isolated from skin tissue removed from the breast of a 17-year-old Caucasian female during bilateral reduction mammoplasty. Patient history included breast hypertrophy. Family history included benign hypertension.
SINITUT03	pINCY	Library was constructed using RNA isolated from ileal tumor tissue obtained from a 49-year-old Caucasian female during destruction of peritoneal tissue, peritoneal adhesiolysis, ileum resection, and permanent colostomy. Pathology indicated grade 4 adenocarcinoma. Patient history included benign hypertension. Previous surgeries included total abdominal hysterectomy, bilateral salpingo-oophorectomy, regional lymph node excision, an incidental appendectomy, and dilation and curettage. Family history included benign hypertension, cerebrovascular disease, hyperlipidemia, atherosclerotic coronary artery disease, hyperlipidemia, type II diabetes, and stomach cancer.
SINTNOR01	PCDNA2.1	This random primed library was constructed using RNA isolated from small intestine tissue removed from a 31-year-old Caucasian female during Roux-en-Y gastric bypass. Patient history included clinical obesity.

Table 6 (cont.)

Library	Vector	Library Description
THYRN0T03	pINCY	Library was constructed using RNA isolated from thyroid tissue removed from the left thyroid of a 28-year-old Caucasian female during a complete thyroidectomy. Pathology indicated a small nodule of adenomatous hyperplasia present in the left thyroid. Pathology for the associated tumor tissue indicated dominant follicular adenoma, forming a well-encapsulated mass in the left thyroid.

Table 7

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

Table 7 (cont.)

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

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - a) a polypeptide comprising an amino acid sequence selected from the group consisting of
5 SEQ ID NO:1-20,
 - 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:1-20,
 - c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and
 - 10 d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20.
2. An isolated polypeptide of claim 1 selected from the group consisting of SEQ ID NO:1-20.
- 15 3. An isolated polynucleotide encoding a polypeptide of claim 1.
4. An isolated polynucleotide encoding a polypeptide of claim 2.
5. An isolated polynucleotide of claim 4 selected from the group consisting of SEQ ID
20 NO:21-40.
6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.
- 25 7. A cell transformed with a recombinant polynucleotide of claim 6.
8. A transgenic organism comprising a recombinant polynucleotide of claim 6.
9. A method for producing a polypeptide of claim 1, the method comprising:
 - 30 a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and
 - b) recovering the polypeptide so expressed.

10. An isolated antibody which specifically binds to a polypeptide of claim 1.
11. An isolated polynucleotide selected from the group consisting of:
- a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting
 - 5 of SEQ ID NO:21-40,
 - b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40,
 - c) a polynucleotide complementary to a polynucleotide of a),
 - d) a polynucleotide complementary to a polynucleotide of b), and
 - 10 e) an RNA equivalent of a)-d).
12. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 11.
13. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:
- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex
 - 20 is formed between said probe and said target polynucleotide or fragments thereof, and
 - b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.
14. A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.
15. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:
- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
 - 30 b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.
16. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable

excipient.

17. A composition of claim 16, wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:1-20.

5

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

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

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

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

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

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

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

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

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

25. A method of screening for a compound that specifically binds to the polypeptide of claim

1, said method comprising the steps of:

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.

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

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

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.

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

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

b) detecting altered expression of the target polynucleotide, and

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

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

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

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

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

5

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

- a) combining the biological sample with an antibody of claim 10, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex; and
- b) detecting the complex, wherein the presence of the complex correlates with the presence of the polypeptide in the biological sample.

10

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

- a) a chimeric antibody,
- b) a single chain antibody,
- c) a Fab fragment,
- d) a F(ab')₂ fragment, or
- e) a humanized antibody.

15

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

20

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

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

25

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

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

30

- a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, or an immunogenic fragment thereof, under conditions to elicit

an antibody response;

- b) isolating antibodies from said animal; and
- c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20.

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

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

10

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

- a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, 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 binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20.

20

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

25

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

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

30

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

43. A method for detecting a polypeptide having an amino acid sequence selected from the

group consisting of SEQ ID NO:1-20 in a sample, comprising the steps of:

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

b) detecting specific binding, wherein specific binding indicates the presence of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20 in the sample.

44. A method of purifying a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20 from a sample, the method comprising:

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

b) separating the antibody from the sample and obtaining the purified polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20.

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

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

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

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

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

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

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

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

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

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

55. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.
56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.
- 5 57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.
58. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:14.
59. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:15.
- 10 60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:16.
61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.
- 15 62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.
63. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:19.
64. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:20.
- 20 65. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:21.
66. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:22.
- 25 67. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:23.
68. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:24.
69. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:25.
- 30 70. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:26.
71. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:27.

72. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:28.
73. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:29.
- 5 74. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:30.
75. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:31.
76. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:32.
- 10 77. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:33.
78. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:34.
- 15 79. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:35.
80. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:36.
81. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:37.
- 20 82. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:38.
83. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:39.
- 25 84. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:40.

<110> INCYTE GENOMICS, INC.
YUE, Henry
KHAN, Farrah A.
GURURAJAN, Rajagopal
HAFALIA, April J. A.
WALIA, Narinder K.
PATTERSON, Chandra
RAMKUMAR, Jayalaxmi
GANDHI, Ameena R.
POLICKY, Jennifer L.
BAUGHN, Mariah R.
TRIBOULEY, Catherine M.
THORNTON, Michael
BANDMAN, Olga
NGUYEN, Danniel B.
LU, Yan
BURFORD, Neil
LAL, Preeti
DING, Li
YAO, Monique G.
ELLIOTT, Vicki S.
RECIPON, Shirley A.
KEARNEY, Liam
LU, Dyung Aina M.
GREENWALD, Sara R.
TANG, Y. Tom
XU, Yuming
WALSH, Roderick T.
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Gly Ala Gly Pro Gly	Arg Asp Asp Pro	Gly Arg Lys Ala Ala Ala			
	35	40			45
Ala Gly Gly Ser Gly	Ser Pro Asn Ala	Ala Leu Ser Arg Pro Arg			
	50	55			60
Pro Ala Pro Ala Pro	Gly Asp Ala Pro	Pro Arg Ala Ala Ala Ser			
	65	70			75
Ala Ala Ala Ala Ala	Ala Ala Ala Ala	Gly Thr Glu Gln Val Asp			
	80	85			90
Gly Pro Leu Arg Ala	Gly Pro Ala Asp	Thr Pro Pro Ser Gly Trp			
	95	100			105
Arg Met Gln Cys Leu	Ala Ala Ala Leu	Lys Asp Glu Thr Asn Met			
	110	115			120
Ser Gly Gly Gly Glu	Gln Ala Asp Ile	Leu Pro Ala Asn Tyr Val			
	125	130			135
Val Lys Asp Arg Trp	Lys Val Leu Lys	Lys Ile Gly Gly Gly Gly			
	140	145			150
Phe Gly Glu Ile Tyr	Glu Ala Met Asp	Leu Leu Thr Arg Glu Asn			
	155	160			165
Val Ala Leu Lys Val	Glu Ser Ala Gln	Gln Pro Lys Gln Val Leu			
	170	175			180

