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Flynn et al.(10) **Pub. No.: US 2008/0269254 A1**(43) **Pub. Date: Oct. 30, 2008**(54) **KINASE INHIBITORS USEFUL FOR THE
TREATMENT OF MYELOPROLIFIC
DISEASES AND OTHER PROLIFERATIVE
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<i>C07D 413/14</i>	(2006.01)

(52) **U.S. Cl. 514/256; 544/333**(57) **ABSTRACT**

Compounds of the present invention find utility in the treatment of mammalian cancers and especially human cancers including but not limited to malignant, melanomas, glioblastomas, ovarian cancer, pancreatic cancer, prostate cancer, lung cancers, breast cancers, kidney cancers, cervical carcinomas, metastasis of primary tumor sites, myeloproliferative diseases, leukemias, papillary thyroid carcinoma, non small cell lung cancer, mesothelioma, hypereosinophilic syndrome, gastrointestinal stromal tumors, colonic cancers, ocular diseases characterized by hyperproliferation leading to blindness including various retinopathies, rheumatoid arthritis, asthma, chronic obstructive pulmonary disease, mastocytosis, mast cell leukemia, a disease caused by c-Abl kinase, oncogenic forms thereof, aberrant fusion proteins thereof and polymorphs thereof, or a disease caused by c-Kit kinase, oncogenic forms thereof, aberrant fusion proteins thereof and polymorphs thereof.

KINASE INHIBITORS USEFUL FOR THE TREATMENT OF MYELOPROLIFIC DISEASES AND OTHER PROLIFERATIVE DISEASES

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of Provisional Application 60/913,216 filed Apr. 20, 2007. This provisional application is incorporated by reference herein in its entirety.

SEQUENCE LISTING

[0002] This application contains a Sequence Listing in both paper and computer readable format in accordance with 37 C.F.R. 1.821 (c) and (e), the contents of which are hereby incorporated by reference in their entirety.

FIELD OF THE INVENTION

[0003] The present invention relates to novel kinase inhibitors and modulator compounds useful for the treatment of various diseases. More particularly, the invention is concerned with such compounds, kinase/compound adducts, methods of treating diseases, and methods of synthesis of the compounds. Preferably, the compounds are useful for the modulation of kinase activity of C-Abl, c-Kit, VEGFR, PDGFR kinases, Flt-3, c-Met, FGFR, the HER family and disease causing polymorphs thereof.

BACKGROUND OF THE INVENTION

[0004] Several members of the protein kinase family have been clearly implicated in the pathogenesis of various proliferative and myeloproliferative diseases and thus represent important targets for treatment of these diseases. Some of the proliferative diseases relevant to this invention include cancer, rheumatoid arthritis, atherosclerosis, and retinopathies. Important examples of kinases which have been shown to cause or contribute to the pathogenesis of these diseases include C-Abl kinase and the oncogenic fusion protein bcr-Abl kinase; c-Kit kinase, PDGF receptor kinase; VEGF receptor kinases; and Flt-3 kinase.

[0005] C-Abl kinase is an important non-receptor tyrosine kinase involved in cell signal transduction. This ubiquitously expressed kinase—upon activation by upstream signaling factors including growth factors, oxidative stress, integrin stimulation, and ionizing radiation—localizes to the cell plasma membrane, the cell nucleus, and other cellular compartments including the actin cytoskeleton (Van Etten, *Trends Cell Biol.* (1999) 9: 179). There are two normal isoforms of Abl kinase: Abl-1A and Abl-1B. The N-terminal half of c-Abl kinase is important for autoinhibition of the kinase domain catalytic activity (Pluk et al, *Cell* (2002) 108: 247). Details of the mechanistic aspects of this autoinhibition have recently been disclosed (Nagar et al, *Cell* (2003) 112: 859). The N-terminal myristoyl amino acid residue of Abl-1B has been shown to intramolecularly occupy a hydrophobic pocket formed from alpha-helices in the C-lobe of the kinase domain. Such intramolecular binding induces a novel binding area for intramolecular docking of the SH2 domain and the SH3 domain onto the kinase domain, thereby distorting and inhibiting the catalytic activity of the kinase. Thus, an intricate intramolecular negative regulation of the kinase activity is brought about by these N-terminal regions of c-Abl kinase. An aberrant dysregulated form of c-Abl is formed from a

chromosomal translocation event, referred to as the Philadelphia chromosome (P. C. Nowell et al, *Science* (1960) 132: 1497; J. D. Rowley, *Nature* (1973) 243: 290). This abnormal chromosomal translocation leads aberrant gene fusion between the Abl kinase gene and the breakpoint cluster region (BCR) gene, thus encoding an aberrant protein called bcr-Abl (C. Q. Daley et al, *Science* (1990) 247: 824; M. L. Gishizky et al, *Proc. Natl. Acad. Sci. USA* (1993) 90: 3755; S. Li et al, *J. Exp. Med.* (1999) 189: 1399). The bcr-Abl fusion protein does not include the regulatory myristoylation site (B. Nagar et al, *Cell* (2003) 112: 859) and as a result functions as an oncoprotein which causes chronic myeloid leukemia (CML). CML is a malignancy of pluripotent hematopoietic stem cells. The p210 form of bcr-Abl is seen in 95% of patients with CML, and in 20% of patients with acute lymphocytic leukemia and is exemplified by sequences such as e14a2 and e13a2. The corresponding p190 form, exemplified by the sequence e1a2 has also been identified. A p185 form has also been disclosed and has been linked to being causative of up to 10% of patients with acute lymphocytic leukemia. It will be appreciated by one skilled in the art that “p210 form”, “p190 form” and “p185 form” each describe a closely related group of fusion proteins, and that Sequence ID’s used herein are merely representative of each form and are not meant to restrict the scope solely to those sequences.

[0006] C-KIT (Kit, CD117, stem cell factor receptor) is a 145 kDa transmembrane tyrosine kinase protein that acts as a type-III receptor (Pereira et al. *J. Carcin.* (2005), 4: 19). The c-KIT proto-oncogene, located on chromosome 4q11-21, encodes the c-KIT receptor, whose ligand is the stem cell factor (SCF, steel factor, kit ligand, mast cell growth factor, Morstyn G, et al. *Oncology* (1994) 51(2):205. Yarden Y, et al. *Embo J* (1987) 6(11):3341). The receptor has tyrosine-protein kinase activity and binding of the ligands leads to the autophosphorylation of KIT and its association with substrates such as phosphatidylinositol 3-kinase (PI3K). Tyrosine phosphorylation by protein tyrosine kinases is of particular importance in cellular signalling and can mediate signals for major cellular processes, such as proliferation, differentiation, apoptosis, attachment, and migration. Defects in KIT are a cause of piebaldism, an autosomal dominant genetic developmental abnormality of pigmentation characterized by congenital patches of white skin and hair that lack melanocytes. Gain-of-function mutations of the c-KIT gene and the expression of phosphorylated KIT are found in most gastrointestinal stromal tumors and mastocytosis. Further, almost all gonadal seminomas/dysgerminomas exhibit KIT membranous staining, and several reports have clarified that some (10-25%) have a c-KIT gene mutation (Sakuma, Y. et al. *Cancer Sci* (2004) 95:9, 716). KIT defects have also been associated with testicular tumors including germ cell tumors (GCT) and testicular germ cell tumors (TGCT).

[0007] The role of c-kit expression has been studied in hematologic and solid tumours, such as acute leukemias (Cortes J. et al. *Cancer* (2003) 97(11):2760) and gastrointestinal stromal tumors (GIST, Fletcher C. D. et al. *Hum Pathol* (2002) 33(5):459). The clinical importance of c-kit expression in malignant tumors relies on studies with Gleevec® (imatinib mesylate, ST1571, Novartis Pharma AG Basel, Switzerland) that specifically inhibits tyrosine kinase receptors (Lefevre G. et al. *J Biol Chem* (2004) 279(30):31769). Moreover, a clinically relevant breakthrough has been the finding of anti-tumor effects of this compound in GIST, a group of tumors regarded as being generally resistant to con-

ventional chemotherapy (de Silva C M, Reid R: *Pathol Oncol Res* (2003) 9(1):13-19). GIST most often become Gleevec resistant and molecularly targeted small therapies that target c-KIT mutations remain elusive.

[0008] c-MET is a unique receptor tyrosine kinase (RTK) located on chromosome 7p and activated via its natural ligand hepatocyte growth factor. c-MET is found mutated in a variety of solid tumors (Ma P. C. et al. *Cancer Metastasis* (2003) 22:309). Mutations in the tyrosine kinase domain are associated with hereditary papillary renal cell carcinomas (Schmidt L. et al. *Nat. Genet.* (1997) 16:68; Schmidt L., et al. *Oncogene* (1999) 18:2343), whereas mutations in the sema and juxtamembrane domains are often found in small cell lung cancers (SCLC; Ma P. C. et al. *Cancer Res* (2003) 63:6272). Many activating mutations are also found in breast cancers (Nakopoulou et al. *Histopath* (2000) 36(4): 313). The paucity of tumor types for which c-Met mediated growth has been implicated suggests this is a target ideally suited for modulation by specific c-MET small molecule inhibitors.

[0009] The TPR-MET oncogene is a transforming variant of the c-MET RTK and was initially identified after treatment of a human osteogenic sarcoma cell line transformed by the chemical carcinogen N-methyl-N'-nitro-N-nitrosoguanidine (Park M. et al. *Cell* (1986) 45:895). The TPR-MET fusion oncoprotein is the result of a chromosomal translocation, placing the TPR3 locus on chromosome 1 upstream of a portion of the c-MET gene on chromosome 7 encoding only for the cytoplasmic region. Studies suggest that TPR-MET is detectable in experimental cancers (e.g. Yu J. et al. *Cancer* (2000) 88:1801). Dimerization of the M_r 65,000 TPR-MET oncoprotein through a leucine zipper motif encoded by TPR leads to constitutive activation of the c-MET kinase (Zhen Z. et al. *Oncogene* (1994) 9:1691). TPR-MET acts to activate wild-type c-MET RTK and can activate crucial cellular growth pathways, including the Ras pathway (Aklilu F. et al. *Am J Physiol* (1996) 271:E277) and the phosphatidylinositol 3-kinase (PI3K)/AKT pathway (Ponzetto C. et al. *Mol Cell Biol* (1993) 13:4600). Conversely, in contrast to c-MET RTK, TPR-MET is ligand independent, lacks the CBL binding site in the juxtamembrane region in c-MET, and is mainly cytoplasmic. c-Met immunohistochemical expression seems to be associated with abnormal β -catenin expression, and provides good prognostic and predictive factors in breast cancer patients.

[0010] The majority of small molecule kinase inhibitors that have been reported have been shown to bind in one of three ways. Most of the reported inhibitors interact with the ATP binding domain of the active site and exert their effects by competing with ATP for occupancy. Other inhibitors have been shown to bind to a separate hydrophobic region of the protein known as the "DFG-in-conformation" pocket wherein such a binding mode by the inhibitor causes the kinase to adopt the "DFG-out" conformation, and still others have been shown to bind to both the ATP domain and the "DFG-in-conformation" pocket again causing the kinase to adopt the "DFG-out" conformation. Examples specific to inhibitors of Raf kinases can be found in Lowinger et al, *Current Pharmaceutical Design* (2002) 8: 2269; Dumas, J. et al, *Current Opinion in Drug Discovery & Development* (2004) 7: 600; Dumas, J. et al, WO 2003068223 A1 (2003); Dumas, J., et al, WO 9932455 A1 (1999), and Wan, P. T. C., et al, *Cell* (2004) 116: 855.

[0011] Physiologically, kinases are regulated by a common activation/deactivation mechanism wherein a specific activa-

tion loop sequence of the kinase protein binds into a specific pocket on the same protein which is referred to as the switch control pocket. Such binding occurs when specific amino acid residues of the activation loop are modified for example by phosphorylation, oxidation, or nitrosylation. The binding of the activation loop into the switch pocket results in a conformational change of the protein into its active form (Huse, M. and Kuriyan, J. *Cell* (109) 275)

SUMMARY OF THE INVENTION

[0012] Compounds of the present invention find utility in the treatment of mammalian cancers and especially human cancers including but not limited to malignant, melanomas, glioblastomas, ovarian cancer, pancreatic cancer, prostate cancer, lung cancers, breast cancers, kidney cancers, cervical carcinomas, metastasis of primary tumor sites, myeloproliferative diseases, leukemias, papillary thyroid carcinoma, non small cell lung cancer, mesothelioma, hypereosinophilic syndrome, gastrointestinal stromal tumors, colonic cancers, ocular diseases characterized by hyperproliferation leading to blindness including various retinopathies, rheumatoid arthritis, asthma, chronic obstructive pulmonary disorder, a disease caused by c-Abl kinase, oncogenic forms thereof, aberrant fusion proteins thereof and polymorphs thereof, or a disease caused by c-Kit, oncogenic forms thereof, aberrant fusion proteins thereof and polymorphs thereof.

Section 1—Description of the Preferred Embodiments

[0013] The following descriptions refer to various compounds, stereo-, regioisomers and tautomers of such compounds and individual moieties of the compounds thereof.

[0014] Cycloalkyl refers to monocyclic saturated carbon rings taken from cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl and cyclooctanyl;

[0015] Aryl refers to monocyclic or fused bicyclic ring systems characterized by delocalized π electrons (aromaticity) shared among the ring carbon atoms of at least one carbocyclic ring; preferred aryl rings are taken from phenyl, naphthyl, tetrahydronaphthyl, indenyl, and indanyl;

[0016] Heteroaryl refers to monocyclic or fused bicyclic ring systems characterized by delocalized π electrons (aromaticity) shared among the ring carbon or heteroatoms including nitrogen, oxygen, or sulfur of at least one carbocyclic or heterocyclic ring; heteroaryl rings are taken from, but not limited to, pyrrolyl, furyl, thienyl, oxazolyl, thiazolyl, isoxazolyl, isothiazolyl, imidazolyl, pyrazolyl, oxadiazolyl, thiadiazolyl, triazolyl, tetrazolyl, pyridinyl, pyrimidinyl, pyrazinyl, pyridazinyl, triazinyl, indolyl, indolinyl, isoindolyl, isoindolinyl, indazolyl, benzofuranyl, benzothienyl, benzothiazolyl, benzothiazolonyl, benzoxazolyl, benzoxazolonyl, benzisoxazolyl, benzisotilazolyl, benzimidazolyl, benzimidazolonyl, benztriazolyl, imidazopyridinyl, pyrazolopyridinyl, imidazolopyridinyl, thiazolopyridinyl, thiazolopyridinyl, oxazolopyridinyl, oxazolopyridinyl, isoxazolopyridinyl, isothiazolopyridinyl, triazolopyridinyl, imidazopyrimidinyl, pyrazolopyrimidinyl, imidazolopyrimidinyl, thiazolopyrimidinyl, thiazolopyrimidinyl, oxazolopyrimidinyl, isoxazolopyrimidinyl, isothiazolopyrimidinyl, triazolopyrimidinyl, dihydropurinonyl, pyrrolopyrimidinyl, purinyl, pyrazolopyrimidinyl, phthalimidyl, phthalimidinyl, pyrazinylpyridinyl, pyridinopyrimidinyl, pyrimidinopyrimidinyl, cinnolinyl, quinoxalinyl, quinazolinyl, quinolinyl, isoquinolinyl,

phthalazinyl, benzodioxyl, benzisothiazoline-1,1,3-trionyl, dihydroquinolyl, tetrahydroquinolyl, dihydroisoquinolyl, tetrahydroisoquinolyl, benzoazepinyl, benzodiazepinyl, benzoxapinyl, and benzoxazepinyl;

[0017] Heterocyclyl refers to monocyclic rings containing carbon and heteroatoms taken from oxygen, nitrogen, or sulfur and wherein there is not delocalized π electrons (aromaticity) shared among the ring carbon or heteroatoms; heterocyclyl rings include, but are not limited to, oxetanyl, azetadanyl, tetrahydrofuranyl, pyrrolidinyl, oxazolanyl, oxazolidinyl, thiazolanyl, thiazolidinyl, pyranyl, thiopyranyl, tetrahydropyranyl, dioxalanyl, piperidinyl, morpholinyl, thiomorpholinyl, thiomorpholinyl S-oxide, thiomorpholinyl S-dioxide, piperazinyl, azepinyl, oxepinyl, diazepinyl, tropanyl, and homotropanyl;

[0018] Poly-aryl refers to two or more monocyclic or fused aryl bicyclic ring systems characterized by delocalized π electrons (aromaticity) shared among the ring carbon atoms of at least one carbocyclic ring wherein the rings contained therein are optionally linked together;

[0019] Poly-heteroaryl refers to two or more monocyclic or fused bicyclic systems characterized by delocalized π electrons (aromaticity) shared among the ring carbon or heteroatoms including nitrogen, oxygen, or sulfur of at least one carbocyclic or heterocyclic ring wherein the rings contained therein are optionally linked together, wherein at least one of the monocyclic or fused bicyclic rings of the poly-heteroaryl system is taken from heteroaryl as defined broadly above and the other rings are taken from either aryl, heteroaryl, or heterocyclyl as defined broadly above;

[0020] Poly-heterocyclyl refers to two or more monocyclic or fused bicyclic ring systems containing carbon and heteroatoms taken from oxygen, nitrogen, or sulfur and wherein there is not delocalized π electrons (aromaticity) shared among the ring carbon or heteroatoms wherein the rings contained therein are optionally linked, wherein at least one of the monocyclic or fused bicyclic rings of the poly-heteroaryl system is taken from heterocyclyl as defined broadly above and the other rings are taken from either aryl, heteroaryl, or heterocyclyl as defined broadly above;

[0021] Alkyl refers to straight or branched chain C1-C6alkyls;

[0022] Halogen refers to fluorine, chlorine, bromine, and iodine;

[0023] Alkoxy refers to —O-(alkyl) wherein alkyl is defined as above;

[0024] Alkoxyalkyl refers to -(alkyl)-O-(alkyl) wherein alkyl is defined as above;

[0025] Alkoxy-carbonyl refers to —C(O)O-(alkyl) wherein alkyl is defined as above;

[0026] Carboxyl-C1-C6alkyl refers to -(C1-C6alkyl)-CO₂H wherein alkyl is defined as above;

[0027] Substituted in connection with a moiety refers to the fact that a further substituent may be attached to the moiety to any acceptable location on the moiety.

[0028] The term salts embraces pharmaceutically acceptable salts commonly used to form alkali metal salts of free acids and to form addition salts of free bases. The nature of the salt is not critical, provided that it is pharmaceutically-acceptable. Suitable pharmaceutically-acceptable acid addition salts may be prepared from an inorganic acid or from an organic acid. Examples of such inorganic acids are hydrochloric, hydrobromic, hydroiodic, nitric, carbonic, sulfuric and phosphoric acid. Appropriate organic acids may be

selected from aliphatic, cycloaliphatic, aromatic, arylaliphatic, and heterocyclyl containing carboxylic acids and sulfonic acids, examples of which are formic, acetic, propionic, succinic, glycolic, gluconic, lactic, malic, tartaric, citric, ascorbic, glucuronic, maleic, fumaric, pyruvic, aspartic, glutamic, benzoic, aithranilic, mesylic, stearic, salicylic, p-hydroxybenzoic, phenylacetic, mandelic, embonic (pamoic), methanesulfonic, ethanesulfonic, benzenesulfonic, pantothenic, toluenesulfonic, 2-hydroxyethanesulfonic, sulfanilic, cyclohexylaminosulfonic, algenic, 3-hydroxybutyric, galactaric and galacturonic acid. Suitable pharmaceutically-acceptable salts of free acid-containing compounds of Formula I include metallic salts and organic salts. More preferred metallic salts include, but are not limited to appropriate alkali metal (group Ia) salts, alkaline earth metal (group IIa) salts and other physiological acceptable metals. Such salts can be made from aluminum, calcium, lithium, magnesium, potassium, sodium and zinc. Preferred organic salts can be made from primary amines, secondary amines, tertiary amines and quaternary ammonium salts, including in part, tromethamine, diethylamine, tetra-N-methylammonium, N,N'-dibenzylethylenediamine, chloroprocaine, choline, diethanolamine, ethylenediamine, meglumine (N-methylglucamine) and procaine.

[0029] The term prodrug refers to derivatives of active compounds which revert in vivo into the active form. For example, a carboxylic acid form of an active drug may be esterified to create a prodrug, and the ester is subsequently converted in vivo to revert to the carboxylic acid form. See Ettmayer et. al, *J. Med. Chem* (2004) 47: 2393 and Lorenzi et. al, *J. Pharm. Exp. Therapeutics* (2005) 883 for reviews.

[0030] Structural, chemical and stereochemical definitions are broadly taken from IUPAC recommendations, and more specifically from Glossary of Terms used in Physical Organic Chemistry (IUPAC Recommendations 1994) as summarized by P. Müller, *Pure Appl. Chem.*, 66, 1077-1184 (1994) and Basic Terminology of Stereochemistry (IUPAC Recommendations 1996) as summarized by G. P. Moss *Pure and Applied Chemistry*, 68, 2193-2222 (1996). Specific definitions are as follows:

[0031] Atropisomers are defined as a subclass of conformers which can be isolated as separate chemical species and which arise from restricted rotation about a single bond.

[0032] Regioisomers or structural isomers are defined as isomers involving the same atoms in different arrangements.

[0033] Enantiomers are defined as one of a pair of molecular entities which are mirror images of each other and non-superimposable.

[0034] Diastereomers or diastereoisomers are defined as stereoisomers other than enantiomers. Diastereomers or diastereoisomers are stereoisomers not related as mirror images. Diastereoisomers are characterized by differences in physical properties, and by some differences in chemical behavior towards achiral as well as chiral reagents

[0035] Tautomerism is defined as isomerism of the general form

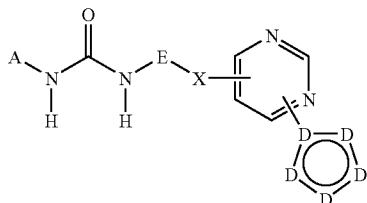


where the isomers (called tautomers) are readily interconvertible; the atoms connecting the groups X, Y, Z are typically any of C, H, O, or S, and G is a group which becomes an electrofuge or nucleofuge during isomerization. The commonest case, when the electrofuge is H⁺, is also known as "prototropy".

[0036] Tautomers are defined as isomers that arise from tautomerism, independent of whether the isomers are isolable.

1. First Aspect of the Invention—Compounds, Methods, Preparations and Adducts

[0037]



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[0038] and wherein the pyrimidine ring may be optionally substituted with one or more R20 moieties;

[0039] each D is individually taken from the group consisting of C, CH, C—R20, N-Z3, N, O and S, such that the resultant ring is taken from the group consisting of pyrazolyl, triazolyl, isoxazolyl, isothiazolyl, oxazolyl, imidazolyl, and thiadiazolyl;

[0040] wherein E is selected from the group consisting of phenyl, pyridyl, and pyrimidinyl;

[0041] E may be optionally substituted with one or two R16 moieties;

[0042] wherein A is a ring system selected from the group consisting of cyclopentyl, cyclohexyl, G1, G2, and G3;

[0043] G1 is a heteroaryl taken from the group consisting of pyrrolyl, furyl, thienyl, oxazolyl, thiazolyl, isoxazol-4-yl, isoxazol-5-yl, isothiazolyl, imidazolyl, pyrazolyl, oxadiazolyl, thiadiazolyl, triazolyl, and tetrazolyl;

[0044] G2 is a fused bicyclic heteroaryl taken from the group consisting of indolyl, indolyl, isoindolyl, isoindolyl, indazolyl, benzofuranyl, benzothienyl, benzothiazolyl, benzothiazolonyl, benzoxazolyl, benzoxazolonyl, benzisoxazolyl, benzisothiazolyl, benzimidazolyl, benzimidazolonyl, benztriazolyl, imidazopyridinyl, pyrazolopyridinyl, imidazolopyridinyl, thiazolopyridinyl, thiazolonopyridinyl, oxazolopyridinyl, oxazolopyridinyl, isoxazolopyridinyl, isothiazolopyridinyl, triazolopyridinyl, imidazopyrimidinyl, pyrazolopyrimidinyl, imidazolopyrimidinyl, thiazolopyrimidinyl, thiazolonopyrimidinyl, oxazolopyrimidinyl, oxazolopyrimidinyl, isoxazolopyrimidinyl, isothiazolopyrimidinyl, triazolopyrimidinyl, dihydropurinyl, pyrrolopyrimidinyl, purinyl, pyrazolopyrimidinyl, phthalimidyl, phthalimidinyl, pyrazinylpyridinyl, pyridinopyrimidinyl, pyrimidinopyrimidinyl, cinnolinyl, quinoxalinyl, quinazolinyl, quinolinyl, isoquinolinyl, phthalazinyl, benzodioxyl, benzisothiazoline-1,1,3-trionyl, dihydroquinolinyl, tetrahydroquinolinyl, dihydroisoquinolinyl, tetrahydroisoquinolinyl, benzoazepinyl, benzodiazepinyl, benzoxapinyl, and benzoxazepinyl;

[0045] G3 is a heterocyclyl taken from the group consisting of oxetanyl, azetadanyl, tetrahydrofuranyl, pyrrolidinyl, oxazolyl, oxazolidinyl, imidazolonyl, pyranyl, thiopyranyl, tetrahydropyranyl, dioxalinyl, piperidinyl, morpholinyl, thiomorpholinyl, thiomorpholinyl S-oxide, thiomorpholinyl S-dioxide, piperazinyl, azepinyl, oxepinyl, diazepinyl, tropanyl, and homotropanyl;

[0046] the A ring may be optionally substituted with one or two R2 moieties;

[0047] X is selected from the group consisting of —O—, —S(CH₂)—, —N(R3)(CH₂)_n—, —(CH₂)_p—, and wherein the carbon atoms of —(CH₂)_n—, —(CH₂)_p—, of X may be further substituted by oxo or one or more C1-C6alkyl moieties;

[0048] when A, G1, G2 or G6 has one or more substitutable sp²-hybridized carbon atoms, each respective sp² hybridized carbon atom may be optionally substituted with a Z1 substituent;

[0049] when A, G1, G2 or G3 has one or more substitutable sp³-hybridized carbon atoms, each respective sp³ hybridized carbon atom may be optionally substituted with a Z2 substituent; when A, G1, G2 or G3 has one or more substitutable nitrogen atoms, each respective nitrogen atom may be optionally substituted with a Z4 substituent;

[0050] each Z1 is independently and individually selected from the group consisting of C1-6alkyl, branched C3-C7alkyl, C3-C8cycloalkyl, halogen, fluoroC1-C6alkyl wherein the alkyl moiety can be partially or fully fluorinated, cyano, C1-C6alkoxy, fluoroC1-C6alkoxy wherein the alkyl moiety can be partially or fully fluorinated, —(CH₂)_nOH, oxo, C1-C6alkoxyC1-C6alkyl, (R4)₂N(CH₂)_n—, (R3)₂N(CH₂)_n—, (R4)₂N(CH₂)_qN(R4)(CH₂)_n—, (R4)₂N(CH₂)_qO(CH₂)_n—, (R3)₂NC(O)—, (R4)₂NC(O)—, (R4)₂NC(O)C1-C6alkyl—, —(R4)NC(O)R8, C1-C6alkoxycarbonyl-, -carboxyC1-C6alkyl, C1-C6alkoxycarbonylC1-C6alkyl-, (R3)₂NSO₂—, —SOR3, (R4)₂NSO₂—, —N(R4)SO₂R8, —O(CH₂)_qOC1-C6alkyl, —SO₂R3, —SOR4, —C(O)R8, —C(O)R6, —C(=NOH)R6, —C(=NOR3)R6, —(CH₂)_nN(R4)C(O)R8, —N(R3)(CH₂)_qO-alkyl, —N(R3)(CH₂)_qN(R4)₂, nitro, —CH(OH)CH(OH)R4, —C(=NH)N(R4)₂, —C(=NOR3)N(R4)₂, —NHC(=NH)R8, R17 substituted G3, R17 substituted pyrazolyl and R17 substituted imidazolyl;

[0051] In the event that Z1 contains an alkyl or alkylene moiety, such moieties may be further substituted with one or more C1-C6alkyls;

[0052] each Z2 is independently and individually selected from the group consisting of aryl, C1-C6alkyl, C3-C8cycloalkyl, branched C3-C7alkyl, hydroxyl, hydroxyC1-C6alkyl-, cyano, (R3)₂N—, (R4)₂N—, (R4)₂NC1-C6alkyl-, (R4)₂NC2-C6alkylN(R4)(CH₂)_n—, (R4)₂NC2-C6alkylO(CH₂)_n—, (R3)₂NC(O)—, (R4)₂NC(O)—, (R4)₂NC(O)C1-C6alkyl-, carboxyl, -carboxyC1-C6alkyl, C1-C6alkoxycarbonyl-, C1-C6alkoxycarbonylC1-C6alkyl-, (R3)₂NSO₂—, (R4)₂NSO₂—, —SO₂R8, —(CH₂)_nN(R4)C(O)R8, —C(O)R8, —O, —NOH, and —N(OR6);

[0053] in the event that Z2 contains an alkyl or alkylene moiety, such moieties may be further substituted with one or more C1-C6alkyls;

[0054] each Z3 is independently and individually selected from the group consisting of H, C1-C6alkyl, branched C3-C7alkyl, C3-C8cycloalkyl, fluoroC1-C6alkyl wherein the alkyl moiety can be partially or fully fluorinated, hydroxyC2-C6alkyl-, C1-C6alkoxycarbonyl-, —C(O)R8, R5C(O)(CH₂)_n—, (R4)₂NC(O)—, (R4)₂NC(O)C1-C6alkyl-, R8C(O)N(R4)(CH₂)_q—, (R3)₂NSO₂—, (R4)₂NSO₂—, —(CH₂)_qN(R3)₂, and —(CH₂)_qN(R4)₂;

[0055] each Z4 is independently and individually selected from the group consisting of C1-C6alkyl, branched C3-C7alkyl, hydroxyC2-C6alkyl-, C1-C6alkoxyC2-C6alkyl-, (R4)₂N-C2-C6alkyl-, (R4)₂N-C2-C6alkylN(R4)-C2-

C6alkyl-, (R4)₂N-C2-C6alkyl-O-C2-C6alkyl-(R4)₂NC(O)C1-C6alkyl-, carboxyC1-C6alkyl-, C1-C6alkoxycarbonylC1-C6alkyl-, -C2-C6alkylN(R4)C(O)R8, R8-C(=NR3)—, —SO₂R8, and —COR8;

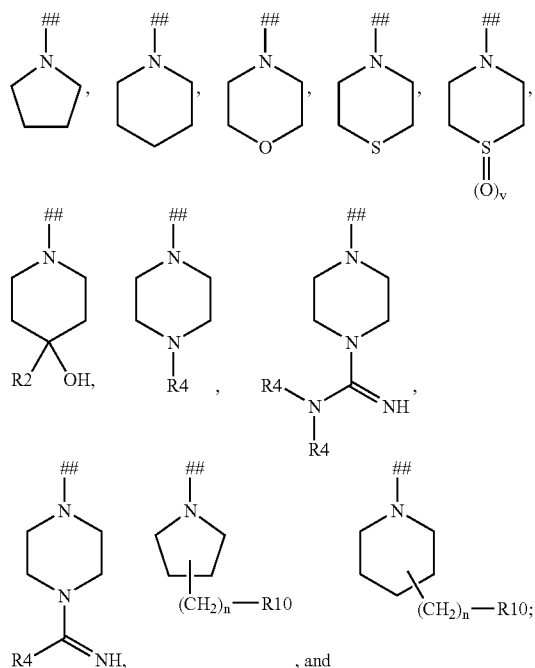
[0056] in the event that Z4 contains an alkyl or alkylene moiety, such moieties may be further substituted with one or more C1-C6alkyls;

