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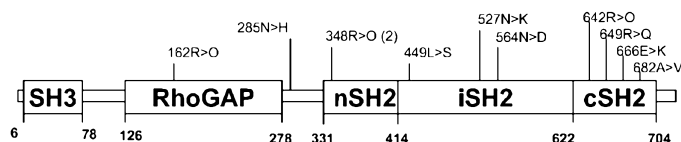
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(54) Title: GENETIC VARIATIONS ASSOCIATED WITH TUMORS

FIGURE 3

Somatic mutations in PIK3R1



Sample	p85 α (PIK3R1)	PTEN
Colon 1	HETSUB.285N>H, 527N>K, 564N>D	HETSUB.31N>H, 28I>M
Colon 2	HETSUB.162R>O, 666E>K	HETSUB.232R>O
Colon 3	HETSUB.642R>O	
Colon 4	HETSUB.348R>O	
Colon 5	HETSUB.348R>O, 574R>I	
Colon 6	HETSUB.682A>V	
Colon 7	HETSUB.649R>Q	
Breast	HETSUB.449L>S	

- 6.4% (7/108) of colorectal cancers have p85 α mutation
- 1.6% (1/62) of breast cancers have p85 α mutation

(57) Abstract: Nucleotide and amino acid variations associated with tumors are provided. Methods for detecting variations and for diagnosing and treating tumors are provided.



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GENETIC VARIATIONS ASSOCIATED WITH TUMORS

CROSS-REFERENCE TO RELATED APPLICATIONS

5 This application claims the benefit of U.S. Provisional Application No. 60/863,106, filed October 26, 2006, and U.S. Provisional Application No. 60/917,814, filed May 14, 2007, the disclosures of which are incorporated herein by reference in their entirety.

FIELD OF THE INVENTION

The present invention generally relates to genetic variations associated with tumors.

BACKGROUND

10 Cancers may arise when cells accumulate somatic mutations that ultimately confer a growth advantage to the cells. Somatic mutations include, e.g., nucleotide base substitutions, deletions, insertions, amplifications, and rearrangements. Identification of somatic mutations that occur in cancer provides valuable information regarding the development of cancer.

15 Such information is also useful for the identification of diagnostic markers and therapeutic targets in cancer. (See, e.g., Bamford et al. (2004) *British Journal of Cancer* 91:355-358.) The identification of somatic mutations associated with cancer has proven valuable in clinical settings, e.g., in distinguishing patient populations that are responsive to a particular therapy. (See, e.g., Lynch et al. (2004) *N. Engl. J. Med.* 350:2129-2139; O'Hare (2004) *Blood* 20 104:2532-2539.) Thus, a continuing need exists to identify somatic mutations that occur in cancer.

 Germline variations, or polymorphisms, are heritable variations that are present in an organism's genome. Polymorphisms include restriction fragment length polymorphisms (RFLPs), short tandem repeats (STRs), and single nucleotide polymorphisms (SNPs).

25 Germline variations may be associated with susceptibility to certain diseases, including cancer. (See, e.g., Vierimaa et al. (2006) *Science* 312:1228-1230; Landi et al. (2006) *Science* 313:521-522; Zhu et al. (2004) *Cancer Research* 64:2251-2257.) Thus, a continuing need exists to identify polymorphisms associated with cancer.

 The inventions described herein meet the above-described needs and provides other
30 benefits.

SUMMARY

A first aspect provides a method for predicting whether a tumor will respond to a therapeutic agent that targets a protein in the PI3K pathway, the method comprising detecting in the tumor (i) a nucleotide substitution in a coding sequence of a PIK3R1 polynucleotide or (ii) an amino acid substitution in a PIK3R1 polypeptide, which nucleotide or amino acid substitution results in activation of a PIK3CA polypeptide, wherein the presence of the substitution indicates that the tumor will respond to the therapeutic agent.

A second aspect provides a method of treating a tumor comprising an amino acid substitution in a PIK3R1 polypeptide, wherein the amino acid substitution results in activation of a PIK3CA polypeptide, the method comprising detecting the amino acid substitution and administering to a mammal having the tumor an effective amount of a pharmaceutical formulation comprising an antagonist of PI3K signaling.

A third aspect provides use of an antagonist of PI3K signaling in the manufacture of a medicament for treating a tumor comprising an amino acid substitution in a PIK3R1 polypeptide, wherein treating comprises detecting the amino acid substitution, and wherein the amino acid substitution results in activation of a PIK3CA polypeptide.

The compositions and methods of the disclosure are based, in part, on the discovery of novel variations in polynucleotides derived from tumor samples.

Disclosed herein is an isolated polynucleotide comprising (a) a PRO polynucleotide or fragment thereof that is at least about 10 nucleotides in length, wherein the PRO polynucleotide or fragment thereof comprises a nucleotide variation at a nucleotide position selected from Figure 1, or (b) the complement of (a). In one embodiment, the nucleotide variation occurs in SEQ ID NOs:1-78. In another embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, the isolated polynucleotide is a primer. In another embodiment, the isolated polynucleotide is an oligonucleotide.

Also disclosed is an oligonucleotide, wherein the oligonucleotide is (a) an allele-specific oligonucleotide that hybridizes to a region of a PRO polynucleotide comprising a nucleotide variation at a nucleotide position selected from Figure 1, or (b) the complement of (a). In one embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, the allele-specific oligonucleotide is an allele-specific

primer. In another embodiment, a kit is disclosed comprising the oligonucleotide and at least one enzyme. In one such embodiment, the at least one enzyme is a polymerase. In another such embodiment, the at least one enzyme is a ligase. In another embodiment, a microarray comprising the oligonucleotide is disclosed.

Also disclosed is a method of detecting the absence or presence of a nucleotide variation at a nucleotide position selected from Figure 1, the method comprising (a) contacting nucleic acid suspected of comprising the nucleotide variation with an allele-specific oligonucleotide that is specific for the nucleotide variation under conditions suitable for hybridization of the allele-specific oligonucleotide to the nucleic acid; and (b) detecting the absence or presence of allele-specific hybridization. In one embodiment, the nucleotide variation is a nucleotide change selected from Figure 1.

Also disclosed is a method of amplifying a nucleic acid comprising a nucleotide variation at a nucleotide position selected from Figure 1, the method comprising (a) contacting the nucleic acid with a primer that hybridizes to the nucleic acid at a sequence 3' of the nucleotide variation, and (b) extending the primer to generate an amplification product comprising the nucleotide variation. In one embodiment, the nucleotide variation is a nucleotide change selected from Figure 1.

In another embodiment, a method of determining the genotype of a biological sample from a mammal is disclosed, the method comprising detecting the absence or presence of a nucleotide variation at a nucleotide position selected from Figure 1 in nucleic acid material derived from the biological sample. In one embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, the biological sample is suspected of comprising tumor cells. In another embodiment, the biological sample is a tumor. In one such embodiment, the tumor is derived from a tissue selected from the tissues listed in column 6 of Figure 2. In another such embodiment, the tumor is a selected from a tumor listed in column 7 of Figure 2. In another embodiment, the detecting comprises carrying out a process selected from a primer extension assay; an allele-specific primer extension assay; an allele-specific nucleotide incorporation assay; an allele-specific oligonucleotide hybridization assay; a 5' nuclease assay; an assay employing molecular beacons; and an oligonucleotide ligation assay.

Also disclosed is a method of classifying a tumor in a mammal, the method comprising detecting the presence of a variation in a PRO or PRO polynucleotide in a

biological sample derived from the mammal, wherein the biological sample is known to or suspected of comprising tumor cells. In one embodiment, the tumor cells are derived from a tissue selected from the tissues listed in column 6 of Figure 2. In another embodiment, the tumor cells are cells of a tumor selected from the tumors listed in column 7 of Figure 2. In another embodiment, the variation is a nucleotide variation. In one such embodiment, the nucleotide variation is at a nucleotide position selected from Figure 1. In one such embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, the detecting comprises carrying out a process selected from a primer extension assay; an allele-specific primer extension assay; an allele-specific nucleotide incorporation assay; an allele-specific oligonucleotide hybridization assay; a 5' nuclease assay; an assay employing molecular beacons; and an oligonucleotide ligation assay. In another embodiment, the variation is an amino acid variation. In one such embodiment, the amino acid variation is in a PRO functional domain selected from Figure 2. In one such embodiment, the amino acid variation is at an amino acid position selected from Figure 1. In one such embodiment, the amino acid variation is an amino acid change selected from Figure 1.

In another embodiment, an amino acid variation is in a PIK3R1 polypeptide, wherein said amino acid variation increases activity of a PIK3CA polypeptide. In another embodiment, an amino acid variation is in a PIK3R1 polypeptide at an amino acid position selected from 162R, 285N, 348R, 380L, 449L, 527N, 543R, 564N, 642R, 649R, 666E, 669H, and 682A. In one such embodiment, the amino acid variation is an amino acid change selected from 162R>O, 285N>H, 348R>O, 449L>S, 527N>K, 543R>I, 564N>D, 642R>O, 649R>Q, 666E>K, and 682A>V. In another embodiment, a nucleotide variation is in a PIK3R1 polynucleotide at a nucleotide position selected from nucleotide 895A, 1084C, 1623T, 1732A, 1988G, 1966C, 2038G, 2087C, 526C, 1182A, 1388T, 1670G, and 2047C. In one such embodiment, the nucleotide variation is a nucleotide change selected from 895A>C, 1084C>T, 1623T>G, 1732A>G, 1988G>A, 1966C>T, 2038G>A, 2087C>T, 526C>T, 1388T>C, and 1670G>T.