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

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Ser Ser Trp His Ser Pro Leu Leu Gln Ser Pro Cys Val Glu Glu
      605                      610                      615
Glu Gln Ser Arg Gly Met Gly Val Pro Ser Ser Pro Val Arg Ala
      620                      625                      630
Pro Pro Asp Ser Pro Thr Thr Pro Val Arg Ser Leu Arg Tyr Arg
      635                      640                      645
Arg Val Asn Ser Pro Glu Ser Glu Arg Leu Ser Thr Ala Asp Gly
      650                      655                      660
Arg Val Glu Leu Pro Glu Arg Arg Trp Val Trp Gly Gln Gly His
      665                      670                      675
Gly Trp Gly Pro Arg Pro Ser Pro Pro Ser Arg Gly Trp Ser Gly
      680                      685                      690
Gly Lys Val Arg Cys Val Ala Glu Val Gly Arg Pro Trp Glu Val
      695                      700                      705
Leu Arg Gly Leu Tyr Leu Gly Leu Gly Ser Asp Ser Val Gly Ala
      710                      715                      720
Arg Asp Arg Ala Trp Glu Asn Gln Trp Gly Ile Gln Arg Gly Pro
      725                      730                      735
Gly Ser Cys Gln Glu Thr
      740

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<210> 5

<211> 645

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477585CD1

<400> 5

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

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

	605	610	615
Ser Asp Cys Phe	Glu Val Asp Gln Leu	Leu Tyr Phe Glu Glu	Gln
	620	625	630
Leu Leu Ile Thr	Met Gly Lys Glu Pro	Thr Leu Gln Asn His	Leu
	635	640	645

<210> 6

<211> 623

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477587CD1

<400> 6

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

	290		295		300
Ala Pro Asn Pro	Ala Glu Arg Pro Ser	Leu Asp His Leu Leu Gln			
	305		310		315
Asp Asp Phe Phe	Thr Gln Gly Phe Thr	Pro Asp Arg Leu Pro Ala			
	320		325		330
His Ser Cys His	Ser Pro Pro Ile Phe	Ala Ile Pro Pro Pro Leu			
	335		340		345
Gly Arg Ile Phe	Arg Lys Val Gly Gln	Arg Leu Leu Thr Gln Cys			
	350		355		360
Arg Pro Pro Cys	Pro Phe Thr Pro Lys	Glu Ala Ser Gly Pro Gly			
	365		370		375
Glu Gly Gly Pro	Asp Pro Asp Ser Met	Glu Trp Asp Gly Glu Ser			
	380		385		390
Ser Leu Ser Ala	Lys Glu Val Pro Cys	Leu Glu Gly Pro Ile His			
	395		400		405
Leu Val Ala Gln	Gly Thr Leu Gln Ser	Asp Leu Ala Ala Thr Gln			
	410		415		420
Asp Pro Leu Gly	Glu Gln Gln Pro Ile	Leu Trp Ala Pro Lys Trp			
	425		430		435
Val Asp Tyr Ser	Ser Lys Tyr Gly Phe	Gly Tyr Gln Leu Leu Asp			
	440		445		450
Gly Gly Arg Thr	Gly Arg His Pro His	Gly Pro Ala Thr Pro Arg			
	455		460		465
Arg Tyr Leu Leu	Ser Thr Tyr Cys Ala	His Leu Gln Val Leu Pro			
	470		475		480
Ala Cys Gln Val	Cys Tyr Met Pro Asn	Cys Gly Arg Leu Glu Ala			
	485		490		495
Phe Ala Leu Arg	Asp Val Pro Gly Leu	Leu Gly Ala Lys Leu Ala			
	500		505		510
Val Leu Gln Leu	Phe Ala Gly Cys Leu	Arg Arg Arg Leu Arg Glu			
	515		520		525
Glu Gly Thr Leu	Pro Thr Pro Val Pro	Pro Ala Gly Pro Gly Leu			
	530		535		540
Cys Leu Leu Arg	Phe Leu Ala Ser Glu	His Ala Leu Leu Leu Leu			
	545		550		555
Phe Ser Asn Gly	Met Val Gln Val Ser	Phe Ser Gly Val Pro Ala			
	560		565		570
Gln Leu Val Leu	Ser Gly Glu Gly Glu	Gly Leu Gln Leu Thr Leu			
	575		580		585
Trp Glu Gln Gly	Ser Pro Gly Thr Ser	Tyr Ser Leu Asp Val Pro			
	590		595		600
Arg Ser His Gly	Cys Ala Pro Thr Thr	Gly Gln His Leu His His			
	605		610		615
Ala Leu Arg Met	Leu Gln Ser Ile				
	620				

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<211> 797

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7594537CD1

<400> 7

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

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

<210> 8

<211> 749

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 70467491CD1

<400> 8

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

	365		370		375
Leu Asp Ala Ser Asp Ser Ser Ser Ser Ser Asn Leu Ser Leu Ala					
	380		385		390
Lys Val Arg Pro Ser Ser Asp Leu Asn Asn Ser Thr Gly Gln Ser					
	395		400		405
Pro His His Lys Val Gln Arg Ser Val Ser Ser Ser Gln Lys Gln					
	410		415		420
Arg Arg Tyr Ser Asp His Ala Gly Pro Ala Ile Pro Ser Val Val					
	425		430		435
Ala Tyr Pro Lys Arg Ser Gln Thr Ser Thr Ala Asp Ser Asp Leu					
	440		445		450
Lys Glu Asp Gly Ile Ser Ser Arg Lys Ser Ser Gly Ser Ala Val					
	455		460		465
Gly Gly Lys Gly Ile Ala Pro Ala Ser Pro Met Leu Gly Asn Ala					
	470		475		480
Ser Asn Pro Asn Lys Ala Asp Ile Pro Glu Arg Lys Lys Ser Ser					
	485		490		495
Thr Val Pro Ser Ser Asn Thr Ala Ser Gly Gly Met Thr Arg Arg					
	500		505		510
Asn Thr Tyr Val Cys Ser Glu Arg Thr Thr Ala Asp Arg His Ser					
	515		520		525
Val Ile Gln Asn Gly Lys Glu Asn Ser Thr Ile Pro Asp Gln Arg					
	530		535		540
Thr Pro Val Ala Ser Thr His Ser Ile Ser Ser Ala Ala Thr Pro					
	545		550		555
Asp Arg Ile Arg Phe Pro Arg Gly Thr Ala Ser Arg Ser Thr Phe					
	560		565		570
His Gly Gln Pro Arg Glu Arg Arg Thr Ala Thr Tyr Asn Gly Pro					
	575		580		585
Pro Ala Ser Pro Ser Leu Ser His Glu Ala Thr Pro Leu Ser Gln					
	590		595		600
Thr Arg Ser Arg Gly Ser Thr Asn Leu Phe Ser Lys Leu Thr Ser					
	605		610		615
Lys Leu Thr Arg Arg Leu Pro Thr Glu Tyr Glu Arg Asn Gly Arg					
	620		625		630
Tyr Glu Gly Ser Ser Arg Asn Val Ser Ala Glu Gln Lys Asp Glu					
	635		640		645
Asn Lys Glu Ala Lys Pro Arg Ser Leu Arg Phe Thr Trp Ser Met					
	650		655		660
Lys Thr Thr Ser Ser Met Asp Pro Gly Asp Met Met Arg Glu Ile					
	665		670		675
Arg Lys Val Leu Asp Ala Asn Asn Cys Asp Tyr Glu Gln Arg Glu					
	680		685		690
Arg Phe Leu Leu Phe Cys Val His Gly Asp Gly His Ala Glu Asn					
	695		700		705
Leu Val Gln Trp Glu Met Glu Val Cys Lys Leu Pro Arg Leu Ser					
	710		715		720
Leu Asn Gly Val Arg Phe Lys Arg Ile Ser Gly Thr Ser Ile Ala					
	725		730		735
Phe Lys Asn Ile Ala Ser Lys Ile Ala Asn Glu Leu Lys Leu					
	740		745		