[0057] each R2 is selected from the group consisting of H, C1-C6alkyl, branched C3-C8alkyl, R19 substituted C3-C8cycloalkyl-, fluoroC1-C6alkyl- wherein the alkyl is fully or partially fluorinated, halogen, cyano, C1-C6alkoxy-, and fluoroC1-C6alkoxy- wherein the alkyl group is fully or partially fluorinated, hydroxyl substituted C1-C6alkyl-, hydroxyl substituted branched C3-C8alkyl-, cyano substituted C1-C6alkyl-, cyano substituted branched C3-C8alkyl-, (R3)₂NC(O)C1-C6alkyl-, and (R3)₂NC(O)C3-C8 branched alkyl-;

[0058] wherein each R3 is independently and individually selected from the group consisting of H, C1-C6alkyl, branched C3-C7alkyl, and C3-C8cycloalkyl;

[0059] each R4 is independently and individually selected from the group consisting of H, C1-C6alkyl, hydroxyC1-C6alkyl-, dihydroxyC1-C6alkyl-, C1-C6alkoxyC1-C6alkyl-, branched C3-C7alkyl, branched hydroxyC1-C6alkyl-, branched C1-C6alkoxyC1-C6alkyl-, branched dihydroxyC1-C6alkyl-, —(CH₂)_pN(R7)₂, —(CH₂)_pC(O)N(R7)₂, —(CH₂)_nC(O)OR3, and R19 substituted C3-C8cycloalkyl-;

[0060] each R5 is independently and individually selected from the group consisting of



[0061] and wherein the symbol (##) is the point of attachment to Z3;

[0062] each R6 is independently and individually selected from the group consisting of C1-C6alkyl, branched C3-C7alkyl, and R19 substituted C3-C8cycloalkyl-;

[0063] each R7 is independently and individually selected from the group consisting of H, C1-C6alkyl, hydroxyC2-

C6alkyl-, dihydroxyC2-C6alkyl-, C1-C6alkoxyC2-C6alkyl-, branched C3-C7alkyl, branched hydroxyC2-C6alkyl-, branched C1-C6alkoxyC2-C6alkyl-, branched dihydroxyC2-C6alkyl-, —(CH₂)_nC(O)OR3, R19 substituted C3-C8cycloalkyl- and —(CH₂)_nR17;

[0064] each R8 is independently and individually selected from the group consisting of C1-C6alkyl, branched C3-C7alkyl, fluoroC1-C6alkyl- wherein the alkyl moiety is partially or fully fluorinated, R19 substituted C3-C8cycloalkyl-, —OH, C1-C6alkoxy, —N(R3)₂, and —N(R4)₂;

[0065] each R10 is independently and individually selected from the group consisting of —CO₂H, —CO₂C1-C6alkyl-, —C(O)N(R4)₂, OH, C1-C6alkoxy, and —N(R4)₂;

[0066] each R16 is independently and individually selected from the group consisting of H, C1-C6alkyl, branched C3-C7alkyl, R19 substituted C3-C8cycloalkyl-, halogen, fluoroC1-C6alkyl- wherein the alkyl moiety can be partially or fully fluorinated, cyano, hydroxyl, C1-C6alkoxy, fluoroC1-C6alkoxy- wherein the alkyl moiety can be partially or fully fluorinated, —N(R3)₂, —N(R4)₂, R3 substituted C2-C3alkynyl- and nitro;

[0067] each R17 is independently and individually selected from the group consisting of H, C1-C6alkyl, branched C3-C7alkyl, R19 substituted C3-C8cycloalkyl-, halogen, fluoroC1-C6alkyl- wherein the alkyl moiety can be partially or fully fluorinated, cyano, hydroxyl, C1-C6alkoxy, fluoroC1-C6alkoxy- wherein the alkyl moiety can be partially or fully fluorinated, —N(R3)₂, —N(R4)₂, and nitro;

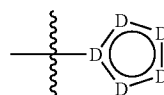
[0068] each R19 is independently and individually selected from the group consisting of H, OH and C1-C6alkyl;

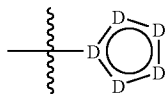
[0069] each R20 is independently and individually selected from the group consisting of C1-C6alkyl, branched C3-C7alkyl, R19 substituted C3-C8cycloalkyl-, halogen, fluoroC1-C6alkyl- wherein the alkyl moiety can be partially or fully fluorinated, cyano, hydroxyl, C1-C6alkoxy, fluoroC1-C6alkoxy- wherein the alkyl moiety can be partially or fully fluorinated, —N(R3)₂, —N(R4)₂, —N(R3)C(O)R3, —C(O)N(R3)₂ and nitro and wherein two R4 moieties independently and individually taken from the group consisting of C1-C6alkyl, branched C3-C6alkyl, hydroxyalkyl-, and alkoxyalkyl and attached to the same nitrogen heteroatom may cyclize to form a C3-C7 heterocycl ring;

[0070] k is 0 or 1; n is 0-6; p is 1-4; q is 2-6; r is 0 or 1; t is 1-3; v is 1 or 2; x is 0-2;

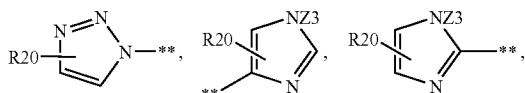
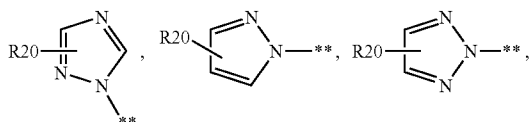
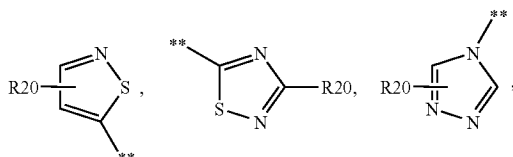
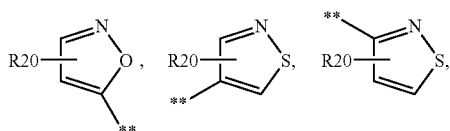
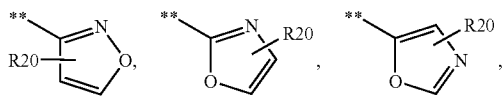
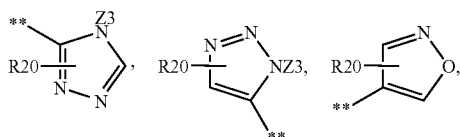
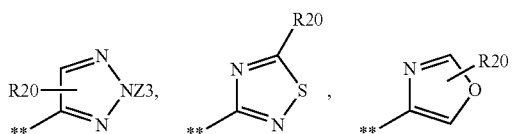
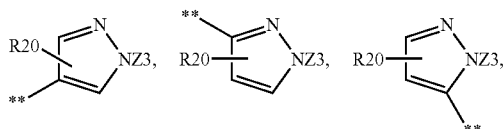
[0071] and stereo-, regioisomers and tautomers of such compounds.

1.1 Compounds of Formula Ia which Exemplify Preferred D Moieties

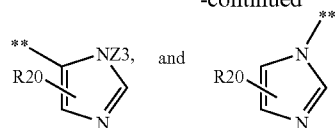




moieties of the formula:



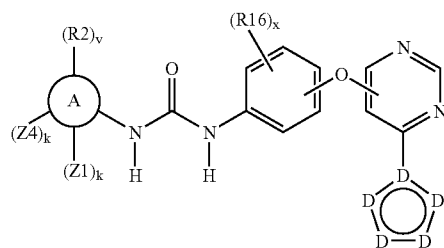
-continued



wherein the symbol (**) indicates the point of attachment to the pyrimidine ring.

1.1.1 Compounds of Formula Ia which Exemplify Preferred A Moieties

[0073] In a preferred embodiment of compounds of formula Ia, said compounds have structures of formula Ib

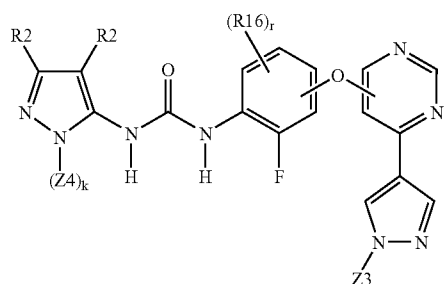


Ib

wherein A is any possible isomer of pyrazole.

1.1.2 Compounds of Formula Ia which Exemplify Preferred A, D, and R16 Moieties

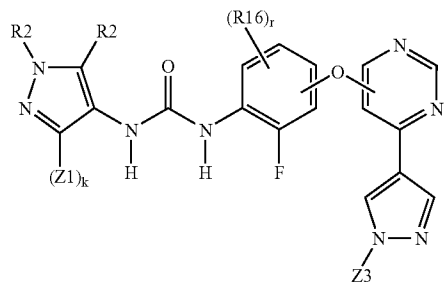
[0074] In a more preferred embodiment of compounds of formula Ib, said compounds have structures of formula Ic



Ic

1.1.3 Compounds of Formula Ia which Exemplify Preferred A, D, and R16 Moieties

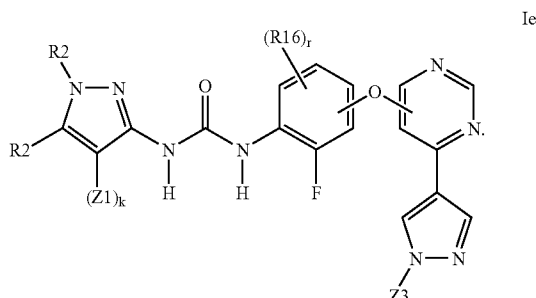
[0075] In a more preferred embodiment of compounds of formula Ib, said compounds have structures of formula Id



Id

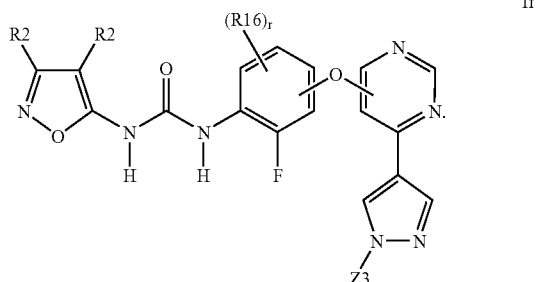
1.1.4 Compounds of Formula Ia which Exemplify Preferred A, D, and R16 Moieties

[0076] In a more preferred embodiment of compounds of formula Ib, said compounds have structures of formula Ie



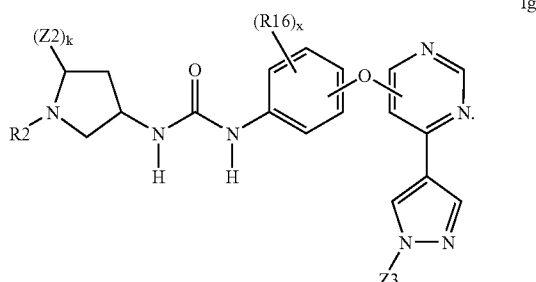
1.1.5 Compounds of Formula Ia which Exemplify Preferred A, D, and R16 Moieties

[0077] In a more preferred embodiment of compounds of formula Ia, said compounds have structures of formula If



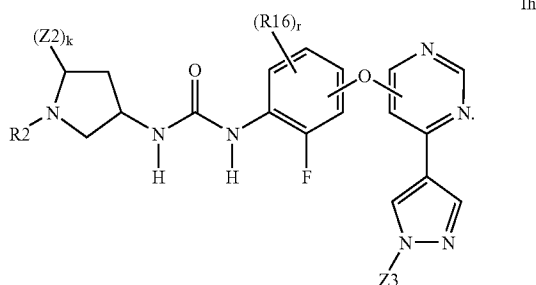
Compounds of Formula Ia which Exemplify Preferred A and D Moieties

[0078] In a more preferred embodiment of compounds of formula Ia, said compounds have structures of formula Ig



1.1.7 Compounds of Formula Ia which Exemplify Preferred A, D, and R16 Moieties

[0079] In a more preferred embodiment of compounds of formula Ia, said compounds have structures of formula Ih



1.1.8 Most Preferred Compounds of Formula Ia

[0080] 1-(1-tert-butyl-1H-pyrazol-4-yl)-3-(2-fluoro-4-methyl-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea, 1-(1-tert-butyl-1H-pyrazol-4-yl)-3-(2-fluoro-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea, 1-(3-tert-butyl-1-methyl-1H-pyrazol-5-yl)-3-(2-fluoro-4-methyl-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea, and 1-(3-tert-butyl-1-methyl-1H-pyrazol-5-yl)-3-(2-fluoro-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea.

1.2 Methods

1.2a Methods of Protein Modulation

[0081] The invention includes methods of modulating kinase activity of a variety of kinases, e.g. C-Abl kinase, bcr-Abl kinase, Flt-3, VEGFR-2 kinase mutants, c-Met, c-Kit, PDGFR and the HER family of kinases. The kinases may be wildtype kinases, oncogenic forms thereof, aberrant fusion proteins thereof or polymorphs of any of the foregoing. The method comprises the step of contacting the kinase species with compounds of the invention and especially those set forth in sections section 1. The kinase species may be activated or unactivated, and the species may be modulated by phosphorylations, sulfation, fatty acid acylations glycosylations, nitrosylation, cystinylation (i.e. proximal cysteine residues in the kinase react with each other to form a disulfide bond) or oxidation. The kinase activity may be selected from the group consisting of catalysis of phospho transfer reactions, inhibition of phosphorylation, oxidation or nitrosylation of said kinase by another enzyme, enhancement of dephosphorylation, reduction or denitrosylation of said kinase by another enzyme, kinase cellular localization, and recruitment of other proteins into signaling complexes through modulation of kinase conformation.

1.2b Treatment Methods

[0082] The methods of the invention also include treating individuals suffering from a condition selected from the group consisting of cancer and hyperproliferative diseases. These methods comprise administering to such individuals compounds of the invention, and especially those of section 1, said diseases including, but not limited to, malignant melanomas, glioblastomas, ovarian cancer, pancreatic cancer, prostate cancer, lung cancers, breast cancers, kidney cancers, cervical carcinomas, metastasis of primary tumor secondary sites, myeloproliferative diseases, leukemias, papillary thyroid carcinoma, non small cell lung cancer, mesothelioma, hypereosinophilic syndrome, gastrointestinal stromal tumors, colonic cancers, ocular diseases characterized by hyperproliferation leading to blindness including various retinopathies including diabetic retinopathy and age-related macular degeneration, rheumatoid arthritis, asthma, chronic obstructive pulmonary disorder, mastocytosis, mast cell leukemia, a disease caused by c-Abl kinase, oncogenic forms thereof, aberrant fusion proteins thereof and polymorphs thereof, or a disease caused by a c-Kit kinase, oncogenic forms thereof, aberrant fusion proteins thereof and polymorphs thereof. The administration method is not critical, and may be from the group consisting of oral, parenteral, inhalation, and subcutaneous.

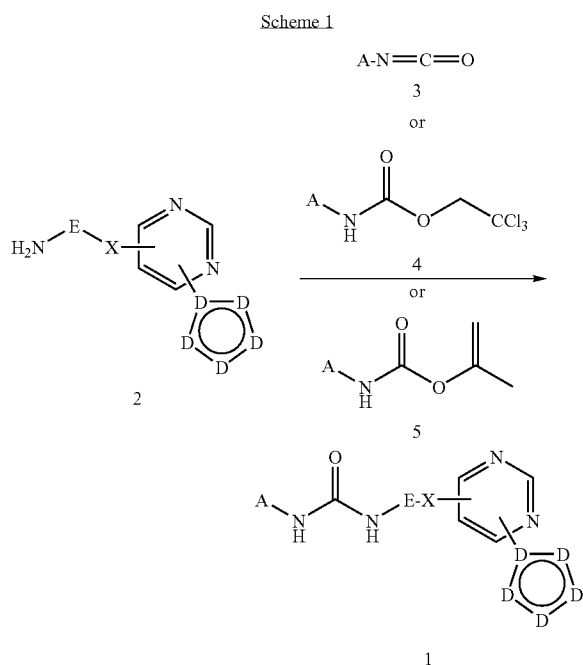
1.3 Pharmaceutical Preparations

[0083] The compounds of the invention, especially those of section 1 may form a part of a pharmaceutical composition by combining one or more such compounds with a pharmaceutically acceptable carrier. Additionally, the compositions may include an additive selected from the group consisting of adjuvants, excipients, diluents, and stabilizers.

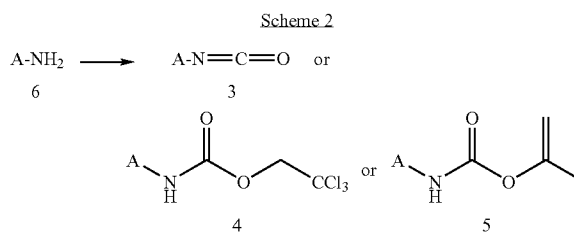
Section 2. Synthesis of Compounds of the Present Invention

[0084] The compounds of the invention are available by the general synthetic methods illustrated in the Schemes below and the accompanying examples.

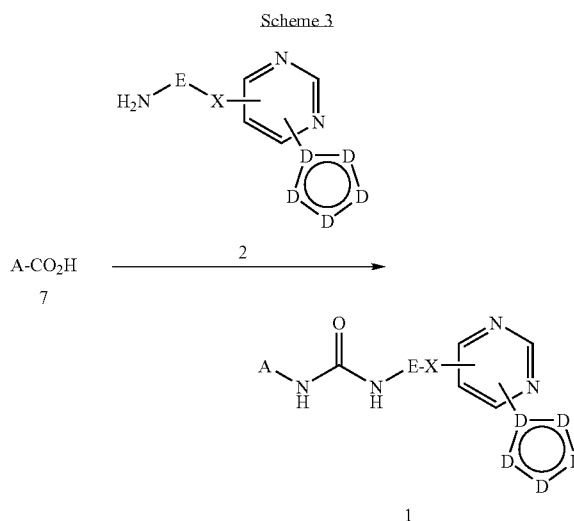
[0085] As indicated in Scheme 1, ureas of general formula 1 can be readily prepared by the union of amines of general formula 2 with isocyanates 3 or isocyanate surrogates 4 (trichloroethyl carbamates) or 5 (isopropenyl carbamates). Preferred conditions for the preparation of compounds of general formula 1 involve heating a solution of 4 or 5 with 2 in the presence of a tertiary base such as diisopropylethylamine, triethylamine or N-methylpyrrolidine in a solvent such as dimethylformamide, dimethylsulfoxide, tetrahydrofuran or 1,4-dioxane at a temperature between 50 and 100° C. for a period of time ranging from 1 hour to 2 days.



[0086] As shown in Scheme 2, isocyanates 3 can be prepared from amines A-NH₂ 6 with phosgene, or a phosgene equivalent such as diphosgene, triphosgene, or N,N-dicarbonylimidazole. Trichloroethyl carbamates 4 and isopropenyl carbamates 5 are readily prepared from amines A-NH₂ (6) by reaction with trichloroethyl chloroformate or isopropenyl chloroformate by standard conditions familiar to those skilled in the art. Preferred conditions for the preparation of 4 and 5 include treatment of compound 6 with the appropriate chloroformate in the presence of pyridine in an aprotic solvent such as dichloromethane or in the presence of aqueous hydroxide or carbonate in a biphasic aqueous/ethyl acetate solvent system.

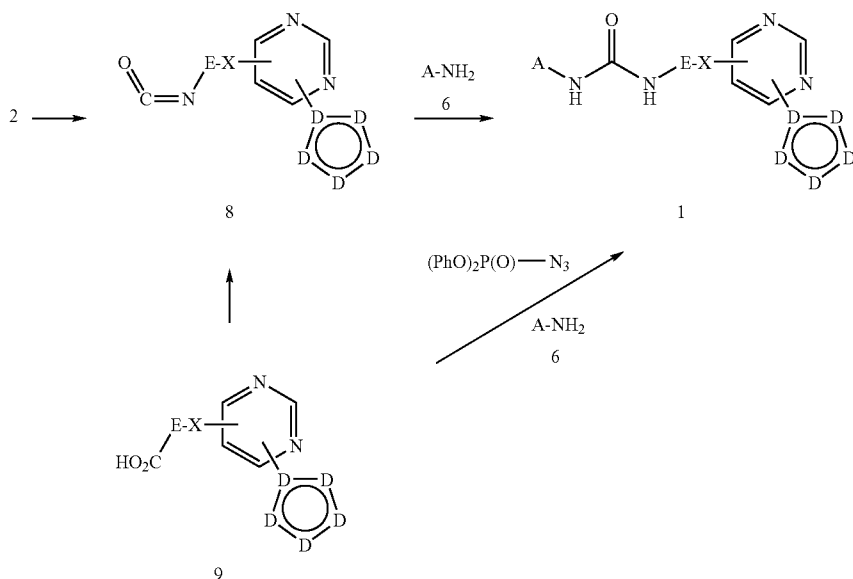


[0087] Additionally, compounds of formula 1 can also be prepared from carboxylic acids 7 by the intermediacy of in-situ generated acyl azides (Curtius rearrangement) as indicated in Scheme 3. Preferred conditions for Scheme 3 include the mixing of acid 7 with amine 2 and diphenylphosphoryl azide in a solvent such as 1,4-dioxane or dimethylformamide in the presence of base, such as triethylamine, and raising the temperature of the reaction to about 80-120° C. to affect the Curtius rearrangement.



[0088] By analogy to Schemes 1 and 3 above, it will be recognized by those skilled in the art that the compounds of formula 1 can also be prepared by the union of amines A-NH₂ 6 with isocyanates 8 (Scheme 4). Isocyanates 8 can be prepared from general amines 2 by standard synthetic methods. Suitable methods for example, include reaction of 2 with phosgene, or a phosgene equivalent such as diphosgene, triphosgene, or N,N-dicarbonylimidazole. In addition to the methods above for converting amines 2 into isocyanates 8, the isocyanates 8 can also be prepared in situ by the Curtius rearrangement and variants thereof. Those skilled in the art will further recognize that isocyanates 8 need not be isolated, but may be simply generated in situ. Accordingly, acid 9 can be converted to compounds of formula 1 either with or without isolation of 8. Preferred conditions for the direct conversion of acid 9 to compounds of formula 1 involve the mixing of acid 9, amine A-NH₂ 6, diphenylphosphoryl azide and a suitable base, for example triethylamine, in an aprotic solvent, for example dioxane. Heating said mixture to a temperature of between 80 and 120° C. provides the compounds of formula 1.

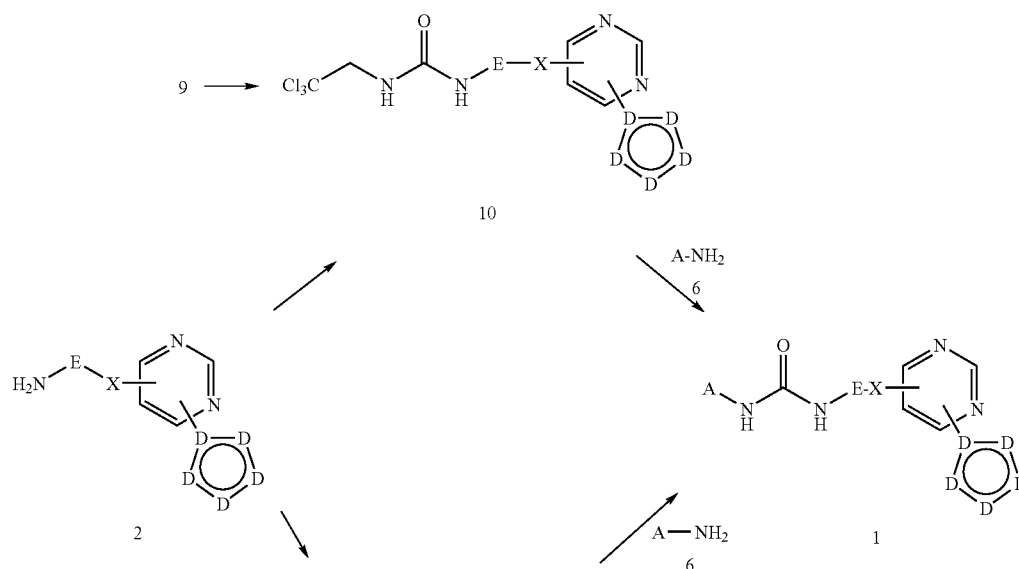
Scheme 4

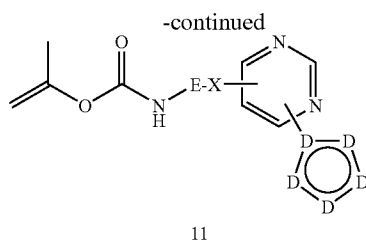


[0089] Additionally, compounds of formula 1 can also be prepared from amines 2 by first preparing stable isocyanate equivalents, such as carbamates (Scheme 5). Especially preferred carbamates include trichloroethyl carbamates (10) and isopropenyl carbamates (11) which are readily prepared from amine 2 by reaction with trichloroethyl chloroformate or isopropenyl chloroformate respectively using standard conditions familiar to those skilled in the art. Further reaction of

carbamates 10 or 11 with amine A-NH₂ 6 provides compounds of formula 1. Those skilled in the art will further recognize that certain carbamates can also be prepared from acid 9 by Curtius rearrangement and trapping with an alcoholic co-solvent. For example, treatment of acid 9 (Scheme 5) with diphenylphosphoryl azide and trichloroethanol at elevated temperature provides trichloroethyl carbamate 10.

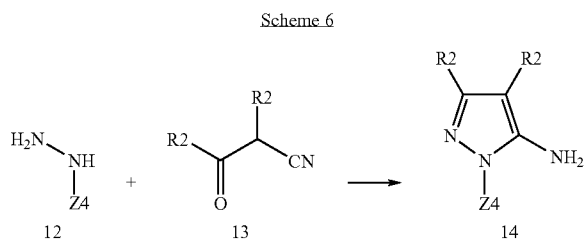
Scheme 5



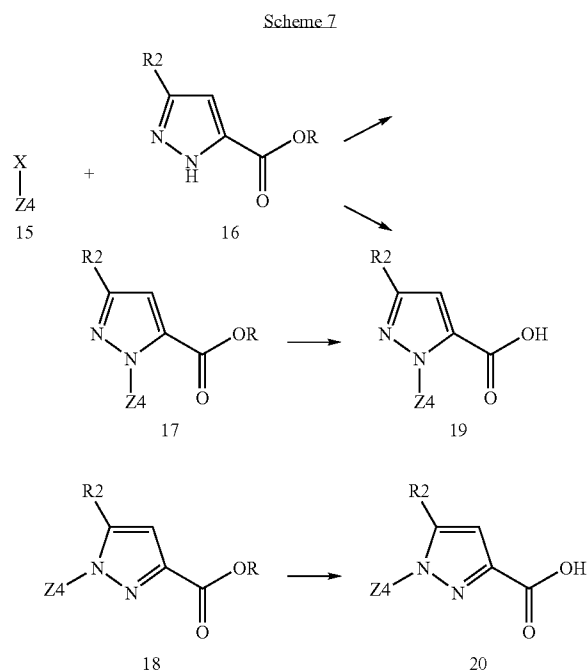


[0090] Many methods exist for the preparation of amines $A-NH_2$ 6 and acids $A-CO_2H$ 7, depending on the nature of the A-moiety. Indeed, many such amines (6) and acids (7) useful for the preparation of compounds of formula 1 are available from commercial vendors. Some non-limiting preferred synthetic methods for the preparation of amines 6 and acids 7 are outlined in the following schemes and accompanying examples.

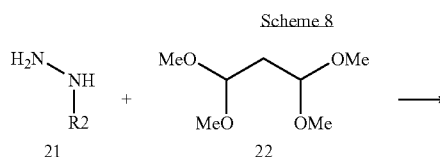
[0091] As illustrated in Scheme 6, Z4-substituted pyrazol-5-yl amines 14 (a preferred aspect of $A-NH_2$ 6, Scheme 2) are available by the condensation of hydrazines 12 and beta-keto nitriles 13 in the presence of a strong acid. Preferred conditions for this transformation are by heating in ethanolic HCl. Many such hydrazines 12 are commercially available. Others can be prepared by conditions familiar to those skilled in the art, for example by the diazotization of amines followed by reduction or, alternately from the reduction of hydrazones prepared from carbonyl precursors.

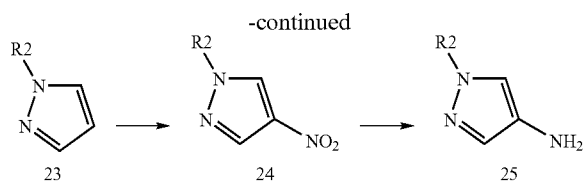


[0092] Another preferred method for constructing Z4-substituted pyrazoles is illustrated by the general preparation of pyrazole acids 19 and 20. (Scheme 7), aspects of general acid $A-CO_2H$ 7 (Scheme 3). As indicated in Scheme 7, pyrazole 5-carboxylic esters 17 and 18 can be prepared by the alkylation of pyrazole ester 16 with Z4-X 15D wherein X represents a leaving group on a Z4 moiety such as a halide, triflate, or other sulfonate. Preferred conditions for the alkylation of pyrazole 16 include the use of strong bases such as sodium hydride, potassium tert-butoxide and the like in polar aprotic solvents such as dimethylsulfoxide, dimethylformamide or tetrahydrofuran. Z4-substituted pyrazoles 17 and 18 are isomers of one another and can both be prepared in the same reactions vessel and separated by purification methods familiar to those skilled in the art. The esters 17 and 18 in turn can be converted to acids 19 and 20 using conditions familiar to those skilled in the art, for example saponification in the case of ethyl esters, hydrogenation in the case of benzyl esters or acidic hydrolysis in the case of tert-butyl esters.

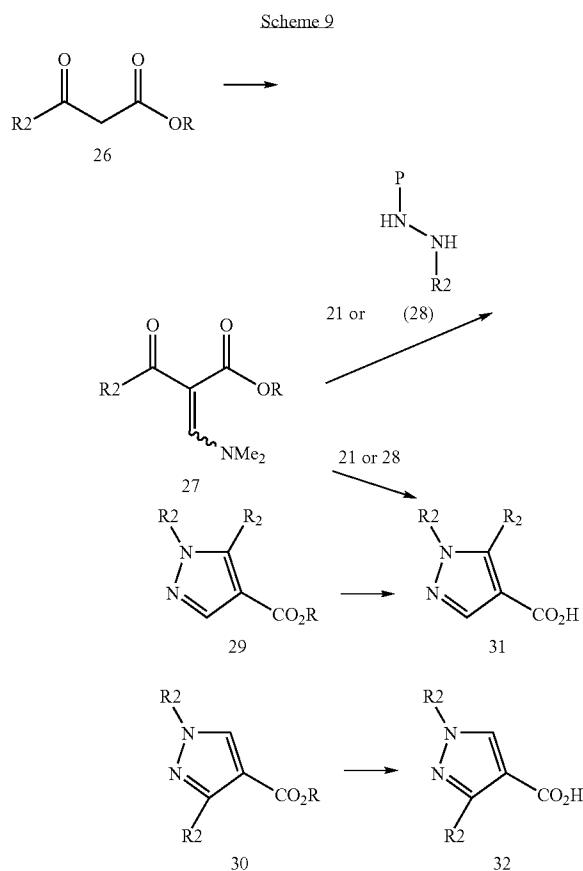


[0093] Scheme 8 illustrates the preparation of pyrazole amine 25, a further example of general amine $A-NH_2$ 6. Acid-catalyzed condensation of R2-substituted hydrazine 21 with 1,1,3,3-tetramethoxypropane 22 provides R2-substituted pyrazole 23. Those skilled in the art will further recognize that R2-substituted pyrazole 23 can also be prepared by direct alkylation of pyrazole. Pyrazole 23 can be regioselectively nitrated to provide nitro-pyrazole 24 by standard conditions familiar to those skilled in the art. Finally, hydrogenation of nitro-pyrazole 24 employing a hydrogenation catalyst such as palladium or nickel provides pyrazole amine 25, an example of general amine $A-NH_2$ 6.