In another embodiment, an amino acid variation is in a PIK3CA polypeptide at an amino acid position selected from 471P, 38R, 726E, and 12G. In another embodiment, a nucleotide variation is in a PIK3CA polynucleotide at a nucleotide position selected from 1568C, 269C, 2333G and 192G. In another embodiment, an amino acid variation is in a

PTEN polypeptide at an amino acid position selected from 28I, 232R, 31N, 3A, and 260Q. In another embodiment, a nucleotide variation is in a PTEN polynucleotide at a nucleotide position selected from 1115T, 1725C, 1122A, 1039C, and 1809C.

Also disclosed is a method for predicting whether a tumor will respond to a therapeutic agent that targets a PRO or a PRO polynucleotide, the method comprising determining whether the tumor comprises a variation in a PRO or PRO polynucleotide, wherein the presence of a variation indicates that the tumor will respond to the therapeutic agent. In one embodiment, the tumor is derived from a tissue selected from the tissues listed in column 6 of Figure 2. In another embodiment, the tumor is selected from a tumor listed in column 7 of Figure 2. In another embodiment, the variation is a nucleotide variation. In one such embodiment, the nucleotide variation is at a nucleotide position selected from Figure 1. In one such embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, the variation is an amino acid variation. In one such embodiment, the amino acid variation is in a PRO functional domain selected from Figure 2. In another such embodiment, the amino acid variation is at an amino acid position selected from Figure 1. In one such embodiment, the amino acid variation is an amino acid change selected from Figure 1.

These and further embodiments are described in the following written description.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a table of nucleotide and amino acid variations identified in selected genes from tumors, as described in Example A.

Figure 2 provides additional information regarding the variations reported in Figure 1.

5 Figure 3 shows somatic mutations discovered in PIK3R1, which encodes p85 α , as described in Example B.

Figure 4 shows the frequency of somatic mutations in various genes across different types of cancer, as described in Example B.

DETAILED DESCRIPTION OF EMBODIMENTS

10 I. DEFINITIONS

For purposes of interpreting this specification, the following definitions will apply and whenever appropriate, terms used in the singular will also include the plural and vice versa. In the event that any definition set forth below conflicts with any document incorporated herein by reference, the definition set forth below shall control.

15 The term "polynucleotide" or "nucleic acid," as used interchangeably herein, refers to polymers of nucleotides of any length, and include DNA and RNA. The nucleotides can be deoxyribonucleotides, ribonucleotides, modified nucleotides or bases, and/or their analogs, or any substrate that can be incorporated into a polymer by DNA or RNA polymerase. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and their
20 analogs. If present, modification to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component. Other types of modifications include, for example, "caps", substitution of one or more of the naturally occurring nucleotides with an analog,
25 internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoamidates, cabamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), those containing pendant moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing
30 chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., alpha anomeric nucleic acids, etc.), as well as unmodified forms of the polynucleotide(s). Further, any of the hydroxyl groups ordinarily

present in the sugars may be replaced, for example, by phosphonate groups, phosphate groups, protected by standard protecting groups, or activated to prepare additional linkages to additional nucleotides, or may be conjugated to solid supports. The 5' and 3' terminal OH can be phosphorylated or substituted with amines or organic capping groups moieties of from 1 to 5 20 carbon atoms. Other hydroxyls may also be derivatized to standard protecting groups. Polynucleotides can also contain analogous forms of ribose or deoxyribose sugars that are generally known in the art, including, for example, 2'-O-methyl-2'-O-allyl, 2'-fluoro- or 2'-azido-ribose, carbocyclic sugar analogs, α -anomeric sugars, epimeric sugars such as arabinose, xyloses or lyxoses, pyranose sugars, furanose sugars, sedoheptuloses, acyclic 10 analogs and abasic nucleoside analogs such as methyl riboside. One or more phosphodiester linkages may be replaced by alternative linking groups. These alternative linking groups include, but are not limited to, embodiments wherein phosphate is replaced by P(O)S("thioate"), P(S)S("dithioate"), "(O)NR₂("amidate"), P(O)R, P(O)OR', CO or CH₂("formacetal"), in which each R or R' is independently H or substituted or unsubstituted alkyl 15 (1-20 C) optionally containing an ether (--O--) linkage, aryl, alkenyl, cycloalkyl, cycloalkenyl or araldyl. Not all linkages in a polynucleotide need be identical. The preceding description applies to all polynucleotides referred to herein, including RNA and DNA.

"Oligonucleotide," as used herein, refers to short, single stranded polynucleotides that are at least about seven nucleotides in length and less than about 250 nucleotides in length. 20 Oligonucleotides may be synthetic. The terms "oligonucleotide" and "polynucleotide" are not mutually exclusive. The description above for polynucleotides is equally and fully applicable to oligonucleotides.

The term "primer" refers to a single stranded polynucleotide that is capable of hybridizing to a nucleic acid and allowing the polymerization of a complementary nucleic acid, generally by providing a free 3'-OH group. 25

The term "PRO" refers to a protein encoded by any of the genes listed in Figure 1, including wild-type and variant forms thereof. Such forms include "full-length," unprocessed forms of PRO; forms of PRO that result from cellular processing; naturally occurring PRO variants, e.g., PRO resulting from alternative splicing, allelic variations, or spontaneous 30 mutation; and fragments or variants of a native PRO that maintain at least one biological activity of PRO, unless otherwise indicated.

The term “PRO polynucleotide” or “nucleic acid encoding PRO” refers to a gene or coding sequence (e.g., an mRNA or cDNA coding sequence) that encodes a PRO, unless otherwise indicated.

The term “nucleotide variation” refers to a change in a nucleotide sequence (e.g., an insertion, deletion, inversion, or substitution of one or more nucleotides, such as a single nucleotide polymorphism (SNP)) relative to a reference sequence (e.g., a wild type sequence). The term also encompasses the corresponding change in the complement of the nucleotide sequence, unless otherwise indicated. A nucleotide variation may be a somatic mutation or a germline polymorphism.

The term “amino acid variation” refers to a change in an amino acid sequence (e.g., an insertion, substitution, or deletion of one or more amino acids, such as an internal deletion or an N- or C-terminal truncation) relative to a reference sequence.

The term “variation” refers to either a nucleotide variation or an amino acid variation.

The term “a nucleotide variation at a nucleotide position selected from Figure 1” and grammatical variants thereof refer to a nucleotide variation in a PRO polynucleotide sequence at any of the nucleotide positions listed in column 6 of Figure 1, including but not limited to the specific nucleotide changes listed in column 6 of Figure 1. For example and for purposes of illustration, with reference to column 6 in the fifth data row of Figure 1, a nucleotide variation at nucleotide position 505 of an AKT2 polynucleotide encompasses any change at that nucleotide position, including but not limited to the specific nucleotide change, i.e., the G/T substitution, indicated in column 6. The term also encompasses the corresponding change in the complement of the nucleotide sequence, unless otherwise indicated.

The term “a nucleotide change selected from Figure 1” and grammatical variants thereof refer to any of the specific nucleotide changes listed in column 6 of Figure 1. For purposes of illustration, an example of a nucleotide change selected from Figure 1 is the G/T substitution at nucleotide position 505 of an AKT2 polynucleotide, as shown in column 6 in the fifth data row of Figure 1.

The term “an amino acid variation at an amino acid position selected from Figure 1” and grammatical variants thereof refer to an amino acid variation in a PRO amino acid sequence at any of the amino acid positions listed in column 7 of Figure 1, including but not limited to the specific amino acid changes listed in column 7 of Figure 1. For example and for purposes of illustration, with reference to column 7 in the fifth data row of Figure 1, an

amino acid variation at amino acid position 101 of AKT2 encompasses any change at that amino acid position, including but not limited to the specific amino acid change, i.e., the R>L substitution, indicated in column 7.

The term “an amino acid change selected from Figure 1” and grammatical variants thereof refer to any of the specific amino acid changes listed in column 7 of Figure 1. For purposes of illustration, an example of an amino acid change selected from Figure 1 is the R>L substitution at amino acid position 101 of AKT2, as shown in column 7 in the fifth data row of Figure 1.

The term “PRO functional domain” refers to any of the protein domains listed in column 5 of Figure 2.

The term “activating variation” refers to a variation in a gene or coding sequence that results in a more active form of the encoded polypeptide, relative to the wild type polypeptide.

The term “array” or “microarray” refers to an ordered arrangement of hybridizable array elements, preferably polynucleotide probes (e.g., oligonucleotides), on a substrate. The substrate can be a solid substrate, such as a glass slide, or a semi-solid substrate, such as nitrocellulose membrane.

The term “amplification” refers to the process of producing one or more copies of a reference nucleic acid sequence or its complement. Amplification may be linear or exponential (e.g., PCR). A “copy” does not necessarily mean perfect sequence complementarity or identity relative to the template sequence. For example, copies can include nucleotide analogs such as deoxyinosine, intentional sequence alterations (such as sequence alterations introduced through a primer comprising a sequence that is hybridizable, but not fully complementary, to the template), and/or sequence errors that occur during amplification.

The term “allele-specific oligonucleotide” refers to an oligonucleotide that hybridizes to a region of a target nucleic acid that comprises a nucleotide variation (generally a substitution). “Allele-specific hybridization” means that, when an allele-specific oligonucleotide is hybridized to its target nucleic acid, a nucleotide in the allele-specific oligonucleotide specifically base pairs with the nucleotide variation. An allele-specific oligonucleotide capable of allele-specific hybridization with respect to a particular nucleotide variation is said to be “specific for” that variation.

The term “allele-specific primer” refers to an allele-specific oligonucleotide that is a primer.

The term “primer extension assay” refers to an assay in which nucleotides are added to a nucleic acid, resulting in a longer nucleic acid, or “extension product,” that is detected
5 directly or indirectly.