<210> 9

<211> 386

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7478559CD1

<400> 9

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

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380

385

<210> 10

<211> 342

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1698381CD1

<400> 10

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

Val Leu Gln Leu Lys Phe Asp His Leu Pro Asn Ile
 335 340

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<211> 1164

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7474637CD1

<400> 11

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

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

	740		745		750
Ala Thr Pro Phe	Ile Asp Pro Asp Leu	Asp Ser Val Asp Gly Tyr			
	755		760		765
Ser Glu Lys Cys	Val Met Asn Asn Tyr	Phe Gly Ile Gly Leu Asp			
	770		775		780
Ala Lys Ile Ser	Leu Glu Phe Asn Asn	Lys Arg Glu Glu His Pro			
	785		790		795
Glu Lys Cys Arg	Ser Arg Thr Lys Asn	Leu Met Trp Tyr Gly Val			
	800		805		810
Leu Gly Thr Arg	Glu Leu Leu Gln Arg	Ser Tyr Lys Asn Leu Glu			
	815		820		825
Gln Arg Val Gln	Leu Glu Cys Asp Gly	Gln Tyr Ile Pro Leu Pro			
	830		835		840
Ser Leu Gln Gly	Ile Ala Val Leu Asn	Ile Pro Ser Tyr Ala Gly			
	845		850		855
Gly Thr Asn Phe	Trp Gly Gly Thr Lys	Glu Asp Asp Ile Phe Ala			
	860		865		870
Ala Pro Ser Phe	Asp Asp Lys Ile Leu	Glu Val Val Ala Ile Phe			
	875		880		885
Asp Ser Met Gln	Met Ala Val Ser Arg	Val Ile Lys Leu Gln His			
	890		895		900
His Arg Ile Ala	Gln Cys Arg Thr Val	Lys Ile Thr Ile Phe Gly			
	905		910		915
Asp Glu Gly Val	Pro Val Gln Val Asp	Gly Glu Ala Trp Val Gln			
	920		925		930
Pro Pro Gly Ile	Ile Lys Ile Val His	Lys Asn Arg Ala Gln Met			
	935		940		945
Leu Thr Arg Asp	Arg Ala Phe Glu Ser	Thr Leu Lys Ser Trp Glu			
	950		955		960
Asp Lys Gln Lys	Cys Asp Ser Gly Lys	Pro Val Leu Arg Thr His			
	965		970		975
Leu Tyr Ile His	His Ala Ile Asp Leu	Ala Thr Glu Glu Val Ser			
	980		985		990
Gln Met Gln Leu	Cys Ser Gln Ala Ala	Glu Glu Leu Ile Thr Arg			
	995		1000		1005
Ile Cys Asp Ala	Ala Thr Ile His Cys	Leu Leu Glu Gln Glu Leu			
	1010		1015		1020
Ala His Ala Val	Asn Ala Cys Ser His	Ala Leu Asn Lys Ala Asn			
	1025		1030		1035
Pro Arg Cys Pro	Glu Ser Leu Thr Arg	Asp Thr Ala Thr Glu Ile			
	1040		1045		1050
Ala Ile Asn Val	Lys Ala Leu Tyr Asn	Glu Thr Glu Ser Leu Leu			
	1055		1060		1065
Val Gly Arg Val	Pro Leu Gln Leu Glu	Ser Pro His Glu Glu Arg			
	1070		1075		1080
Val Ser Asn Ala	Leu His Ser Val Glu	Val Glu Leu Gln Lys Leu			
	1085		1090		1095
Thr Glu Ile Pro	Trp Leu Tyr Tyr Ile	Leu His Pro Asn Glu Asp			
	1100		1105		1110
Glu Glu Pro Pro	Met Asp Cys Thr Lys	Arg Asn Asn Arg Ser Thr			
	1115		1120		1125
Val Phe Arg Ile	Val Pro Lys Phe Lys	Lys Glu Lys Val Gln Lys			
	1130		1135		1140
Gln Lys Thr Ser	Ser Gln Pro Gly Ser	Gly Asp Thr Glu Ser Gly			
	1145		1150		1155
Ser Cys Glu Ala	Asn Ser Pro Gly Asn				

1160

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 <211> 268
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> Incyte ID No: 7170260CD1

<400> 12

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

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<220>
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<223> Incyte ID No: 1797506CD1

<400> 13

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

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				395					400				405	
Leu	Leu	Ile	Gly	His	His	Glu	Leu	Pro	Pro	Val	Leu	His	Thr	Thr
				410					415					420
Met	Leu	Arg	Val	His	Pro	Thr	Leu	Gly	Ser	Gly	Thr	Ala	Glu	Thr
				425					430					435
Arg	Pro	Pro	Glu	Asn	Thr	Gln	Ala	Pro	Ala	Phe	Phe	Leu	Glu	Leu
				440					445					450
Leu	Ser	Leu	Ser	Arg	Glu	Lys	Leu	Trp	Asp	Ser	Glu	Leu	His	Pro
				455					460					465
Glu	Glu	Lys	Thr	Pro	Asp	Ser	Tyr	Leu	Gly	Leu	Gly	Pro	Gln	Asp
				470					475					480
Leu	Leu	Ala	Ala	Ser	Leu	Thr	Ala	Val	Leu	Leu	Gly	Gly	Trp	Ile
				485					490					495
Leu	Phe	Val	Met	Arg	Gln	Gln	Gln	Glu	Thr	Pro	Leu	Ala	Pro	Ala
				500					505					510
Asp	Phe	Ala	His	Ile	Ser	Gln	Asp	Ala	Gln	Ser	Leu	His	Ser	Gly
				515					520					525
Ala	Ser	Arg	Arg	Ser	Gln	Lys	Arg	Leu	Gln	Ser	Pro	Ser	Pro	Glu
				530					535					540
Ser	Pro	Pro	Ser	Ser	Pro	Pro	Ala	Glu	Gln	Leu	Thr	Val	Val	Gly
				545					550					555
Lys	Ile	Ser	Phe	Asn	Pro	Lys	Asp	Val	Leu	Gly	Arg	Gly	Ala	Gly
				560					565					570
Gly	Thr	Phe	Val	Phe	Arg	Gly	Gln	Phe	Glu	Gly	Arg	Ala	Val	Ala
				575					580					585
Val	Lys	Arg	Leu	Leu	Arg	Glu	Cys	Phe	Gly	Leu	Val	Arg	Arg	Glu
				590					595					600
Val	Gln	Leu	Leu	Gln	Glu	Ser	Asp	Arg	His	Pro	Asn	Val	Leu	Arg
				605					610					615
Tyr	Phe	Cys	Thr	Glu	Arg	Gly	Pro	Gln	Phe	His	Tyr	Ile	Ala	Leu
				620					625					630
Glu	Leu	Cys	Arg	Ala	Ser	Leu	Gln	Glu	Tyr	Val	Glu	Asn	Pro	Asp
				635					640					645
Leu	Asp	Arg	Gly	Gly	Leu	Glu	Pro	Glu	Val	Val	Leu	Gln	Gln	Leu
				650					655					660
Met	Ser	Gly	Leu	Ala	His	Leu	His	Ser	Leu	His	Ile	Val	His	Arg
				665					670					675
Asp	Leu	Lys	Pro	Gly	Asn	Ile	Leu	Ile	Thr	Gly	Pro	Asp	Ser	Gln
				680					685					690
Gly	Leu	Gly	Arg	Val	Val	Leu	Ser	Asp	Phe	Gly	Leu	Cys	Lys	Lys
				695					700					705
Leu	Pro	Ala	Gly	Arg	Cys	Ser	Phe	Ser	Leu	His	Ser	Gly	Ile	Pro
				710					715					720
Gly	Thr	Glu	Gly	Trp	Met	Ala	Pro	Glu	Leu	Leu	Gln	Leu	Leu	Pro
				725					730					735
Pro	Asp	Ser	Pro	Thr	Ser	Ala	Val	Asp	Ile	Phe	Ser	Ala	Gly	Cys
				740					745					750
Val	Phe	Tyr	Tyr	Val	Leu	Ser	Gly	Gly	Ser	His	Pro	Phe	Gly	Asp
				755					760					765
Ser	Leu	Tyr	Arg	Gln	Ala	Asn	Ile	Leu	Thr	Gly	Ala	Pro	Cys	Leu
				770					775					780
Ala	His	Leu	Glu	Glu	Glu	Val	His	Asp	Lys	Val	Val	Ala	Arg	Asp
				785					790					795
Leu	Val	Gly	Ala	Met	Leu	Ser	Pro	Leu	Pro	Gln	Pro	Arg	Pro	Ser
				800					805					810
Ala	Pro	Gln	Val	Leu	Ala	His	Pro	Phe	Phe	Trp	Ser	Arg	Ala	Lys