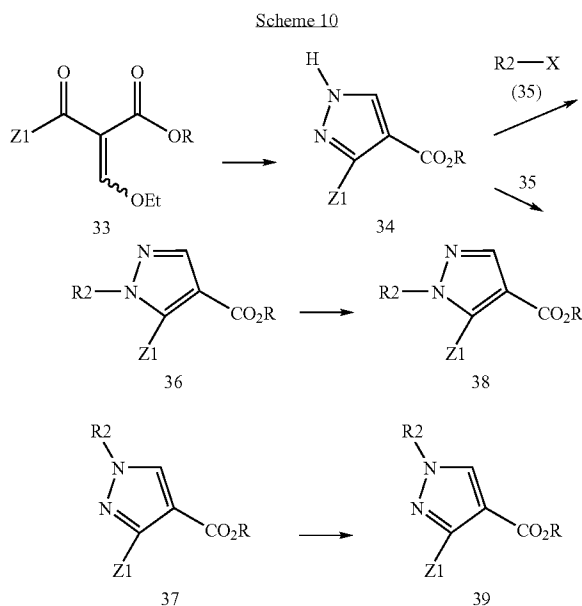




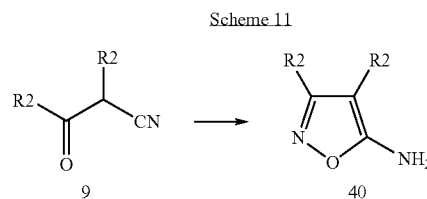
[0094] Additional pyrazoles useful for the synthesis of compounds of formula 1 can be prepared as described in Scheme 9. Thus, keto-ester 26 can be reacted with N,N-dimethylformamide dimethyl acetal to provide 27. Reaction of 27 with either 21 or 28 (wherein P is an acid-labile protecting group) in the presence of acid provides 29 or 30. In practice, both 29 and 30 can be obtained from the same reaction and can be separated by standard chromatographic conditions. In turn, esters 29 and 30 can be converted to acids 31 and 32 respectively as previously described in Scheme 7.



[0095] In a manner similar to Scheme 9, NH-pyrazole 34 can be prepared by reaction of acrylate 33 with hydrazine (Scheme 10). Alkylation of 34 with R²-X 35 as described above for Scheme 7 provides mixtures of pyrazole esters 36 and 37 which are separable by standard chromatographic techniques. Further conversion of esters 36 and 37 to acids 38 and 39 can be accomplished as described above in Scheme 7.



[0096] General amines 6 containing an isoxazole ring can be prepared as described in Scheme 11. Thus, by analogy to Scheme 6, reaction of keto-nitrile 9 with hydroxylamine can provide the 5-aminoisoxazole 40. Preferred conditions for the formation of 5-aminoisoxazole 40 include the treatment of 9 with hydroxylamine in the presence of aqueous sodium hydroxide, optionally in the presence of an alcoholic co-solvent at a temperature between 0 and 100° C.

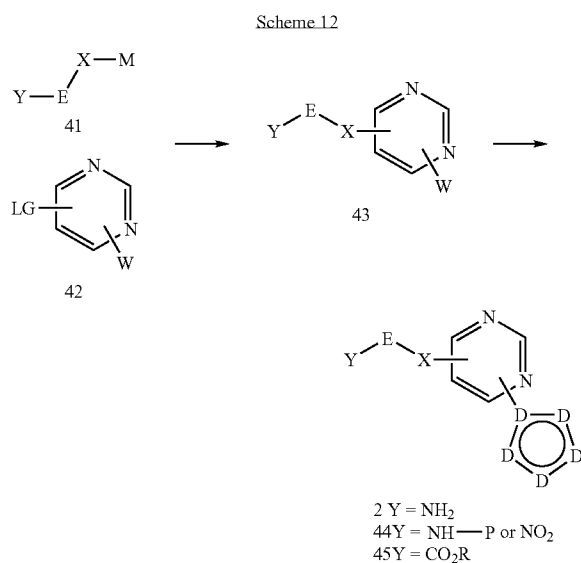


[0097] Amines 2 useful for the invention can be synthesized according to methods commonly known to those skilled in the art. Amines of general formula 2 contain three rings and can be prepared by the stepwise union of three monocyclic subunits as illustrated in the following non-limiting Schemes. Scheme 12 illustrates one mode of assembly in which an E-containing subunit 41 is combined with the central pyridine ring 42 to provide the bicyclic intermediate 43. In one aspect this general Scheme, the "M" moiety of 41, represents a hydrogen atom of a heteroatom on the X linker that participates in a nucleophilic aromatic substitution reaction with monocycle 42. Such reactions may be facilitated by the presence of bases (for example, potassium tert-butoxide), thus M may also represent a suitable counterion (for example potassium, sodium, lithium, or cesium) within an alkoxide, sulfide or amide moiety. Alternately, the "M" group can represent a metallic species (for example, copper, boron, tin, zirconium, aluminum, magnesium, lithium, silicon, etc.) on a carbon

atom of the X moiety that can undergo a transition-metal-mediated coupling with monocycle 42.

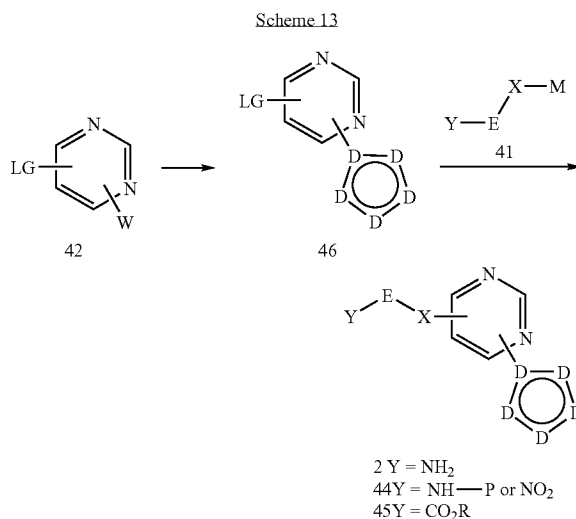
[0098] The “Y” group of monocyclic species 41 is an amine or an amine surrogate, such as an amine masked by a protecting group (“P” in formula 44), a nitro group, or a carboxy acid or ester that can be used to prepare an amine via known rearrangement. Examples of suitable protecting groups “P” include but are not limited to tert-butoxycarbonyl (Boc), benzyloxycarbonyl (Cbz), and acetamide. In the instances wherein the “Y”-group of intermediate 41 is not an amine, the products of Scheme 12 will be amine surrogates such as 44 or 45 that can be converted to amine 2 by a deprotection, reduction or rearrangement (for example, Curtius rearrangement) familiar to those skilled in the art.

[0099] In these instances, the “LG” of monocycle 42 represents a moiety that can either be directly displaced in a nucleophilic substitution reaction (with or without additional activation) or can participate in a transition-mediated union with fragment 41. The W group of monocycle 42 or bicycle 43 represents a moiety that allows the attachment of the pyrazole. In one aspect, the “W” group represents a halogen atom that will participate in a transition-metal-mediated coupling with a pre-formed heterocyclic reagent (for example a boronic acid or ester, or heteroaryl stannane) to give rise to amine 2. In another aspect, the “W” group of 42 and 43 represents a functional group that can be converted to a five-membered heterocycle by an annulation reaction. Non-limiting examples of such processes would include the conversion of a cyano, formyl, carboxy, acetyl, or alkynyl moiety into a five-membered heterocycle moiety. It will be understood by those skilled in the art that such annulations may in fact be reaction sequences and that the reaction arrows in Scheme 12 may represent either a single reaction or a reaction sequence. Additionally, the “W” group of 43 may represent a leaving group (halogen or triflate) that can be displaced by a nucleophilic nitrogen atom of a pyrazole, triazole or imidazole ring.

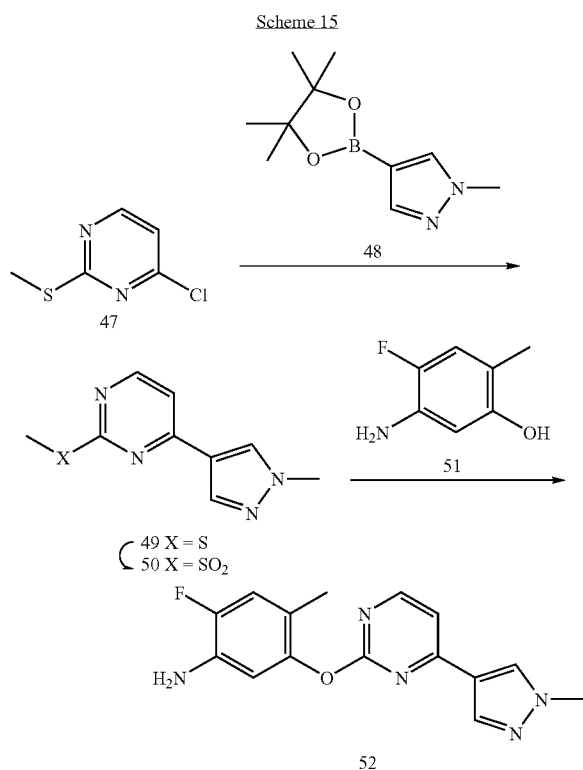


[0100] Scheme 13 illustrates another general method of preparing amines 2 by first attaching the 5-membered heterocycle to the pyrimidine ring (42). As before, the “LG” of monocycle 42 represents a moiety that can either be directly

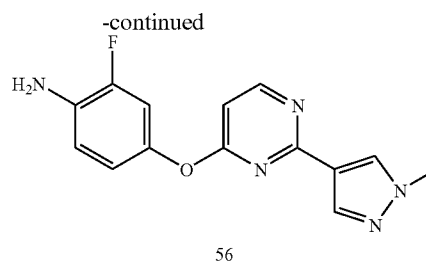
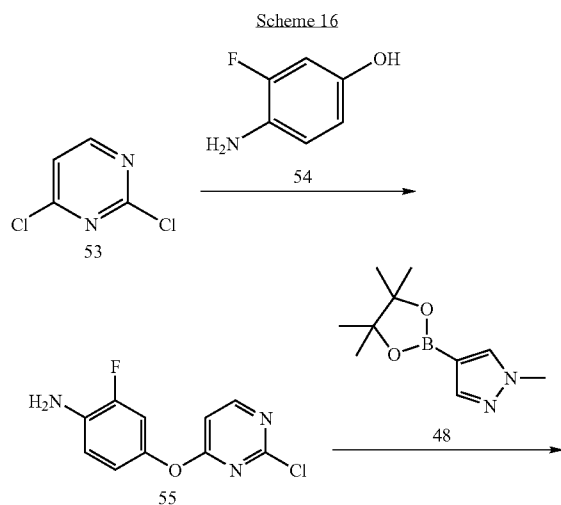
displaced in a nucleophilic substitution reaction (with or without additional activation) or can participate in a transition-mediated union with fragment 41. The “W” group of monocycle 42 represents a moiety that allows the attachment of a 5-membered heterocycle. In one aspect, the “W” group represents a halogen atom that will participate in a transition-metal-mediated coupling with a pre-formed heterocyclic reagent (for example, a boronic acid or ester, or heteroaryl stannane) to give rise to amine 2. In another aspect, the “W” group of 42 represents a functional group that can be converted to a five-membered heterocycle by an annulation reaction. Additionally, the “W” group of 42 may represent a leaving group (halogen or triflate) that can be displaced by a nucleophilic nitrogen atom of a pyrazole, triazole or imidazole ring. After conversion of 49 to 46, the “LG” moiety can be replaced with an “X” linkage to the E-sub-unit to provide the tricyclic amine 2, as described above in Scheme 12. Those skilled in the art will recognize that amines 2 may be accessed directly from the union of 46 and 41 or may arise indirectly via the intermediacy of 44 or 45, as described previously.



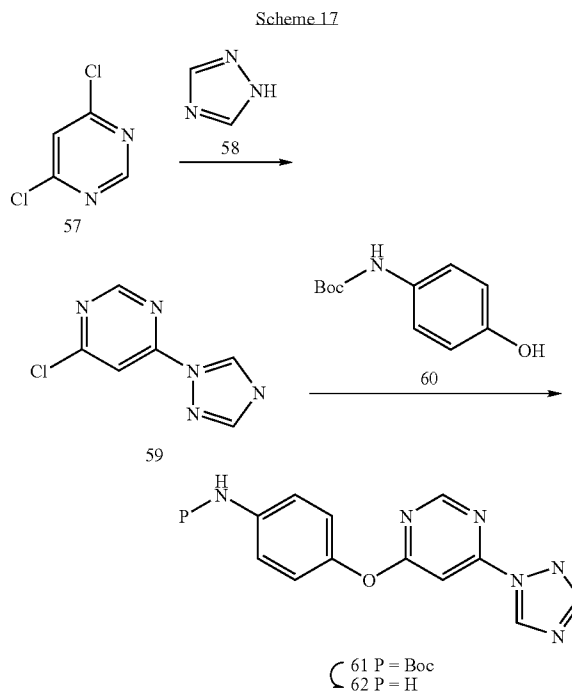
[0101] A specific example of Scheme 13 is illustrated by the preparation of amine 55 in Scheme 14. Thus, commercially available pyrimidine 47, an example of general intermediate 42, undergoes a palladium-catalyzed coupling with the commercially available pyrazole boronate 48 to provide the bicycle 49, an example of general intermediate 46. Oxidation of the sulfide moiety of 49 (The “LG” group of general intermediate 46) with m-chloroperbenzoic acid firer activates this moiety toward nucleophilic displacement and gives rise to intermediate 50. Treatment of sulfone 50 with phenol 51 in the presence of a base provides tricyclic amine 52, an example of general amine 2. Preferred bases for the later transformation include potassium carbonate and potassium tert-butoxide in polar aprotic solvents such as dimethylformamide or dimethylacetamide.



[0102] Similarly, Scheme 16 illustrates the preparation amine 56 as a non-limiting example of general Scheme 12. Thus, 2,4-dichloropyrimidine (53) can be reacted with phenol 54 in the presence of a base to provide 55, an example of general intermediate 43 (Scheme 12). Further reaction of chloropyrimidine 55 with pyrazole boronate 48 in the presence of palladium catalyst provides amine 56, an example of general amine 2.



[0103] As an additional example of general Scheme 13, Scheme 17 illustrates the preparation of amine 62, an additional example of general amine 2. In this instance, 4,6-dichloropyrimidine (57), an example of general pyrimidine 42 (Scheme 13) wherein “W” is chloro, is reacted with 1,2,4-triazole 58 to provide 59, an example of general intermediate 46 (Scheme 13) wherein “LG” is chloro. Further reaction of 59 with phenol 60 provides the Boc-protected amine 61, corresponding to general intermediate 44 (Scheme 13 wherein “P” is tert-butoxycarbonyl [Boc]). Treatment of 61 with an acid, for example trifluoroacetic acid, provides amine 62, an example of general amine 2.

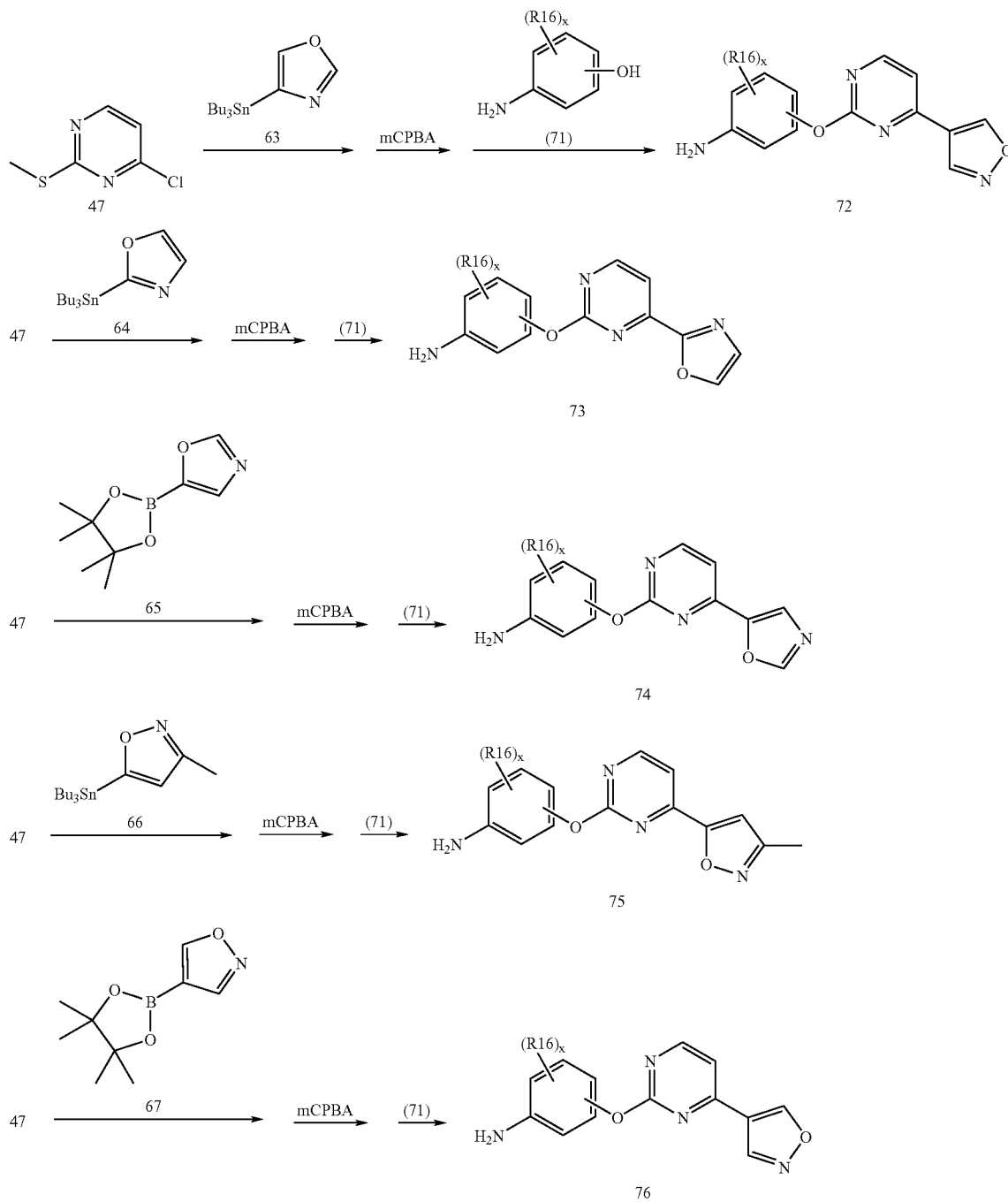


[0104] As indicated in Scheme 18, additional non-limiting examples of general amine 2 can also be prepared from chloropyrimidine 47 by the three step sequence of Scheme 15 (Step 1: palladium-catalyzed cross-coupling reaction; Step 2: Sulfide oxidation to sulfone; Step 3: Displacement of sulfone with phenol 71, wherein R16 is an optional substituent as described above and x is 0-2). Suzuki cross-coupling reactions using readily available boronates or Stille cross-coupling reactions using readily available stannanes are interchangeable for Step 1. Thus, in a 3-step sequence as indicated

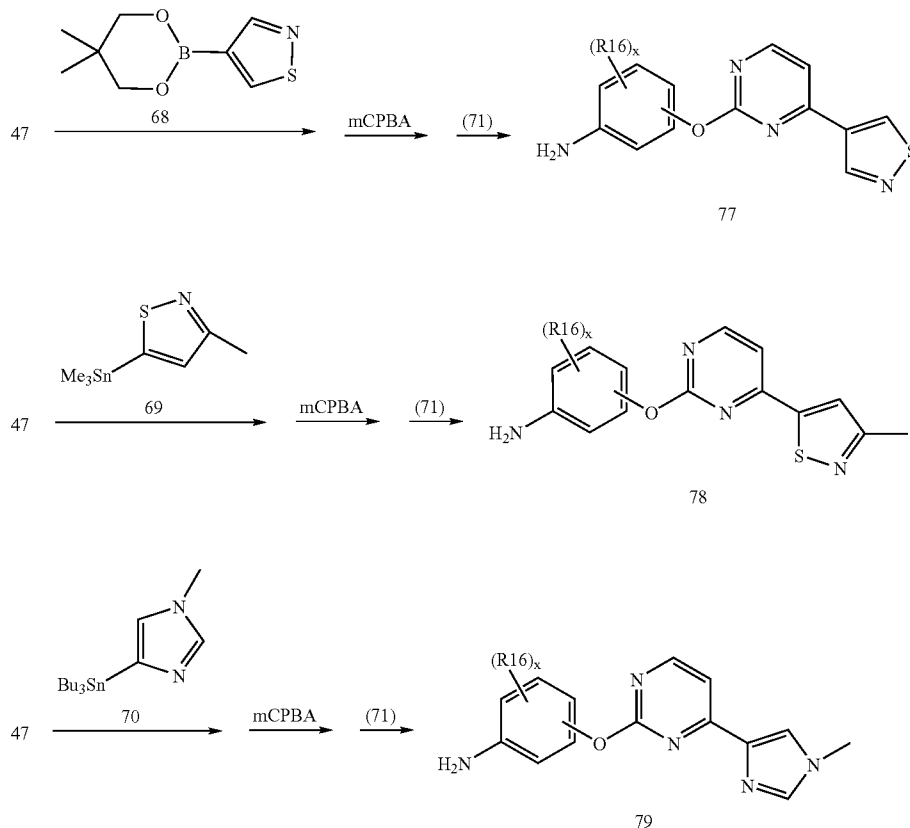
in Scheme 18, chloropyrimidine 47, can be combined with tributylstannane 63 (see: Cheng et al., *Biorg. Med. Chem. Lett.*, 2006, 2076), stannane 64 (Aldrich Chemical), boronate 65 (BoroPharm), tributylstannane 66 (see: Sakamoto, et al. *Tetrahedron*, 1991, 5111), boronate 67 (Frontier Scientific),

boronate 68 (see: Blackaby, et al., U.S. Pat. No. 7,030,128), trimethylstannane 69 (see: Wentland, et al. *J. Med. Chem.*, 1993, 1580) or stannane 70 (see: Nicolaou, et. al., *Chem. Med. Chem.*, 2006, 41) to provide general amines 72-79 respectively.

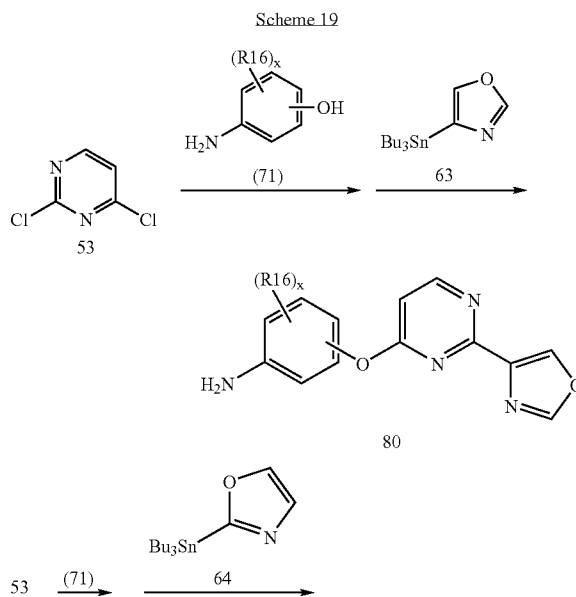
Scheme 18

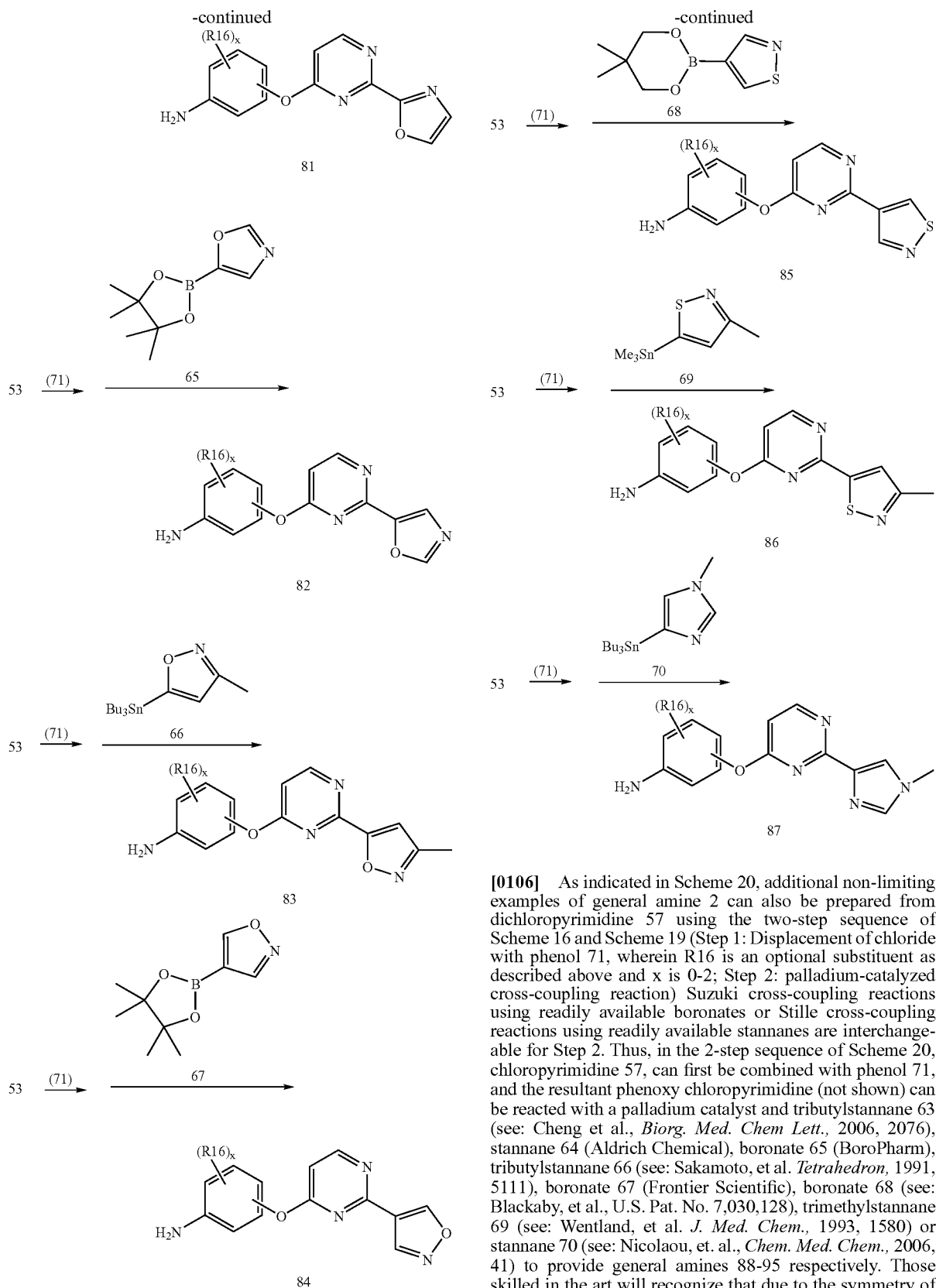


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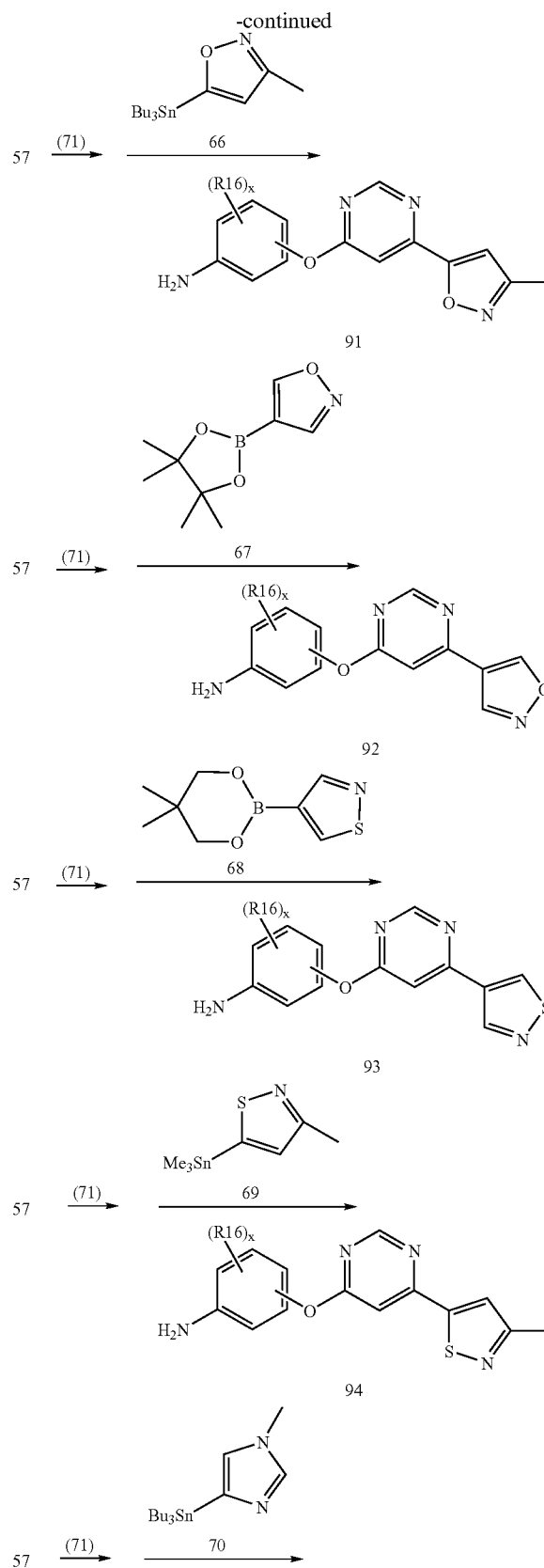
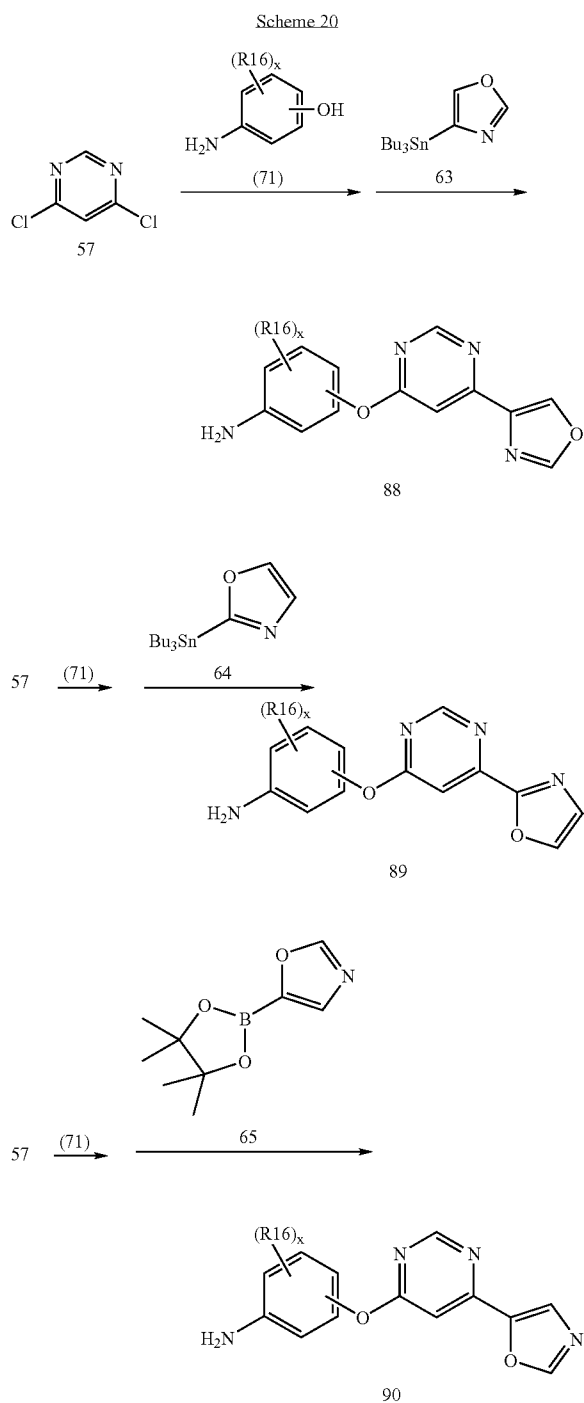
[0105] As indicated in Scheme 19, additional non-limiting examples of general amine 2 can also be prepared from dichloropyrimidine 53 by the two-step sequence of Scheme 16 (Step 1: Displacement of chloride with phenol 71, wherein R16 is an optional substituent as described above and x is 0-2; Step 2: palladium-catalyzed cross-coupling reaction). Suzuki cross-coupling reactions using readily available boronates or Stille cross-coupling reactions using readily available stannanes are interchangeable for Step 2. Thus, in the 2-step sequence of Scheme 19, chloropyrimidine 53, can first be combined with phenol 71, and the resultant phenoxy chloropyrimidine (not shown) can be reacted with a palladium catalyst and tributylstannane 63 (see: Cheng et al., *Biorg. Med Chem Lett.*, 2006, 2076), stannane 64 (Aldrich Chemical), boronate 65 (BoroPharm), tributylstannane 66 (see: Sakamoto, et al. *Tetrahedron*, 1991, 5111), boronate 67 (Frontier Scientific), boronate 68 (see: Blackaby, et al., U.S. Pat. No. 7,030,128), trimethylstannane 69 (see: Wentland, et al. *J. Med. Chem.*, 1993, 1580) or stannane 70 (see: Nicolaou, et. al., *Chem. Med. Chem.*, 2006, 41) to provide general amines 80-87 respectively.