The term “allele-specific nucleotide incorporation assay” refers to a primer extension assay in which a primer is (a) hybridized to target nucleic acid at a region that is 3’ of a nucleotide variation and (b) extended by a polymerase, thereby incorporating into the extension product a nucleotide that is complementary to the nucleotide variation.

10 The term “allele-specific primer extension assay” refers to a primer extension assay in which an allele-specific primer is hybridized to a target nucleic acid and extended.

The term “allele-specific oligonucleotide hybridization assay” refers to an assay in which (a) an allele-specific oligonucleotide is hybridized to a target nucleic acid and (b) hybridization is detected directly or indirectly.

15 The term “5’ nuclease assay” refers to an assay in which hybridization of an allele-specific oligonucleotide to a target nucleic acid allows for nucleolytic cleavage of the hybridized probe, resulting in a detectable signal.

The term “assay employing molecular beacons” refers to an assay in which hybridization of an allele-specific oligonucleotide to a target nucleic acid results in a level of
20 detectable signal that is higher than the level of detectable signal emitted by the free oligonucleotide.

The term “oligonucleotide ligation assay” refers to an assay in which an allele-specific oligonucleotide and a second oligonucleotide are hybridized adjacent to one another on a target nucleic acid and ligated together (either directly or indirectly through intervening
25 nucleotides), and the ligation product is detected directly or indirectly.

The term “target sequence,” “target nucleic acid,” or “target nucleic acid sequence” refers generally to a polynucleotide sequence of interest in which a nucleotide variation is suspected or known to reside, including copies of such target nucleic acid generated by amplification.

30 The term “detection” includes any means of detecting, including direct and indirect detection.

The term “diagnosis” is used herein to refer to the identification or classification of a molecular or pathological state, disease or condition. For example, “diagnosis” may refer to

identification of a particular type of cancer, e.g., a lung cancer. "Diagnosis" may also refer to the classification of a particular type of cancer, e.g., by histology (e.g., a non small cell lung carcinoma), by molecular features (e.g., a lung cancer characterized by nucleotide and/or amino acid variation(s) in a particular gene or protein), or both.

5 The term "prognosis" is used herein to refer to the prediction of the likelihood of cancer-attributable death or progression, including, for example, recurrence, metastatic spread, and drug resistance, of a neoplastic disease, such as cancer.

 The term "prediction" is used herein to refer to the likelihood that a patient will respond either favorably or unfavorably to a drug or set of drugs. In one embodiment, the prediction relates to the extent of those responses. In another embodiment, the prediction relates to whether and/or the probability that a patient will survive following treatment, for example treatment with a particular therapeutic agent and/or surgical removal of the primary tumor, and/or chemotherapy for a certain period of time without cancer recurrence. The predictive methods of the invention can be used clinically to make treatment decisions by choosing the most appropriate treatment modalities for any particular patient. The predictive methods of the present invention are valuable tools in predicting if a patient is likely to respond favorably to a treatment regimen, such as a given therapeutic regimen, including for example, administration of a given therapeutic agent or combination, surgical intervention, chemotherapy, etc., or whether long-term survival of the patient, following a therapeutic regimen is likely.

 The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are associated with a measurable degree of abnormal cell proliferation. In one embodiment, the cell proliferative disorder is cancer.

 "Tumor," as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues. The terms "cancer," "cancerous," "cell proliferative disorder," "proliferative disorder" and "tumor" are not mutually exclusive as referred to herein.

 The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth and proliferation. Examples of cancer include, but are not limited to, carcinoma, lymphoma (e.g., Hodgkin's and non-Hodgkin's lymphoma), blastoma, sarcoma, and leukemia. More particular examples of cancers include squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, squamous carcinoma of the lung, cancer of the peritoneum,

hepatocellular cancer, renal cell carcinoma, gastrointestinal cancer, gastric cancer, esophageal cancer, pancreatic cancer, glioma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, rectal cancer, lung cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, melanoma, leukemia and other lymphoproliferative disorders, and various types of head and neck cancer.

The term "lung tumor" refers to any tumor of the lung, including but not limited to small-cell lung carcinoma and non-small cell lung carcinoma, the latter including but not limited to adenocarcinoma, squamous carcinoma, and large cell carcinoma.

The term "neoplasm" or "neoplastic cell" refers to an abnormal tissue or cell that proliferates more rapidly than corresponding normal tissues or cells and continues to grow after removal of the stimulus that initiated the growth.

A "lung tumor cell" refers to a lung tumor cell, either in vivo or in vitro, and encompasses cells derived from primary lung tumors or metastatic lung tumors, as well as cell lines derived from such cells.

As used herein, "treatment" (and variations such as "treat" or "treating") refers to clinical intervention in an attempt to alter the natural course of the individual or cell being treated, and can be performed either for prophylaxis or during the course of clinical pathology. Desirable effects of treatment include preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis.

An "individual," "subject" or "patient" is a vertebrate. In certain embodiments, the vertebrate is a mammal. Mammals include, but are not limited to, farm animals (such as cows), sport animals, pets (such as cats, dogs, and horses), primates (including human and non-human primates), and rodents (e.g., mice and rats). In certain embodiments, a mammal is a human.

An "effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic or prophylactic result.

A "therapeutically effective amount" of a substance/molecule of the invention may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the substance/molecule, to elicit a desired response in the individual. A

therapeutically effective amount encompasses an amount in which any toxic or detrimental effects of the substance/molecule are outweighed by the therapeutically beneficial effects. A "prophylactically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired prophylactic result. Typically, but not necessarily, since a prophylactic dose is used in subjects prior to or at an earlier stage of disease, the prophylactically effective amount would be less than the therapeutically effective amount.

The term "long-term" survival is used herein to refer to survival for at least 1 year, 5 years, 8 years, or 10 years following therapeutic treatment.

The term "increased resistance" to a particular therapeutic agent or treatment option, when used in accordance with the invention, means decreased response to a standard dose of the drug or to a standard treatment protocol.

The term "decreased sensitivity" to a particular therapeutic agent or treatment option, when used in accordance with the invention, means decreased response to a standard dose of the agent or to a standard treatment protocol, where decreased response can be compensated for (at least partially) by increasing the dose of agent, or the intensity of treatment.

"Patient response" can be assessed using any endpoint indicating a benefit to the patient, including, without limitation, (1) inhibition, to some extent, of tumor growth, including slowing down or complete growth arrest; (2) reduction in the number of tumor cells; (3) reduction in tumor size; (4) inhibition (i.e., reduction, slowing down or complete stopping) of tumor cell infiltration into adjacent peripheral organs and/or tissues; (5) inhibition (i.e. reduction, slowing down or complete stopping) of metastasis; (6) enhancement of anti-tumor immune response, which may, but does not have to, result in the regression or rejection of the tumor; (7) relief, to some extent, of one or more symptoms associated with the tumor; (8) increase in the length of survival following treatment; and/or (9) decreased mortality at a given point of time following treatment.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully inhibits or neutralizes a biological activity of a polypeptide, such as PRO, or that partially or fully inhibits the transcription or translation of a nucleic acid encoding the polypeptide. Exemplary antagonist molecules include, but are not limited to, antagonist antibodies, polypeptide fragments, oligopeptides, organic molecules (including small molecules), and anti-sense nucleic acids.

The term "agonist" is used in the broadest sense, and includes any molecule that partially or fully mimics a biological activity of a polypeptide, such as PRO, or that increases

the transcription or translation of a nucleic acid encoding the polypeptide. Exemplary agonist molecules include, but are not limited to, agonist antibodies, polypeptide fragments, oligopeptides, organic molecules (including small molecules), PRO polynucleotides, PRO polypeptides, and PRO-Fc fusions.

5 A “therapeutic agent that targets a PRO or a PRO polynucleotide” means any agent that affects the expression and/or activity of PRO or a PRO polynucleotide including, but not limited to, any of the PRO agonists or antagonists described herein, including such therapeutic agents that are already known in the art as well as those that are later developed.

 The term "cytotoxic agent" as used herein refers to a substance that inhibits or
10 prevents a cellular function and/or causes cell death or destruction. The term is intended to include radioactive isotopes (e.g., At²¹¹, I¹³¹, I¹²⁵, Y⁹⁰, Re¹⁸⁶, Re¹⁸⁸, Sm¹⁵³, Bi²¹², P³², Pb²¹² and radioactive isotopes of Lu), chemotherapeutic agents (e.g., methotrexate, adriamycin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents, enzymes and fragments thereof
15 such as nucleolytic enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof, and the various antitumor or anticancer agents disclosed below. Other cytotoxic agents are described below. A “tumoricidal” agent causes destruction of tumor cells.