	815		820		825
Gln Leu Gln Phe	Phe Gln Asp Val Ser Asp Trp Leu Glu Lys	Glu			
	830		835		840
Ser Glu Gln Glu	Pro Leu Val Arg Ala Leu Glu Ala Gly Gly	Cys			
	845		850		855
Ala Val Val Arg	Asp Asn Trp His Glu His Ile Ser Met Pro	Leu			
	860		865		870
Gln Thr Asp Leu	Arg Lys Phe Arg Ser Tyr Lys Gly Thr Ser	Val			
	875		880		885
Arg Asp Leu Leu	Arg Ala Val Arg Asn Lys Lys His His Tyr	Arg			
	890		895		900
Glu Leu Pro Val	Glu Val Arg Gln Ala Leu Gly Gln Val Pro	Asp			
	905		910		915
Gly Phe Val Gln	Tyr Phe Thr Asn Arg Phe Pro Arg Leu Leu	Leu			
	920		925		930
His Thr His Arg	Ala Met Arg Ser Cys Ala Ser Glu Ser Leu	Phe			
	935		940		945
Leu Pro Tyr Tyr	Pro Pro Asp Ser Glu Ala Arg Arg Pro Cys	Pro			
	950		955		960
Gly Ala Thr Gly	Arg				
	965				

<210> 14

<211> 329

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 1851973CD1

<400> 14

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

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Thr Leu Asn Arg Asp Ile Asn Met Met Asp Ile Leu Thr Thr Pro
      185                      190                      195
Ser Met Ala Lys Pro Arg Gln Asp Tyr Ser Arg Thr Pro Gly Gln
      200                      205                      210
Val Leu Ser Leu Ile Ser Ser Leu Gly Phe Asn Thr Pro Ile Ala
      215                      220                      225
Glu Lys Asn Gln Asp Pro Ala Asn Ile Leu Ser Ala Cys Leu Ser
      230                      235                      240
Glu Thr Ser Gln Leu Ser Gln Gly Leu Val Cys Pro Met Ser Val
      245                      250                      255
Asp Gln Lys Asp Thr Thr Pro Tyr Ser Ser Lys Leu Leu Lys Ser
      260                      265                      270
Cys Leu Glu Thr Val Ala Ser Asn Pro Gly Met Pro Val Lys Cys
      275                      280                      285
Leu Thr Ser Asn Leu Leu Gln Ser Arg Lys Arg Leu Ala Thr Ser
      290                      295                      300
Ser Ala Ser Ser Gln Ser His Thr Phe Ile Ser Ser Val Glu Ser
      305                      310                      315
Glu Cys His Ser Ser Pro Lys Trp Glu Lys Asp Cys Gln Val
      320                      325

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<210> 15

<211> 945

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7474604CD1

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

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

	605	610	615
Val His Asp Glu	Ala Glu Glu Ser Glu	Asp Asp Phe Glu Glu	Met
	620	625	630
Asn Leu Ser Leu	Leu Ser Ala Arg Ser	Phe Pro Arg Lys Ala	Ser
	635	640	645
Gln Thr Ser Ile	Phe Leu Gln Glu Trp	Asp Ile Pro Phe Glu	Gln
	650	655	660
Leu Glu Ile Gly	Glu Leu Ile Gly Lys	Gly Arg Phe Gly Gln	Val
	665	670	675
Tyr His Gly Arg	Trp His Gly Glu Val	Ala Ile Arg Leu Ile	Asp
	680	685	690
Ile Glu Arg Asp	Asn Glu Asp Gln Leu	Lys Ala Phe Lys Arg	Glu
	695	700	705
Val Met Ala Tyr	Arg Gln Thr Arg His	Glu Asn Val Val Leu	Phe
	710	715	720
Met Gly Ala Cys	Met Ser Pro Pro His	Leu Ala Ile Ile Thr	Ser
	725	730	735
Leu Cys Lys Gly	Arg Thr Leu Tyr Ser	Val Val Arg Asp Ala	Lys
	740	745	750
Ile Val Leu Asp	Val Asn Lys Thr Arg	Gln Ile Ala Gln Glu	Ile
	755	760	765
Val Lys Gly Met	Gly Tyr Leu His Ala	Lys Gly Ile Leu His	Lys
	770	775	780
Asp Leu Lys Ser	Lys Asn Val Phe Tyr	Asp Asn Gly Lys Val	Val
	785	790	795
Ile Thr Asp Phe	Gly Leu Phe Ser Ile	Ser Gly Val Leu Gln	Ala
	800	805	810
Gly Arg Arg Glu	Asp Lys Leu Arg Ile	Gln Asn Gly Trp Leu	Cys
	815	820	825
His Leu Ala Pro	Glu Ile Ile Arg Gln	Leu Ser Pro Asp Thr	Glu
	830	835	840
Glu Asp Lys Leu	Pro Phe Ser Lys His	Ser Asp Val Phe Ala	Leu
	845	850	855
Gly Thr Ile Trp	Tyr Glu Leu His Ala	Arg Glu Trp Pro Phe	Lys
	860	865	870
Thr Gln Pro Ala	Glu Ala Ile Ile Trp	Gln Met Gly Thr Gly	Met
	875	880	885
Lys Pro Asn Leu	Ser Gln Ile Gly Met	Gly Lys Glu Ile Ser	Asp
	890	895	900
Ile Leu Leu Phe	Cys Trp Ala Phe Glu	Gln Glu Glu Arg Pro	Thr
	905	910	915
Phe Thr Lys Leu	Met Asp Met Leu Glu	Lys Leu Pro Lys Arg	Asn
	920	925	930
Arg Arg Leu Ser	His Pro Gly His Phe	Trp Lys Ser Ala Glu	Leu
	935	940	945