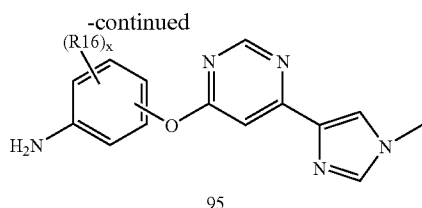




[0106] As indicated in Scheme 20, additional non-limiting examples of general amine 2 can also be prepared from dichloropyrimidine 57 using the two-step sequence of Scheme 16 and Scheme 19 (Step 1: Displacement of chloride with phenol 71, wherein R16 is an optional substituent as described above and x is 0-2; Step 2: palladium-catalyzed cross-coupling reaction) Suzuki cross-coupling reactions using readily available boronates or Stille cross-coupling reactions using readily available stannanes are interchangeable for Step 2. Thus, in the 2-step sequence of Scheme 20, chloropyrimidine 57, can first be combined with phenol 71, and the resultant phenoxy chloropyrimidine (not shown) can be reacted with a palladium catalyst and tributylstannane 63 (see: Cheng et al., *Biorg. Med. Chem. Lett.*, 2006, 2076), stannane 64 (Aldrich Chemical), boronate 65 (BoroPharm), tributylstannane 66 (see: Sakamoto, et al. *Tetrahedron*, 1991, 5111), boronate 67 (Frontier Scientific), boronate 68 (see: Blackaby, et al., U.S. Pat. No. 7,030,128), trimethylstannane 69 (see: Wentland, et al. *J. Med. Chem.*, 1993, 1580) or stannane 70 (see: Nicolaou, et. al., *Chem. Med. Chem.*, 2006, 41) to provide general amines 88-95 respectively. Those skilled in the art will recognize that due to the symmetry of dichloropyrimidine 57, the general amine products of

Scheme 20 can also be prepared by reversing the order of the 2-step sequence (Step 1: Palladium-catalyzed cross-coupling reaction of 57 with 63-70; Step 2: Displacement of chloride with phenol 71).





[0107] Additional synthetic methods for the preparation of compounds of formula 1 are found in the following examples.

Section 3

EXAMPLES

General Method A

[0108] To a stirring solution of the carboxylic acid (0.24 mmol) and TEA (1.2 mmol) in 1,4-dioxane (4.5 mL) at RT was added DPPA (0.29 mmol). After stirring for 0.5 h at RT, the appropriate amine (0.71 mmol) was added and the reaction was stirred with heating at 100° C. for 2 h. The reaction was cooled to RT, diluted with brine (15 mL) and extracted with EtOAc (3×30 mL). The combined organic layers were dried (MgSO₄) and concentrated. The residue was purified by chromatography to afford the target compound.

Example A1

[0109] 4-Fluoro-2-methyl-phenol (25 g, 0.2 mol) was added to a solution of sodium hydroxide (9.7 g, 0.24 mol) in water (160 mL) and the resultant solution was cooled to 0° C. Methyl chloroformate (24.2 g, 0.26 mol) was added dropwise at 0° C. At the completion of the reaction, the pH was adjusted to pH 8 with saturated aqueous Na₂CO₃ and then mixture was extracted with ethyl acetate (3×300 mL). The combined organic extracts were washed with water and brine, dried (MgSO₄) and were concentrated under reduced pressure to provide carbonic acid 4-fluoro-2-methyl-phenyl ester methyl ester (30 g, 82% yield). ¹H NMR (300 MHz, DMSO-d₆): δ 7.22-7.13 (m, 2 H), 7.05 (m, 1H), 3.81 (s, 1H), 2.12 (s, 3H).

[0110] To a solution of carbonic acid 4-fluoro-2-methyl-phenyl ester methyl ester (15 g, 81.5 mmol) in conc. sulfuric acid (100 mL) at 0° C. was added powdered KNO₃ (8.3 g, 82.2 mmol) in several portions. The reaction mixture was stirred for 1 hour at 0° C. and was then poured into ice water and extracted with ethyl acetate (3×100 mL). The extracts were washed with water and brine, dried (MgSO₄), concentrated in vacuo and purified by silica gel chromatography to provide carbonic acid 4-fluoro-2-methyl-5-nitro-phenyl ester methyl ester (2.0 g, 11% yield). ¹H NMR (300 MHz, DMSO-d₆): δ 8.14 (d, J=6.9, 1H), 7.60 (d, J=12.0 Hz, 1H), 3.86 (s, 3H), 2.25 (s, 3H).

[0111] To a solution of aqueous sodium hydroxide (1.2 N, 20 mL, 24 mmol) was added 4-fluoro-2-methyl-5-nitro-phenyl ester methyl ester (2.0 g, 8.7 mmol), then the resultant mixture was refluxed for 2 hours. The reaction was cooled to RT and partitioned between EtOAc and water. The organic layer was washed with water and brine, dried (MgSO₄), and concentrated in vacuo to provide 4-fluoro-2-methyl-5-nitro-phenol (1.4 g, 93% yield). ¹H NMR (300 MHz, DMSO-d₆): δ 10.33 (s, 1H), 7.45 (d, J=6.6, 1H), 7.32 (d, J=12.3 Hz, 1H), 2.19 (s, 3H).

[0112] A mixture of 4-fluoro-2-methyl-5-nitro-phenol (1.4 g, 8.2 mmol) and 10% Pd/C (0.3 g, 20%/w) in MeOH (80 mL) was stirred under H₂ (30 psi) for 2 h. The Pd/C was removed by filtration and the filtrate was concentrated to give 5-amino-4-fluoro-2-methyl-phenol (0.68 g, 62% yield). ¹H NMR (300 MHz, DMSO-d₆): δ 8.75 (s, 1H), 6.62 (d, J=12.0 Hz, 1H), 6.21 (d, J=8.1 Hz, 1H), 4.69 (s, 2H), 1.93 (s, 3H).

[0113] The mixture of 2-methanesulfonyl-4-(1-methyl-1H-pyrazol-4-yl)-pyrimidine and 2-methanesulfinyl-4-(1-methyl-1H-pyrazol-4-yl)-pyrimidine from Example A10 (1 g, 4.2 mmol), 5-amino-4-fluoro-2-methylphenol (1.2 g, 8.5 mmol) and K₂CO₃ (1.2 g, 8.6 mmol) were combined in DMF (10 mL) using a procedure analogous to Example A10 to provide 2-fluoro-4-methyl-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)benzenamine (420 mg). ¹H NMR (400 MHz, DMSO-d₆): δ 8.42 (d, J=5.2 Hz, 1H), 8.39 (s, 1H), 8.07 (s, 1H), 7.40 (d, J=5.2 Hz, 1H), 6.90 (d, J=9.6 Hz, 1H), 6.47 (d, J=8.4 Hz, 1H), 5.02 (br s, 2H), 3.88 (s, 3H), 1.88 (s, 3H); MS (ESI) m/z: 300.2 (M+H⁺).

Example A2

[0114] Methyl chloroformate (77.3 g, 0.82 mol) was added dropwise to a -10° C. solution of 2-chloro-4-fluorophenol (100 g, 0.68 mol) and sodium hydroxide (32.8 g, 0.82 mol) in water (550 mL). After complete addition, the precipitated solid was collected by filtration and washed with water to give 2-chloro-4-fluorophenyl methyl carbonate (110 g, 79% yield). ¹H NMR (300 MHz, DMSO-d₆): δ 7.62 (dd, J=8.1, 2.7 Hz, 1H), 7.50 (dd, J=9.0, 5.4 Hz, 1H), 7.30 (td, J=8.1, 3.0 Hz, 1H), 3.86 (s, 3H); MS (ESI) m/z: 205.2 (M+H⁺).

[0115] To a suspension of 2-chloro-4-fluorophenyl methyl carbonate (110 g, 0.54 mol) in conc. H₂SO₄ (50 mL) was slowly added a mixture comprised of conc. H₂SO₄ (40 mL) and fuming HNO₃ (40.8 mL, 0.89 mol). The resultant mixture was stirred for 30 min at 0° C. The reaction mixture was poured into ice water and the precipitated solid was collected by filtration and washed with water to give 2-chloro-4-fluoro-5-nitrophenyl methyl carbonate (120 g, 90% yield). ¹H NMR (400 MHz, DMSO-d₆): δ 8.45 (d, J=7.2 Hz, 1H), 8.12 (d, J=10.8 Hz, 1H), 3.89 (s, 3H); MS (ESI) m/z: 250.1 (M+H⁺).

[0116] 2-Chloro-4-fluoro-5-nitrophenyl methyl carbonate (120 g 0.48 mol) was combined with a solution of sodium hydroxide (22.7 g, 0.57 mol) in water (300 mL) and the resultant mixture was refluxed for 4 h. The insoluble solids were removed by filtration and the filtrate was acidified with dilute HCl. The precipitated solid was collected by filtration and washed with water to give 2-chloro-4-fluoro-5-nitrophenol (90 g, 98% yield). ¹H NMR (400 MHz, DMSO-d₆): δ 11.18 (s, 1H), 8.10 (d, J=10.4 Hz, 1H), 7.62 (d, J=7.2 Hz, 1H); MS (ESI) m/z: 192.1 (M+H⁺).

[0117] 2-Chloro-4-fluoro-5-nitrophenol (85 g, 0.45 mol) and 10% Pd/C (25 g, 0.023 mol) were combined in EtOH and hydrogenated (50 psi) for 12 h. The reaction mixture was filtered. The filtrate was concentrated in vacuo and purified by silica gel chromatography to provide 3-amino-4-fluorophenol (40 g 70%, yield). ¹H NMR (400 MHz, DMSO-d₆): δ 8.87 (s, 1H), 6.70 (dd, J=11.2, 8.8 Hz, 1H), 6.14 (dd, J=7.8, 2.4 Hz, 1H), 5.84 (m, 1H), 4.92 (s, 2H); MS (ESI) m/z: 128.2 (M+H⁺).

[0118] 4-Chloro-2-methylsulfonyl-pyrimidine (1.4 g, 8.8 mmol), 1-methyl-4-(4,4,5,5-tetramethyl-[1,3,2]dioxaborolan-2-yl)-1H-pyrazole (2.0 g, 1.1 eq), Na₂CO₃ (2.8 g, 3 eq) and Pd(PPh₃)₄ (500 mg, 0.43 mmol) were combined in a solvent comprised of toluene/EtOH/H₂O (4/4/1, 20 mL). The

reaction mixture was purged with argon and heated to 100° C. overnight. The reaction was filtered to remove insolubles and the filtrate was concentrated in vacuo. The residue was purified by silica gel chromatography to provide 4-(1-methyl-1H-pyrazol-4-yl)-2-(methylthio)pyrimidine contaminated with triphenylphosphine oxide (2.0 g, >100% yield). ¹H NMR (300 MHz, DMSO-*d*₆): δ 8.49 (d, J=5.1 Hz, 1H), 8.46 (s, 1H), 8.12 (s, 1H), 7.38 (d, J=5.1 Hz, 1H), 3.89 (s, 3H), 2.52 (s, 3H).

[0119] A solution of 4-(1-methyl-1H-pyrazol-4-yl)-2-methylsulfanyl-pyrimidine (2.0 g crude, 8.8 mmol) in dichloromethane (20 mL) was treated with *m*-CPBA (3.0 g, 17.4 mmol) portionwise at RT. The reaction was stirred 2 h and was quenched with saturated aqueous Na₂SO₃ (3 mL). The mixture was partitioned with saturated aq Na₂CO₃ and the organics were washed with brine, dried (Na₂SO₄), and concentrated to provide a mixture (2.0 g) of 2-methanesulfonyl-4-(1-methyl-1H-pyrazol-4-yl)-pyrimidine and 2-methanesulfinyl-4-(1-methyl-1H-pyrazol-4-yl)-pyrimidine with a molar ratio of 1:0.3. ¹H NMR (400 MHz, DMSO-*d*₆): δ 8.83 (d, J=5.2 Hz, 1H), 8.82 (d, J=5.2 Hz, 0.24 H), 8.57 (s, 1H), 8.57 (s, 0.24H), 8.21 (s, 1H), 8.21 (s, 0.23H), 7.80 (d, J=5.6 Hz, 1H), 7.80 (d, J=5.6 Hz, 0.25H), 3.48 (s, 3H), 2.88 (s, 0.7H).

[0120] The above mixture of 2-methanesulfonyl-4-(1-methyl-1H-pyrazol-4-yl)-pyrimidine and 2-methanesulfinyl-4-(1-methyl-1H-pyrazol-4-yl)-pyrimidine (1 g, 4.2 mmol), 4-amino-3-fluoro-phenol (1.1 g, 8.6 mmol) and K₂CO₃ (1.2 g, 8.6 mmol) in DMF (10 mL) was heated at 100° C. for 12 h. The reaction was partitioned between H₂O and EtOAc (3×50 mL). The combined organics were dried (Na₂SO₄), concentrated in vacuo and chromatographed to 2-fluoro-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)benzenamine (402 mg). ¹H NMR (400 MHz, DMSO-*d*₆): δ 8.44 (d, J=5.2 Hz, 1H), 8.39 (s, 1H), 8.07 (s, 1H), 7.41 (d, J=5.2 Hz, 1H), 6.98 (t, J=9.6 Hz, 1H), 6.53 (dd, J=5.6, 2.0 Hz, 1H), 6.28 (d, J=8.4 Hz, 1H), 5.25 (br s, 2H), 3.88 (s, 3H). MS (ESI) *m/z*: 286.2 (M+H⁺).

Example B1

[0121] *t*-Butylhydrazine and 1,1,1,3-tetramethoxypropane were combined according to literature procedures to yield 1-*t*-butyl-1H-pyrazol-4-amine. See Ger. Offen., DE3332270, 21 Mar. 1985.

Example 1

[0122] To a biphasic solution of Example A1 (0.071 g, 0.23 mmol) in EtOAc (5 mL) and NaHCO₃ (10 mL) was added prop-1-en-2-yl carbonochloridate (0.043 g, 0.35 mmol) and the mixture was stirred for 2 h at RT. The layers were separated and the aqueous layer was extracted with EtOAc (1×5 mL). The combined organics were washed with brine, dried (Na₂SO₄) and concentrated in vacuo to afford prop-1-en-2-yl 2-fluoro-4-methyl-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenylcarbamate as an off-white solid. MS (ESI) *m/z*: 384.2 (M+H⁺).

[0123] A solution of prop-1-en-2-yl 2-fluoro-4-methyl-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenylcarbamate, Example B1 (0.033 g, 0.237 mmol) and DBU (catalytic) was dissolved in THF (2 mL) and stirred at 55° C. for 6 h. Solvents were removed and the crude residue was purified by column chromatography (methanol/CH₂Cl₂) to afford 1-(1-*t*-butyl-1H-pyrazol-4-yl)-3-(2-fluoro-4-methyl-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)

phenyl)urea as a white solid. (0.089 mg, 81% yield). ¹H NMR (400 MHz, DMSO-*d*₆): δ 8.66 (s, 1H), 8.50 (d, J=1.6 Hz, 1H), 8.44 (d, J=5.2 Hz, 1H), 8.42 (s, 1H), 8.09 (s, 1H), 7.91 (d, J=7.2 Hz, 1H), 7.77 (s, 1H), 7.44 (d, J=5.2 Hz, 1H), 7.36 (s, 1H), 7.18 (d, J=12.0 Hz, 1H), 3.87 (s, 3H), 2.01 (s, 3H), 1.46 (s, 9H); MS (ESI) *m/z*: 465.3 (M+H⁺).

Example 2

[0124] To a biphasic solution of Example A1 (0.075 g, 0.26 mmol) in EtOAc (5 mL) and NaHCO₃ (10 mL) was added prop-1-en-2-yl carbonochloridate (0.048 g, 0.35 mmol) and the mixture was stirred for 2 h at RT. The layers were separated and the aqueous layer was extracted with EtOAc (1×5 mL). The combined organics were washed with brine, dried (Na₂SO₄) and concentrated in vacuo to afford prop-1-en-2-yl 2-fluoro-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenylcarbamate as an off-white solid. MS (ESI) *m/z*: 370.2 (M+H⁺).

[0125] A solution of prop-1-en-2-yl 2-fluoro-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenylcarbamate, Example B1 (0.037 g, 0.26 mmol), DBU (catalytic) in THF (2 mL) was stirred at 55° C. for 6 h. Solvents were removed and the crude residue was purified by column chromatography (methanol/CH₂Cl₂) to afford 1-(1-*t*-butyl-1H-pyrazol-4-yl)-3-(2-fluoro-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea as a white solid. (0.089 mg, 75% yield). ¹H NMR (400 MHz, DMSO-*d*₆): δ 8.73 (s, 1H), 8.61 (d, J=2.4 Hz, 1H), 8.46 (d, J=5.2 Hz, 1H), 8.42 (s, 1H), 8.10 (s, 1H), 8.04 (dd, J=7.2 Hz, 2.8 Hz, 1H), 7.79 (s, 1H), 7.45 (d, J=5.2 Hz, 1H), 7.38 (s, 1H), 7.26 (dd, J=10.8 Hz, 8.8 Hz, 1H), 6.81-6.78 (m, 1H), 3.87 (s, 3H), 1.46 (s, 9H); MS (ESI) *m/z*: 451.2 (M+H⁺).

Example 3

[0126] Using General Method A, 3-*t*-butyl-1-methyl-1H-pyrazole-5-carboxylic acid (0.074 g, 0.4 mmol), Example A1 (0.081 g, 0.27 mmol), triethylamine (0.0892 g, 0.8 mmol) and DPPA (0.15 g, 0.54 mmol) were combined and purified via chromatography (EtOAc/hexanes) to afford 1-(3-*t*-butyl-1-methyl-1H-pyrazol-5-yl)-3-(2-fluoro-4-methyl-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea as white solid (0.07 g, 54% yield). ¹H NMR (400 MHz, DMSO-*d*₆): δ 8.88 (s, 1H), 8.82 (d, J=2.4 Hz, 1H), 8.44 (d, J=4.8 Hz, 1H), 8.42 (s, 1H), 8.08 (s, 1H), 7.89 (d, J=7.6 Hz, 1H), 7.44 (d, J=5.2 Hz, 1H), 7.22 (d, J=11.6 Hz, 1H), 6.02 (s, 1H), 3.87 (s, 3H), 3.57 (s, 3H), 2.02 (s, 3H), 1.15 (s, 9H); MS (ESI) *m/z*: 479.3 (M+H⁺).

Example 4

[0127] Using General Method A, 3-*t*-butyl-1-methyl-1H-pyrazole-5-carboxylic acid (0.072 g, 0.39 mmol), Example A2 (0.075 g, 0.26 mmol), triethylamine (0.08 g, 0.79 mmol) and DPPA (0.14 g, 0.52 mmol) were combined and purified via chromatography (EtOAc/hexanes) to afford 1-(3-*t*-butyl-1-methyl-1H-pyrazol-5-yl)-3-(2-fluoro-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea as white solid (0.062 g, 51% yield). ¹H NMR (400 MHz, DMSO-*d*₆): δ 8.95 (s, 1H), 8.93 (d, J=2.0 Hz, 1H), 8.46 (d, J=5.2 Hz, 1H), 8.42 (s, 1H), 8.08 (s, 1H), 8.02 (dd, J=6.8 Hz, 2.8 Hz, 1H), 7.45 (d, J=5.2 Hz, 1H), 7.30 (dd, J=11.2 Hz, 2 Hz, 1H), 6.87-6.83 (m, 1H), 6.04 (s, 1H), 3.87 (s, 3H), 3.58 (s, 3H), 1.16 (s, 9H); MS (ESI) *m/z*: 465.3 (M+H⁺).

dazol-4-yl)pyrimidin-4-yloxy)phenyl)urea, 1-(1-tert-butyl-1H-pyrazol-4-yl)-3-(2-fluoro-4-(6-(1-methyl-1H-1,2,3-triazol-4-yl)pyrimidin-4-yloxy)phenyl)urea, 1-(4-(6-(1H-1,2,4-triazol-1-yl)pyrimidin-4-yloxy)-2-fluorophenyl)-3-(1-tert-butyl-1H-pyrazol-4-yl)urea, 1-(4-(6-(4H-1,2,4-triazol-3-yl)pyrimidin-4-yloxy)-2-fluorophenyl)-3-(1-tert-butyl-1H-pyrazol-4-yl)urea, 1-(4-(6-(1H-1,2,3-triazol-1-yl)pyrimidin-4-yloxy)-2-fluorophenyl)-3-(1-tert-butyl-1H-pyrazol-4-yl)urea, 1-(4-(6-(1,3,4-thiadiazol-2-yl)pyrimidin-4-yloxy)-2-fluorophenyl)-3-(1-tert-butyl-1H-pyrazol-4-yl)urea, 1-(5-(4-(1H-pyrazol-4-yl)pyrimidin-2-yloxy)-2-fluorophenyl)-3-(3-tert-butylisoxazol-5-yl)urea, 1-(5-(4-(1H-pyrazol-4-yl)pyrimidin-2-yloxy)-2-fluorophenyl)-3-(1-tert-butyl-1H-pyrazol-3-yl)urea, 1-(5-(4-(1H-pyrazol-4-yl)pyrimidin-2-yloxy)-2-fluorophenyl)-3-(5-tert-butylthiophen-3-yl)urea, 1-(5-(4-(1H-pyrazol-4-yl)pyrimidin-2-yloxy)-2-fluorophenyl)-3-(1-tert-butyl-1H-imidazol-4-yl)urea, 1-(5-(4-(1H-pyrazol-4-yl)pyrimidin-2-yloxy)-2-fluorophenyl)-3-(3-tert-butyl-1-methyl-1H-pyrazol-5-yl)urea, 1-(1-tert-butyl-1H-pyrazol-4-yl)-3-(2-fluoro-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea, 1-(1-tert-butyl-1H-pyrazol-3-yl)-3-(2-fluoro-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea, 1-(5-tert-butylthiophen-3-yl)-3-(2-fluoro-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea, 1-(5-(4-(1H-pyrazol-4-yl)pyrimidin-2-yloxy)-2-fluoro-4-methylphenyl)-3-(3-tert-butyl-1-methyl-1H-pyrazol-5-yl)urea, 1-(5-(4-(1H-pyrazol-4-yl)pyrimidin-2-yloxy)-2-fluoro-4-methylphenyl)-3-(3-tert-butylisoxazol-5-yl)urea, H-pyrazol-4-yl)urea, 1-(5-(4-(1H-pyrazol-4-yl)pyrimidin-2-yloxy)-2-fluoro-4-methylphenyl)-3-(1-tert-butyl-1H-pyrazol-3-yl)urea, 1-(5-(4-(1H-pyrazol-4-yl)pyrimidin-2-yloxy)-2-fluoro-4-methylphenyl)-3-(5-tert-butylthiophen-3-yl)urea, 1-(5-(4-(1H-pyrazol-4-yl)pyrimidin-2-yloxy)-2-fluoro-4-methylphenyl)-3-(1-tert-butyl-1H-imidazol-4-yl)urea, 1-(1-tert-butyl-1H-pyrazol-4-yl)-3-(2-fluoro-4-methyl-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea, 1-(1-tert-butyl-1H-pyrazol-3-yl)-3-(2-fluoro-4-methyl-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea, and 1-(5-tert-butylthiophen-3-yl)-3-(2-fluoro-4-methyl-5-(4-(1-methyl-1H-pyrazol-4-yl)pyrimidin-2-yloxy)phenyl)urea.

Section 4. Biological Data

Abl Kinase (SEQ ID NO: 1) Assay

[0130] Activity of Abl kinase (SEQ ID NO:1) was determined by following the production of ADP from the kinase reaction through coupling with the pyruvate kinase/lactate dehydrogenase system (e.g., Schindler, et al. Science (2000) 289, 1938-1942). In this assay, the oxidation of NADH (thus the decrease at $A_{340\text{ nm}}$) was continuously monitored spectrophotometrically. The reaction mixture (100 μ l) contained Abl kinase (1 μ M, Abl from deCode Genetics), peptide substrate (EAIYAAPFAKKK, 0.2 mM), MgCl₂ (10 mM), pyruvate

kinase (4 units), lactate dehydrogenase (0.7 units), phosphoenol pyruvate (1 mM), and NADH (0.28 mM) in 90 mM Tris buffer containing 0.2% octyl-glucoside and 3.5% DMSO, pH 7.5. Test compounds were incubated with Abl (SEQ ID NO:1) and other reaction reagents at 30° C. for 2 h before ATP (500 μ M) was added to start the reaction. The absorption at 340 nm was monitored continuously for 2 hours at 30° C. on Polarstar Optima plate reader (BMG). The reaction rate was calculated using the 1.0 to 2.0 h time frame. Percent inhibition was obtained by comparison of reaction rate with that of a control (i.e. with no test compound). IC₅₀ values were calculated from a series of percent inhibition values determined at a range of inhibitor concentrations using software routines as implemented in the GraphPad Prism software package.

Abl kinase

(SEQ ID NO:1)

GTSMDPSSPNYDKWEMERTDITMKHKLGGGQYGEVYEGVWKKYSLTVAVK
TLKEDTMEVEEFLKEAAVMKEIKHPNLVQLLGVCCTREPPFYIIIEFTMTYG
NLLDYLRECNRQEVNAVVLVLLMATQISAMEYLEKKNFIIHRDLAARNCLV
GENHLVKVADFGLSRLMTGDTYTAHAGAKFPIKWTAPESLAYNKFSIKSD
VWAFGVLLWEIATYGMSPYPGIDLSQVYELLEKDYRMERPEGCPKVEYEL
MRACQWNPNSDRPSFAEIHQAFETMFQE

Abl Kinase (SEQ ID NO:2) Assay

[0131] Activity of T315I Abl kinase (SEQ ID NO:2) was determined by following the production of ADP from the kinase reaction through coupling with the pyruvate kinase/lactate dehydrogenase system (e.g., Schindler, et al. Science (2000) 289, 1938-1942). In this assay, the oxidation of NADH (thus the decrease at $A_{340\text{ nm}}$) was continuously monitored spectrophotometrically. The reaction mixture (100 μ l) contained Abl kinase (4.4 nM, M315I Abl from deCode Genetics), peptide substrate (EAIYAAPFAKKK, 0.2 mM), MgCl₂ (10 mM), pyruvate kinase (4 units), lactate dehydrogenase (0.7 units), phosphoenol pyruvate (1 mM), and NADH (0.28 mM) in 90 mM Tris buffer containing 0.2% octyl-glucoside and 1% DMSO, pH 7.5. Test compounds were incubated with T315I Abl (SEQ ID NO:2) and other reaction reagents at 30° C. for 1 h before ATP (500 μ M) was added to start the reaction. The absorption at 340 nm was monitored continuously for 2 hours at 30° C. on Polarstar Optima plate reader (BMG). The reaction rate was calculated using the 1.0 to 2.0 h time frame. Percent inhibition was obtained by comparison of reaction rate with that of a control (i.e. with no test compound). IC₅₀ values were calculated from a series of percent inhibition values determined at a range of inhibitor concentrations using software routines as implemented in the GraphPad Prism software package.