20 A “toxin” is any substance capable of having a detrimental effect on the growth or proliferation of a cell.

 A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include alkylating agents such as thiotepa and CYTOXAN® cyclophosphamide; alkyl sulfonates such as busulfan, improsulfan and
25 piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, triethylenephosphoramide, triethylenethiophosphoramide and trimethylolomelamine; acetogenins (especially bullatacin and bullatacinone); delta-9-tetrahydrocannabinol (dronabinol, MARINOL®); beta-lapachone; lapachol; colchicines; betulinic acid; a
30 camptothecin (including the synthetic analogue topotecan (HYCAMTIN®), CPT-11 (irinotecan, CAMPTOSAR®), acetylcamptothecin, scoplectin, and 9-aminocamptothecin); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); podophyllotoxin; podophyllinic acid; teniposide; cryptophycins (particularly

cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CB1-TM1); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosoureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, and ranimustine; antibiotics such as the enediyne antibiotics (e. g., calicheamicin, especially calicheamicin gamma II and calicheamicin omega I (see, e.g., Agnew, *Chem Intl. Ed. Engl.*, 33: 183-186 (1994))); dynemicin, including dynemicin A; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antibiotic chromophores), aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, carabycin, carminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, ADRIAMYCIN® doxorubicin (including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins such as mitomycin C, mycophenolic acid, nogalamycin, olivomycins, peplomycin, porfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; androgens such as calusterone, dromostanolone propionate, epitio stanol, mepitio stanol, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; eniluracil; amsacrine; bestabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elfornithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidainine; maytansinoids such as maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidanmol; nitraerine; pentostatin; phenamet; pirarubicin; losoxantrone; 2-ethylhydrazide; procarbazine; PSK® polysaccharide complex (JHS Natural Products, Eugene, OR); razoxane; rhizoxin; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2''-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethan; vindesine (ELDISINE®, FILDESIN®); dacarbazine; mannomustine; mitobronitol; mitolactol;

pipobroman; gacytosine; arabinoside ("Ara-C"); thiotepa; taxoids, e.g., TAXOL® paclitaxel (Bristol-Myers Squibb Oncology, Princeton, N.J.), ABRAXANE™ Cremophor-free, albumin-engineered nanoparticle formulation of paclitaxel (American Pharmaceutical Partners, Schaumburg, Illinois), and TAXOTERE® docetaxel (Rhône-Poulenc Rorer, Antony, France); chloranbucil; gemcitabine (GEMZAR®); 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine (VELBAN®); platinum; etoposide (VP-16); ifosfamide; mitoxantrone; vincristine (ONCOVIN®); oxaliplatin; leucovovin; vinorelbine (NAVELBINE®); novantrone; edatrexate; daunomycin; aminopterin; ibandronate; topoisoemrase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoids such as retinoic acid; capecitabine (XELODA®); pharmaceutically acceptable salts, acids or derivatives of any of the above; as well as combinations of two or more of the above such as CHOP, an abbreviation for a combined therapy of cyclophosphamide, doxorubicin, vincristine, and prednisolone, and FOLFOX, an abbreviation for a treatment regimen with oxaliplatin (ELOXATIN™) combined with 5-FU and leucovovin.

Also included in this definition are anti-hormonal agents that act to regulate, reduce, block, or inhibit the effects of hormones that can promote the growth of cancer, and are often in the form of systemic, or whole-body treatment. They may be hormones themselves. Examples include anti-estrogens and selective estrogen receptor modulators (SERMs), including, for example, tamoxifen (including NOLVADEX® tamoxifen), EVISTA® raloxifene, droloxifene, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and FARESTON® toremifene; anti-progesterones; estrogen receptor down-regulators (ERDs); agents that function to suppress or shut down the ovaries, for example, leutinizing hormone-releasing hormone (LHRH) agonists such as LUPRON® and ELIGARD® leuprolide acetate, goserelin acetate, buserelin acetate and triptorelin; other anti-androgens such as flutamide, nilutamide and bicalutamide; and aromatase inhibitors that inhibit the enzyme aromatase, which regulates estrogen production in the adrenal glands, such as, for example, 4(5)-imidazoles, aminoglutethimide, MEGASE® megestrol acetate, AROMASIN® exemestane, formestane, fadrozole, RIVISOR® vorozole, FEMARA® letrozole, and ARIMIDEX® anastrozole. In addition, such definition of chemotherapeutic agents includes bisphosphonates such as clodronate (for example, BONEFOS® or OSTAC®), DIDROCAL® etidronate, NE-58095, ZOMETA® zoledronic acid/zoledronate, FOSAMAX® alendronate, AREDIA® pamidronate, SKELID® tiludronate, or ACTONEL® risedronate; as well as

troxacitabine (a 1,3-dioxolane nucleoside cytosine analog); antisense oligonucleotides, particularly those that inhibit expression of genes in signaling pathways implicated in aberrant cell proliferation, such as, for example, PKC-alpha, Raf, H-Ras, and epidermal growth factor receptor (EGF-R); vaccines such as THERATOPE® vaccine and gene therapy vaccines, for example, ALLOVECTIN® vaccine, LEUVECTIN® vaccine, and VAXID® vaccine; LURTOTECAN® topoisomerase I inhibitor; ABARELIX® rmRH; lapatinib ditosylate (an ErbB-2 and EGFR dual tyrosine kinase small-molecule inhibitor also known as GW572016); and pharmaceutically acceptable salts, acids or derivatives of any of the above.

A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell (such as a cell expressing PRO) either in vitro or in vivo. Thus, the growth inhibitory agent may be one which significantly reduces the percentage of cells (such as a cell expressing PRO) in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxanes, and topoisomerase II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in The Molecular Basis of Cancer, Mendelsohn and Israel, eds., Chapter 1, entitled "Cell cycle regulation, oncogenes, and antineoplastic drugs" by Murakami et al. (WB Saunders: Philadelphia, 1995), especially p. 13. The taxanes (paclitaxel and docetaxel) are anticancer drugs both derived from the yew tree. Docetaxel (TAXOTERE®, Rhone-Poulenc Rorer), derived from the European yew, is a semisynthetic analogue of paclitaxel (TAXOL®, Bristol-Myers Squibb). Paclitaxel and docetaxel promote the assembly of microtubules from tubulin dimers and stabilize microtubules by preventing depolymerization, which results in the inhibition of mitosis in cells.

As used herein, the term "EGFR inhibitor" refers to compounds that bind to or otherwise interact directly with EGFR and prevent or reduce its signaling activity, and is alternatively referred to as an "EGFR antagonist." Examples of such agents include antibodies and small molecules that bind to EGFR. Examples of antibodies which bind to EGFR include MA b 579 (ATCC CRL HB 8506), MA b 455 (ATCC CRL HB8507), MA b 225 (ATCC CRL 8508), MA b 528 (ATCC CRL 8509) (see, US Patent No. 4,943, 533, Mendelsohn *et al.*) and variants thereof, such as chimerized 225 (C225 or Cetuximab;

ERBITUX[®]) and reshaped human 225 (H225) (see, WO 96/40210, Imclone Systems Inc.); IMC-11F8, a fully human, EGFR-targeted antibody (Imclone); antibodies that bind type II mutant EGFR (US Patent No. 5,212,290); humanized and chimeric antibodies that bind EGFR as described in US Patent No. 5,891,996; and human antibodies that bind EGFR, such as ABX-EGF or Panitumumab (see WO98/50433, Abgenix/Amgen); EMD 55900 (Stragliotto *et al.* *Eur. J. Cancer* 32A:636-640 (1996)); EMD7200 (matuzumab) a humanized EGFR antibody directed against EGFR that competes with both EGF and TGF- α for EGFR binding (EMD/Merck); human EGFR antibody, HuMax-EGFR (GenMab); fully human antibodies known as E1.1, E2.4, E2.5, E6.2, E6.4, E2.11, E6.3 and E7.6.3 and described in US 6,235,883; MDX-447 (Medarex Inc); and mAb 806 or humanized mAb 806 (Johns *et al.*, *J. Biol. Chem.* 279(29):30375-30384 (2004)). The anti-EGFR antibody may be conjugated with a cytotoxic agent, thus generating an immunoconjugate (see, *e.g.*, EP659,439A2, Merck Patent GmbH). EGFR antagonists include small molecules such as compounds described in US Patent Nos: 5,616,582, 5,457,105, 5,475,001, 5,654,307, 5,679,683, 6,084,095, 6,265,410, 6,455,534, 6,521,620, 6,596,726, 6,713,484, 5,770,599, 6,140,332, 5,866,572, 6,399,602, 6,344,459, 6,602,863, 6,391,874, 6,344,455, 5,760,041, 6,002,008, and 5,747,498, as well as the following PCT publications: WO98/14451, WO98/50038, WO99/09016, and WO99/24037. Particular small molecule EGFR antagonists include OSI-774 (CP-358774, erlotinib, TARCEVA[®] Genentech/OSI Pharmaceuticals); PD 183805 (CI 1033, 2-propenamide, N-[4-[(3-chloro-4-fluorophenyl)amino]-7-[3-(4-morpholinyl)propoxy]-6-quinazolinyl]-, dihydrochloride, Pfizer Inc.); ZD1839, gefitinib (IRESSA[™]) 4-(3'-Chloro-4'-fluoroanilino)-7-methoxy-6-(3-morpholinopropoxy)quinazoline, AstraZeneca); ZM 105180 ((6-amino-4-(3-methylphenyl-amino)-quinazoline, Zeneca); BIBX-1382 (N8-(3-chloro-4-fluoro-phenyl)-N2-(1-methyl-piperidin-4-yl)-pyrimido[5,4-d]pyrimidine-2,8-diamine, Boehringer Ingelheim); PKI-166 ((R)-4-[4-[(1-phenylethyl)amino]-1H-pyrrolo[2,3-d]pyrimidin-6-yl]-phenol); (R)-6-(4-hydroxyphenyl)-4-[(1-phenylethyl)amino]-7H-pyrrolo[2,3-d]pyrimidine); CL-387785 (N-[4-[(3-bromophenyl)amino]-6-quinazolinyl]-2-butyramide); EKB-569 (N-[4-[(3-chloro-4-fluorophenyl)amino]-3-cyano-7-ethoxy-6-quinolinyl]-4-(dimethylamino)-2-butenamide) (Wyeth); AG1478 (Pfizer); AG1571 (SU 5271; Pfizer); dual EGFR/HER2 tyrosine kinase inhibitors such as lapatinib (TYKERB[®], GSK572016 or N-[3-chloro-4-[(3-fluorophenyl)methoxy]phenyl]6[[[2methylsulfonyl)ethyl]amino]methyl]-2-furanyl]-4-quinazolinamine; Glaxo-SmithKline).