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<211> 1009

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7474721CD1

<400> 16

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

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	410		415		420
Arg Tyr Thr Val	Arg Val Ala Val Leu	Asn Gly Val Ser Gly	Pro		
	425		430		435
Ala Ala Ala Leu	Val Pro Val Gly Ala	Val Ser Ile Asn Pro	Gly		
	440		445		450
Thr Val Gly Pro	Val Pro Val Ala Gly	Val Ile Arg Asp Arg	Val		
	455		460		465
Glu Pro Gln Ser	Val Ser Leu Ser Trp	Arg Glu Pro Ile Pro	Ala		
	470		475		480
Gly Ala Pro Gly	Ala Asn Asp Thr Glu	Tyr Glu Ile Arg Tyr	Tyr		
	485		490		495
Glu Lys Val Gln	Ser Glu Gln Thr Tyr	Ser Met Val Lys Thr	Gly		
	500		505		510
Ala Pro Thr Val	Thr Val Thr Asn Leu	Lys Pro Ala Thr Arg	Tyr		
	515		520		525
Val Phe Gln Ile	Arg Ala Ala Ser Pro	Gly Pro Ser Trp Glu	Ala		
	530		535		540
Gln Ser Phe Asn	Pro Ser Ile Glu Val	Gln Thr Leu Gly Glu	Ala		
	545		550		555
Ala Ser Gly Ser	Arg Asp Gln Ser Pro	Ala Ile Val Val Thr	Val		
	560		565		570
Val Thr Ile Ser	Ala Leu Leu Val Leu	Gly Ser Val Met Ser	Val		
	575		580		585
Leu Ala Ile Trp	Arg Arg Pro Cys Ser	Tyr Gly Lys Gly Gly	Gly		
	590		595		600
Asp Ala His Asp	Glu Glu Glu Leu Tyr	Phe His Phe Lys Val	Pro		
	605		610		615
Thr Arg Arg Thr	Phe Leu Asp Pro Gln	Ser Cys Gly Asp Leu	Leu		
	620		625		630
Gln Ala Val His	Leu Phe Ala Lys Glu	Leu Asp Ala Lys Ser	Val		
	635		640		645
Thr Leu Glu Arg	Ser Leu Gly Gly Gly	Arg Phe Gly Glu Leu	Cys		
	650		655		660
Cys Gly Cys Leu	Gln Leu Pro Gly Arg	Gln Glu Leu Leu Val	Ala		
	665		670		675
Val His Met Leu	Arg Asp Ser Ala Ser	Asp Ser Gln Arg Leu	Gly		
	680		685		690
Phe Leu Ala Glu	Ala Leu Thr Leu Gly	Gln Phe Asp His Ser	His		
	695		700		705
Ile Val Arg Leu	Glu Gly Val Val Thr	Arg Gly Ser Thr Leu	Met		
	710		715		720
Ile Val Thr Glu	Tyr Met Ser His Gly	Ala Leu Asp Gly Phe	Leu		
	725		730		735
Arg Arg His Glu	Gly Gln Leu Val Ala	Gly Gln Leu Met Gly	Leu		
	740		745		750
Leu Pro Gly Leu	Ala Ser Ala Met Lys	Tyr Leu Ser Glu Met	Gly		
	755		760		765
Tyr Val His Arg	Gly Leu Ala Ala Arg	His Val Leu Val Ser	Ser		
	770		775		780
Asp Leu Val Cys	Lys Ile Ser Gly Phe	Gly Arg Gly Pro Arg	Asp		
	785		790		795
Arg Ser Glu Ala	Val Tyr Thr Thr Met	Ser Gly Arg Ser Pro	Ala		
	800		805		810
Leu Trp Ala Ala	Pro Glu Thr Leu Gln	Phe Gly His Phe Ser	Ser		
	815		820		825
Ala Ser Asp Val	Trp Ser Phe Gly Ile	Ile Met Trp Glu Val	Met		

	830		835		840
Ala Phe Gly Glu Arg Pro Tyr Trp Asp Met Ser Gly Gln Asp Val					
	845		850		855
Ile Lys Ala Val Glu Asp Gly Phe Arg Leu Pro Pro Pro Arg Asn					
	860		865		870
Cys Pro Asn Leu Leu His Arg Leu Met Leu Asp Cys Trp Gln Lys					
	875		880		885
Asp Pro Gly Glu Arg Pro Arg Phe Ser Gln Ile His Ser Ile Leu					
	890		895		900
Ser Lys Met Val Gln Asp Pro Glu Pro Pro Lys Cys Ala Leu Thr					
	905		910		915
Thr Cys Pro Arg Pro Pro Thr Pro Leu Ala Asp Arg Ala Phe Ser					
	920		925		930
Thr Phe Pro Ser Phe Gly Ser Val Gly Ala Trp Leu Glu Ala Leu					
	935		940		945
Asp Leu Cys Arg Tyr Lys Asp Ser Phe Ala Ala Ala Gly Tyr Gly					
	950		955		960
Ser Leu Glu Ala Val Ala Glu Met Thr Ala Gln Arg Asp Leu Val					
	965		970		975
Ser Leu Gly Ile Ser Leu Ala Glu His Arg Glu Ala Leu Leu Ser					
	980		985		990
Gly Ile Ser Ala Leu Gln Ala Arg Val Leu Gln Leu Gln Gly Gln					
	995		1000		1005
Gly Val Gln Val					

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<211> 917

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7478815CD1

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

Gly	Leu	Thr	Phe	Ser	Phe	Pro	Cys	Arg	Gln	Thr	Lys	Leu	Glu	Glu
				155					160					165
Gly	Val	Leu	Leu	Ser	Trp	Thr	Lys	Lys	Phe	Lys	Ala	Arg	Gly	Val
				170					175					180
Gln	Asp	Thr	Asp	Val	Val	Ser	Arg	Leu	Thr	Lys	Ala	Met	Arg	Arg
				185					190					195
His	Lys	Asp	Met	Asp	Val	Asp	Ile	Leu	Ala	Leu	Val	Asn	Asp	Thr
				200					205					210
Val	Gly	Thr	Met	Met	Thr	Cys	Ala	Tyr	Asp	Asp	Pro	Tyr	Cys	Glu
				215					220					225
Val	Gly	Val	Ile	Ile	Gly	Thr	Gly	Thr	Asn	Ala	Cys	Tyr	Met	Glu
				230					235					240
Asp	Met	Ser	Asn	Ile	Asp	Leu	Val	Glu	Gly	Asp	Glu	Gly	Arg	Met
				245					250					255
Cys	Ile	Asn	Thr	Glu	Trp	Gly	Ala	Phe	Gly	Asp	Asp	Gly	Ala	Leu
				260					265					270
Glu	Asp	Ile	Arg	Thr	Glu	Phe	Asp	Arg	Glu	Leu	Asp	Leu	Gly	Ser
				275					280					285
Leu	Asn	Pro	Gly	Lys	Gln	Leu	Phe	Glu	Lys	Met	Ile	Ser	Gly	Leu
				290					295					300
Tyr	Leu	Gly	Glu	Leu	Val	Arg	Leu	Ile	Leu	Leu	Lys	Met	Ala	Lys
				305					310					315
Ala	Gly	Leu	Leu	Phe	Gly	Gly	Glu	Lys	Ser	Ser	Ala	Leu	His	Thr
				320					325					330
Lys	Gly	Lys	Ile	Glu	Thr	Arg	His	Val	Ala	Ala	Met	Glu	Lys	Tyr
				335					340					345
Lys	Glu	Gly	Leu	Ala	Asn	Thr	Arg	Glu	Ile	Leu	Val	Asp	Leu	Gly
				350					355					360
Leu	Glu	Pro	Ser	Glu	Ala	Asp	Cys	Ile	Ala	Val	Gln	His	Val	Cys
				365					370					375
Thr	Ile	Val	Ser	Phe	Arg	Ser	Ala	Asn	Leu	Cys	Ala	Ala	Ala	Leu
				380					385					390
Ala	Ala	Ile	Leu	Thr	Arg	Leu	Arg	Glu	Asn	Lys	Lys	Val	Glu	Arg
				395					400					405
Leu	Arg	Thr	Thr	Val	Gly	Met	Asp	Gly	Thr	Leu	Tyr	Lys	Ile	His
				410					415					420
Pro	Gln	Tyr	Pro	Lys	Arg	Leu	His	Lys	Val	Val	Arg	Lys	Leu	Val
				425					430					435
Pro	Ser	Cys	Asp	Val	Arg	Phe	Leu	Leu	Ser	Glu	Ser	Gly	Ser	Thr
				440					445					450
Lys	Gly	Ala	Ala	Met	Val	Thr	Ala	Val	Ala	Ser	Arg	Val	Gln	Ala
				455					460					465
Gln	Arg	Lys	Gln	Ile	Asp	Arg	Val	Leu	Ala	Leu	Phe	Gln	Leu	Thr
				470					475					480
Arg	Glu	Gln	Leu	Val	Asp	Val	Gln	Ala	Lys	Met	Arg	Ala	Glu	Leu
				485					490					495
Glu	Tyr	Gly	Leu	Lys	Lys	Lys	Ser	His	Gly	Leu	Ala	Thr		