Abl T315I kinase

(SEQ ID NO:2)

GTSMDPSSPNYDKWEMERTDITMKHKLGGGQYGEVYEGVWKKYSLTVAVKTLKEDTMEVE
EFLKEAAVMKEIKHPNLVQLLGVCCTREPPFYIIIEFTMTYGNLLDYLRECNRQEVNAVVLV
YMATQISAMEYLEKKNFIIHRDLAARNCLVGENHLVKVADFGLSRLMTGDTYTAHAGAKF
PIKWTAPESLAYNKFSIKSDVWAFGVLLWEIATYGMSPYPGIDLSQVYELLEKDYRMERP

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EGCPEKVYELMRACWQWNPSPDRPSFAEIHQAFETMFQE

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(SEQ ID NO:3)

MVDPVGFAEAWKAQFPDSEPPRMELRSVGDIEQELERCKASIRRLEQEVNQERFRMIYLQ
TL LAKEKKS YDRQWGFRRAAQAPDGASEPRASASRPQAPADGADPPPAEEPEARPDGE
GSPGKARPGTARRPGAAASGERDDRGPPASVAALRSNFERIRKGGHQPADA EKPFYVNV
EFHHERGLVKVNDKEVSDRISLGSQAMQMERKKSQHGAGSSVG DASRPPYRGRSSESSC
GVDGDYEDAE LNPRFLKDN LIDANGGSRPPWPPLEYQPYQSIYVGGIMEGEGKGPLLRSQ
STSEQEKRLTWPRRSYS PRSFEDCGGYTPDCSSNENLTSSEEDFSSGQSSRVSPSPTY
RMFRDKSRSPSQNSQQSFDSSSPPTPQCHKRRHCPVVVSEATIVGVRKTGQIWPNDEG
AFHGADAGSGFTPPGYGCAADRAEEQRRHQDGLPYIDDSPPSSPHLSSKGRGSRDALVSG
ALKSTKASELDLEKGLEMRKWVLSGILASEETYL SHLEALLPMKPLKAAATTSQPVLTS
QQIETIFFKVP ELYEIHKESYDGLFPRVQQWSHQQRVGDLFQKLASQLGVYRAFVDNYGV
AMEMAEKCCQANAQFAEISENLARSNKDAKDPTTKNSLETLLYKPVDRVTRSTLVLHDL
LKHTPASHPDHPLQDALRISQNFLSSINEEITPRRQSM TVKKGEHRQLKDSFMVELVE
GARKLRHVFLFTDLLCTKLKKQSGGKTQQYDCKWYIPLTDLSPQM VDELEAVPNIPLVP
DEELDALKIKISQIKSDIQREKRANKGSKATERLKKLSEQESLLLLMSPMAFRVHSRN
GKSYTFLISSDYERA EWRENIREQQKKCFRSFSLTSVELQMLTNSCVKLQTVHSIPLTIN
KEDDESPLYGFLNVIVHSATGFKQSSKALQRPVASDFEPQGLSEARWNSKENLLAGPS
ENDPNLFVALYDFVASGDNLTLSITKGEKRLVLYNHNGEWCEAQTKNGQGWVPSNYITPV
NSLEKHSWYHGPVSRNAAEYPLSSGINGSFLVRESESSPSQRSISLRYEGRVYHYRINTA
SDGKLYVSSSERFNTLAE LVHHSTVADGLITTLHYPAKRNKPTVYGVSPNYDKWEMER
TDITMKHKLGGGQYGEVYEGVWKYSLTVAVKTLKEDTMEVEEFLKEAAMKEIKHPNLV
QLLGVC TREPPFYIITEFMTYGNLLDYLR CNRQEVNAVVL LLYMATQISSAMEYLEKKNF
IHRDLAARNCLVGENHLVKVADFGLSRLMTGDTYTAHAGAKFPIKWTAPESLAYNKFSIK
SDVWAFGVL LWEIATYGMSPYPGIDRSQVYELLEKDYRMKRPEGCEKVYELMRACWQWNP
PSDRPSFAEIHQAFETMFQESSISDEVEKELGKGVRGAVTTLQAPELPTKTRTSRRAA
EHRD TTDVPEMPHSGKGQGESDPLDHEPAVSPLLP RKERGPPEGGLNEDERLLPKDKKTNL
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SCVPHGAKDTEWRSVTLPRDLQSTGRQFDSSTFGGHKSEK PALPRKRAGENRSDQVTRGT
VTPPRLVKKNEEADEVFKDIMESSPGSSPPNLTPKPLRRQVTVAPASGLPHKEEAWKG
SALGTPAAAEFVTPTSKAGSGAPRGTSKGP AEESRVR RHKHSSESPGRDKGKLSKLKPAP
PPPPAASAGKAGKPSQRPGQEAAGEAVLGAKTKATSLVDAVNSDAKPSQPAEGLKKPV
LPATPKPHPAKPSGTPI SPAPVPLSTLPSASSALAGDQPSSTAFIPLISTRVSLRKTROP
PERASGAI TKGVLDSTEALCLAISGNSEQMASHSAVLEAGKNLYTFCVSYVDSIQQMRN
KFAFREAINKLNNLRELQICPASAGSGPAATQDFSKLLSSVKEISDIVQR

BCR-Ab1 p210-e13a2

(SEQ ID NO:4)

MVDPVGFAEAWKAQFPDSEPPMEELRSVGDIEQELERCKASIRRLEQEVNQERFRMIYLQ

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TLLAKEKKS YDRQ R W G F R R A A Q A P D G A S E P R A S A S R P Q P A P A D G A D P P P A E E P E A R P D G E
G S P G K A R P G T A R R P G A A A S G E R D D R G P P A S V A A L R S N F E R I R K G H G Q P G A D A E K P F Y V N V
E F H H E R G L V K V N D K E V S D R I S S L G S Q A M Q M E R K K S Q H G A G S S V G D A S R P P Y R G R S S E S S C
G V D G D Y E D A E L N P R F L K D N L I D A N G G S R P P W P P L E Y Q P Y Q S I Y V G G I M E G E G K G P L L R S Q
S T S E Q E K R L T W P R R S Y S P R S F E D C G G Y T P D C S S N E N L T S S E E D F S S G Q S S R V S P S P T T Y
R M F R D K S R S P S Q N S Q Q S F D S S S P T P Q C H K R H R H C P V V V S E A T I V G R K T G Q I W P N D D E G
A F H G D A D G S F G T P P G Y G C A A D R A E E Q R R H Q D G L P Y I D D S P S S S P H L S S K G R G S R D A L V S G
A L K S T K A S E L D L E K G L E M R K W L S G I L A S E E T Y L S H L E A L L P M K P L K A A A T T S Q P V L T S
Q Q I E T I F F K V P E L Y E I H K E S Y D G L F P R V Q Q W S H Q Q R V G D L F Q K L A S Q L G V Y R A F V D N Y G V
A M E M A E K C C Q A N A Q F A E I S E N L R A R S N K D A K D P T K N S L E T L L Y K P V D R V T R S T L V L H D L
L K H T P A S H P D H P L L Q D A L R I S Q N F L S S I N E E I T P R R Q S M T V K K G E H R Q L L K D S F M V E L V E
G A R K L R H V F L F T D L L L C T K L K K Q S G G K T Q Q Y D C K W Y I P L T D L S F Q M V D E L E A V P N I P L V P
D E E L D A L K I K I S Q I K S D I Q R E K R A N K G S K A T E R L K K K L S E Q E S L L L M S P S M A F R V H S R N
G K S Y T F L I S S D Y E R A E W R E N I R E Q Q K C F R S F S L T S V E L Q M L T N S C V K L Q T V H S I P L T I N
K E E A L Q R P V A S D F E P Q L S E A A R W N S K E N L L A G P S E N D P N L F V A L Y D F V A S G D N T L S I T K
G E K L R V L G Y N H N G E W C E A Q T K N G Q G W V P S N Y I T P V N S L E K H S W Y H G P V S R N A A E Y P L S S G
I N G S F L V R E S E S P S Q R S I S L R Y E G R V Y H R I N T A S D G K L Y V S E S E R F N T L A E L V H H H S T
V A D G L I T T L H Y P A P K R N K P T V Y G V S P N Y D K W E M E R T D I T M K H K L G G G Q Y G E V Y E G V W K K Y
S L T V A V K T L K E D T M E V E E F L K E A A V M K E I K H P N L V Q L L G V C T R E P P F Y I I T E F M T Y G N L L
D Y L R E C N R Q E V N A V V L L Y M A T Q I S S A M E Y L E K K N F I H R D L A A R N C L V G E N H L V K V A D F G L
S R L M T G D T Y T A H A G A K P P I K W T A P E S L A Y N K F S I K S D V W A F G V L L W E I A T Y G M S P Y P G I D
R S Q V Y E L L E K D Y R M K R P E G C P E K V Y E L M R A C W Q W N P S D R P S F A E I H Q A F E T M F Q E S S I S D
E V E K E L G K Q G V R G A V T T L L Q A P E L P T K T R T S R R A A E H R D T T D V P E M P H S K G Q G E S D P L D H
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D G Q P E R R G A G E E E G R D I S N G A L A F T P L D T A D P A K S P K P S N G A G V P N G A L R E S G G S G F R S P
H L W K S S T L T S S R L A T G E E E G G S S K R F L R S C S V S C V P H G A K D T E W R S V T L P R D L Q S T G
R Q P D S S T F G G H K S E K P A L P R K R A G E N R S D Q V T R G T V T P P P R L V K K N E A A D E V F K D I M E S
S P G S S P N L T P K P L R R Q V T V A P A S G L P H K E A W K G S A L G T P A A A E P V T P T S K A G S G A P R G
T S K G P A E E S R V R R H K H S E S P G R D K G K L S K L K P A P P P P P A A S A G A G K P S Q R P G Q E A A G
E A V L G A K T K A T S L V D A V N S D A A K P S Q P A E G L K K P V L P A T P K P H P A K P S G T P I S P A P V P L S
T L P S A S A L A G D Q P S S T A F I P L I S T R V S L R K T R Q P P E R A S G A I T K G V V L D S T E A L C L A I S
G N S E Q M A S H A V L E A G K N L Y T F C V S Y V D S I Q Q M R N K F A F R E A I N K L E N N L R E L Q I C P A S A
G S G P A A T Q D F S K L L S S V K E I S D I V Q R

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(SEQ ID NO:5)

M V D P V G F A E A W K A Q P D S E P P R M E L R S V G D I E Q E L E R C K A S I R R L E Q E V N Q E R F R M I Y L Q
T L L A K E K K S Y D R Q R W G F R R A A Q A P D G A S E P R A S A S R P Q P A P A D G A D P P P A E E P E A R P D G E
G S P G K A R P G T A R R P G A A A S G E R D D R G P P A S V A A L R S N F E R I R K G H G Q P G A D A E K P F Y V N V
E F H H E R G L V K V N D K E V S D R I S S L G S Q A M Q M E R K K S Q H G A G S S V G D A S R P P Y R G R S S E S S C
G V D G D Y E D A E L N P R F L K D N L I D A N G G S R P P W P P L E Y Q P Y Q S I Y V G G I M E G E G K G P L L R S Q

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STSEQEKRLTWPRRSYSPRSFEDCGGGYTPDCSSNENLTSSEEDFSSGQSSRVSPSPTTY
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LSSGINGSFLVRESESSPSQRSISLRYEGRVYHYRINTASDGKLYVSSSRFNTLAELVH
HHSTVADGLITTLHYPAKRNKPTVYGVSPNYDKWEMERTDITMKHKLGGGQYGEVYEGV
WKYSLTVAVKTLKEDTMEVEEFLKEAAVMKEIKHPNLVQLLGVCTREPPFYIITEFMTY
GNLLDYLRECNREQVNAVLLYMATQISSAMEYLEKKFIHRDLAARNCLVGENHLVKVA
DFGLSRLMTGDTYTAHAGAKFPIKWTAPESLAYNKFSIKSDVWAFGVLLWEIATYGMSPY
PGIDRSQVYELLEKDYRMKRPEGCEKQVYELMPACWQWNPDRPSFAEIHQAFETMFQES
SISDEVEKELGKQVGRGAVTTLQAPELPTKTRTSRRAAEHRDITDVPMPHSGKGQESD
PLDHEPAVSPLLPRKERGPPEGGLNEDERLLPKDKKTNLFSALIKKKKTAPTTPKRSSS
FREMDOGPERRGAGEEEGRDISNGALAFPLDTADPAKSPKPSNGAGVPNGALRESGGSG
FRSPHLWKKSSTLTSSRLATGEEEGGSSSKRFLRSCSVSCVPHGAKDTEWRSVTLPRDL
QSTGRQFDSSTFGGHKSEKPALPRKRAGENRSDQVTRGTVTPPPRLVKNEEADEVFKD
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APRGTSKGPAEESRVRHKHSSESPGRDKGLSKLKPA PPPPAASAGKAGGKPSQRPQG
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LAISGNSEQMASHSAVLEAGKNLYTFCVSYVDSIQQMRNKFAFREAINKLENNLRELQIC
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BCR-Ab1 p210-e14a2 T315I
(SEQ ID NO:6)
MVDPVGFAEAWKAQFPDSEPPRMELRSVGDIEQELERCKASIRRLEQEVNQERFRMIYLQ
TL LAKEKSYDRQRWFRRAAQAPDGASEPRASASRPQAPADGADPPPAEEPEARPDGE
GSPGKARPGTARRPGAAASGERDDRGPPASVAALRSNFERIRKGHGQPGADAEPFYVNV
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GVDGDYEDAE LNPRFLKDNLIDANGSRPPWPPLYQPYQSIYVGGIMEGEGKGPLRSQ
STSEQEKRLTWPRRSYSPRSFEDCGGGYTPDCSSNENLTSSEEDFSSGQSSRVSPSPTTY
RMFRDKSRSPSQNSQQSFDSSSPPTPQCHKRHRHCPVVVSEATIVGVRKTGQIWPNDDEG
AFHGDA DGSFGTPPGYGCAADRAEEQRRHQDGLPYIDDSPSSPHLSSKGRGSRDALVSG
ALKSTKASELDLEKGLEMRKWVLSGILASEETYL SHLEALLPMKPLKAAATTSQPV LTS
QQIETIFFKVP ELYEIHKESYDGLFPRVQQWQSHQQRVGD LFKLASQLGVYRAFDNYGV
AMEMA EKCQANAQFAEISENLRARSNKDAKDP TT KNSLETLLYKPVDRVTRSTLV LHDL
LKHTPASHPDHPLQDALRISQNFLSSINEEITPRRQSM TVKKGEHRQLKDSFMV ELVE
GARKLRHVFLFTDLLCTKLKKQSGGKTQQYDCKWYIPLTDLSPQM VDELEAVNIP LVP
DEELDALKIKISQIKSDIQREKRANKGSKATERLKKLSEQES LLLMSPSMAFRVHSRN
GKSYTFLISSDYERA EWRENIREQQKKCFRSFSLTSVELQMLTNSCVKLQTVHSIPLTIN
KEDDES PGLYGLNVIVHSATGFKQSSKALQRPVASFEPQGLSEAARWNSKENLLAGPS

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ENDPNLFVALYDFVASGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNQGNVPSNYITPV
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 PSDRPSFAEIHQAFETMFQESSISDEVEKELGKQGVRAVTTLLQAPELPTKTRTSRRAA
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 PKPSNGAGVPNGALRESGGSGFRSPHLWKKSSTLTSSRLATGEEEGGSSSKRFLRSCSV
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 PPPPAASAGKAGGKPSQRPQGEAAGEAVLGAKTKATSLVDVNSDAAKPSQPAEGLKKPV
 LPATPKPHPAKPSGTPISPAPVPLSTLPSASSALAGDQPSSTAFIPLISTRVSLRKTRQP
 PERASGAITKGVVLDSTEALCLAISGNSEQMASHSAVLEAGKNLYTFCVSYVDSIQQMRN
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 BCR-Ab1 p210-e13a2 T315I (SEQ ID NO: 7)
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 GSPGKARPGTARRPGAAASGERDRGPPASVAALRSNFERIRKGGHQPADAEPFYVNV
 EFHHERGLVKVNDKEVSDRISSLGSAQMERKKSQHGAGSSVGDAERPPYRGRSSESSC
 GVDGDYEDAELNPRFLKDNLIDANGGSRPWPPLYEQPYQSIYVGGIMEGEGKGLLRSQ
 STSEQEKRLTWPRRSYSRPFEDCGGYTPDCSSNENLTSSEEDFSSGQSSRVSPSTTY
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 ALKSTKASELDLEKGLEMRKWVLSGILASEETYLHLEALLPMKPLKAAATTSQPVLTS
 QQIETIFFKVPPELYEIHKESYDGLFPRVQWQSHQQRVGDLEFQKLASQLGVYRAFVDNYGV
 AMEMAEKCCQANAQFAEISENLRARSNKDAKDPTTKNSLETLLYKPVDRVTRSTLVLHDL
 LKHTPASHPDHPLLQDALRISQNFLSSINEETPRRQSMTVKKGHRQLLKDSFMVELVE
 GARKLRHVFLFTDLLLCTKLKKQSGGKTQQYDCKWYIPLTDLSFQMVDELEAVPNIPLVP
 DEELDALKIKISQIKSDIQREKRANKGSKATERLKKLSEQESLLLLMSPSMAFRVHSRN
 GKSFTFLISSDYERAWEWRENIREQQKKCFRFSLSLTVLQMLTNSCVKLQTVHSIPLTIN
 KEEALQRPVASFEPQGLSEAARWNSKENLLAGPSENDPNLFVALYDFVASGDNTLSITK
 GEKLRVLGYNHNGEWCEAQTKNQGWVPSNYITPVNSLEKHSWYHGPVSRNAAEYPLSSG
 INGSFLVRESESSPSQRSISLRYEGRVYHYRINTASDGKLYVSSSERFNTLAELVHHHST
 VADGLITTLHYPAKRNKPTVYGVSPNYDKWEMERTDI TMKHKLGGGQYGEVYEGVWKY
 SLTVAVKTLKEDTMEVEEFLKEAAVMKEIKHPNLVQLLGVCTREPPFYIIIEFMTYGNLL

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DYLRECNRQEVNAVVLlyMATQISSAMEYLEKKNF IHRDLAARNCLVGENHLVKVADFGL
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EVEKELGKQGVRGAVTTLLQAPELPTKTRTSRRAAEHRD TTDVPEMPHSGKGESDPLDH
EPAVSPLLPRKERGPPEGGLNEDERLLPKDKKTNLFSALIKKKKTAPT PPKRSSSFREM
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SPGSSPNNLT PKPLRRQVT VAPASGLPHKEEAWKGSALGTAAAEPVTPTS KAGSGAPRG
TSKGPAEESRVR RHKSSES PGRDKGKLSKLPAPPPPPAASAGKAGKPSQRPQGEAAG
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GNSEQMASHSAVLEAGKNLYTFCVSYVDSIQQMRNKFAFREAINKLENNLRELQICPASA
GSGPAATQDFSKLLSSVKEISDIVQR

BCR-Abl p190-e1a2

(SEQ ID NO:8)

MVDPVGFAEAWKAQFPDSEPPRMELRSVGDIEQELERCKASIRRLQE EVNQERFRMIYLQ
TLLAKEKKS YDRQWGFRRAAQAPDGASEPRASASRPQAPADGADPPAE EPEARPDGE
GSPGKARPGTARRPGAAASGERDDRGPPASVAALRSNFERIRK GHGQPGADAEKPFYVNV
EFHHERGLVKVKDKEVSDRISSLG SQAMQMERKKSQHGAGSSVGDASRP PYRGRSSESSC
GVDGDYEDAE LNPRFLKDNLIDANGGSRPPWPPLEYQPYQSIYVGGIMEGEGKGPLRSQ
STSEQEKRLTWPRRSYSR SFEDCGGYTPDCSSNENLTSSEEDFSSGQSSRVSPSPTY
RMFRDKSRSPSQNSQQSFDSSSPPTPQCHKRHRHCPVVVSEATIVGVRKTGQIWPNDDEG
AFHGDAEALQRPVASFEPQGLSEAARWNSKENLLAGPSENDPNLFVALYDFVASGDNTL
SITKGEKLRVLGYNHNGEWCEAQTKNGQGWVPSNYITPVNSLEKHSWYHGVPVRNAEYP
LSSGINGSFLVRESESSPQRSISLRYEGRVYHYRINTASDGKLYVSSSRPNTLAE LVH
HHSTVADGLITTLHPAPKR NKPTVYGVSPNYDKWEMERTDITMKHKLGGGQYGEVYEGV
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DFGLSRLMTGDTYTAHAGAKFPIKWTAPESLAYNKFSIKSDVWAFGVLLWEIATYGMSPY
PGIDRSQVYELLEKDYRMKRPEGCEKVYELMRACWQWNP SDRPSFAEIHQAFETMFQES
SISDEVEKELGKQGVRGAVTTLLQAPELPTKTRTSRRAAEHRD TTDVPEMPHSGKGESD
PLDHEPAVSPLLPRKERGPPEGGLNEDERLLPKDKKTNLFSALIKKKKTAPT PPKRSSS
FREM DQGQERRGAGEEEGRDISNGALAF TPLDTADPAKSPKPSNGAGVPNGALRESGGSG
FRSPHLWKKSTLTSSRLATGEEEGGSSSKRFLRSCSVSCVPHGAKDTEWRSVTLRPDL
QSTGRQFDSSTFGGHKSEKPALPRKRAGENRSDQVTRGTVTPPRLVKNEEADEVFKD
IMESSPGSSPNNLT PKPLRRQVT VAPASGLPHKEEAWKGSALGTAAAEPVTPTS KAGSG
APRGTSKGPAEESRVR RHKSSES PGRDKGKLSKLPAPPPPPAASAGKAGKPSQRPQ
EAAGEAVLGAKTKATSLVDAVNSDAAKPSQPAEGLKKPVLPATPKHPAKPSGTPISPAP

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VPLSTLPSASSALAGDQPSSTAFIPLISTRVSLRKTRQPPERASGAIKGVVLDSTEALC
 LAISGNSEQMASHSAVLEAGKNLYTFCVSYVDSIQQMRNKFAPFREAINKLENNLRELQIC
 PASAGSGPAATQDESKLLSSVKEISDIVQR

C-Kit Kinase (SEQ ID NO:9) Assay

[0132] Activity of c-Kit kinase (SEQ ID NO:9) was determined by following the production of ADP from the kinase reaction through coupling with the pyruvate kinase/lactate dehydrogenase system (e.g., Schindler, et al. Science (2000) 289, 1938-1942). In this assay, the oxidation of NADH (thus the decrease at A340 nm) was continuously monitored spectrophotometrically. The reaction mixture (100 μ l) contained c-Kit (cKIT residues T544-V976, from ProQinase, 5.4 nM), polyE4Y (1 mg/ml), MgCl₂ (10 mM), pyruvate kinase (4 units), lactate dehydrogenase (0.7 units), phosphoenol pyruvate (1 mM), and NADH (0.28 mM) in 90 mM Tris buffer containing 0.2% octyl-glucoside and 1% DMSO, pH 7.5. Test compounds were incubated with C-Met (SEQ ID NO:9) and other reaction reagents at 22° C. for <2 min before ATP (200 μ M) was added to start the reaction. The absorption at 340 nm was monitored continuously for 0.5 hours at 30° C. on Polarstar Optima plate reader (BMG). The reaction rate was calculated using the 0 to 0.5 h time frame. Percent inhibition was obtained by comparison of reaction rate with that of a control (i.e. with no test compound). IC₅₀ values were calculated from a series of percent inhibition values determined at a range of inhibitor concentrations using software routines as implemented in the GraphPad Prism software package.

c-Kit with N-terminal GST fusion

(SEQ ID NO:9)

LGWYKIKGLVQPTRLLLEYLEEKYEELHYERDEGDKWRNKKFELGLEFPN
 LPYYIDGDKVLTQSMIAIRYADKHNLGGCPKERAETSMLEGAVIDIRYG
 VSRAYSXKDFETLKVDFLSKLPKMFEDRLCHKTYLNGDHVTHPDFML
 YDALDVVLYMDPMCLDAPKLVCFKKRIEAIQIDKYLKSSKYIWPLQGW
 QATFGGGDHPKSDLVPRHNQTSLYKKAGSAAVLEENLYFQQTYKYLQK
 PMYEVQWKVVEEINGNNYVYIDPTQLPYDHKWEPFNRLSFGKTLGAGAF
 GKVVEATAYGLIKSDAAMTVAVKMLKPSAHLTEREALMSELKVLVSYLGNH
 MNIVNLLGACTIGGPTLVITEYCCYGDLLNFLRRKRDSFICSKQEDHAEA
 ALYKNLLHSSKSSCSDSTNEYMDMKPGVSYVVPVKADKRRSVRIGSYIER
 DVTPEIMDEDELALDLEDLLSFSYQVAKGMAFLASKNCIHRDLAARNILL
 THGRITKICDFGLARDIKNDSNYVVGKNARLPVKWMAPEIFNCVYTFES
 DVWSYGIFLWELFSLGSSPYPGMPVDSKFYKMIKEGFRMLSPEHAPAEMY
 DIMKTCWDADPLKRPFTKQIVQLEIKQISESTNHIYSLANCSNRPQKPV
 VDHVSVRINSVGSTASSQPLLVHDDV

C-Met Kinase (SEQ ID NO:10) Assay

[0133] Activity of C-Met kinase (SEQ ID NO:10) was determined by following the production of ADP from the kinase reaction through coupling with the pyruvate kinase/lactate dehydrogenase system (e.g., Schindler, et al. Science

(2000) 289, 1938-1942). In this assay, the oxidation of NADH (thus the decrease at A340 nm) was continuously monitored spectrophotometrically. The reaction mixture (100 μ l) contained C-Met (c-Met residues: 956-1390, from Invitrogen, catalogue #PV3143, 6 nM), polyE4Y (1 mg/ml), MgCl₂ (10 mM), pyruvate kinase (4 units), lactate dehydrogenase (0.7 units), phosphoenol pyruvate (1 mM), and NADH (0.28 mM) in 90 mM Tris buffer containing 0.25 mM DTT, 0.2% octyl-glucoside and 1% DMSO, pH 7.5. Test compounds were incubated with C-Met (SEQ ID NO:10) and other reaction reagents at 22° C. for 0.5 h before ATP (100 μ M) was added to start the reaction. The absorption at 340 nm was monitored continuously for 2 hours at 30° C. on Polarstar Optima plate reader (BMG). The reaction rate was calculated using the 1.0 to 2.0 h time frame. Percent inhibition was obtained by comparison of reaction rate with that of a control (i.e. with no test compound). IC₅₀ values were calculated from a series of percent inhibition values determined at a range of inhibitor concentrations using software routines as implemented in the GraphPad Prism software package.

cMet Kinase

(SEQ ID NO:10)

MSYYHHHHHDYDIPTTENLYFQGAMLVPRGSPWIPFTMKRKQIKDLGS
 ELVRDYARVHTPHLDRLVSARSVSPTEMTVSNESVDYRATFPEDQFPNSS
 QNGSCRQVQYPLTDMSPILTSGLSDISSPLLQNTVHIDLALNPVLQAV
 QHVVIGPSSSLIVHFNEVIGRGHFGCVYHGTLDDNDGKKIHCAVKSILNRIT
 DIGEVSQFLTEGIIMKDFSHPNVLSLLGICLRSEGSPVLVPLPMKHGDLR
 NFIRNETHNPTVKDLIGFGIQVAKGMKYLASKKFVHRDLAARNCLMDEKF
 TVKVADPGLARDMYDKEYYSVHNKTGAKLPVKWMALESQTQKFTTKSDV
 WSGVLLWELMTRGAPPYPDVNTFDITVYLLQGRRLQLQPEYCPDPLYEVM
 LKCWHPKAEMRPSFSELVSRIASIFSTFGEHYVHVNATVYVNVKCVAPYP
 SLLSSEDNADDEVDTTPASFWETS

[0134] The biochemical IC₅₀ values of other compounds disclosed herein are at least 10 μ M against Abl enzyme.

Cell Culture

[0135] BaF3 cells (parental or transfected with the following: wild type p210 BCR-Abl and T3151 p210 BCR-Abl) was obtained from Professor Richard Van Etten (New England Medical Center, Boston, Mass.). Briefly, cells were grown in RPMI 1640 supplemented with 10% characterized fetal bovine serum (HyClone, Logan, Utah) at 37 degrees Celsius, 5% CO₂, 95% humidity. Cells were allowed to expand until reaching 80% saturation at which point they were subcultured or harvested for assay use.

Cell Proliferation Assay

[0136] A serial dilution of test compound was dispensed into a 96 well black clear bottom plate (Corning, Corning,

N.Y.). For each cell line, three thousand cells were added per well in complete growth medium. Plates were incubated for 72 hours at 37 degrees Celsius, 5% CO₂, 95% humidity. At the end of the incubation period Cell Titer Blue (Promega, Madison, Wis.) was added to each well and an additional 4.5 hour

incubation at 37 degrees Celsius, 5% CO₂, 95% humidity was performed. Plates were then read on a BMG Fluostar Optima (BMG, Durham, N.C.) using an excitation of 544 nM and an emission of 612 nM. Data was analyzed using Prism software (Graphpad, San Diego, Calif.) to calculate IC₅₀'s.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 10

<210> SEQ ID NO 1

<211> LENGTH: 278

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

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35 40 45
Val Lys Thr Leu Lys Glu Asp Thr Met Glu Val Glu Glu Phe Leu Lys
50 55 60
Glu Ala Ala Val Met Lys Glu Ile Lys His Pro Asn Leu Val Gln Leu
65 70 75 80
Leu Gly Val Cys Thr Arg Glu Pro Pro Phe Tyr Ile Ile Thr Glu Phe
85 90 95
Met Thr Tyr Gly Asn Leu Leu Asp Tyr Leu Arg Glu Cys Asn Arg Gln
100 105 110
Glu Val Asn Ala Val Val Leu Leu Tyr Met Ala Thr Gln Ile Ser Ser
115 120 125
Ala Met Glu Tyr Leu Glu Lys Lys Asn Phe Ile His Arg Asp Leu Ala
130 135 140
Ala Arg Asn Cys Leu Val Gly Glu Asn His Leu Val Lys Val Ala Asp
145 150 155 160
Phe Gly Leu Ser Arg Leu Met Thr Gly Asp Thr Tyr Thr Ala His Ala
165 170 175
Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ser Leu Ala Tyr
180 185 190
Asn Lys Phe Ser Ile Lys Ser Asp Val Trp Ala Phe Gly Val Leu Leu
195 200 205
Trp Glu Ile Ala Thr Tyr Gly Met Ser Pro Tyr Pro Gly Ile Asp Leu
210 215 220
Ser Gln Val Tyr Glu Leu Leu Glu Lys Asp Tyr Arg Met Glu Arg Pro
225 230 235 240
Glu Gly Cys Pro Glu Lys Val Tyr Glu Leu Met Arg Ala Cys Trp Gln
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<210> SEQ ID NO 2

<211> LENGTH: 278

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Gly Glu Val Tyr Glu Gly Val Trp Lys Lys Tyr Ser Leu Thr Val Ala
35     40     45
Val Lys Thr Leu Lys Glu Asp Thr Met Glu Val Glu Glu Phe Leu Lys
50     55     60
Glu Ala Ala Val Met Lys Glu Ile Lys His Pro Asn Leu Val Gln Leu
65     70     75     80
Leu Gly Val Cys Thr Arg Glu Pro Pro Phe Tyr Ile Ile Ile Glu Phe
85     90     95
Met Thr Tyr Gly Asn Leu Leu Asp Tyr Leu Arg Glu Cys Asn Arg Gln
100    105    110
Glu Val Asn Ala Val Val Leu Leu Tyr Met Ala Thr Gln Ile Ser Ser
115    120    125
Ala Met Glu Tyr Leu Glu Lys Lys Asn Phe Ile His Arg Asp Leu Ala
130    135    140
Ala Arg Asn Cys Leu Val Gly Glu Asn His Leu Val Lys Val Ala Asp
145    150    155    160
Phe Gly Leu Ser Arg Leu Met Thr Gly Asp Thr Tyr Thr Ala His Ala
165    170    175
Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ser Leu Ala Tyr
180    185    190
Asn Lys Phe Ser Ile Lys Ser Asp Val Trp Ala Phe Gly Val Leu Leu
195    200    205
Trp Glu Ile Ala Thr Tyr Gly Met Ser Pro Tyr Pro Gly Ile Asp Leu
210    215    220
Ser Gln Val Tyr Glu Leu Leu Glu Lys Asp Tyr Arg Met Glu Arg Pro
225    230    235    240
Glu Gly Cys Pro Glu Lys Val Tyr Glu Leu Met Arg Ala Cys Trp Gln
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Glu Thr Met Phe Gln Glu
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<210> SEQ ID NO 3
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<212> TYPE: PRT
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20     25     30
Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35     40     45

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Lys	Glu	Lys	Lys	Ser	Tyr	Asp	Arg	Gln	Arg	Trp	Gly	Phe	Arg	Arg	Ala
65					70					75					80
Ala	Gln	Ala	Pro	Asp	Gly	Ala	Ser	Glu	Pro	Arg	Ala	Ser	Ala	Ser	Arg
				85					90					95	
Pro	Gln	Pro	Ala	Pro	Ala	Asp	Gly	Ala	Asp	Pro	Pro	Pro	Ala	Glu	Glu
			100					105					110		
Pro	Glu	Ala	Arg	Pro	Asp	Gly	Glu	Gly	Ser	Pro	Gly	Lys	Ala	Arg	Pro
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Gly	Thr	Ala	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Ser	Gly	Glu	Arg	Asp	Asp
	130					135						140			
Arg	Gly	Pro	Pro	Ala	Ser	Val	Ala	Ala	Leu	Arg	Ser	Asn	Phe	Glu	Arg
145					150					155					160
Ile	Arg	Lys	Gly	His	Gly	Gln	Pro	Gly	Ala	Asp	Ala	Glu	Lys	Pro	Phe
				165					170					175	
Tyr	Val	Asn	Val	Glu	Phe	His	His	Glu	Arg	Gly	Leu	Val	Lys	Val	Asn
		180						185					190		
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		195					200					205			
Gln	Met	Glu	Arg	Lys	Lys	Ser	Gln	His	Gly	Ala	Gly	Ser	Ser	Val	Gly
	210					215					220				
Asp	Ala	Ser	Arg	Pro	Pro	Tyr	Arg	Gly	Arg	Ser	Ser	Glu	Ser	Ser	Cys
225					230					235					240
Gly	Val	Asp	Gly	Asp	Tyr	Glu	Asp	Ala	Glu	Leu	Asn	Pro	Arg	Phe	Leu
				245				250						255	
Lys	Asp	Asn	Leu	Ile	Asp	Ala	Asn	Gly	Gly	Ser	Arg	Pro	Pro	Trp	Pro
		260						265					270		
Pro	Leu	Glu	Tyr	Gln	Pro	Tyr	Gln	Ser	Ile	Tyr	Val	Gly	Gly	Ile	Met
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Glu	Gly	Glu	Gly	Lys	Gly	Pro	Leu	Leu	Arg	Ser	Gln	Ser	Thr	Ser	Glu
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Gln	Glu	Lys	Arg	Leu	Thr	Trp	Pro	Arg	Arg	Ser	Tyr	Ser	Pro	Arg	Ser
305					310					315					320
Phe	Glu	Asp	Cys	Gly	Gly	Gly	Tyr	Thr	Pro	Asp	Cys	Ser	Ser	Asn	Glu
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Asn	Leu	Thr	Ser	Ser	Glu	Glu	Asp	Phe	Ser	Ser	Gly	Gln	Ser	Ser	Arg
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Val	Ser	Pro	Ser	Pro	Thr	Thr	Tyr	Arg	Met	Phe	Arg	Asp	Lys	Ser	Arg
		355					360					365			
Ser	Pro	Ser	Gln	Asn	Ser	Gln	Gln	Ser	Phe	Asp	Ser	Ser	Ser	Pro	Pro
	370					375				380					
Thr	Pro	Gln	Cys	His	Lys	Arg	His	Arg	His	Cys	Pro	Val	Val	Val	Ser
385					390					395					400
Glu	Ala	Thr	Ile	Val	Gly	Val	Arg	Lys	Thr	Gly	Gln	Ile	Trp	Pro	Asn
			405					410						415	
Asp	Asp	Glu	Gly	Ala	Phe	His	Gly	Asp	Ala	Asp	Gly	Ser	Phe	Gly	Thr
		420						425					430		
Pro	Pro	Gly	Tyr	Gly	Cys	Ala	Ala	Asp	Arg	Ala	Glu	Glu	Gln	Arg	Arg
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His	Gln	Asp	Gly	Leu	Pro	Tyr	Ile	Asp	Asp	Ser	Pro	Ser	Ser	Ser	Pro