A "tyrosine kinase inhibitor" is a molecule which inhibits tyrosine kinase activity of a tyrosine kinase such as a HER receptor. Examples of such inhibitors include the EGFR-targeted drugs noted in the preceding paragraph; small molecule HER2 tyrosine kinase inhibitor such as TAK165 available from Takeda; CP-724,714, an oral selective inhibitor of the ErbB2 receptor tyrosine kinase (Pfizer and OSI); dual-HER inhibitors such as EKB-569 (available from Wyeth) which preferentially binds EGFR but inhibits both HER2 and EGFR-overexpressing cells; lapatinib (GSK572016; available from Glaxo-SmithKline), an oral HER2 and EGFR tyrosine kinase inhibitor; PKI-166 (available from Novartis); pan-HER inhibitors such as canertinib (CI-1033; Pharmacia); Raf-1 inhibitors such as antisense agent ISIS-5132 available from ISIS Pharmaceuticals which inhibit Raf-1 signaling; non-HER targeted TK inhibitors such as imatinib mesylate (GLEEVEC™, available from Glaxo SmithKline); multi-targeted tyrosine kinase inhibitors such as sunitinib (SUTENT®, available from Pfizer); VEGF receptor tyrosine kinase inhibitors such as vatalanib (PTK787/ZK222584, available from Novartis/Schering AG); MAPK extracellular regulated kinase I inhibitor CI-1040 (available from Pharmacia); quinazolines, such as PD 153035, 4-(3-chloroanilino) quinazoline; pyridopyrimidines; pyrimidopyrimidines; pyrrolopyrimidines, such as CGP 59326, CGP 60261 and CGP 62706; pyrazolopyrimidines, 4-(phenylamino)-7H-pyrrolo[2,3-d] pyrimidines; curcumin (diferuloyl methane, 4,5-bis (4-fluoroanilino)phthalimide); tyrphostines containing nitrothiophene moieties; PD-0183805 (Warner-Lambers); antisense molecules (*e.g.* those that bind to HER-encoding nucleic acid); quinoxalines (US Patent No. 5,804,396); tyrphostins (US Patent No. 5,804,396); ZD6474 (Astra Zeneca); PTK-787 (Novartis/Schering AG); pan-HER inhibitors such as CI-1033 (Pfizer); Affinitac (ISIS 3521; Isis/Lilly); imatinib mesylate (GLEEVEC™); PKI 166 (Novartis); GW2016 (Glaxo SmithKline); CI-1033 (Pfizer); EKB-569 (Wyeth); Semaxinib (Pfizer); ZD6474 (AstraZeneca); PTK-787 (Novartis/Schering AG); INC-1C11 (Imclone); or as described in any of the following patent publications: US Patent No. 5,804,396; WO 1999/09016 (American Cyanamid); WO 1998/43960 (American Cyanamid); WO 1997/38983 (Warner Lambert); WO 1999/06378 (Warner Lambert); WO 1999/06396 (Warner Lambert); WO 1996/30347 (Pfizer, Inc); WO 1996/33978 (Zeneca); WO 1996/3397 (Zeneca); and WO 1996/33980 (Zeneca).

"Antibodies" (Abs) and "immunoglobulins" (Igs) refer to glycoproteins having similar structural characteristics. While antibodies exhibit binding specificity to a specific antigen, immunoglobulins include both antibodies and other antibody-like molecules which generally

lack antigen specificity. Polypeptides of the latter kind are, for example, produced at low levels by the lymph system and at increased levels by myelomas.

The terms "antibody" and "immunoglobulin" are used interchangeably in the broadest sense and include monoclonal antibodies (*e.g.*, full length or intact monoclonal antibodies), polyclonal antibodies, monovalent antibodies, multivalent antibodies, multispecific antibodies (*e.g.*, bispecific antibodies so long as they exhibit the desired biological activity) and may also include certain antibody fragments (as described in greater detail herein). An antibody can be chimeric, human, humanized and/or affinity matured.

The term "anti-PRO antibody" or "an antibody that binds to PRO" refers to an antibody that is capable of binding PRO with sufficient affinity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting PRO. Preferably, the extent of binding of an anti-PRO antibody to an unrelated, non-PRO protein is less than about 10% of the binding of the antibody to PRO as measured, *e.g.*, by a radioimmunoassay (RIA). In certain embodiments, an antibody that binds to PRO has a dissociation constant (K_d) of $\leq 1\mu\text{M}$, $\leq 100\text{ nM}$, $\leq 10\text{ nM}$, $\leq 1\text{ nM}$, or $\leq 0.1\text{ nM}$. In certain embodiments, an anti-PRO antibody binds to an epitope of PRO that is conserved among PRO from different species.

The terms "full length antibody," "intact antibody" and "whole antibody" are used herein interchangeably to refer to an antibody in its substantially intact form, not antibody fragments as defined below. The terms particularly refer to an antibody with heavy chains that contain the Fc region.

"Antibody fragments" comprise a portion of an intact antibody, preferably comprising the antigen binding region thereof. Examples of antibody fragments include Fab, Fab', F(ab')_2 , and Fv fragments; diabodies; linear antibodies; single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an F(ab')_2 fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is a minimum antibody fragment which contains a complete antigen-binding site. In one embodiment, a two-chain Fv species consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. Collectively, the six CDRs of an Fv confer antigen-binding specificity to the antibody. However, even a single variable

domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment contains the heavy- and light-chain variable domains and also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

"Single-chain Fv" or "scFv" antibody fragments comprise the VH and VL domains of antibody, wherein these domains are present in a single polypeptide chain. Generally, the scFv polypeptide further comprises a polypeptide linker between the VH and VL domains which enables the scFv to form the desired structure for antigen binding. For a review of scFv see Pluckthun, in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) in the same polypeptide chain (VH-VL). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies may be bivalent or bispecific. Diabodies are described more fully in, for example, EP 404,097; WO93/1161; Hudson et al. (2003) *Nat. Med.* 9:129-134; and Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90: 6444-6448 (1993). Triabodies and tetrabodies are also described in Hudson et al. (2003) *Nat. Med.* 9:129-134.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible mutations, e.g., naturally occurring mutations, that may be present in minor amounts. Thus, the modifier "monoclonal" indicates the character of the antibody as not being a mixture of discrete antibodies. In certain embodiments, such a monoclonal antibody typically includes an antibody comprising a polypeptide sequence that binds a target, wherein the target-binding polypeptide sequence was obtained by a process that includes the selection of a single target

binding polypeptide sequence from a plurality of polypeptide sequences. For example, the selection process can be the selection of a unique clone from a plurality of clones, such as a pool of hybridoma clones, phage clones, or recombinant DNA clones. It should be understood that a selected target binding sequence can be further altered, for example, to improve affinity for the target, to humanize the target binding sequence, to improve its production in cell culture, to reduce its immunogenicity *in vivo*, to create a multispecific antibody, etc., and that an antibody comprising the altered target binding sequence is also a monoclonal antibody of this invention. In contrast to polyclonal antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody of a monoclonal antibody preparation is directed against a single determinant on an antigen. In addition to their specificity, monoclonal antibody preparations are advantageous in that they are typically uncontaminated by other immunoglobulins.

The modifier “monoclonal” indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by a variety of techniques, including, for example, the hybridoma method (e.g., Kohler et al., *Nature*, 256: 495 (1975); Harlow et al., *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling et al., in: *Monoclonal Antibodies and T-Cell Hybridomas* 563-681 (Elsevier, N.Y., 1981)), recombinant DNA methods (see, e.g., U.S. Patent No. 4,816,567), phage display technologies (see, e.g., Clackson et al., *Nature*, 352: 624-628 (1991); Marks et al., *J. Mol. Biol.* 222: 581-597 (1992); Sidhu et al., *J. Mol. Biol.* 338(2): 299-310 (2004); Lee et al., *J. Mol. Biol.* 340(5): 1073-1093 (2004); Fellouse, *Proc. Natl. Acad. Sci. USA* 101(34): 12467-12472 (2004); and Lee et al., *J. Immunol. Methods* 284(1-2): 119-132(2004), and technologies for producing human or human-like antibodies in animals that have parts or all of the human immunoglobulin loci or genes encoding human immunoglobulin sequences (see, e.g., WO98/24893; WO96/34096; WO96/33735; WO91/10741; Jakobovits et al., *Proc. Natl. Acad. Sci. USA* 90: 2551 (1993); Jakobovits et al., *Nature* 362: 255-258 (1993); Bruggemann et al., *Year in Immunol.* 7:33 (1993); U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016; Marks et al., *Bio.Technology* 10: 779-783 (1992); Lonberg et al., *Nature* 368: 856-859 (1994); Morrison, *Nature* 368: 812-813 (1994); Fishwild et al., *Nature Biotechnol.* 14: 845-851 (1996);

Neuberger, *Nature Biotechnol.* 14: 826 (1996) and Lonberg and Huszar, *Intern. Rev. Immunol.* 13: 65-93 (1995).

The monoclonal antibodies herein specifically include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (U.S. Patent No. 4,816,567; and Morrison *et al.*, *Proc. Natl. Acad. Sci. USA* 81:6851-6855 (1984)).

"Humanized" forms of non-human (*e.g.*, murine) antibodies are chimeric antibodies that contain minimal sequence derived from non-human immunoglobulin. In one embodiment, a humanized antibody is a human immunoglobulin (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit, or nonhuman primate having the desired specificity, affinity, and/or capacity. In some instances, framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications may be made to further refine antibody performance. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin, and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally will also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992). See also the following review articles and references cited therein: Vaswani and Hamilton, *Ann. Allergy, Asthma & Immunol.* 1:105-115 (1998); Harris, *Biochem. Soc. Transactions* 23:1035-1038 (1995); Hurler and Gross, *Curr. Op. Biotech.* 5:428-433 (1994).