Glu	Glu	Leu	Phe	Asp	His	Ile	Val	Gln	Cys	Ile	Ala	Asp	Phe	Leu	575	580	585
Asp	Tyr	Met	Gly	Leu	Lys	Gly	Ala	Ser	Leu	Pro	Leu	Gly	Phe	Thr	590	595	600
Phe	Ser	Phe	Pro	Cys	Arg	Gln	Met	Ser	Ile	Asp	Lys	Gly	Thr	Leu	605	610	615
Ile	Gly	Trp	Thr	Lys	Gly	Phe	Lys	Ala	Thr	Asp	Cys	Glu	Gly	Glu	620	625	630
Asp	Val	Val	Asp	Met	Leu	Arg	Glu	Ala	Ile	Lys	Arg	Arg	Asn	Glu	635	640	645
Phe	Asp	Leu	Asp	Ile	Val	Ala	Val	Val	Asn	Asp	Thr	Val	Gly	Thr	650	655	660
Met	Met	Thr	Cys	Gly	Tyr	Glu	Asp	Pro	Asn	Cys	Glu	Ile	Gly	Leu	665	670	675
Ile	Ala	Gly	Thr	Gly	Ser	Asn	Met	Cys	Tyr	Met	Glu	Asp	Met	Arg	680	685	690
Asn	Ile	Glu	Met	Val	Glu	Gly	Gly	Glu	Gly	Lys	Met	Cys	Ile	Asn	695	700	705
Thr	Glu	Trp	Gly	Gly	Phe	Gly	Asp	Asn	Gly	Cys	Ile	Asp	Asp	Ile	710	715	720
Arg	Thr	Arg	Tyr	Asp	Thr	Glu	Val	Asp	Glu	Gly	Ser	Leu	Asn	Pro	725	730	735
Gly	Lys	Gln	Arg	Tyr	Glu	Lys	Met	Thr	Ser	Gly	Met	Tyr	Leu	Gly	740	745	750
Glu	Ile	Val	Arg	Gln	Ile	Leu	Ile	Asp	Leu	Thr	Lys	Gln	Gly	Leu	755	760	765
Leu	Phe	Arg	Gly	Gln	Ile	Ser	Glu	Arg	Leu	Arg	Thr	Arg	Gly	Ile	770	775	780
Phe	Glu	Thr	Lys	Phe	Leu	Ser	Gln	Ile	Glu	Ser	Asp	Arg	Leu	Ala	785	790	795
Leu	Leu	Gln	Val	Arg	Arg	Ile	Leu	Gln	Gln	Leu	Gly	Leu	Asp	Ser	800	805	810
Thr	Cys	Glu	Asp	Ser	Ile	Val	Val	Lys	Glu	Val	Cys	Gly	Ala	Val	815	820	825
Ser	Arg	Arg	Ala	Ala	Gln	Leu	Cys	Gly	Ala	Gly	Leu	Ala	Ala	Ile	830	835	840
Val	Glu	Lys	Arg	Arg	Glu	Asp	Gln	Gly	Leu	Glu	His	Leu	Arg	Ile	845	850	855
Thr	Val	Gly	Val	Asp	Gly	Thr	Leu	Tyr	Lys	Leu	His	Pro	His	Phe	860	865	870
Ser	Arg	Ile	Leu	Gln	Glu	Thr	Val	Lys	Glu	Leu	Ala	Pro	Arg	Cys	875	880	885
Asp	Val	Thr	Phe	Met	Leu	Ser	Glu	Asp	Gly	Ser	Gly	Lys	Gly	Ala	890	895	900
Ala	Leu	Ile	Thr	Ala	Val	Ala	Lys	Arg	Leu	Gln	Gln	Ala	Gln	Lys	905	910	915

Glu Asn

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<211> 2380

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477141CD1

<400> 18

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

	395		400		405
Ala Val Thr Gly	Arg Met Val Thr Leu Thr Trp Asn Pro Pro Arg				
	410		415		420
Ser Leu Asp Met	Ala Ile Asp Pro Asp Ser Leu Thr Tyr Thr Val				
	425		430		435
Gln His Gln Val	Leu Gly Ser Asp Gln Trp Thr Ala Leu Val Thr				
	440		445		450
Gly Leu Arg Glu	Pro Gly Trp Ala Ala Thr Gly Leu Arg Lys Gly				
	455		460		465
Val Gln His Ile	Phe Arg Val Leu Ser Thr Thr Val Lys Ser Ser				
	470		475		480
Ser Lys Pro Ser	Pro Pro Ser Glu Pro Val Gln Leu Leu Glu His				
	485		490		495
Gly Pro Thr Leu	Glu Glu Ala Pro Ala Met Leu Asp Lys Pro Asp				
	500		505		510
Ile Val Tyr Val	Val Glu Gly Gln Pro Ala Ser Val Thr Val Thr				
	515		520		525
Phe Asn His Val	Glu Ala Gln Val Val Trp Arg Ser Cys Arg Gly				
	530		535		540
Ala Leu Leu Glu	Ala Arg Ala Gly Val Tyr Glu Leu Ser Gln Pro				
	545		550		555
Asp Asp Asp Gln	Tyr Cys Leu Arg Ile Cys Arg Val Ser Arg Arg				
	560		565		570
Asp Met Gly Ala	Leu Thr Cys Thr Ala Arg Asn Arg His Gly Thr				
	575		580		585
Gln Thr Cys Ser	Val Thr Leu Glu Leu Ala Glu Ala Pro Arg Phe				
	590		595		600
Glu Ser Ile Met	Glu Asp Val Glu Val Gly Ala Gly Glu Thr Ala				
	605		610		615
Arg Phe Ala Val	Val Val Glu Gly Lys Pro Leu Pro Asp Ile Met				
	620		625		630
Trp Tyr Lys Asp	Glu Val Leu Leu Thr Glu Ser Ser His Val Ser				
	635		640		645
Phe Val Tyr Glu	Glu Asn Glu Cys Ser Leu Val Val Leu Ser Thr				
	650		655		660
Gly Ala Gln Asp	Gly Gly Val Tyr Thr Cys Thr Ala Gln Asn Leu				
	665		670		675
Ala Gly Glu Val	Ser Cys Lys Ala Glu Leu Ala Val His Ser Ala				
	680		685		690
Gln Thr Ala Met	Glu Val Glu Gly Val Gly Glu Asp Glu Asp His				
	695		700		705
Arg Gly Arg Arg	Leu Ser Asp Phe Tyr Asp Ile His Gln Glu Ile				
	710		715		720
Gly Arg Gly Ala	Phe Ser Tyr Leu Arg Arg Ile Val Glu Arg Ser				
	725		730		735
Ser Gly Leu Glu	Phe Ala Ala Lys Phe Ile Pro Ser Gln Ala Lys				
	740		745		750
Pro Lys Ala Ser	Ala Arg Arg Glu Ala Arg Leu Leu Ala Arg Leu				
	755		760		765
Gln His Asp Cys	Val Leu Tyr Phe His Glu Ala Phe Glu Arg Arg				
	770		775		780
Arg Gly Leu Val	Ile Val Thr Glu Leu Cys Thr Glu Glu Leu Leu				
	785		790		795
Glu Arg Ile Ala	Arg Lys Pro Thr Val Cys Glu Ser Glu Ile Arg				
	800		805		810
Ala Tyr Met Arg	Gln Val Leu Glu Gly Ile His Tyr Leu His Gln				