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

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Gln	Lys	Lys	Cys	Phe	Arg	Ser	Phe	Ser	Leu	Thr	Ser	Val	Glu	Leu	Gln
865					870					875					880
Met	Leu	Thr	Asn	Ser	Cys	Val	Lys	Leu	Gln	Thr	Val	His	Ser	Ile	Pro
			885						890					895	
Leu	Thr	Ile	Asn	Lys	Glu	Asp	Asp	Glu	Ser	Pro	Gly	Leu	Tyr	Gly	Phe
		900						905					910		
Leu	Asn	Val	Ile	Val	His	Ser	Ala	Thr	Gly	Phe	Lys	Gln	Ser	Ser	Lys
	915						920					925			
Ala	Leu	Gln	Arg	Pro	Val	Ala	Ser	Asp	Phe	Glu	Pro	Gln	Gly	Leu	Ser
	930						935				940				
Glu	Ala	Ala	Arg	Trp	Asn	Ser	Lys	Glu	Asn	Leu	Leu	Ala	Gly	Pro	Ser
945					950					955					960
Glu	Asn	Asp	Pro	Asn	Leu	Phe	Val	Ala	Leu	Tyr	Asp	Phe	Val	Ala	Ser
				965					970					975	
Gly	Asp	Asn	Thr	Leu	Ser	Ile	Thr	Lys	Gly	Glu	Lys	Leu	Arg	Val	Leu
		980						985					990		
Gly	Tyr	Asn	His	Asn	Gly	Glu	Trp	Cys	Glu	Ala	Gln	Thr	Lys	Asn	Gly
		995					1000					1005			
Gln	Gly	Trp	Val	Pro	Ser	Asn	Tyr	Ile	Thr	Pro	Val	Asn	Ser	Leu	
	1010						1015					1020			
Glu	Lys	His	Ser	Trp	Tyr	His	Gly	Pro	Val	Ser	Arg	Asn	Ala	Ala	
	1025						1030					1035			
Glu	Tyr	Pro	Leu	Ser	Ser	Gly	Ile	Asn	Gly	Ser	Phe	Leu	Val	Arg	
	1040						1045					1050			
Glu	Ser	Glu	Ser	Ser	Pro	Ser	Gln	Arg	Ser	Ile	Ser	Leu	Arg	Tyr	
	1055						1060					1065			
Glu	Gly	Arg	Val	Tyr	His	Tyr	Arg	Ile	Asn	Thr	Ala	Ser	Asp	Gly	
	1070						1075					1080			
Lys	Leu	Tyr	Val	Ser	Ser	Glu	Ser	Arg	Phe	Asn	Thr	Leu	Ala	Glu	
	1085						1090					1095			
Leu	Val	His	His	His	Ser	Thr	Val	Ala	Asp	Gly	Leu	Ile	Thr	Thr	
	1100						1105					1110			
Leu	His	Tyr	Pro	Ala	Pro	Lys	Arg	Asn	Lys	Pro	Thr	Val	Tyr	Gly	
	1115						1120					1125			
Val	Ser	Pro	Asn	Tyr	Asp	Lys	Trp	Glu	Met	Glu	Arg	Thr	Asp	Ile	
	1130						1135					1140			
Thr	Met	Lys	His	Lys	Leu	Gly	Gly	Gly	Gln	Tyr	Gly	Glu	Val	Tyr	
	1145						1150					1155			
Glu	Gly	Val	Trp	Lys	Lys	Tyr	Ser	Leu	Thr	Val	Ala	Val	Lys	Thr	
	1160						1165					1170			
Leu	Lys	Glu	Asp	Thr	Met	Glu	Val	Glu	Glu	Phe	Leu	Lys	Glu	Ala	
	1175						1180					1185			
Ala	Val	Met	Lys	Glu	Ile	Lys	His	Pro	Asn	Leu	Val	Gln	Leu	Leu	
	1190						1195					1200			
Gly	Val	Cys	Thr	Arg	Glu	Pro	Pro	Phe	Tyr	Ile	Ile	Thr	Glu	Phe	
	1205						1210					1215			
Met	Thr	Tyr	Gly	Asn	Leu	Leu	Asp	Tyr	Leu	Arg	Glu	Cys	Asn	Arg	
	1220						1225					1230			
Gln	Glu	Val	Asn	Ala	Val	Val	Leu	Leu	Tyr	Met	Ala	Thr	Gln	Ile	
	1235						1240					1245			

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

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1625	1630	1635
Arg Asp Leu Gln Ser Thr Gly 1640	Arg Gln Phe Asp Ser 1645	Ser Ser Thr Phe 1650
Gly Gly His Lys Ser Glu Lys 1655	Pro Ala Leu Pro Arg 1660	Lys Arg Ala 1665
Gly Glu Asn Arg Ser Asp Gln 1670	Val Thr Arg Gly Thr 1675	Val Thr Pro 1680
Pro Pro Arg Leu Val Lys Lys 1685	Asn Glu Glu Ala Ala 1690	Asp Glu Val 1695
Phe Lys Asp Ile Met Glu Ser 1700	Ser Pro Gly Ser Ser 1705	Pro Pro Asn 1710
Leu Thr Pro Lys Pro Leu Arg 1715	Arg Gln Val Thr Val 1720	Ala Pro Ala 1725
Ser Gly Leu Pro His Lys Glu 1730	Glu Ala Trp Lys Gly 1735	Ser Ala Leu 1740
Gly Thr Pro Ala Ala Ala Glu 1745	Pro Val Thr Pro Thr 1750	Ser Lys Ala 1755
Gly Ser Gly Ala Pro Arg Gly 1760	Thr Ser Lys Gly Pro 1765	Ala Glu Glu 1770
Ser Arg Val Arg Arg His Lys 1775	His Ser Ser Glu Ser 1780	Pro Gly Arg 1785
Asp Lys Gly Lys Leu Ser Lys 1790	Leu Lys Pro Ala Pro 1795	Pro Pro Pro 1800
Pro Ala Ala Ser Ala Gly Lys 1805	Ala Gly Gly Lys Pro 1810	Ser Gln Arg 1815
Pro Gly Gln Glu Ala Ala Gly 1820	Glu Ala Val Leu Gly 1825	Ala Lys Thr 1830
Lys Ala Thr Ser Leu Val Asp 1835	Ala Val Asn Ser Asp 1840	Ala Ala Lys 1845
Pro Ser Gln Pro Ala Glu Gly 1850	Leu Lys Lys Pro Val 1855	Leu Pro Ala 1860
Thr Pro Lys Pro His Pro Ala 1865	Lys Pro Ser Gly Thr 1870	Pro Ile Ser 1875
Pro Ala Pro Val Pro Leu Ser 1880	Thr Leu Pro Ser Ala 1885	Ser Ser Ala 1890
Leu Ala Gly Asp Gln Pro Ser 1895	Ser Thr Ala Phe Ile 1900	Pro Leu Ile 1905
Ser Thr Arg Val Ser Leu Arg 1910	Lys Thr Arg Gln Pro 1915	Pro Glu Arg 1920
Ala Ser Gly Ala Ile Thr Lys 1925	Gly Val Val Leu Asp 1930	Ser Thr Glu 1935
Ala Leu Cys Leu Ala Ile Ser 1940	Gly Asn Ser Glu Gln 1945	Met Ala Ser 1950
His Ser Ala Val Leu Glu Ala 1955	Gly Lys Asn Leu Tyr 1960	Thr Phe Cys 1965
Val Ser Tyr Val Asp Ser Ile 1970	Gln Gln Met Arg Asn 1975	Lys Phe Ala 1980
Phe Arg Glu Ala Ile Asn Lys 1985	Leu Glu Asn Asn Leu 1990	Arg Glu Leu 1995
Gln Ile Cys Pro Ala Ser Ala 2000	Gly Ser Gly Pro Ala 2005	Ala Thr Gln 2010

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Asp Phe Ser Lys Leu Leu Ser Ser Val Lys Glu Ile Ser Asp Ile
 2015 2020 2025

Val Gln Arg
 2030

<210> SEQ ID NO 4
 <211> LENGTH: 2006
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

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Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
 35 40 45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
 50 55 60

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
 65 70 75 80

Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
 85 90 95

Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
 100 105 110

Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
 115 120 125

Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
 130 135 140

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

Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
 165 170 175

Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
 180 185 190

Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
 195 200 205

Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
 210 215 220

Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
 225 230 235 240

Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
 245 250 255

Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
 260 265 270

Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Ile Met
 275 280 285

Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
 290 295 300

Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
 305 310 315 320

Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu

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

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

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Tyr 1130	Gly	Glu	Val	Tyr	Glu	Gly	Val	Trp	Lys	Lys	Tyr	Ser	Leu	Thr
						1135					1140			
Val	Ala	Val	Lys	Thr	Leu	Lys	Glu	Asp	Thr	Met	Glu	Val	Glu	Glu
	1145					1150					1155			
Phe	Leu	Lys	Glu	Ala	Ala	Val	Met	Lys	Glu	Ile	Lys	His	Pro	Asn
	1160					1165					1170			
Leu	Val	Gln	Leu	Leu	Gly	Val	Cys	Thr	Arg	Glu	Pro	Pro	Phe	Tyr
	1175					1180					1185			
Ile	Ile	Thr	Glu	Phe	Met	Thr	Tyr	Gly	Asn	Leu	Leu	Asp	Tyr	Leu
	1190					1195					1200			
Arg	Glu	Cys	Asn	Arg	Gln	Glu	Val	Asn	Ala	Val	Val	Leu	Leu	Tyr
	1205					1210					1215			
Met	Ala	Thr	Gln	Ile	Ser	Ser	Ala	Met	Glu	Tyr	Leu	Glu	Lys	Lys
	1220					1225					1230			
Asn	Phe	Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Leu	Val	Gly
	1235					1240					1245			
Glu	Asn	His	Leu	Val	Lys	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	Leu
	1250					1255					1260			
Met	Thr	Gly	Asp	Thr	Tyr	Thr	Ala	His	Ala	Gly	Ala	Lys	Phe	Pro
	1265					1270					1275			
Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ser	Leu	Ala	Tyr	Asn	Lys	Phe	Ser
	1280					1285					1290			
Ile	Lys	Ser	Asp	Val	Trp	Ala	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile
	1295					1300					1305			
Ala	Thr	Tyr	Gly	Met	Ser	Pro	Tyr	Pro	Gly	Ile	Asp	Arg	Ser	Gln
	1310					1315					1320			
Val	Tyr	Glu	Leu	Leu	Glu	Lys	Asp	Tyr	Arg	Met	Lys	Arg	Pro	Glu
	1325					1330					1335			
Gly	Cys	Pro	Glu	Lys	Val	Tyr	Glu	Leu	Met	Arg	Ala	Cys	Trp	Gln
	1340					1345					1350			
Trp	Asn	Pro	Ser	Asp	Arg	Pro	Ser	Phe	Ala	Glu	Ile	His	Gln	Ala
	1355					1360					1365			
Phe	Glu	Thr	Met	Phe	Gln	Glu	Ser	Ser	Ile	Ser	Asp	Glu	Val	Glu
	1370					1375					1380			
Lys	Glu	Leu	Gly	Lys	Gln	Gly	Val	Arg	Gly	Ala	Val	Thr	Thr	Leu
	1385					1390					1395			
Leu	Gln	Ala	Pro	Glu	Leu	Pro	Thr	Lys	Thr	Arg	Thr	Ser	Arg	Arg
	1400					1405					1410			
Ala	Ala	Glu	His	Arg	Asp	Thr	Thr	Asp	Val	Pro	Glu	Met	Pro	His
	1415					1420					1425			
Ser	Lys	Gly	Gln	Gly	Glu	Ser	Asp	Pro	Leu	Asp	His	Glu	Pro	Ala
	1430					1435					1440			
Val	Ser	Pro	Leu	Leu	Pro	Arg	Lys	Glu	Arg	Gly	Pro	Pro	Glu	Gly
	1445					1450					1455			
Gly	Leu	Asn	Glu	Asp	Glu	Arg	Leu	Leu	Pro	Lys	Asp	Lys	Lys	Thr
	1460					1465					1470			
Asn	Leu	Phe	Ser	Ala	Leu	Ile	Lys	Lys	Lys	Lys	Lys	Thr	Ala	Pro
	1475					1480					1485			
Thr	Pro	Pro	Lys	Arg	Ser	Ser	Ser	Phe	Arg	Glu	Met	Asp	Gly	Gln
	1490					1495					1500			
Pro	Glu	Arg	Arg	Gly	Ala	Gly	Glu	Glu	Glu	Gly	Arg	Asp	Ile	Ser

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1505	1510	1515
Asn Gly Ala Leu Ala Phe Thr Pro Leu Asp Thr Ala Asp Pro Ala		
1520	1525	1530
Lys Ser Pro Lys Pro Ser Asn Gly Ala Gly Val Pro Asn Gly Ala		
1535	1540	1545
Leu Arg Glu Ser Gly Gly Ser Gly Phe Arg Ser Pro His Leu Trp		
1550	1555	1560
Lys Lys Ser Ser Thr Leu Thr Ser Ser Arg Leu Ala Thr Gly Glu		
1565	1570	1575
Glu Glu Gly Gly Gly Ser Ser Ser Lys Arg Phe Leu Arg Ser Cys		
1580	1585	1590
Ser Val Ser Cys Val Pro His Gly Ala Lys Asp Thr Glu Trp Arg		
1595	1600	1605
Ser Val Thr Leu Pro Arg Asp Leu Gln Ser Thr Gly Arg Gln Phe		
1610	1615	1620
Asp Ser Ser Thr Phe Gly Gly His Lys Ser Glu Lys Pro Ala Leu		
1625	1630	1635
Pro Arg Lys Arg Ala Gly Glu Asn Arg Ser Asp Gln Val Thr Arg		
1640	1645	1650
Gly Thr Val Thr Pro Pro Pro Arg Leu Val Lys Lys Asn Glu Glu		
1655	1660	1665
Ala Ala Asp Glu Val Phe Lys Asp Ile Met Glu Ser Ser Pro Gly		
1670	1675	1680
Ser Ser Pro Pro Asn Leu Thr Pro Lys Pro Leu Arg Arg Gln Val		
1685	1690	1695
Thr Val Ala Pro Ala Ser Gly Leu Pro His Lys Glu Glu Ala Trp		
1700	1705	1710
Lys Gly Ser Ala Leu Gly Thr Pro Ala Ala Ala Glu Pro Val Thr		
1715	1720	1725
Pro Thr Ser Lys Ala Gly Ser Gly Ala Pro Arg Gly Thr Ser Lys		
1730	1735	1740
Gly Pro Ala Glu Glu Ser Arg Val Arg Arg His Lys His Ser Ser		
1745	1750	1755
Glu Ser Pro Gly Arg Asp Lys Gly Lys Leu Ser Lys Leu Lys Pro		
1760	1765	1770
Ala Pro Pro Pro Pro Pro Ala Ala Ser Ala Gly Lys Ala Gly Gly		
1775	1780	1785
Lys Pro Ser Gln Arg Pro Gly Gln Glu Ala Ala Gly Glu Ala Val		
1790	1795	1800
Leu Gly Ala Lys Thr Lys Ala Thr Ser Leu Val Asp Ala Val Asn		
1805	1810	1815
Ser Asp Ala Ala Lys Pro Ser Gln Pro Ala Glu Gly Leu Lys Lys		
1820	1825	1830
Pro Val Leu Pro Ala Thr Pro Lys Pro His Pro Ala Lys Pro Ser		
1835	1840	1845
Gly Thr Pro Ile Ser Pro Ala Pro Val Pro Leu Ser Thr Leu Pro		
1850	1855	1860
Ser Ala Ser Ser Ala Leu Ala Gly Asp Gln Pro Ser Ser Thr Ala		
1865	1870	1875
Phe Ile Pro Leu Ile Ser Thr Arg Val Ser Leu Arg Lys Thr Arg		
1880	1885	1890

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Gln Pro Pro Glu Arg Ala Ser Gly Ala Ile Thr Lys Gly Val Val
1895 1900 1905

Leu Asp Ser Thr Glu Ala Leu Cys Leu Ala Ile Ser Gly Asn Ser
1910 1915 1920

Glu Gln Met Ala Ser His Ser Ala Val Leu Glu Ala Gly Lys Asn
1925 1930 1935

Leu Tyr Thr Phe Cys Val Ser Tyr Val Asp Ser Ile Gln Gln Met
1940 1945 1950

Arg Asn Lys Phe Ala Phe Arg Glu Ala Ile Asn Lys Leu Glu Asn
1955 1960 1965

Asn Leu Arg Glu Leu Gln Ile Cys Pro Ala Ser Ala Gly Ser Gly
1970 1975 1980

Pro Ala Ala Thr Gln Asp Phe Ser Lys Leu Leu Ser Ser Val Lys
1985 1990 1995

Glu Ile Ser Asp Ile Val Gln Arg
2000 2005

<210> SEQ ID NO 5
 <211> LENGTH: 1530
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
1 5 10 15

Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
20 25 30

Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
35 40 45

Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
50 55 60

Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65 70 75 80

Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
85 90 95

Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
100 105 110

Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
115 120 125

Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
130 135 140

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

Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
165 170 175

Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
180 185 190

Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
195 200 205

Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
210 215 220

Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys

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225	230	235	240
Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu	245	250	255
Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro	260	265	270
Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Ile Met	275	280	285
Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu	295	300	
Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser	310	315	320
Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu	325	330	335
Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg	340	345	350
Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg	355	360	365
Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro	375	380	
Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser	390	395	400
Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn	405	410	415
Asp Asp Glu Gly Ala Phe His Gly Asp Ala Glu Ala Leu Gln Arg Pro	420	425	430
Val Ala Ser Asp Phe Glu Pro Gln Gly Leu Ser Glu Ala Ala Arg Trp	435	440	445
Asn Ser Lys Glu Asn Leu Leu Ala Gly Pro Ser Glu Asn Asp Pro Asn	455	460	
Leu Phe Val Ala Leu Tyr Asp Phe Val Ala Ser Gly Asp Asn Thr Leu	470	475	480
Ser Ile Thr Lys Gly Glu Lys Leu Arg Val Leu Gly Tyr Asn His Asn	485	490	495
Gly Glu Trp Cys Glu Ala Gln Thr Lys Asn Gly Gln Gly Trp Val Pro	500	505	510
Ser Asn Tyr Ile Thr Pro Val Asn Ser Leu Glu Lys His Ser Trp Tyr	515	520	525
His Gly Pro Val Ser Arg Asn Ala Ala Glu Tyr Pro Leu Ser Ser Gly	530	535	540
Ile Asn Gly Ser Phe Leu Val Arg Glu Ser Glu Ser Ser Pro Ser Gln	550	555	560
Arg Ser Ile Ser Leu Arg Tyr Glu Gly Arg Val Tyr His Tyr Arg Ile	565	570	575
Asn Thr Ala Ser Asp Gly Lys Leu Tyr Val Ser Ser Glu Ser Arg Phe	580	585	590
Asn Thr Leu Ala Glu Leu Val His His His Ser Thr Val Ala Asp Gly	595	600	605
Leu Ile Thr Thr Leu His Tyr Pro Ala Pro Lys Arg Asn Lys Pro Thr	615	620	
Val Tyr Gly Val Ser Pro Asn Tyr Asp Lys Trp Glu Met Glu Arg Thr	630	635	640

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Asp	Ile	Thr	Met	Lys	His	Lys	Leu	Gly	Gly	Gln	Tyr	Gly	Glu	Val	645	650	655	
Tyr	Glu	Gly	Val	Trp	Lys	Lys	Tyr	Ser	Leu	Thr	Val	Ala	Val	Lys	Thr	660	665	670
Leu	Lys	Glu	Asp	Thr	Met	Glu	Val	Glu	Glu	Phe	Leu	Lys	Glu	Ala	Ala	675	680	685
Val	Met	Lys	Glu	Ile	Lys	His	Pro	Asn	Leu	Val	Gln	Leu	Leu	Gly	Val	690	695	700
Cys	Thr	Arg	Glu	Pro	Pro	Phe	Tyr	Ile	Ile	Thr	Glu	Phe	Met	Thr	Tyr	705	710	715
Gly	Asn	Leu	Leu	Asp	Tyr	Leu	Arg	Glu	Cys	Asn	Arg	Gln	Glu	Val	Asn	725	730	735
Ala	Val	Val	Leu	Leu	Tyr	Met	Ala	Thr	Gln	Ile	Ser	Ser	Ala	Met	Glu	740	745	750
Tyr	Leu	Glu	Lys	Lys	Asn	Phe	Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	755	760	765
Cys	Leu	Val	Gly	Glu	Asn	His	Leu	Val	Lys	Val	Ala	Asp	Phe	Gly	Leu	770	775	780
Ser	Arg	Leu	Met	Thr	Gly	Asp	Thr	Tyr	Thr	Ala	His	Ala	Gly	Ala	Lys	785	790	795
Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ser	Leu	Ala	Tyr	Asn	Lys	Phe	805	810	815
Ser	Ile	Lys	Ser	Asp	Val	Trp	Ala	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	820	825	830
Ala	Thr	Tyr	Gly	Met	Ser	Pro	Tyr	Pro	Gly	Ile	Asp	Arg	Ser	Gln	Val	835	840	845
Tyr	Glu	Leu	Leu	Glu	Lys	Asp	Tyr	Arg	Met	Lys	Arg	Pro	Glu	Gly	Cys	850	855	860
Pro	Glu	Lys	Val	Tyr	Glu	Leu	Met	Arg	Ala	Cys	Trp	Gln	Trp	Asn	Pro	865	870	875
Ser	Asp	Arg	Pro	Ser	Phe	Ala	Glu	Ile	His	Gln	Ala	Phe	Glu	Thr	Met	885	890	895
Phe	Gln	Glu	Ser	Ser	Ile	Ser	Asp	Glu	Val	Glu	Lys	Glu	Leu	Gly	Lys	900	905	910
Gln	Gly	Val	Arg	Gly	Ala	Val	Thr	Thr	Leu	Leu	Gln	Ala	Pro	Glu	Leu	915	920	925
Pro	Thr	Lys	Thr	Arg	Thr	Ser	Arg	Arg	Ala	Ala	Glu	His	Arg	Asp	Thr	930	935	940
Thr	Asp	Val	Pro	Glu	Met	Pro	His	Ser	Lys	Gly	Gln	Gly	Glu	Ser	Asp	945	950	955
Pro	Leu	Asp	His	Glu	Pro	Ala	Val	Ser	Pro	Leu	Leu	Pro	Arg	Lys	Glu	965	970	975
Arg	Gly	Pro	Pro	Glu	Gly	Gly	Leu	Asn	Glu	Asp	Glu	Arg	Leu	Leu	Pro	980	985	990
Lys	Asp	Lys	Lys	Thr	Asn	Leu	Phe	Ser	Ala	Leu	Ile	Lys	Lys	Lys	Lys	995	1000	1005
Lys	Thr	Ala	Pro	Thr	Pro	Pro	Lys	Arg	Ser	Ser	Ser	Phe	Arg	Glu		1010	1015	1020
Met	Asp	Gly	Gln	Pro	Glu	Arg	Arg	Gly	Ala	Gly	Glu	Glu	Glu	Gly		1025	1030	1035

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Arg Asp 1040	Ile Ser Asn Gly 1045	Ala Leu Ala Phe Thr 1050	Pro Leu Asp Thr 1055
Ala Asp 1055	Pro Ala Lys Ser 1060	Lys Pro Ser Asn Gly 1065	Ala Gly Val 1070
Pro Asn 1070	Gly Ala Leu Arg 1075	Ser Gly Gly Ser Gly 1080	Phe Arg Ser 1085
Pro His 1085	Leu Trp Lys Lys 1090	Ser Thr Leu Thr Ser 1095	Ser Arg Leu 1100
Ala Thr 1100	Gly Glu Glu Glu 1105	Gly Gly Ser Ser Ser 1110	Lys Arg Phe 1115
Leu Arg 1115	Ser Cys Ser Val 1120	Cys Val Pro His Gly 1125	Ala Lys Asp 1130
Thr Glu 1130	Trp Arg Ser Val 1135	Leu Pro Arg Asp Leu 1140	Gln Ser Thr 1145
Gly Arg 1145	Gln Phe Asp Ser 1150	Thr Phe Gly Gly His 1155	Lys Ser Glu 1160
Lys Pro 1160	Ala Leu Pro Arg 1165	Arg Ala Gly Glu Asn 1170	Arg Ser Asp 1175
Gln Val 1175	Thr Arg Gly Thr 1180	Thr Pro Pro Pro Arg 1185	Leu Val Lys 1190
Lys Asn 1190	Glu Glu Ala Ala 1195	Glu Val Phe Lys Asp 1200	Ile Met Glu 1205
Ser Ser 1205	Pro Gly Ser Ser 1210	Pro Asn Leu Thr Pro 1215	Lys Pro Leu 1220
Arg Arg 1220	Gln Val Thr Val 1225	Pro Ala Ser Gly Leu 1230	Pro His Lys 1235
Glu Glu 1235	Ala Trp Lys Gly 1240	Ala Leu Gly Thr Pro 1245	Ala Ala Ala 1250
Glu Pro 1250	Val Thr Pro Thr 1255	Lys Ala Gly Ser Gly 1260	Ala Pro Arg 1265
Gly Thr 1265	Ser Lys Gly Pro 1270	Glu Glu Ser Arg Val 1275	Arg Arg His 1280
Lys His 1280	Ser Ser Glu Ser 1285	Pro Gly Arg Asp Lys 1290	Lys Leu Ser 1295
Lys Leu 1295	Lys Pro Ala Pro 1300	Pro Pro Pro Ala Ala 1305	Ser Ala Gly 1310
Lys Ala 1310	Gly Gly Lys Pro 1315	Gln Arg Pro Gly Gln 1320	Glu Ala Ala 1325
Gly Glu 1325	Ala Val Leu Gly 1330	Lys Thr Lys Ala Thr 1335	Ser Leu Val 1340
Asp Ala 1340	Val Asn Ser Asp 1345	Ala Lys Pro Ser Gln 1350	Pro Ala Glu 1355
Gly Leu 1355	Lys Lys Pro Val 1360	Pro Ala Thr Pro Lys 1365	Pro His Pro 1370
Ala Lys 1370	Pro Ser Gly Thr 1375	Ile Ser Pro Ala Pro 1380	Val Pro Leu 1385
Ser Thr 1385	Leu Pro Ser Ala 1390	Ser Ala Leu Ala Gly 1395	Asp Gln Pro 1400
Ser Ser 1400	Thr Ala Phe Ile 1405	Leu Ile Ser Thr Arg 1410	Val Ser Leu 1415
Arg Lys 1420	Thr Arg Gln Pro 1425	Glu Arg Ala Ser Gly 1430	Ala Ile Thr 1435

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1415	1420	1425
Lys Gly Val Val Leu Asp Ser Thr Glu Ala Leu Cys Leu Ala Ile		
1430	1435	1440
Ser Gly Asn Ser Glu Gln Met Ala Ser His Ser Ala Val Leu Glu		
1445	1450	1455
Ala Gly Lys Asn Leu Tyr Thr Phe Cys Val Ser Tyr Val Asp Ser		
1460	1465	1470
Ile Gln Gln Met Arg Asn Lys Phe Ala Phe Arg Glu Ala Ile Asn		
1475	1480	1485
Lys Leu Glu Asn Asn Leu Arg Glu Leu Gln Ile Cys Pro Ala Ser		
1490	1495	1500
Ala Gly Ser Gly Pro Ala Ala Thr Gln Asp Phe Ser Lys Leu Leu		
1505	1510	1515
Ser Ser Val Lys Glu Ile Ser Asp Ile Val Gln Arg		
1520	1525	1530

<210> SEQ ID NO 6

<211> LENGTH: 2031

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

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

Gly	Val	Asp	Gly	Asp	Tyr	Glu	Asp	Ala	Glu	Leu	Asn	Pro	Arg	Phe	Leu
				245					250					255	
Lys	Asp	Asn	Leu	Ile	Asp	Ala	Asn	Gly	Gly	Ser	Arg	Pro	Pro	Trp	Pro
				260				265					270		
Pro	Leu	Glu	Tyr	Gln	Pro	Tyr	Gln	Ser	Ile	Tyr	Val	Gly	Gly	Ile	Met
				275			280					285			
Glu	Gly	Glu	Gly	Lys	Gly	Pro	Leu	Leu	Arg	Ser	Gln	Ser	Thr	Ser	Glu
				290		295					300				
Gln	Glu	Lys	Arg	Leu	Thr	Trp	Pro	Arg	Arg	Ser	Tyr	Ser	Pro	Arg	Ser
				305	310					315					320
Phe	Glu	Asp	Cys	Gly	Gly	Gly	Tyr	Thr	Pro	Asp	Cys	Ser	Ser	Asn	Glu
				325				330						335	
Asn	Leu	Thr	Ser	Ser	Glu	Glu	Asp	Phe	Ser	Ser	Gly	Gln	Ser	Ser	Arg
				340				345					350		
Val	Ser	Pro	Ser	Pro	Thr	Thr	Tyr	Arg	Met	Phe	Arg	Asp	Lys	Ser	Arg
				355			360					365			
Ser	Pro	Ser	Gln	Asn	Ser	Gln	Gln	Ser	Phe	Asp	Ser	Ser	Ser	Pro	Pro
				370		375					380				
Thr	Pro	Gln	Cys	His	Lys	Arg	His	Arg	His	Cys	Pro	Val	Val	Val	Ser
				385	390					395					400
Glu	Ala	Thr	Ile	Val	Gly	Val	Arg	Lys	Thr	Gly	Gln	Ile	Trp	Pro	Asn
				405				410						415	
Asp	Asp	Glu	Gly	Ala	Phe	His	Gly	Asp	Ala	Asp	Gly	Ser	Phe	Gly	Thr
				420				425					430		
Pro	Pro	Gly	Tyr	Gly	Cys	Ala	Ala	Asp	Arg	Ala	Glu	Glu	Gln	Arg	Arg
				435			440					445			
His	Gln	Asp	Gly	Leu	Pro	Tyr	Ile	Asp	Asp	Ser	Pro	Ser	Ser	Ser	Pro
				450		455					460				
His	Leu	Ser	Ser	Lys	Gly	Arg	Gly	Ser	Arg	Asp	Ala	Leu	Val	Ser	Gly
				465	470					475					480
Ala	Leu	Lys	Ser	Thr	Lys	Ala	Ser	Glu	Leu	Asp	Leu	Glu	Lys	Gly	Leu
				485				490						495	
Glu	Met	Arg	Lys	Trp	Val	Leu	Ser	Gly	Ile	Leu	Ala	Ser	Glu	Glu	Thr
				500				505					510		
Tyr	Leu	Ser	His	Leu	Glu	Ala	Leu	Leu	Leu	Pro	Met	Lys	Pro	Leu	Lys
				515			520					525			
Ala	Ala	Ala	Thr	Thr	Ser	Gln	Pro	Val	Leu	Thr	Ser	Gln	Gln	Ile	Glu
				530		535					540				
Thr	Ile	Phe	Phe	Lys	Val	Pro	Glu	Leu	Tyr	Glu	Ile	His	Lys	Glu	Ser
				545	550					555					560
Tyr	Asp	Gly	Leu	Phe	Pro	Arg	Val	Gln	Gln	Trp	Ser	His	Gln	Gln	Arg
				565				570						575	
Val	Gly	Asp	Leu	Phe	Gln	Lys	Leu	Ala	Ser	Gln	Leu	Gly	Val	Tyr	Arg
				580				585					590		
Ala	Phe	Val	Asp	Asn	Tyr	Gly	Val	Ala	Met	Glu	Met	Ala	Glu	Lys	Cys
				595			600					605			
Cys	Gln	Ala	Asn	Ala	Gln	Phe	Ala	Glu							