A "human antibody" is one which comprises an amino acid sequence corresponding to that of an antibody produced by a human and/or has been made using any of the techniques for making human antibodies as disclosed herein. Such techniques include screening human-

derived combinatorial libraries, such as phage display libraries (see, e.g., Marks *et al.*, *J. Mol. Biol.*, 222: 581-597 (1991) and Hoogenboom *et al.*, *Nucl. Acids Res.*, 19: 4133-4137 (1991)); using human myeloma and mouse-human heteromyeloma cell lines for the production of human monoclonal antibodies (see, e.g., Kozbor *J. Immunol.*, 133: 3001 (1984); Brodeur *et al.*, *Monoclonal Antibody Production Techniques and Applications*, pp. 51-63 (Marcel Dekker, Inc., New York, 1987); and Boerner *et al.*, *J. Immunol.*, 147: 86 (1991)); and generating monoclonal antibodies in transgenic animals (e.g., mice) that are capable of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production (see, e.g., Jakobovits *et al.*, *Proc. Natl. Acad. Sci USA*, 90: 2551 (1993); Jakobovits *et al.*, *Nature*, 362: 255 (1993); Bruggermann *et al.*, *Year in Immunol.*, 7: 33 (1993)). This definition of a human antibody specifically excludes a humanized antibody comprising antigen-binding residues from a non-human animal.

An "affinity matured" antibody is one with one or more alterations in one or more CDRs thereof which result in an improvement in the affinity of the antibody for antigen, compared to a parent antibody which does not possess those alteration(s). In one embodiment, an affinity matured antibody has nanomolar or even picomolar affinities for the target antigen. Affinity matured antibodies are produced by procedures known in the art. Marks *et al.* *Bio/Technology* 10:779-783 (1992) describes affinity maturation by VH and VL domain shuffling. Random mutagenesis of HVR and/or framework residues is described by: Barbas *et al. Proc Nat. Acad. Sci. USA* 91:3809-3813 (1994); Schier *et al. Gene* 169:147-155 (1995); Yelton *et al. J. Immunol.* 155:1994-2004 (1995); Jackson *et al., J. Immunol.* 154(7):3310-9 (1995); and Hawkins *et al, J. Mol. Biol.* 226:889-896 (1992).

A "blocking antibody" or an "antagonist antibody" is one which inhibits or reduces a biological activity of the antigen it binds. Certain blocking antibodies or antagonist antibodies partially or completely inhibit the biological activity of the antigen.

A "small molecule" or "small organic molecule" is defined herein as an organic molecule having a molecular weight below about 500 Daltons.

A "PRO-binding oligopeptide" or an "oligopeptide that binds PRO" is an oligopeptide that is capable of binding PRO with sufficient affinity such that the oligopeptide is useful as a diagnostic and/or therapeutic agent in targeting PRO. In certain embodiments, the extent of binding of a PRO-binding oligopeptide to an unrelated, non-PRO protein is less than about 10% of the binding of the PRO-binding oligopeptide to PRO as measured, e.g., by

a surface plasmon resonance assay. In certain embodiments, a PRO-binding oligopeptide has a dissociation constant (K_d) of $\leq 1\mu\text{M}$, $\leq 100\text{ nM}$, $\leq 10\text{ nM}$, $\leq 1\text{ nM}$, or $\leq 0.1\text{ nM}$.

A "PRO-binding organic molecule" or "an organic molecule that binds PRO" is an organic molecule other than an oligopeptide or antibody as defined herein that is capable of binding PRO with sufficient affinity such that the organic molecule is useful as a diagnostic and/or therapeutic agent in targeting PRO. In certain embodiments, the extent of binding of a PRO-binding organic molecule to an unrelated, non-PRO protein is less than about 10% of the binding of the PRO-binding organic molecule to PRO as measured, e.g., by a surface plasmon resonance assay. In certain embodiments, a PRO-binding organic molecule has a dissociation constant (K_d) of $\leq 1\mu\text{M}$, $\leq 100\text{ nM}$, $\leq 10\text{ nM}$, $\leq 1\text{ nM}$, or $\leq 0.1\text{ nM}$.

The dissociation constant (K_d) of any molecule that binds a target polypeptide may conveniently be measured using a surface plasmon resonance assay. Such assays may employ a BIAcoreTM-2000 or a BIAcoreTM-3000 (BIAcore, Inc., Piscataway, NJ) at 25°C with immobilized target polypeptide CM5 chips at ~10 response units (RU). Briefly, carboxymethylated dextran biosensor chips (CM5, BIAcore Inc.) are activated with *N*-ethyl-*N'*-(3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and *N*-hydroxysuccinimide (NHS) according to the supplier's instructions. Target polypeptide is diluted with 10 mM sodium acetate, pH 4.8, to 5 $\mu\text{g/ml}$ (~0.2 μM) before injection at a flow rate of 5 $\mu\text{l/minute}$ to achieve approximately 10 response units (RU) of coupled protein. Following the injection of target polypeptide, 1 M ethanolamine is injected to block unreacted groups. For kinetics measurements, two-fold serial dilutions of the binding molecule (0.78 nM to 500 nM) are injected in PBS with 0.05% Tween 20 (PBST) at 25°C at a flow rate of approximately 25 $\mu\text{l/min}$. Association rates (k_{on}) and dissociation rates (k_{off}) are calculated using a simple one-to-one Langmuir binding model (BIAcore Evaluation Software version 3.2) by simultaneously fitting the association and dissociation sensorgrams. The equilibrium dissociation constant (K_d) is calculated as the ratio $k_{\text{off}}/k_{\text{on}}$. See, e.g., Chen, Y., et al., (1999) *J. Mol. Biol.* 293:865-881. If the on-rate of an antibody exceeds $10^6\text{ M}^{-1}\text{ s}^{-1}$ by the surface plasmon resonance assay above, then the on-rate can be determined by using a fluorescent quenching technique that measures the increase or decrease in fluorescence emission intensity (excitation = 295 nm; emission = 340 nm, 16 nm band-pass) at 25°C of a 20 nM antibody (Fab form) in PBS, pH 7.2, in the presence of increasing concentrations of antigen as measured in a spectrometer, such as a stop-flow equipped spectrophotometer (Aviv

Instruments) or a 8000-series SLM-Aminco spectrophotometer (ThermoSpectronic) with a stirred cuvette.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of an agent, e.g., a drug, to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

The word "label" when used herein refers to a detectable compound or composition. The label may be detectable by itself (*e.g.*, radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which results in a detectable product. Radionuclides that can serve as detectable labels include, for example, I-131, I-123, I-125, Y-90, Re-188, Re-186, At-211, Cu-67, Bi-212, and Pd-109.

An "isolated" biological molecule, such as a nucleic acid, polypeptide, or antibody, is one which has been identified and separated and/or recovered from at least one component of its natural environment.

II. DESCRIPTION OF CERTAIN EMBODIMENTS

Nucleotide and amino acid variations associated with tumors are provided herein. These variations provide biomarkers for cancer and/or predispose or contribute to tumorigenesis or tumor promotion. Accordingly, the variations disclosed herein are useful in a variety of settings, e.g., in methods and compositions related to cancer diagnosis and therapy.

A. Variations

One hundred-fifty three genes from a panel of 708 tumor specimens were analyzed for variations, as further described in Example A. The variations identified by that analysis are listed in the table shown in Figure 1. The first column of the table ("VARIANT ID") lists the identification numbers assigned to each variation. The second and third columns ("UNQ ID" and "DNA ID") list additional gene-specific identification numbers. The fourth column ("GENE") lists the genes in which variations were identified. The fifth column ("GENE DESCRIPTION (HUGO)") provides a brief description from the Human Genome Organisation (HUGO) of each gene listed in the fourth column. *See* Wain et al. (2002) *Genomics* 79:464-470.

The sixth column ("NT_CHGE") lists the nucleotide change found in each gene. In this study, the nucleotide changes were primarily single nucleotide substitutions, although deletions and insertions were also found. The term "HETSUB" in the sixth column stands for "heterozygous substitution," meaning that both the indicated variation and the wild type allele were detected in the tumor sample. The term "HOMSUB" stands for "homozygous substitution," meaning that the indicated variation was detected in the tumor sample, and the wild type allele was not detected in the tumor sample. This may occur, for example, if the tumor has undergone loss of heterozygosity (e.g., where one copy of a given gene contains a variation, and the other copy contains a deletion in the corresponding gene). The term "HOMDEL" (see, e.g., Variant ID 3561 in EGFR) stands for homozygous deletion, meaning that the indicated variation is a deletion that was detected in the tumor sample, and the wild type allele was not detected in the tumor sample. The term "HETDEL" (see, e.g., Variant ID 39041 in EGFR) stands for heterozygous deletion, meaning that the indicated variation is a deletion that was detected in the tumor sample, and the wild type allele was also detected in the tumor sample. The term "HETINS" (see, e.g., Variant ID 60761 in CBLC) stands for heterozygous insertion, meaning that the indicated variation is an insertion that was detected in the tumor sample, and the wild type allele was also detected in the tumor sample.

In the sixth column, nucleotide numbers refer to nucleotide positions in the cDNA sequences corresponding to the indicated genes. For example, in the fifth data row, Variant ID 21270 is a heterozygous substitution designated "505G>T," indicating that a "G" has been substituted by a "T" in one copy of the AKT2 gene, with the substitution occurring at a genomic position corresponding to nucleotide 505 of the cDNA sequence (SEQ ID NO:2) of the AKT2 gene. For each gene listed in Figure 1, the corresponding cDNA sequences and their translations are provided in the sequence listing, as indicated in Table 1 below.