	815		820		825
Ser His Val Leu	His Leu Asp Val Lys	Pro Glu Asn Leu Leu	Val		
	830		835		840
Trp Asp Gly Ala	Ala Gly Glu Gln Gln	Val Arg Ile Cys Asp	Phe		
	845		850		855
Gly Asn Ala Gln	Glu Leu Thr Pro Gly	Glu Pro Gln Tyr Cys	Gln		
	860		865		870
Tyr Gly Thr Pro	Glu Phe Val Ala Pro	Glu Ile Val Asn Gln	Ser		
	875		880		885
Pro Val Ser Gly	Val Thr Asp Ile Trp	Pro Val Gly Val Val	Ala		
	890		895		900
Phe Leu Cys Leu	Thr Gly Ile Ser Pro	Phe Val Gly Glu Asn	Asp		
	905		910		915
Arg Thr Thr Leu	Met Asn Ile Arg Asn	Tyr Asn Val Ala Phe	Glu		
	920		925		930
Glu Thr Thr Phe	Leu Ser Leu Ser Arg	Glu Ala Arg Gly Phe	Leu		
	935		940		945
Ile Lys Val Leu	Val Gln Asp Arg Leu	Arg Pro Thr Ala Glu	Glu		
	950		955		960
Thr Leu Glu His	Pro Trp Phe Lys Thr	Gln Ala Lys Gly Ala	Glu		
	965		970		975
Val Ser Thr Asp	His Leu Lys Leu Phe	Leu Ser Arg Arg Arg	Trp		
	980		985		990
Gln Arg Ser Gln	Ile Ser Tyr Lys Cys	His Leu Val Leu Arg	Pro		
	995		1000		1005
Ile Pro Glu Leu	Leu Arg Ala Pro Pro	Glu Arg Val Trp Val	Thr		
	1010		1015		1020
Met Pro Arg Arg	Pro Pro Ser Gly Gly	Leu Ser Ser Ser Ser			
	1025		1030		1035
Asp Ser Glu Glu	Glu Glu Leu Glu Glu	Leu Pro Ser Val Pro	Arg		
	1040		1045		1050
Pro Leu Gln Pro	Glu Phe Ser Gly Ser	Arg Val Ser Leu Thr	Asp		
	1055		1060		1065
Ile Pro Thr Glu	Asp Glu Ala Leu Gly	Thr Pro Glu Thr Gly	Ala		
	1070		1075		1080
Ala Thr Pro Met	Asp Trp Gln Glu Gln	Gly Arg Ala Pro Ser	Gln		
	1085		1090		1095
Asp Gln Glu Ala	Pro Ser Pro Glu Ala	Leu Pro Ser Pro Gly	Gln		
	1100		1105		1110
Glu Pro Ala Ala	Gly Ala Ser Pro Arg	Arg Gly Glu Leu Arg	Arg		
	1115		1120		1125
Gly Ser Ser Ala	Glu Ser Ala Leu Pro	Arg Ala Gly Pro Arg	Glu		
	1130		1135		1140
Leu Gly Arg Gly	Leu His Lys Ala Ala	Ser Val Glu Leu Pro	Gln		
	1145		1150		1155
Arg Arg Ser Pro	Gly Pro Gly Ala Thr	Arg Leu Ala Arg Gly	Gly		
	1160		1165		1170
Leu Gly Glu Gly	Glu Tyr Ala Gln Arg	Leu Gln Ala Leu Arg	Gln		
	1175		1180		1185
Arg Leu Leu Arg	Gly Gly Pro Glu Asp	Gly Lys Val Ser Gly	Leu		
	1190		1195		1200
Arg Gly Pro Leu	Leu Glu Ser Leu Gly	Gly Arg Ala Arg Asp	Pro		
	1205		1210		1215
Arg Met Ala Arg	Ala Ala Ser Ser Glu	Ala Ala Pro His His	Gln		
	1220		1225		1230
Pro Pro Leu Glu	Asn Arg Gly Leu Gln	Lys Ser Ser Ser Phe	Ser		

1235	1240	1245
Gln Gly Glu Ala Glu Pro Arg Gly Arg His Arg Arg Ala Gly Ala		
1250	1255	1260
Pro Leu Glu Ile Pro Val Ala Arg Leu Gly Ala Arg Arg Leu Gln		
1265	1270	1275
Glu Ser Pro Ser Leu Ser Ala Leu Ser Glu Ala Gln Pro Ser Ser		
1280	1285	1290
Pro Ala Arg Pro Ser Ala Pro Lys Pro Ser Thr Pro Lys Ser Ala		
1295	1300	1305
Glu Pro Ser Ala Thr Thr Pro Ser Asp Ala Pro Gln Pro Pro Ala		
1310	1315	1320
Pro Gln Pro Ala Gln Asp Lys Ala Pro Glu Pro Arg Pro Glu Pro		
1325	1330	1335
Val Arg Ala Ser Lys Pro Ala Pro Pro Pro Gln Ala Leu Gln Thr		
1340	1345	1350
Leu Ala Leu Pro Leu Thr Pro Tyr Ala Gln Ile Ile Gln Ser Leu		
1355	1360	1365
Gln Leu Ser Gly His Ala Gln Gly Pro Ser Gln Gly Pro Ala Ala		
1370	1375	1380
Pro Pro Ser Glu Pro Lys Pro His Ala Ala Val Phe Ala Arg Val		
1385	1390	1395
Ala Ser Pro Pro Pro Gly Ala Pro Glu Lys Arg Val Pro Ser Ala		
1400	1405	1410
Gly Gly Pro Pro Val Leu Ala Glu Lys Ala Arg Val Pro Thr Val		
1415	1420	1425
Pro Pro Arg Pro Gly Ser Ser Leu Ser Ser Ser Ile Glu Asn Leu		
1430	1435	1440
Glu Ser Glu Ala Val Phe Glu Ala Lys Phe Lys Arg Ser Arg Glu		
1445	1450	1455
Ser Pro Leu Ser Leu Gly Leu Arg Leu Leu Ser Arg Ser Arg Ser		
1460	1465	1470
Glu Glu Arg Gly Pro Phe Arg Gly Ala Glu Glu Glu Asp Gly Ile		
1475	1480	1485
Tyr Arg Pro Ser Pro Ala Gly Thr Pro Leu Glu Leu Val Arg Arg		
1490	1495	1500
Pro Glu Arg Ser Arg Ser Val Gln Asp Leu Arg Ala Val Gly Glu		
1505	1510	1515
Pro Gly Leu Val Arg Arg Leu Ser Leu Ser Leu Ser Gln Arg Leu		
1520	1525	1530
Arg Arg Thr Pro Pro Ala Gln Arg His Pro Ala Trp Glu Ala Arg		
1535	1540	1545
Gly Gly Asp Gly Glu Ser Ser Glu Gly Gly Ser Ser Ala Arg Gly		
1550	1555	1560
Ser Pro Val Leu Ala Met Arg Arg Arg Leu Ser Phe Thr Leu Glu		
1565	1570	1575
Arg Leu Ser Ser Arg Leu Gln Arg Ser Gly Ser Ser Glu Asp Ser		
1580	1585	1590
Gly Gly Ala Ser Gly Arg Ser Thr Pro Leu Phe Gly Arg Leu Arg		
1595	1600	1605
Arg Ala Thr Ser Glu Gly Glu Ser Leu Arg Arg Leu Gly Leu Pro		
1610	1615	1620
His Asn Gln Leu Ala Ala Gln Ala Gly Ala Thr Thr Pro Ser Ala		
1625	1630	1635
Glu Ser Leu Gly Ser Glu Ala Ser Ala Thr Ser Gly Ser Ser Ala		
1640	1645	1650
Pro Gly Glu Ser Arg Ser Arg Leu Arg Trp Gly Phe Ser Arg Pro		