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645					650					655					
Leu	His	Asp	Leu	Leu	Lys	His	Thr	Pro	Ala	Ser	His	Pro	Asp	His	Pro
			660					665					670		
Leu	Leu	Gln	Asp	Ala	Leu	Arg	Ile	Ser	Gln	Asn	Phe	Leu	Ser	Ser	Ile
		675					680					685			
Asn	Glu	Glu	Ile	Thr	Pro	Arg	Arg	Gln	Ser	Met	Thr	Val	Lys	Lys	Gly
	690					695					700				
Glu	His	Arg	Gln	Leu	Leu	Lys	Asp	Ser	Phe	Met	Val	Glu	Leu	Val	Glu
705					710					715					720
Gly	Ala	Arg	Lys	Leu	Arg	His	Val	Phe	Leu	Phe	Thr	Asp	Leu	Leu	Leu
				725					730					735	
Cys	Thr	Lys	Leu	Lys	Lys	Gln	Ser	Gly	Gly	Lys	Thr	Gln	Gln	Tyr	Asp
			740					745					750		
Cys	Lys	Trp	Tyr	Ile	Pro	Leu	Thr	Asp	Leu	Ser	Phe	Gln	Met	Val	Asp
		755					760					765			
Glu	Leu	Glu	Ala	Val	Pro	Asn	Ile	Pro	Leu	Val	Pro	Asp	Glu	Glu	Leu
	770					775					780				
Asp	Ala	Leu	Lys	Ile	Lys	Ile	Ser	Gln	Ile	Lys	Ser	Asp	Ile	Gln	Arg
785					790					795					800
Glu	Lys	Arg	Ala	Asn	Lys	Gly	Ser	Lys	Ala	Thr	Glu	Arg	Leu	Lys	Lys
				805					810					815	
Lys	Leu	Ser	Glu	Gln	Glu	Ser	Leu	Leu	Leu	Leu	Met	Ser	Pro	Ser	Met
			820					825					830		
Ala	Phe	Arg	Val	His	Ser	Arg	Asn	Gly	Lys	Ser	Tyr	Thr	Phe	Leu	Ile
		835					840					845			
Ser	Ser	Asp	Tyr	Glu	Arg	Ala	Glu	Trp	Arg	Glu	Asn	Ile	Arg	Glu	Gln
		850				855					860				
Gln	Lys	Lys	Cys	Phe	Arg	Ser	Phe	Ser	Leu	Thr	Ser	Val	Glu	Leu	Gln
865					870					875					880
Met	Leu	Thr	Asn	Ser	Cys	Val	Lys	Leu	Gln	Thr	Val	His	Ser	Ile	Pro
			885						890					895	
Leu	Thr	Ile	Asn	Lys	Glu	Asp	Asp	Glu	Ser	Pro	Gly	Leu	Tyr	Gly	Phe
			900					905					910		
Leu	Asn	Val	Ile	Val	His	Ser	Ala	Thr	Gly	Phe	Lys	Gln	Ser	Ser	Lys
		915					920					925			
Ala	Leu	Gln	Arg	Pro	Val	Ala	Ser	Asp	Phe	Glu	Pro	Gln	Gly	Leu	Ser
	930					935					940				
Glu	Ala	Ala	Arg	Trp	Asn	Ser	Lys	Glu	Asn	Leu	Leu	Ala	Gly	Pro	Ser
945					950					955					960
Glu	Asn	Asp	Pro	Asn	Leu	Phe	Val	Ala	Leu	Tyr	Asp	Phe	Val	Ala	Ser
				965					970					975	
Gly	Asp	Asn	Thr	Leu	Ser	Ile	Thr	Lys	Gly	Glu	Lys	Leu	Arg	Val	Leu
			980					985					990		
Gly	Tyr	Asn	His	Asn	Gly	Glu	Trp	Cys	Glu	Ala	Gln	Thr	Lys	Asn	Gly
		995					1000					1005			
Gln	Gly	Trp	Val	Pro	Ser	Asn	Tyr	Ile	Thr	Pro	Val	Asn	Ser	Leu	
	1010					1015					1020				
Glu	Lys	His	Ser	Trp	Tyr	His	Gly	Pro	Val	Ser	Arg	Asn	Ala	Ala	
	1025					1030					1035				
Glu	Tyr	Pro	Leu	Ser	Ser	Gly	Ile	Asn	Gly	Ser	Phe	Leu	Val	Arg	
	1040					1045					1050				

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Glu Ser	Glu Ser Ser Pro	Ser	Gln Arg Ser Ile	Ser	Leu Arg Tyr
1055		1060		1065	
Glu Gly	Arg Val Tyr His	Tyr	Arg Ile Asn Thr	Ala	Ser Asp Gly
1070		1075		1080	
Lys Leu	Tyr Val Ser Ser	Glu	Ser Arg Phe Asn	Thr	Leu Ala Glu
1085		1090		1095	
Leu Val	His His His Ser	Thr	Val Ala Asp Gly	Leu	Ile Thr Thr
1100		1105		1110	
Leu His	Tyr Pro Ala Pro	Lys	Arg Asn Lys Pro	Thr	Val Tyr Gly
1115		1120		1125	
Val Ser	Pro Asn Tyr Asp	Lys	Trp Glu Met Glu	Arg	Thr Asp Ile
1130		1135		1140	
Thr Met	Lys His Lys Leu	Gly	Gly Gly Gln Tyr	Gly	Glu Val Tyr
1145		1150		1155	
Glu Gly	Val Trp Lys Lys	Tyr	Ser Leu Thr Val	Ala	Val Lys Thr
1160		1165		1170	
Leu Lys	Glu Asp Thr Met	Glu	Val Glu Glu Phe	Leu	Lys Glu Ala
1175		1180		1185	
Ala Val	Met Lys Glu Ile	Lys	His Pro Asn Leu	Val	Gln Leu Leu
1190		1195		1200	
Gly Val	Cys Thr Arg Glu	Pro	Pro Phe Tyr Ile	Ile	Ile Glu Phe
1205		1210		1215	
Met Thr	Tyr Gly Asn Leu	Leu	Asp Tyr Leu Arg	Glu	Cys Asn Arg
1220		1225		1230	
Gln Glu	Val Asn Ala Val	Val	Leu Leu Tyr Met	Ala	Thr Gln Ile
1235		1240		1245	
Ser Ser	Ala Met Glu Tyr	Leu	Glu Lys Lys Asn	Phe	Ile His Arg
1250		1255		1260	
Asp Leu	Ala Ala Arg Asn	Cys	Leu Val Gly Glu	Asn	His Leu Val
1265		1270		1275	
Lys Val	Ala Asp Phe Gly	Leu	Ser Arg Leu Met	Thr	Gly Asp Thr
1280		1285		1290	
Tyr Thr	Ala His Ala Gly	Ala	Lys Phe Pro Ile	Lys	Trp Thr Ala
1295		1300		1305	
Pro Glu	Ser Leu Ala Tyr	Asn	Lys Phe Ser Ile	Lys	Ser Asp Val
1310		1315		1320	
Trp Ala	Phe Gly Val Leu	Leu	Trp Glu Ile Ala	Thr	Tyr Gly Met
1325		1330		1335	
Ser Pro	Tyr Pro Gly Ile	Asp	Arg Ser Gln Val	Tyr	Glu Leu Leu
1340		1345		1350	
Glu Lys	Asp Tyr Arg Met	Lys	Arg Pro Glu Gly	Cys	Pro Glu Lys
1355		1360		1365	
Val Tyr	Glu Leu Met Arg	Ala	Cys Trp Gln Trp	Asn	Pro Ser Asp
1370		1375		1380	
Arg Pro	Ser Phe Ala Glu	Ile	His Gln Ala Phe	Glu	Thr Met Phe
1385		1390		1395	
Gln Glu	Ser Ser Ile Ser	Asp	Glu Val Glu Lys	Glu	Leu Gly Lys
1400		1405		1410	
Gln Gly	Val Arg Gly Ala	Val	Thr Thr Leu Leu	Gln	Ala Pro Glu
1415		1420		1425	

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Leu 1430	Pro	Thr	Lys	Thr	Arg	Thr 1435	Ser	Arg	Arg	Ala	Ala 1440	Glu	His	Arg
Asp 1445	Thr	Thr	Asp	Val	Pro	Glu 1450	Met	Pro	His	Ser	Lys 1455	Gly	Gln	Gly
Glu 1460	Ser	Asp	Pro	Leu	Asp	His 1465	Glu	Pro	Ala	Val	Ser 1470	Pro	Leu	Leu
Pro 1475	Arg	Lys	Glu	Arg	Gly	Pro 1480	Pro	Glu	Gly	Gly	Leu 1485	Asn	Glu	Asp
Glu 1490	Arg	Leu	Leu	Pro	Lys	Asp 1495	Lys	Lys	Thr	Asn	Leu 1500	Phe	Ser	Ala
Leu 1505	Ile	Lys	Lys	Lys	Lys	Lys 1510	Thr	Ala	Pro	Thr	Pro 1515	Pro	Lys	Arg
Ser 1520	Ser	Ser	Phe	Arg	Glu	Met 1525	Asp	Gly	Gln	Pro	Glu 1530	Arg	Arg	Gly
Ala 1535	Gly	Glu	Glu	Glu	Gly	Arg 1540	Asp	Ile	Ser	Asn	Gly 1545	Ala	Leu	Ala
Phe 1550	Thr	Pro	Leu	Asp	Thr	Ala 1555	Asp	Pro	Ala	Lys	Ser 1560	Pro	Lys	Pro
Ser 1565	Asn	Gly	Ala	Gly	Val	Pro 1570	Asn	Gly	Ala	Leu	Arg 1575	Glu	Ser	Gly
Gly 1580	Ser	Gly	Phe	Arg	Ser	Pro 1585	His	Leu	Trp	Lys	Lys 1590	Ser	Ser	Thr
Leu 1595	Thr	Ser	Ser	Arg	Leu	Ala 1600	Thr	Gly	Glu	Glu	Glu 1605	Gly	Gly	Gly
Ser 1610	Ser	Ser	Lys	Arg	Phe	Leu 1615	Arg	Ser	Cys	Ser	Val 1620	Ser	Cys	Val
Pro 1625	His	Gly	Ala	Lys	Asp	Thr 1630	Glu	Trp	Arg	Ser	Val 1635	Thr	Leu	Pro
Arg 1640	Asp	Leu	Gln	Ser	Thr	Gly 1645	Arg	Gln	Phe	Asp	Ser 1650	Ser	Thr	Phe
Gly 1655	Gly	His	Lys	Ser	Glu	Lys 1660	Pro	Ala	Leu	Pro	Arg 1665	Lys	Arg	Ala
Gly 1670	Glu	Asn	Arg	Ser	Asp	Gln 1675	Val	Thr	Arg	Gly	Thr 1680	Val	Thr	Pro
Pro 1685	Pro	Arg	Leu	Val	Lys	Lys 1690	Asn	Glu	Glu	Ala	Ala 1695	Asp	Glu	Val
Phe 1700	Lys	Asp	Ile	Met	Glu	Ser 1705	Ser	Pro	Gly	Ser	Ser 1710	Pro	Pro	Asn
Leu 1715	Thr	Pro	Lys	Pro	Leu	Arg 1720	Arg	Gln	Val	Thr	Val 1725	Ala	Pro	Ala
Ser 1730	Gly	Leu	Pro	His	Lys	Glu 1735	Glu	Ala	Trp	Lys	Gly 1740	Ser	Ala	Leu
Gly 1745	Thr	Pro	Ala	Ala	Ala	Glu 1750	Pro	Val	Thr	Pro	Thr 1755	Ser	Lys	Ala
Gly 1760	Ser	Gly	Ala	Pro	Arg	Gly 1765	Thr	Ser	Lys	Gly	Pro 1770	Ala	Glu	Glu
Ser 1775	Arg	Val	Arg	Arg	His	Lys 1780	His	Ser	Ser	Glu	Ser 1785	Pro	Gly	Arg
Asp 1790	Lys	Gly	Lys	Leu	Ser	Lys 1795	Leu	Lys	Pro	Ala	Pro 1800	Pro	Pro	Pro
Pro	Ala	Ala	Ser	Ala	Gly	Lys	Ala	Gly	Gly	Lys	Pro	Ser	Gln	Arg

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1805	1810	1815
Pro Gly Gln Glu Ala Ala Gly	Glu Ala Val Leu Gly	Ala Lys Thr
1820	1825	1830
Lys Ala Thr Ser Leu Val Asp	Ala Val Asn Ser Asp	Ala Ala Lys
1835	1840	1845
Pro Ser Gln Pro Ala Glu Gly	Leu Lys Lys Pro Val	Leu Pro Ala
1850	1855	1860
Thr Pro Lys Pro His Pro Ala	Lys Pro Ser Gly Thr	Pro Ile Ser
1865	1870	1875
Pro Ala Pro Val Pro Leu Ser	Thr Leu Pro Ser Ala	Ser Ser Ala
1880	1885	1890
Leu Ala Gly Asp Gln Pro Ser	Ser Thr Ala Phe Ile	Pro Leu Ile
1895	1900	1905
Ser Thr Arg Val Ser Leu Arg	Lys Thr Arg Gln Pro	Pro Glu Arg
1910	1915	1920
Ala Ser Gly Ala Ile Thr Lys	Gly Val Val Leu Asp	Ser Thr Glu
1925	1930	1935
Ala Leu Cys Leu Ala Ile Ser	Gly Asn Ser Glu Gln	Met Ala Ser
1940	1945	1950
His Ser Ala Val Leu Glu Ala	Gly Lys Asn Leu Tyr	Thr Phe Cys
1955	1960	1965
Val Ser Tyr Val Asp Ser Ile	Gln Gln Met Arg Asn	Lys Phe Ala
1970	1975	1980
Phe Arg Glu Ala Ile Asn Lys	Leu Glu Asn Asn Leu	Arg Glu Leu
1985	1990	1995
Gln Ile Cys Pro Ala Ser Ala	Gly Ser Gly Pro Ala	Ala Thr Gln
2000	2005	2010
Asp Phe Ser Lys Leu Leu Ser	Ser Val Lys Glu Ile	Ser Asp Ile
2015	2020	2025
Val Gln Arg		
2030		

<210> SEQ ID NO 7
 <211> LENGTH: 2006
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

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

Pro	Glu	Ala	Arg	Pro	Asp	Gly	Glu	Gly	Ser	Pro	Gly	Lys	Ala	Arg	Pro
		115					120					125			
Gly	Thr	Ala	Arg	Arg	Pro	Gly	Ala	Ala	Ala	Ser	Gly	Glu	Arg	Asp	Asp
	130					135					140				
Arg	Gly	Pro	Pro	Ala	Ser	Val	Ala	Ala	Leu	Arg	Ser	Asn	Phe	Glu	Arg
145					150					155					160
Ile	Arg	Lys	Gly	His	Gly	Gln	Pro	Gly	Ala	Asp	Ala	Glu	Lys	Pro	Phe
				165					170					175	
Tyr	Val	Asn	Val	Glu	Phe	His	His	Glu	Arg	Gly	Leu	Val	Lys	Val	Asn
			180					185					190		
Asp	Lys	Glu	Val	Ser	Asp	Arg	Ile	Ser	Ser	Leu	Gly	Ser	Gln	Ala	Met
		195					200					205			
Gln	Met	Glu	Arg	Lys	Lys	Ser	Gln	His	Gly	Ala	Gly	Ser	Ser	Val	Gly
	210					215					220				
Asp	Ala	Ser	Arg	Pro	Pro	Tyr	Arg	Gly	Arg	Ser	Ser	Glu	Ser	Ser	Cys
225					230					235					240
Gly	Val	Asp	Gly	Asp	Tyr	Glu	Asp	Ala	Glu	Leu	Asn	Pro	Arg	Phe	Leu
				245					250					255	
Lys	Asp	Asn	Leu	Ile	Asp	Ala	Asn	Gly	Gly	Ser	Arg	Pro	Pro	Trp	Pro
			260					265					270		
Pro	Leu	Glu	Tyr	Gln	Pro	Tyr	Gln	Ser	Ile	Tyr	Val	Gly	Gly	Ile	Met
		275					280					285			
Glu	Gly	Glu	Gly	Lys	Gly	Pro	Leu	Leu	Arg	Ser	Gln	Ser	Thr	Ser	Glu
	290					295					300				
Gln	Glu	Lys	Arg	Leu	Thr	Trp	Pro	Arg	Arg	Ser	Tyr	Ser	Pro	Arg	Ser
305					310					315					320
Phe	Glu	Asp	Cys	Gly	Gly	Gly	Tyr	Thr	Pro	Asp	Cys	Ser	Ser	Asn	Glu
				325					330					335	
Asn	Leu	Thr	Ser	Ser	Glu	Glu	Asp	Phe	Ser	Ser	Gly	Gln	Ser	Ser	Arg
			340					345					350		
Val	Ser	Pro	Ser	Pro	Thr	Thr	Tyr	Arg	Met	Phe	Arg	Asp	Lys	Ser	Arg
		355					360					365			
Ser	Pro	Ser	Gln	Asn	Ser	Gln	Gln	Ser	Phe	Asp	Ser	Ser	Ser	Pro	Pro
	370					375				380					
Thr	Pro	Gln	Cys	His	Lys	Arg	His	Arg	His	Cys	Pro	Val	Val	Val	Ser
385					390					395					400
Glu	Ala	Thr	Ile	Val	Gly	Val	Arg	Lys	Thr	Gly	Gln	Ile	Trp	Pro	Asn
			405					410						415	
Asp	Asp	Glu	Gly	Ala	Phe	His	Gly	Asp	Ala	Asp	Gly	Ser	Phe	Gly	Thr
			420					425					430		
Pro	Pro	Gly	Tyr	Gly	Cys	Ala	Ala	Asp	Arg	Ala	Glu	Glu	Gln	Arg	Arg
		435				440						445			
His	Gln	Asp	Gly	Leu	Pro	Tyr	Ile	Asp	Asp	Ser	Pro	Ser	Ser	Ser	Pro
	450					455				460					
His	Leu	Ser	Ser	Lys	Gly	Arg									

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515					520					525					
Ala 530	Ala 530	Ala 530	Thr 530	Thr 530	Ser 530	Gln 535	Pro 535	Val 535	Leu 535	Thr 540	Ser 540	Gln 540	Gln 540	Ile 540	Glu 540
Thr 545	Ile 545	Phe 545	Phe 545	Lys 545	Val 550	Pro 550	Glu 550	Leu 550	Tyr 555	Glu 555	Ile 555	His 555	Lys 555	Glu 560	Ser 560
Tyr 565	Asp 565	Gly 565	Leu 565	Phe 565	Pro 565	Arg 565	Val 570	Gln 570	Gln 570	Trp 570	Ser 575	His 575	Gln 575	Gln 575	Arg 575
Val 580	Gly 580	Asp 580	Leu 580	Phe 580	Gln 580	Lys 580	Leu 585	Ala 585	Ser 585	Gln 585	Leu 590	Gly 590	Val 590	Tyr 590	Arg 590
Ala 595	Phe 595	Val 595	Asp 595	Asn 595	Tyr 595	Gly 600	Val 600	Ala 600	Met 600	Glu 605	Met 605	Ala 605	Glu 605	Lys 605	Cys 605
Cys 610	Gln 610	Ala 610	Asn 610	Ala 610	Gln 610	Phe 615	Ala 615	Glu 615	Ile 615	Ser 620	Glu 620	Asn 620	Leu 620	Arg 620	Ala 620
Arg 625	Ser 625	Asn 625	Lys 625	Asp 625	Ala 630	Lys 630	Asp 630	Pro 635	Thr 635	Thr 635	Lys 635	Asn 635	Ser 635	Leu 640	Glu 640
Thr 645	Leu 645	Leu 645	Tyr 645	Lys 645	Pro 645	Val 645	Asp 645	Arg 650	Val 650	Thr 650	Arg 650	Ser 650	Thr 650	Leu 655	Val 655
Leu 660	His 660	Asp 660	Leu 660	Leu 660	Lys 660	His 660	Thr 665	Pro 665	Ala 665	Ser 665	His 665	Pro 670	Asp 670	His 670	Pro 670
Leu 675	Leu 675	Gln 675	Asp 675	Ala 675	Leu 675	Arg 675	Ile 680	Ser 680	Gln 680	Asn 680	Phe 685	Leu 685	Ser 685	Ser 685	Ile 685
Asn 690	Glu 690	Glu 690	Ile 690	Thr 690	Pro 695	Arg 695	Arg 695	Gln 695	Ser 695	Met 695	Thr 700	Val 700	Lys 700	Lys 700	Gly 700
Glu 705	His 705	Arg 705	Gln 705	Leu 705	Leu 710	Lys 710	Asp 710	Ser 710	Phe 715	Met 715	Val 715	Glu 715	Leu 715	Val 720	Glu 720
Gly 725	Ala 725	Arg 725	Lys 725	Leu 725	Arg 725	His 725	Val 725	Phe 730	Leu 730	Phe 730	Thr 730	Asp 735	Leu 735	Leu 735	Leu 735
Cys 740	Thr 740	Lys 740	Leu 740	Lys 740	Lys 740	Gln 740	Ser 745	Gly 745	Gly 745	Lys 745	Thr 745	Gln 750	Gln 750	Tyr 750	Asp 750
Cys 755	Lys 755	Trp 755	Tyr 755	Ile 755	Pro 755	Leu 760	Thr 760	Asp 760	Leu 760	Ser 765	Phe 765	Gln 765	Met 765	Val 765	Asp 765
Glu 770	Leu 770	Glu 770	Ala 770	Val 770	Pro 775	Asn 775	Ile 775	Pro 775	Leu 775	Val 775	Pro 780	Asp 780	Glu 780	Glu 780	Leu 780
Asp 785	Ala 785	Leu 785	Lys 785	Ile 785	Lys 790	Ile 790	Ser 790	Gln 790	Ile 795	Lys 795	Ser 795	Asp 795	Ile 795	Gln 800	Arg 800
Glu 805	Lys 805	Arg 805	Ala 805	Asn 805	Lys 805	Gly 805	Ser 805	Lys 810	Ala 810	Thr 810	Glu 810	Arg 810	Leu 815	Lys 815	Lys 815
Lys 820	Leu 820	Ser 820	Glu 820	Gln 820	Glu 820	Ser 820	Leu 825	Leu 825	Leu 825	Leu 825	Met 825	Ser 830	Pro 830	Ser 830	Met 830
Ala 835	Phe 835	Arg 835	Val 835	His 835	Ser 835	Arg 840	Asn 840	Gly 840	Lys 840	Ser 840	Tyr 845	Thr 845	Phe 845	Leu 845	Ile 845
Ser 850	Ser 850	Asp 850	Tyr 850	Glu 850	Arg 855	Ala 855	Glu 855	Trp 855	Arg 855	Glu 860	Asn 860	Ile 860	Arg 860	Glu 860	Gln 860
Gln 865	Lys 865	Lys 865	Cys 865	Phe 865	Arg 870	Ser 870	Phe 870	Ser 875	Leu 875	Thr 875	Ser 875	Val 875	Glu 875	Leu 880	Gln 880
Met 885	Leu 885	Thr 885	Asn 885	Ser 885	Cys 885	Val 885	Lys 885	Leu 890	Gln 890	Thr 890	Val 890	His 890	Ser 890	Ile 895	Pro 895
Leu 900	Thr 900	Ile 900	Asn 900	Lys 900	Glu 900	Glu 900	Ala 905	Leu 905	Gln 905	Arg 905	Pro 905	Val 910	Ala 910	Ser 910	Asp 910
Phe 915	Glu 915	Pro 915	Gln 915	Gly 915	Leu 915	Ser 920	Glu 920	Ala 920	Ala 920	Arg 920	Trp 925	Asn 925	Ser 925	Lys 925	Glu 925

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Asn Leu Leu Ala Gly Pro Ser Glu Asn Asp Pro Asn Leu Phe Val Ala	
930	935 940
Leu Tyr Asp Phe Val Ala Ser Gly Asp Asn Thr Leu Ser Ile Thr Lys	
945	950 955 960
Gly Glu Lys Leu Arg Val Leu Gly Tyr Asn His Asn Gly Glu Trp Cys	
	965 970 975
Glu Ala Gln Thr Lys Asn Gly Gln Gly Trp Val Pro Ser Asn Tyr Ile	
	980 985 990
Thr Pro Val Asn Ser Leu Glu Lys His Ser Trp Tyr His Gly Pro Val	
	995 1000 1005
Ser Arg Asn Ala Ala Glu Tyr Pro Leu Ser Ser Gly Ile Asn Gly	
1010	1015 1020
Ser Phe Leu Val Arg Glu Ser Glu Ser Ser Pro Ser Gln Arg Ser	
1025	1030 1035
Ile Ser Leu Arg Tyr Glu Gly Arg Val Tyr His Tyr Arg Ile Asn	
1040	1045 1050
Thr Ala Ser Asp Gly Lys Leu Tyr Val Ser Ser Glu Ser Arg Phe	
1055	1060 1065
Asn Thr Leu Ala Glu Leu Val His His His Ser Thr Val Ala Asp	
1070	1075 1080
Gly Leu Ile Thr Thr Leu His Tyr Pro Ala Pro Lys Arg Asn Lys	
1085	1090 1095
Pro Thr Val Tyr Gly Val Ser Pro Asn Tyr Asp Lys Trp Glu Met	
1100	1105 1110
Glu Arg Thr Asp Ile Thr Met Lys His Lys Leu Gly Gly Gly Gln	
1115	1120 1125
Tyr Gly Glu Val Tyr Glu Gly Val Trp Lys Lys Tyr Ser Leu Thr	
1130	1135 1140
Val Ala Val Lys Thr Leu Lys Glu Asp Thr Met Glu Val Glu Glu	
1145	1150 1155
Phe Leu Lys Glu Ala Ala Val Met Lys Glu Ile Lys His Pro Asn	
1160	1165 1170
Leu Val Gln Leu Leu Gly Val Cys Thr Arg Glu Pro Pro Phe Tyr	
1175	1180 1185
Ile Ile Ile Glu Phe Met Thr Tyr Gly Asn Leu Leu Asp Tyr Leu	
1190	1195 1200
Arg Glu Cys Asn Arg Gln Glu Val Asn Ala Val Val Leu Leu Tyr	
1205	1210 1215
Met Ala Thr Gln Ile Ser Ser Ala Met Glu Tyr Leu Glu Lys Lys	
1220	1225 1230
Asn Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val Gly	
1235	1240 1245
Glu Asn His Leu Val Lys Val Ala Asp Phe Gly Leu Ser Arg Leu	
1250	1255 1260
Met Thr Gly Asp Thr Tyr Thr Ala His Ala Gly Ala Lys Phe Pro	
1265	1270 1275
Ile Lys Trp Thr Ala Pro Glu Ser Leu Ala Tyr Asn Lys Phe Ser	
1280	1285 1290
Ile Lys Ser Asp Val Trp Ala Phe Gly Val Leu Leu Trp Glu Ile	
1295	1300 1305

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Ala	Thr	Tyr	Gly	Met	Ser	Pro	Tyr	Pro	Gly	Ile	Asp	Arg	Ser	Gln
1310						1315					1320			
Val	Tyr	Glu	Leu	Leu	Glu	Lys	Asp	Tyr	Arg	Met	Lys	Arg	Pro	Glu
1325						1330					1335			
Gly	Cys	Pro	Glu	Lys	Val	Tyr	Glu	Leu	Met	Arg	Ala	Cys	Trp	Gln
1340						1345					1350			
Trp	Asn	Pro	Ser	Asp	Arg	Pro	Ser	Phe	Ala	Glu	Ile	His	Gln	Ala
1355						1360					1365			
Phe	Glu	Thr	Met	Phe	Gln	Glu	Ser	Ser	Ile	Ser	Asp	Glu	Val	Glu
1370						1375					1380			
Lys	Glu	Leu	Gly	Lys	Gln	Gly	Val	Arg	Gly	Ala	Val	Thr	Thr	Leu
1385						1390					1395			
Leu	Gln	Ala	Pro	Glu	Leu	Pro	Thr	Lys	Thr	Arg	Thr	Ser	Arg	Arg
1400						1405					1410			
Ala	Ala	Glu	His	Arg	Asp	Thr	Thr	Asp	Val	Pro	Glu	Met	Pro	His
1415						1420					1425			
Ser	Lys	Gly	Gln	Gly	Glu	Ser	Asp	Pro	Leu	Asp	His	Glu	Pro	Ala
1430						1435					1440			
Val	Ser	Pro	Leu	Leu	Pro	Arg	Lys	Glu	Arg	Gly	Pro	Pro	Glu	Gly
1445						1450					1455			
Gly	Leu	Asn	Glu	Asp	Glu	Arg	Leu	Leu	Pro	Lys	Asp	Lys	Lys	Thr
1460						1465					1470			
Asn	Leu	Phe	Ser	Ala	Leu	Ile	Lys	Lys	Lys	Lys	Lys	Thr	Ala	Pro
1475						1480					1485			
Thr	Pro	Pro	Lys	Arg	Ser	Ser	Ser	Phe	Arg	Glu	Met	Asp	Gly	Gln
1490						1495					1500			
Pro	Glu	Arg	Arg	Gly	Ala	Gly	Glu	Glu	Glu	Gly	Arg	Asp	Ile	Ser
1505						1510					1515			
Asn	Gly	Ala	Leu	Ala	Phe	Thr	Pro	Leu	Asp	Thr	Ala	Asp	Pro	Ala
1520						1525					1530			
Lys	Ser	Pro	Lys	Pro	Ser	Asn	Gly	Ala	Gly	Val	Pro	Asn	Gly	Ala
1535						1540					1545			
Leu	Arg	Glu	Ser	Gly	Gly	Ser	Gly	Phe	Arg	Ser	Pro	His	Leu	Trp
1550						1555					1560			
Lys	Lys	Ser	Ser	Thr	Leu	Thr	Ser	Ser	Arg	Leu	Ala	Thr	Gly	Glu
1565						1570					1575			
Glu	Glu	Gly	Gly	Gly	Ser	Ser	Ser	Lys	Arg	Phe	Leu	Arg	Ser	Cys
1580						1585					1590			
Ser	Val	Ser	Cys	Val	Pro	His	Gly	Ala	Lys	Asp	Thr	Glu	Trp	Arg
1595						1600					1605			
Ser	Val	Thr	Leu	Pro	Arg	Asp	Leu	Gln	Ser	Thr	Gly	Arg	Gln	Phe
1610						1615					1620			
Asp	Ser	Ser	Thr	Phe	Gly	Gly	His	Lys	Ser	Glu	Lys	Pro	Ala	Leu
1625						1630					1635			
Pro	Arg	Lys	Arg	Ala	Gly	Glu	Asn	Arg	Ser	Asp	Gln	Val	Thr	Arg
1640						1645					1650			
Gly	Thr	Val	Thr	Pro	Pro	Pro	Arg	Leu	Val	Lys	Lys	Asn	Glu	Glu
1655						1660					1665			
Ala	Ala	Asp	Glu	Val	Phe	Lys	Asp	Ile	Met	Glu	Ser	Ser	Pro	Gly
1670						1675					1680			
Ser	Ser	Pro	Pro	Asn	Leu	Thr	Pro	Lys	Pro	Leu	Arg	Arg	Gln	Val