TABLE 1

GENE NAME	cDNA SEQUENCE SEQ ID NO	AMINO ACID SEQUENCE SEQ ID NO:
AKT-1	1	79
AKT2	2	80
ALK	3	81
ARAF	4	82
AXIN1	5	83
AXIN2	6	84
AXL	7	85
BAX	8	86
BCL-XL	9	87
B-raf	10	88
CBL	11	89

CBLB	12	90
CBLC	13	91
CDKN2A (isoform 1)	14	92
CDKN2A (isoform 2)	15	93
CIAS1 (isoform 1)	16	94
CIAS1 (isoform 2)	17	95
cMet	18	96
CXCR4	19	97
DDR2	20	98
DUBA2	21	99
EDG1	22	100
EGFL11	23	101
EGFR	24	102
ERBB3	25	103
ERBB4	26	104
ETBR	27	105
FGFR1	28	106
FGFR2	29	107
FGFR3	30	108
FGFR4	31	109
FRAP1	32	110
GPR73	33	111
Her2	34	112
IGF1-R	35	113
JAG1	36	114
JAG2	37	115
JAK2	38	116
KRAS	39	117
MAP2K1	40	118
MELK	41	119
Notch2	42	120
NOTCH3	43	121
NRP1	44	122
NTC1	45	123
NTRK1	46	124
NTRK2	47	125
NTRK3	48	126
OTUD1	49	127
PAK6	50	128
PDGFRB	51	129
PDK1	52	130
PIK3CA	53	131
PIK3R1	54	132
PIK3R2	55	133
PIK3R4	56	134
PIK3R5	57	135
PLK1	58	136
PRKCB1	59	137
PRKCI	60	138
PTCH	61	139
PTEN	62	140
RB1	63	141
Rem2	64	142
RET	65	143
RON	66	144
SMAD2	67	145
Stk6	68	146
SUFU	69	147

TGFBR1	70	148
TGFBR2	71	149
TP53	72	150
USP21	73	151
USP24	74	152
USP25	75	153
USP28	76	154
USP35	77	155
VEGFR2	78	156

The seventh column ("AA_CHGE") of the table in Figure 1 lists the amino acid changes resulting from the nucleotide changes listed in the previous column. Amino acids are numbered according to their positions in the translated cDNA sequences. Where a nucleotide substitution resulted in a stop codon (i.e., a nonsense mutation), the corresponding amino acid change is indicated by an "O" (e.g., see Variant ID 42019 in AXIN1, indicating an amino acid change of "314G>O"). Where a nucleotide change occurred in a splice site, the designation "INTRONIC" occurs in column six (e.g., see Variant ID 3465 in CBL). Where a nucleotide insertion or deletion resulted in a frame shift, the corresponding amino acid change is indicated by "FS" (e.g., see Variant ID 60761 in CBLC).

Figure 2 provides additional information about the variations reported in Figure 1. The first and second columns of Figure 2 list variant identification numbers and corresponding genes, as provided in the first and fourth columns of Figure 1. The third column ("EFFECT") indicates whether the variation results in a nonsynonymous ("Nonsyn.") or synonymous ("Syn.") amino acid substitution, or a deletion ("Deletion") in the encoded polypeptide. The fourth column ("LOCATION") indicates whether the variation occurs in a coding region ("Coding") or in an intronic region ("Splice Site") of the indicated gene. The fifth column ("DOMAIN") indicates, for some of the variations, the protein domains in which the amino acid changes occur. Protein domains are indicated by Pfam nomenclature. (See, e.g., Bateman et al. (2004) *Nucleic Acids Res.* 32(1):D138-141.) The sixth column indicates the tissue types of the tumors in which the variations were found. The seventh column indicates the particular types of tumors in which the variations were found.

Although the variations described herein were identified in the tumor types indicated in the last column of Figure 2, other types of cancers may be routinely screened to determine whether any of these variations occur in those cancers. The compositions and methods of the present invention are applicable to any cancer comprising a variation in any PRO or PRO polynucleotide selected from those provided in Figure 1.

The variations described herein are all somatic mutations (i.e., the variations were present in DNA derived from their respective tumor samples, but absent from DNA derived from the corresponding patient matched normal samples). Generally, somatic mutations are those that occur only in certain tissue(s), e.g., in tumor tissue, and are not inherited in the germline. Germline polymorphisms are generally found in all tissues.

Variations were found in genes encoding proteins from a variety of protein families. For example, variations were found in a number of genes encoding kinases, including receptor tyrosine kinases (RTKs). Generally, activation of kinases is often associated with cell proliferation and tumor promotion. Thus, variations in genes encoding kinases may be “gain-of-function” mutations that increase kinase activity. Tumors in which such variations are detected may thus be responsive to kinase antagonists. A variety of kinase antagonists are currently known in the art. Such kinase antagonists include, but are not limited to antagonist antibodies and small molecule antagonists, e.g., 3-[2,4-dimethylpyrrol-5-yl)methylidene]-indolin-2-one (“SU5416”); imatinib (Gleevec®), a 2-phenylaminopyrimidine; 1-*tert*-butyl-3-[6-(3,5-dimethoxy-phenyl)-2-(4-diethylamino-butylamino)-pyrido[2,3-d]pyrimidin-7-yl]-urea (“PD173074”) (see, e.g., Moffa et al. (2004) *Mol. Cancer Res.* 2:643-652); and indolinones such as 3-[3-(2-carboxyethyl)-4-methylpyrrol-2-methylidenyl]-2-indolinone (“SU5402”) (see, e.g., Bernard-Pierrot (2004) *Oncogene* 23:9201-9211).

Variations were also found in tumor suppressor genes (e.g., p53 and retinoblastoma). Generally, loss of tumor suppressor function is often associated with cell proliferation and tumor promotion. Thus, variations in genes encoding tumor suppressors may be complete or partial “loss-of-function” mutations that decrease tumor suppressor function. Tumors in which such variations are detected may be responsive to tumor suppressor agonists. A tumor suppressor agonist may be, e.g., an agonist antibody, a polynucleotide encoding a tumor suppressor, the tumor suppressor itself, or a tumor suppressor-Fc fusion.

B. Compositions

In one aspect, an isolated polynucleotide comprising at least a fragment of a PRO polynucleotide is provided, wherein the fragment comprises a nucleotide variation. In one embodiment, the nucleotide variation is at a nucleotide position selected from Figure 1. In one such embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, a fragment of a PRO polynucleotide is at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20

nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length, alternatively at least about 1000 nucleotides in length, and alternatively about the length of the full-length coding sequence. In this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. In another embodiment, the polynucleotide comprises a nucleotide variation in a polynucleotide sequence selected from SEQ ID NO:1-78 or a fragment thereof. In another embodiment, the complement of any of the above polynucleotides is provided. In another embodiment, a PRO encoded by the any of the above polynucleotides is provided.

In one embodiment, an isolated polynucleotide provided herein is detectably labeled, e.g., with a radioisotope, a fluorescent agent, or a chromogenic agent. In another embodiment, an isolated polynucleotide is a primer. In another embodiment, an isolated polynucleotide is an oligonucleotide, e.g., an allele-specific oligonucleotide. In another embodiment, an oligonucleotide may be, for example, from 7-60 nucleotides in length, 9-45 nucleotides in length, 15-30 nucleotides in length, or 18-25 nucleotides in length. In another embodiment, an oligonucleotide may be, e.g., PNA, morpholino-phosphoramidates, LNA, or 2'-alkoxyalkoxy. Oligonucleotides as provided herein are useful, e.g., as hybridization probes for the detection of nucleotide variations.

In another aspect, an allele-specific oligonucleotide is provided that hybridizes to a region of a PRO polynucleotide comprising a nucleotide variation (e.g., a substitution). In one embodiment, the nucleotide variation is at a nucleotide position selected from Figure 1.

In one such embodiment, the nucleotide variation is a nucleotide change selected from Figure

1. The allele-specific oligonucleotide, when hybridized to the region of the PRO polynucleotide, comprises a nucleotide that base pairs with the nucleotide variation. In another embodiment, the complement of an allele-specific oligonucleotide is provided. In another embodiment, a microarray comprises an allele-specific oligonucleotide or its complement. In another embodiment, an allele-specific oligonucleotide or its complement is an allele-specific primer.

An allele-specific oligonucleotide can be used in conjunction with a control oligonucleotide that is identical to the allele-specific oligonucleotide, except that the nucleotide that specifically base pairs with the nucleotide variation is replaced with a nucleotide that specifically base pairs with the corresponding nucleotide present in the wild type PRO polynucleotide. Such oligonucleotides may be used in competitive binding assays under hybridization conditions that allow the oligonucleotides to distinguish between a PRO polynucleotide comprising a nucleotide variation and a PRO polynucleotide comprising the corresponding wild type nucleotide. Using routine methods based on, e.g., the length and base composition of the oligonucleotides, one skilled in the art can arrive at suitable hybridization conditions under which (a) an allele-specific oligonucleotide will preferentially bind to a PRO polynucleotide comprising a nucleotide variation relative to a wild type PRO polynucleotide, and (b) the control oligonucleotide will preferentially bind to a wild type PRO polynucleotide relative to a PRO polynucleotide comprising a nucleotide variation. Exemplary conditions include conditions of high stringency, e.g., hybridization conditions of 5x standard saline phosphate EDTA (SSPE) and 0.5% NaDodSO₄ (SDS) at 55°C, followed by washing with 2X SSPE and 0.1% SDS at 55°C or room temperature.

In another aspect, a binding agent is provided that preferentially binds to a PRO comprising an amino acid variation, relative to a wild-type PRO. In one embodiment, the amino acid variation is at an amino acid position selected from Figure 1. In one such embodiment, the amino acid variation is an amino acid change selected from Figure 1. In another embodiment, the binding agent is an antibody.

In another aspect, diagnostic kits are provided. In one embodiment, a kit comprises any of the foregoing polynucleotides and an enzyme. In one embodiment, the enzyme is at least one enzyme selected from a nuclease, a ligase, and a polymerase.