1655	1660	1665
Arg Lys Asp Lys Gly Leu Ser Pro Pro Asn Leu Ser Ala Ser Val		
1670	1675	1680
Gln Glu Glu Leu Gly His Gln Tyr Val Arg Ser Glu Ser Asp Phe		
1685	1690	1695
Pro Pro Val Phe His Ile Lys Leu Lys Asp Gln Val Leu Leu Glu		
1700	1705	1710
Gly Glu Ala Ala Thr Leu Leu Cys Leu Pro Ala Ala Cys Pro Ala		
1715	1720	1725
Pro His Ile Ser Trp Met Lys Asp Lys Lys Ser Leu Arg Ser Glu		
1730	1735	1740
Pro Ser Val Ile Ile Val Ser Cys Lys Asp Gly Arg Gln Leu Leu		
1745	1750	1755
Ser Ile Pro Arg Ala Gly Lys Arg His Ala Gly Leu Tyr Glu Cys		
1760	1765	1770
Ser Ala Thr Asn Val Leu Gly Ser Ile Thr Ser Ser Cys Thr Val		
1775	1780	1785
Ala Val Ala Arg Val Pro Gly Lys Leu Ala Pro Pro Glu Val Pro		
1790	1795	1800
Gln Thr Tyr Gln Asp Thr Ala Leu Val Leu Trp Lys Pro Gly Asp		
1805	1810	1815
Ser Arg Ala Pro Cys Thr Tyr Thr Leu Glu Arg Arg Val Asp Gly		
1820	1825	1830
Glu Ser Val Trp His Pro Val Ser Ser Gly Ile Pro Asp Cys Tyr		
1835	1840	1845
Tyr Asn Val Thr His Leu Pro Val Gly Val Thr Val Arg Phe Arg		
1850	1855	1860
Val Ala Cys Ala Asn Arg Ala Gly Gln Gly Pro Phe Ser Asn Ser		
1865	1870	1875
Ser Glu Lys Val Phe Val Arg Gly Thr Gln Asp Ser Ser Ala Val		
1880	1885	1890
Pro Ser Ala Ala His Gln Glu Ala Pro Val Thr Ser Arg Pro Ala		
1895	1900	1905
Arg Ala Arg Pro Pro Asp Ser Pro Thr Ser Leu Ala Pro Pro Leu		
1910	1915	1920
Ala Pro Ala Ala Pro Thr Pro Pro Ser Val Thr Val Ser Pro Ser		
1925	1930	1935
Ser Pro Pro Thr Pro Pro Ser Gln Ala Leu Ser Ser Leu Lys Ala		
1940	1945	1950
Val Gly Pro Pro Pro Gln Thr Pro Pro Arg Arg His Arg Gly Leu		
1955	1960	1965
Gln Ala Ala Arg Pro Ala Glu Pro Thr Leu Pro Ser Thr His Val		
1970	1975	1980
Thr Pro Ser Glu Pro Lys Pro Phe Val Leu Asp Thr Gly Thr Pro		
1985	1990	1995
Ile Pro Ala Ser Thr Pro Gln Gly Val Lys Pro Val Ser Ser Ser		
2000	2005	2010
Thr Pro Val Tyr Val Val Thr Ser Phe Val Ser Ala Pro Pro Ala		
2015	2020	2025
Pro Glu Pro Pro Ala Pro Glu Pro Pro Pro Glu Pro Thr Lys Val		
2030	2035	2040
Thr Val Gln Ser Leu Ser Pro Ala Lys Glu Val Val Ser Ser Pro		
2045	2050	2055
Gly Ser Ser Pro Arg Ser Ser Pro Arg Pro Glu Gly Thr Thr Leu		
2060	2065	2070
Arg Gln Gly Pro Pro Gln Lys Pro Tyr Thr Phe Leu Glu Glu Lys		

2075	2080	2085
Ala Arg Gly Arg Phe Gly Val Val Arg Ala Cys Arg Glu Asn Ala		
2090	2095	2100
Thr Gly Arg Thr Phe Val Ala Lys Ile Val Pro Tyr Ala Ala Glu		
2105	2110	2115
Gly Lys Arg Arg Val Leu Gln Glu Tyr Glu Val Leu Arg Thr Leu		
2120	2125	2130
His His Glu Arg Ile Met Ser Leu His Glu Ala Tyr Ile Thr Pro		
2135	2140	2145
Arg Tyr Leu Val Leu Ile Ala Glu Ser Cys Gly Asn Arg Glu Leu		
2150	2155	2160
Leu Cys Gly Leu Ser Asp Arg Phe Arg Tyr Ser Glu Asp Asp Val		
2165	2170	2175
Ala Thr Tyr Met Val Gln Leu Leu Gln Gly Leu Asp Tyr Leu His		
2180	2185	2190
Gly His His Val Leu His Leu Asp Ile Lys Pro Asp Asn Leu Leu		
2195	2200	2205
Leu Ala Pro Asp Asn Ala Leu Lys Ile Val Asp Phe Gly Ser Ala		
2210	2215	2220
Gln Pro Tyr Asn Pro Gln Ala Leu Arg Pro Leu Gly His Arg Thr		
2225	2230	2235
Gly Thr Leu Glu Phe Met Ala Pro Glu Met Val Lys Gly Glu Pro		
2240	2245	2250
Ile Gly Ser Ala Thr Asp Ile Trp Gly Ala Gly Val Leu Thr Tyr		
2255	2260	2265
Ile Met Leu Ser Gly Arg Ser Pro Phe Tyr Glu Pro Asp Pro Gln		
2270	2275	2280
Glu Thr Glu Ala Arg Ile Val Gly Gly Arg Phe Asp Ala Phe Gln		
2285	2290	2295
Leu Tyr Pro Asn Thr Ser Gln Ser Ala Thr Leu Phe Leu Arg Lys		
2300	2305	2310
Val Leu Ser Val His Pro Trp Ser Arg Pro Ser Leu Gln Asp Cys		
2315	2320	2325
Leu Ala His Pro Trp Leu Gln Asp Ala Tyr Leu Met Lys Leu Arg		
2330	2335	2340
Arg Gln Thr Leu Thr Phe Thr Thr Asn Arg Leu Lys Glu Phe Leu		
2345	2350	2355
Gly Glu Gln Arg Arg Arg Arg Ala Glu Ala Ala Thr Arg His Lys		
2360	2365	2370
Val Leu Leu Arg Ser Tyr Pro Gly Gly Pro		
2375	2380	

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<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2190612CD1

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Leu Val Glu Arg Val Ala Ala Ile Asp Val Thr His Leu Glu Glu		
20	25	30

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

Lys	Ser	Met	Leu	Arg	Lys	Arg	Ser	Phe	Gly	Asn	Pro	Phe	Glu	Pro
				455					460					465
Gln	Ala	Arg	Arg	Glu	Glu	Arg	Ser	Met	Ser	Ala	Pro	Gly	Asn	Leu
				470					475					480
Leu	Val	Lys	Glu	Gly	Phe	Gly	Glu	Gly	Gly	Lys	Ser	Pro	Glu	Leu
				485					490					495
Pro	Gly	Val	Gln	Glu	Asp	Glu	Ala	Ala	Ser					
				500					505					

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<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477549CD1

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<210> 23

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<213> Homo sapiens

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<223> Incyte ID No: 7474590CB1

<400> 23

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<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 7474594CB1

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<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477585CB1

<400> 25

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<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 7477587CB1

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<211> 4277
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 7594537CB1

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<211> 2616

<212> DNA

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<221> misc_feature

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<223> Incyte ID No: 1851973CB1

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<213> Homo sapiens

<220>

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<223> Incyte ID No: 7474604CB1

<400> 35

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<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7474721CB1

<400> 36

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<211> 3650

<212> DNA

<213> Homo sapiens

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<211> 7789

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 7477141CB1

<400> 38

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