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

<210> SEQ ID NO 8
 <211> LENGTH: 1530
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

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

-continued

420							425					430				
Val	Ala	Ser	Asp	Phe	Glu	Pro	Gln	Gly	Leu	Ser	Glu	Ala	Ala	Arg	Trp	
435							440					445				
Asn	Ser	Lys	Glu	Asn	Leu	Leu	Ala	Gly	Pro	Ser	Glu	Asn	Asp	Pro	Asn	
450							455					460				
Leu	Phe	Val	Ala	Leu	Tyr	Asp	Phe	Val	Ala	Ser	Gly	Asp	Asn	Thr	Leu	
465							470					475				
Ser	Ile	Thr	Lys	Gly	Glu	Lys	Leu	Arg	Val	Leu	Gly	Tyr	Asn	His	Asn	
485							490					495				
Gly	Glu	Trp	Cys	Glu	Ala	Gln	Thr	Lys	Asn	Gly	Gln	Gly	Trp	Val	Pro	
500							505					510				
Ser	Asn	Tyr	Ile	Thr	Pro	Val	Asn	Ser	Leu	Glu	Lys	His	Ser	Trp	Tyr	
515							520					525				
His	Gly	Pro	Val	Ser	Arg	Asn	Ala	Ala	Glu	Tyr	Pro	Leu	Ser	Ser	Gly	
530							535					540				
Ile	Asn	Gly	Ser	Phe	Leu	Val	Arg	Glu	Ser	Glu	Ser	Ser	Pro	Ser	Gln	
545							550					555				
Arg	Ser	Ile	Ser	Leu	Arg	Tyr	Glu	Gly	Arg	Val	Tyr	His	Tyr	Arg	Ile	
565							570					575				
Asn	Thr	Ala	Ser	Asp	Gly	Lys	Leu	Tyr	Val	Ser	Ser	Glu	Ser	Arg	Phe	
580							585					590				
Asn	Thr	Leu	Ala	Glu	Leu	Val	His	His	His	Ser	Thr	Val	Ala	Asp	Gly	
595							600					605				
Leu	Ile	Thr	Thr	Leu	His	Tyr	Pro	Ala	Pro	Lys	Arg	Asn	Lys	Pro	Thr	
610							615					620				
Val	Tyr	Gly	Val	Ser	Pro	Asn	Tyr	Asp	Lys	Trp	Glu	Met	Glu	Arg	Thr	
625							630					635				
Asp	Ile	Thr	Met	Lys	His	Lys	Leu	Gly	Gly	Gly	Gln	Tyr	Gly	Glu	Val	
645							650					655				
Tyr	Glu	Gly	Val	Trp	Lys	Lys	Tyr	Ser	Leu	Thr	Val	Ala	Val	Lys	Thr	
660							665					670				
Leu	Lys	Glu	Asp	Thr	Met	Glu	Val	Glu	Glu	Phe	Leu	Lys	Glu	Ala	Ala	
675							680					685				
Val	Met	Lys	Glu	Ile	Lys	His	Pro	Asn	Leu	Val	Gln	Leu	Leu	Gly	Val	
690							695					700				
Cys	Thr	Arg	Glu	Pro	Pro	Phe	Tyr	Ile	Ile	Ile	Glu	Phe	Met	Thr	Tyr	
705							710					715				
Gly	Asn	Leu	Leu	Asp	Tyr	Leu	Arg	Glu	Cys	Asn	Arg	Gln	Glu	Val	Asn	
725							730					735				
Ala	Val	Val	Leu	Leu	Tyr	Met	Ala	Thr	Gln	Ile	Ser	Ser	Ala	Met	Glu	
740							745					750				
Tyr	Leu	Glu	Lys	Lys	Asn	Phe	Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	
755							760					765				
Cys	Leu	Val	Gly	Glu	Asn	His	Leu	Val	Lys	Val	Ala	Asp	Phe	Gly	Leu	
770							775					780				
Ser	Arg	Leu	Met	Thr	Gly	Asp	Thr	Tyr	Thr	Ala	His	Ala	Gly	Ala	Lys	
785							790					795				
Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ser	Leu	Ala	Tyr	Asn	Lys	Phe	
805							810					815				
Ser	Ile	Lys	Ser	Asp	Val	Trp	Ala	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	
820							825					830				

-continued

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

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<210> SEQ ID NO 9
<211> LENGTH: 676
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro Thr Arg Leu Leu
1      5      10     15
Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu Tyr Glu Arg Asp
20     25     30

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-continued

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

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Pro Thr Lys Ala Asp Lys Arg Arg Ser Val Arg Ile Gly Ser Tyr Ile
   435                               440                     445

Glu Arg Asp Val Thr Pro Ala Ile Met Glu Asp Asp Glu Leu Ala Leu
   450                               455                     460

Asp Leu Glu Asp Leu Leu Ser Phe Ser Tyr Gln Val Ala Lys Gly Met
  465                               470                     475                     480

Ala Phe Leu Ala Ser Lys Asn Cys Ile His Arg Asp Leu Ala Ala Arg
   485                               490                     495

Asn Ile Leu Leu Thr His Gly Arg Ile Thr Lys Ile Cys Asp Phe Gly
   500                               505                     510

Leu Ala Arg Asp Ile Lys Asn Asp Ser Asn Tyr Val Val Lys Gly Asn
   515                               520                     525

Ala Arg Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Cys
   530                               535                     540

Val Tyr Thr Phe Glu Ser Asp Val Trp Ser Tyr Gly Ile Phe Leu Trp
  545                               550                     555                     560

Glu Leu Phe Ser Leu Gly Ser Ser Pro Tyr Pro Gly Met Pro Val Asp
   565                               570                     575

Ser Lys Phe Tyr Lys Met Ile Lys Glu Gly Phe Arg Met Leu Ser Pro
   580                               585                     590

Glu His Ala Pro Ala Glu Met Tyr Asp Ile Met Lys Thr Cys Trp Asp
   595                               600                     605

Ala Asp Pro Leu Lys Arg Pro Thr Phe Lys Gln Ile Val Gln Leu Ile
   610                               615                     620

Glu Lys Gln Ile Ser Glu Ser Thr Asn His Ile Tyr Ser Asn Leu Ala
  625                               630                     635                     640

Asn Cys Ser Pro Asn Arg Gln Lys Pro Val Val Asp His Ser Val Arg
   645                               650                     655

Ile Asn Ser Val Gly Ser Thr Ala Ser Ser Ser Gln Pro Leu Leu Val
   660                               665                     670

His Asp Asp Val
   675

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<210> SEQ ID NO 10

<211> LENGTH: 474

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

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Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr
  1                               5                               10                     15

Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Leu Val Pro Arg Gly Ser
   20                               25                               30

Pro Trp Ile Pro Phe Thr Met Lys Lys Arg Lys Gln Ile Lys Asp Leu
   35                               40                               45

Gly Ser Glu Leu Val Arg Tyr Asp Ala Arg Val His Thr Pro His Leu
   50                               55                               60

Asp Arg Leu Val Ser Ala Arg Ser Val Ser Pro Thr Thr Glu Met Val
   65                               70                               75                     80

Ser Asn Glu Ser Val Asp Tyr Arg Ala Thr Phe Pro Glu Asp Gln Phe
   85                               90                               95

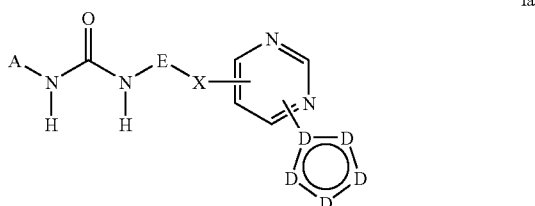
Pro Asn Ser Ser Gln Asn Gly Ser Cys Arg Gln Val Gln Tyr Pro Leu
  100                               105                               110

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-continued

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

1. Compounds of the formula Ia



and wherein the pyrimidine ring may be optionally substituted with one or more R20 moieties;

each D is individually taken from the group consisting of C, CH, C—R20, N-Z3, N, O and S, such that the resultant ring is taken from the group consisting of pyrazolyl, triazolyl, isoxazolyl, isothiazolyl, oxazolyl, imidazolyl, and thiadiazolyl;

wherein E is selected from the group consisting phenyl, pyridyl, and pyrimidinyl;

E may be optionally substituted with one or two R16 moieties;

wherein A is a ring system selected from the group consisting of cyclopentyl, cyclohexyl, G1, G2, and G3;

G1 is a heteroaryl taken from the group consisting of pyrrolyl, furyl, thienyl, oxazolyl, thiazolyl, isoxazol-4-yl, isoxazol-5-yl, isothiazolyl, imidazolyl, pyrazolyl, oxadiazolyl, thiadiazolyl, triazolyl, and tetrazolyl;

G2 is a fused bicyclic heteroaryl taken from the group consisting of indolyl, indolinyl, isoindolyl, isoindolinyl, indazolyl, benzofuranyl, benzothienyl, benzothiazolyl, benzothiazolonyl, benzoxazolyl, benzoxazolonyl, benzisoxazolyl, benzisothiazolyl, benzimidazolyl, benzimidazolonyl, benztriazolyl, imidazopyridinyl, pyrazolopyridinyl, imidazonopyridinyl, thiazolopyridinyl, thiazolonopyridinyl, oxazolopyridinyl, oxazonopyridinyl, isoxazolopyridinyl, isothiazolopyridinyl, triazolopyridinyl, imidazopyrimidinyl, pyrazolopyrimidinyl, imidazonopyrimidinyl, thiazolopyrimidinyl, thiazolonopyrimidinyl, oxazolopyrimidinyl, oxazonopyrimidinyl, isoxazolopyrimidinyl, isothiazolopyrimidinyl, triazolopyrimidinyl, dihydropurinonyl, pyrrolopyrimidinyl, purinyl, pyrazolopyrimidinyl, phthalimidyl, phthalimidinyl, pyrazinylpyridinyl, pyridinopyrimidinyl, pyrimidinopyrimidinyl, cinnolinyl, quinoxalinyl, quinazolinyl, quinolinyl, isoquinolinyl, phthalazinyl, benzodioxyl, benzisothiazoline-1,1,3-trionyl, dihydroquinolinyl, tetrahydroquinolinyl, dihydroisoquinolinyl, tetrahydroisoquinolinyl, benzoxazepinyl, benzodiazepinyl, benzoxapinyl, and benzoxazepinyl;

G3 is a heterocyclyl taken from the group consisting of oxetanyl, azetadanyl, tetrahydrofuranyl, pyrrolidinyl, oxazolonyl, oxazolidinyl, imidazolonyl, pyranlyl, thiopyranlyl, tetrahydropyranlyl, dioxaliny, piperidinyl, morpholinyl, thiomorpholinyl, thiomorpholinyl S-oxide, thiomorpholinyl S-dioxide, piperazinyl, azepinyl, oxepinyl, diazepinyl, tropanyl, and homotropanyl;

the A ring may be optionally substituted with one or two R2 moieties;

X is selected from the group consisting of —O—, —S(CH₂)_n—, —N(R3)(CH₂)_n—, —(CH₂)_p—, and wherein the carbon atoms of —(CH₂)_n—, —(CH₂)_p—, of X may be further substituted by oxo or one or more C1-C6alkyl moieties;

when A, G1, G2 or G3 has one or more substitutable sp²-hybridized carbon atoms, each respective sp² hybridized carbon atom may be optionally substituted with a Z1 substituent;

when A, G1, G2 or G3 has one or more substitutable sp³-hybridized carbon atoms, each respective sp³ hybridized carbon atom may be optionally substituted with a Z2 substituent;

when A, G1, G2 or G3 has one or more substitutable nitrogen atoms, each respective nitrogen atom may be optionally substituted with a Z4 substituent;

each Z1 is independently and individually selected from the group consisting of C1-6alkyl, branched C3-C7alkyl, C3-C8cycloalkyl, halogen, fluoroC1-C6alkyl wherein the alkyl moiety can be partially or fully fluorinated, cyano, C1-C6alkoxy, fluoroC1-C6alkoxy wherein the alkyl moiety can be partially or fully fluorinated, —(CH₂)_nOH, oxo, C1-C6alkoxyC1-C6alkyl, (R4)₂N(CH₂)_n—, (R3)₂N(CH₂)_n—, (R4)₂N(CH₂)_qN(R4)(CH₂)_n—, (R4)₂N(CH₂)_qO(CH₂)_n—, (R3)₂NC(O)—, (R4)₂NC(O)—, (R4)₂NC(O)C1-C6alkyl-, —(R4)NC(O)R8, C1-C6alkoxycarbonyl-, -carboxyC1-C6alkyl, C1-C6alkoxycarbonylC1-C6alkyl-, (R3)₂NSO₂—, —SOR3, (R4)₂NSO₂—, —N(R4)SO₂R8, —O(CH₂)_qOC1-C6alkyl, —SO₃R3, —SOR4, —C(O)R8, —C(O)R6, —C(=NOH)R6, —C(=NOR3)R6, —(CH₂)_nN(R4)C(O)R8, —N(R3)(CH₂)_qO-alkyl, —N(R3)(CH₂)_qN(R4)₂, nitro, —CH(OH)CH(OH)R4, —C(=NH)N(R4)₂, —C(=NOR3)N(R4)₂, and —NHC(=NH)R8, R17 substituted G3, R17 substituted pyrazolyl and R17 substituted imidazolyl;

in the event that Z1 contains an alkyl or alkylene moiety, such moieties may be further substituted with one or more C1-C6alkyls;

each Z2 is independently and individually selected from the group consisting of aryl, C1-C6alkyl, C3-C8cycloalkyl, branched C3-C7alkyl, hydroxyl, hydroxyC1-C6alkyl-, cyano, (R3)₂N—, (R4)₂N—, (R4)₂NC1-C6alkyl-, (R4)₂NC2-C6alkylN(R4)(CH₂)_n—, (R4)₂NC2-C6alkylO(CH₂)_n—, (R4)₂NC(O)—, (R4)₂NC(O)—, (R4)₂NC(O)-C1-C6alkyl-, carboxyl, -carboxyC1-C6alkyl, C1-C6alkoxycarbonyl-, C1-C6alkoxycarbonylC1-C6alkyl-, (R3)₂NSO₂—, (R4)₂NSO₂—, —SO₂R8, —(CH₂)_nN(R4)C(O)R8, —C(O)R8, =O, =NOH, and =N(OR6);

in the event that Z2 contains an alkyl or alkylene moiety, such moieties may be further substituted with one or more C1-C6alkyls;

each Z3 is independently and individually selected from the group consisting of H, C1-C6alkyl, branched C3-C7alkyl, C3-C8cycloalkyl, fluoroC1-C6alkyl wherein the alkyl moiety can be partially or fully fluorinated, hydroxyC2-C6alkyl-, C1-C6alkoxycarbonyl-, —C(O)R8, R5C(O)(CH₂)_n—, (R4)₂NC(O)—, (R4)₂NC(O)C1-C6alkyl-, R8C(O)N(R4)(CH₂)_q—, (R3)₂NSO₂—, (R4)₂NSO₂—, —(CH₂)_qN(R3)₂, and —(CH₂)_qN(R4)₂;

each Z4 is independently and individually selected from the group consisting of C1-C6alkyl, branched

C3-7alkyl, hydroxyC2-C6alkyl-, C1-C6alkoxyC2-C6alkyl-, (R4)₂N-C2-C6alkyl-, (R4)₂N-C2-C6alkylN(R4)-C2-C6alkyl-, (R4)₂N-C2-C6alkyl-O-C2-C6alkyl-, (R4)₂NC(O)C1-C6alkyl-, carboxyC1-C6alkyl-, C1-C6alkoxycarbonylC1-C6alkyl-, -C2-C6alkylN(R4)C(O)R8, R8-C(=NR3)—, —SO₂R8, and —COR8;

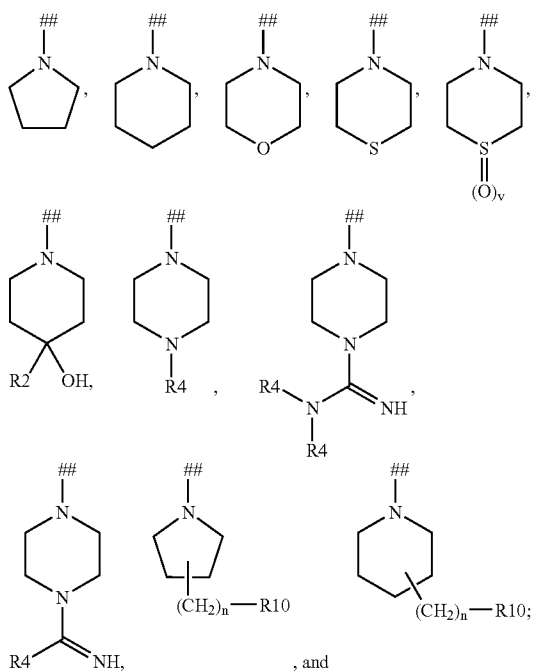
in the event that Z4 contains an alkyl or alkylene moiety, such moieties may be further substituted with one or more C1-C6alkyls;

each R2 is selected from the group consisting of H, C1-C6alkyl, branched C3-C8alkyl, R19 substituted C3-C8cycloalkyl-, fluoroC1-C6alkyl- wherein the alkyl is fully or partially fluorinated, halogen, cyano, C1-C6alkoxy-, and fluoroC1-C6alkoxy- wherein the alkyl group is fully or partially fluorinated, hydroxyl substituted C1-C6alkyl-, hydroxyl substituted branched C3-C8alkyl-, cyano substituted C1-C6alkyl-, cyano substituted branched C3-C8alkyl-, (R3)₂NC(O)C1-C6alkyl- and (R3)₂NC(O)C3-C8 branched alkyl-;

wherein each R3 is independently and individually selected from the group consisting of H, C1-C6alkyl, branched C3-C7alkyl, and C3-C8cycloalkyl;

each R4 is independently and individually selected from the group consisting of H, C1-C6alkyl, hydroxyC1-C6alkyl-, dihydroxyC1-C6alkyl-, C1-C6alkoxyC1-C6alkyl-, branched C3-C7alkyl, branched hydroxyC1-C6alkyl-, branched C1-C6alkoxyC1-C6alkyl-, branched dihydroxyC1-C6alkyl-, —(CH₂)_pN(R7)₂, —(CH₂)_pC(O)N(R7)₂, —(CH₂)_nC(C)OR3, and R19 substituted C3-C8cycloalkyl-;

each R5 is independently and individually selected from the group consisting of



and wherein the symbol (##) is the point of attachment to Z3;

each R6 is independently and individually selected from the group consisting of C1-C6alkyl, branched C3-C7alkyl, and R19 substituted C3-C8cycloalkyl-;

each R7 is independently and individually selected from the group consisting of H, C1-C6alkyl, hydroxyC2-C6alkyl-, dihydroxyC2-C6alkyl-, C1-C6alkoxyC2-C6alkyl-, branched C3-C7alkyl, branched hydroxyC2-C6alkyl-, branched C1-C6alkoxyC2-C6alkyl-, branched dihydroxyC2-C6alkyl-, —(CH₂)_nC(O)OR3, R19 substituted C3-C8cycloalkyl- and —(CH₂)_nR17;

each R8 is independently and individually selected from the group consisting of C1-C6alkyl, branched C3-C7alkyl, fluoroC1-C6alkyl- wherein the alkyl moiety is partially or fully fluorinated, R19 substituted C3-C8cycloalkyl-, —OH, C1-C6alkoxy, —N(R3)₂, and —N(R4)₂;

each R10 is independently and individually selected from the group consisting of —CO₂H, —CO₂C1-C6alkyl-, —C(O)N(R4)₂, OH, C1-C6alkoxy, and —N(R4)₂;

each R16 is independently and individually selected from the group consisting of H, C1-C6alkyl, branched C3-C7alkyl, R19 substituted C3-C8cycloalkyl-, halogen, fluoroC1-C6alkyl- wherein the alkyl moiety can be partially or fully fluorinated, cyano, hydroxyl, C1-C6alkoxy, fluoroC1-C6alkoxy- wherein the alkyl moiety can be partially or fully fluorinated, —N(R3)₂, —N(R4)₂, R3 substituted C2-C3alkynyl- and nitro;

each R17 is independently and individually selected from the group consisting of H, C1-C6alkyl, branched C3-C7alkyl, R19 substituted C3-C8cycloalkyl-, halogen, fluoroC1-C6alkyl- wherein the alkyl moiety can be partially or fully fluorinated, cyano, hydroxyl, C1-C6alkoxy, fluoroC1-C6alkoxy- wherein the alkyl moiety can be partially or fully fluorinated, —N(R3)₂, —N(R4)₂, and nitro;

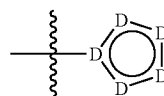
each R19 is independently and individually selected from the group consisting of H, OH and C1-C6alkyl;

each R20 is independently and individually selected from the group consisting of C1-C6alkyl, branched C3-C7alkyl, R19 substituted C3-C8cycloalkyl-, halogen, fluoroC1-C6alkyl- wherein the alkyl moiety can be partially or fully fluorinated, cyano, hydroxyl, C1-C6alkoxy, fluoroC1-C6alkoxy- wherein the alkyl moiety can be partially or fully fluorinated, —N(R3)₂, —N(R4)₂, —N(R3)C(O)R3, —C(O)N(R3)₂ and nitro and wherein two R4 moieties independently and individually taken from the group consisting of C1-C6alkyl, branched C3-C6alkyl, hydroxyalkyl-, and alkoxyalkyl and attached to the same nitrogen heteroatom may cyclize to form a C3-C7 heterocycl ring;

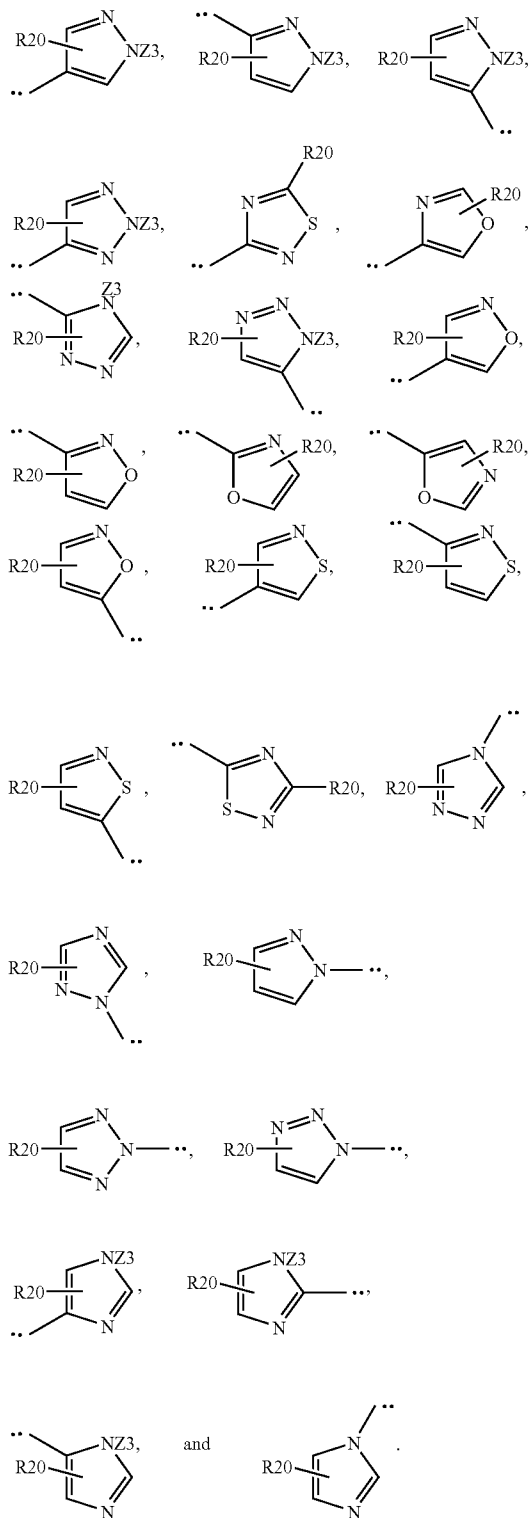
k is 0 or 1; n is 0-6; p is 1-4; q is 2-6; r is 0 or 1; t is 1-3; v is 1 or 2; x is 0-2;

and stereo-, regioisomers and tautomers of such compounds.

2. Compounds of claim 1 wherein

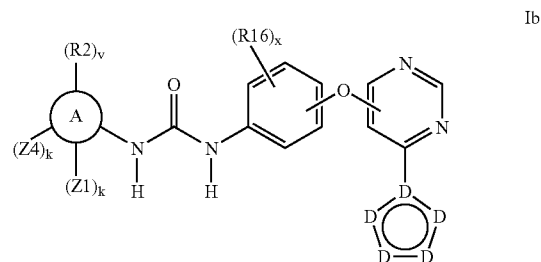


is selected from the group consisting of



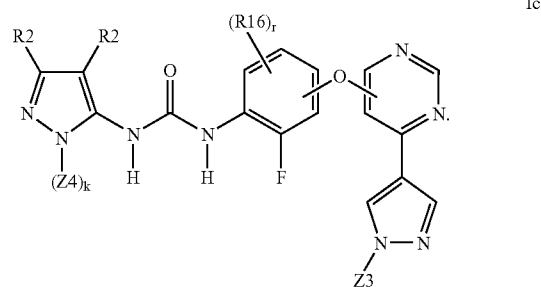
wherein the symbol (**) indicates the point of attachment to the pyrimidine ring.

3. Compounds of claim 2 having formula Ib

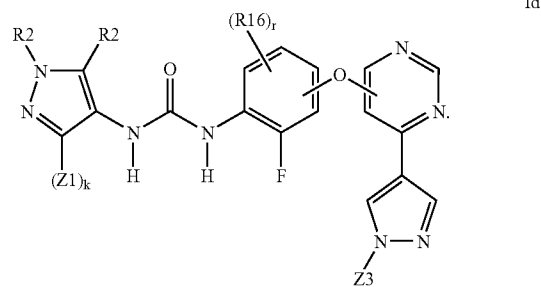


wherein A is any possible isomer of pyrazole.

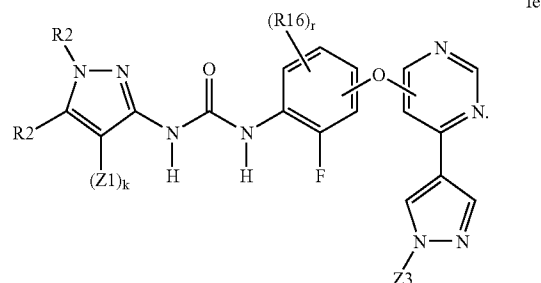
4. Compounds of claim 3 having formula Ic



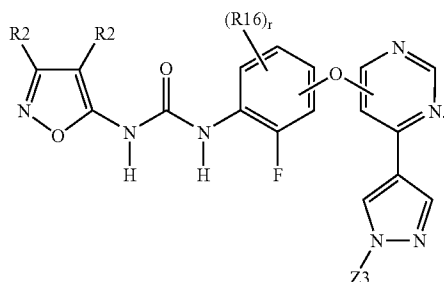
5. Compounds of claim having formula Id



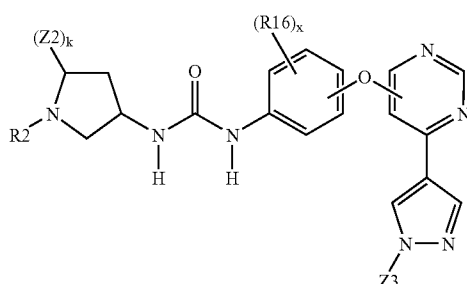
6. Compounds of claim 3 having formula Ie



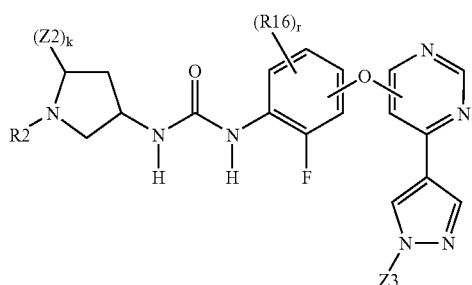
7. Compounds of claim 2 having formula If



8. Compounds of claim 2 having formula Ig



9. Compounds of claim 8 having formula Ih



10. A method of treating mammalian disease wherein the disease etiology or progression is at least partially mediated by the kinase activity of c-Abl kinase, bcr-Abl kinase, Flt-3 kinase, VEGFR-2 kinase mutants, c-Met, PDGFR-alpha kinase, PDGFR-beta kinase, HER-1, HER-2, HER-3, HER-4, FGFR, c-Kit, oncogenic forms thereof, aberrant fusion proteins thereof and polymorphs of any of the foregoing, comprising the step of administering to the mammal a compound of claim 1.

11. A method of claim 10 wherein said kinase is selected from the group consisting of bcr-Abl fusion protein kinases p210, ber-Abl fusion protein kinases p190, bcr-Abl fusion protein kinases bearing the T315I gatekeeper mutant in the Abl kinase domain of p210, bcr-Abl fusion protein kinases bearing the T315I gatekeeper mutant in the Abl kinase domain of p190, and other bcr-Abl polymorphs of any of the foregoing kinases.

12. The method of claim 11, wherein said bcr-Abl fusion protein kinases p210 having SEQ ID NO:3 & SEQ ID NO:4, wherein said bcr-Abl fusion protein kinase p190 has SEQ ID NO:5, wherein said bcr-Abl fusion protein kinases p210 bearing the T315I mutation in the Abl kinase domain has SEQ ID NO:6 & SEQ ID NO:7, and wherein said bcr-Abl fusion protein kinase p190 bearing the T315I mutation in the Abl kinase domain has SEQ ID NO:8.

13. A method of claim 10 wherein said kinase is selected from the group consisting of cKit protein kinase, PDGFR-alpha kinase, and any fusion protein, mutation and polymorphs of any of the foregoing.

14. A method of claim 10 wherein said kinase is selected from the group consisting of c-Met protein kinase, and any fusion protein, mutation and polymorphs of any of the foregoing.

15. A pharmaceutical composition comprising a compound of claim 1, together with a pharmaceutically acceptable carrier, optionally containing an additive selected from the group including adjuvants, excipients, diluents, and stabilizers.

16. A method of treating an individual suffering from a condition selected from the group consisting of cancer, hyperproliferative diseases, metabolic diseases, neurodegenerative diseases, or diseases characterized by angiogenesis, such as solid tumors, melanomas, glioblastomas, ovarian cancer, pancreatic cancer, prostate cancer, lung cancers, breast cancers, renal cancers, hepatic cancers, cervical carcinomas, metastasis of primary tumor sites, myeloproliferative diseases, chronic myelogenous leukemia, leukemias, papillary thyroid carcinoma, non-small cell lung cancer, mesothelioma, hypereosinophilic syndrome, gastrointestinal stromal tumors, colonic cancers, ocular diseases characterized by hyperproliferation leading to blindness including retinopathies, diabetic retinopathy, age-related macular degeneration and hypereosinophilic syndrome, rheumatoid arthritis, asthma, chronic obstructive pulmonary, mastocytosis, mast cell leukemia, or disease a disease caused by c-Kit kinase, oncogenic forms thereof; aberrant fusion proteins thereof and polymorphs thereof, comprising the step of administering to such individual a compound of claim 1.

17. The method of claim 16, said compound being administered by a method selected from the group consisting of oral, parenteral, inhalation, and subcutaneous.

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