C. Methods

5 In one aspect, a method of detecting the presence of a tumor is provided, the method comprising detecting a variation in a PRO or PRO polynucleotide derived from a biological sample. In one embodiment, the biological sample is obtained from a mammal suspected of having a tumor.

10 In another aspect, a method of determining the genotype of a biological sample is provided, the method comprising detecting whether a nucleotide variation is present in a PRO polynucleotide derived from the biological sample. In one embodiment, the nucleotide variation is at a nucleotide position selected from Figure 1. In one such embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, the biological sample is suspected of comprising tumor cells. In another embodiment, the
15 biological sample is a cell line, e.g., an immortalized cell line. In another embodiment, the biological sample is a tumor. In one such embodiment, the genotyping of the tumor provides a basis for classifying the tumor.

In another aspect, a method of identifying tumor cells in a biological sample from a mammal is provided, the method comprising detecting a variation in a PRO or PRO
20 polynucleotide derived from the biological sample. In one embodiment, the variation is a nucleotide variation. In one such embodiment, the nucleotide variation is at a nucleotide position selected from Figure 1. In one such embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, the variation is an amino acid variation. In one such embodiment, the amino acid variation is in a PRO functional
25 domain selected from Figure 2. In another such embodiment, the amino acid variation is at an amino acid position selected from Figure 1. In another such embodiment, the amino acid variation is an amino acid change selected from Figure 1. In another embodiment, the biological sample is a biopsy (e.g., a tissue sample containing cells suspected of being cancerous).

30 In another aspect, a method of diagnosing a tumor in a mammal is provided, the method comprising detecting the presence of a variation in a PRO or PRO polynucleotide derived from a biological sample obtained from the mammal, wherein the biological sample is known to or suspected of comprising tumor cells. In one embodiment, the variation is a

nucleotide variation. In one such embodiment, the nucleotide variation is at a nucleotide position selected from Figure 1. In one such embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, the variation is an amino acid variation. In one such embodiment, the amino acid variation is in a PRO functional domain selected from Figure 2. In another such embodiment, the amino acid variation is at an amino acid position selected from Figure 1. In another such embodiment, the amino acid variation is an amino acid change selected from Figure 1. In another embodiment, the method is a method of classifying a tumor, e.g., as a tumor characterized by a nucleotide or amino acid variation(s) in a particular PRO polynucleotide or PRO.

In another aspect, a method is provided for predicting whether a tumor from a mammal will respond to a therapeutic agent that targets a PRO or PRO polynucleotide, the method comprising determining whether the tumor comprises a variation in a PRO or PRO polynucleotide, wherein the presence of a variation in a PRO or PRO polynucleotide indicates that the tumor will respond to the therapeutic agent. In one embodiment, the variation is a nucleotide variation. In one such embodiment, the nucleotide variation is at a nucleotide position selected from Figure 1. In one such embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, the variation is an amino acid variation. In one such embodiment, the amino acid variation is in a PRO functional domain selected from Figure 2. In another such embodiment, the amino acid variation is at an amino acid position selected from Figure 1. In another such embodiment, the amino acid variation is an amino acid change selected from Figure 1. In another embodiment, the PRO is a kinase (such as a tyrosine kinase, e.g., an RTK). In another embodiment, the PRO is a tumor suppressor.

In another aspect, a method of detecting the absence or presence of a nucleotide variation at a nucleotide position in a nucleic acid encoding a PRO is provided, the method comprising (a) contacting the nucleic acid with any of the polynucleotides described above (section II.B.) under conditions suitable for formation of a hybridization complex between the nucleic acid and the polynucleotide; and (b) detecting whether the polynucleotide specifically base pairs with the nucleic acid at the nucleotide position. In one embodiment, the nucleotide variation is at a nucleotide position selected from Figure 1. In one such embodiment, the nucleotide variation is a nucleotide change selected from Figure 1.

In another aspect, a method of detecting the absence or presence of a nucleotide variation in a nucleic acid encoding a PRO is provided, the method comprising (a) contacting

the nucleic acid with an allele-specific oligonucleotide that is specific for the nucleotide variation under conditions suitable for hybridization of the allele-specific oligonucleotide to the nucleic acid; and (b) detecting the absence or presence of allele-specific hybridization. In one embodiment, the nucleotide variation is at a nucleotide position selected from Figure 1.

- 5 In one such embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, an allele-specific oligonucleotide is an allele-specific primer.

In another aspect, a method of amplifying a nucleic acid comprising a PRO polynucleotide or fragment thereof is provided, wherein the PRO polynucleotide or fragment thereof comprises a nucleotide variation, the method comprising (a) contacting the nucleic
10 acid with a primer that hybridizes to a sequence 3' of the nucleotide variation, and (b) extending the primer to generate an amplification product comprising the nucleotide variation. In one embodiment, the method further comprises contacting the amplification product with a second primer that hybridizes to a sequence 3' of the nucleotide variation, and extending the second primer to generate a second amplification product. In one such
15 embodiment, the method further comprises amplifying the amplification product and second amplification product, e.g., by PCR. In any of the above embodiments, the nucleotide variation is at a nucleotide position selected from Figure 1. In any of the above embodiments, the nucleotide variation is a nucleotide change selected from Figure 1.

In another aspect, a method of assessing the activity of a PRO comprising an amino
20 acid variation is provided, the method comprising (a) determining the activity of the PRO; and (b) comparing the activity of the PRO with the activity of a wild-type PRO. In one embodiment, the activity is kinase activity. In another embodiment, the activity is tumor suppressor activity. In another embodiment, the amino acid variation is in a PRO functional domain selected from Figure 2. In another embodiment, the amino acid variation is at an
25 amino acid position selected from Figure 1. In another embodiment, the amino acid variation is an amino acid change selected from Figure 1.

In another aspect, a method of identifying an agent for the treatment of a tumor is provided, the method comprising (a) contacting a PRO with a test agent, wherein the PRO comprises an amino acid variation, (b) assessing the activity of the PRO in the presence of
30 the test agent with the activity of the PRO in the absence of the test agent, wherein an increase or decrease in the activity of the PRO in the presence of the test agent indicates that the test agent is an agent for the treatment of a tumor. In one embodiment, the amino acid variation is in a PRO functional domain selected from Figure 2. In another embodiment, the

amino acid variation is at an amino acid position selected from Figure 1. In another embodiment, the amino acid variation is an amino acid change selected from Figure 1. In another embodiment, the PRO is a kinase (such as a tyrosine kinase, e.g., an RTK), and a decrease in the activity of the kinase in the presence of the test agent indicates that the test agent is an agent for the treatment of a tumor. In another embodiment, the PRO is a tumor suppressor, and an increase in the activity of the tumor suppressor in the presence of the test agent indicates that the test agent is an agent for the treatment of a tumor.

In another aspect, a method of inhibiting the proliferation of a tumor cell is provided, wherein the tumor cell comprises a PRO having an activating variation, the method comprising exposing the tumor cell to an antagonist of PRO. In one embodiment, the PRO is a kinase, e.g., a receptor tyrosine kinase.

In another aspect, a method of inhibiting the proliferation of a tumor cell is provided, wherein the tumor cell comprises a variation in a PRO that decreases the activity of PRO, the method comprising exposing the tumor cell to an agonist of PRO. In one embodiment, an agonist comprises a PRO polynucleotide or PRO itself. In another embodiment, the PRO is a tumor suppressor.

In another aspect, a method of treating a tumor comprising a variation in a PRO is provided, the method comprising administering to a mammal having the tumor an effective amount of a pharmaceutical formulation comprising an antagonist or agonist of PRO. In one embodiment, the variation is a nucleotide variation. In one such embodiment, the nucleotide variation is at a nucleotide position selected from Figure 1. In one such embodiment, the nucleotide variation is a nucleotide change selected from Figure 1. In another embodiment, the variation is an amino acid variation. In one such embodiment, the amino acid variation is in a PRO functional domain selected from Figure 2. In another such embodiment, the amino acid variation is at an amino acid position selected from Figure 1. In another such embodiment, the amino acid variation is an amino acid change selected from Figure 1. In another embodiment, the PRO is a kinase (such as a tyrosine kinase, e.g., an RTK). In another embodiment, the PRO is a tumor suppressor.

A tumor, according to any of the above methods, may be a tumor selected from a lung tumor (particularly non-small cell lung carcinomas), breast tumor, colon tumor, kidney tumor, liver tumor, bladder tumor, ovarian tumor, stomach tumor, skin tumor (including melanoma and non-melanoma skin cancers), rectal tumor, and lymphoma. In one embodiment, the tumor is derived from a tissue listed in column 6 of Figure 2 (e.g., a lung

tumor, a colon tumor, a cecum tumor, a liver tumor, a stomach tumor, etc.). In another embodiment, the tumor is selected from the specific tumor types listed in column 7 of Figure 2.

A nucleotide variation, according to any of the above methods, may be a somatic mutation or a germline polymorphism.

D. General Techniques

Nucleic acid, according to any of the above methods, may be genomic DNA; RNA transcribed from genomic DNA; or cDNA generated from RNA. Nucleic acid may be derived from a vertebrate, e.g., a mammal. A nucleic acid is said to be "derived from" a particular source if it is obtained directly from that source or if it is a copy of a nucleic acid found in that source.

Nucleic acid includes copies of the nucleic acid, e.g., copies that result from amplification. Amplification may be desirable in certain instances, e.g., in order to obtain a desired amount of material for detecting variations. For example, a PRO polynucleotide or portion thereof may be amplified from nucleic acid material. The amplicons may then be subjected to a variation detection method, such as those described below, to determine whether a variation is present in the amplicon.

Variations may be detected by certain methods known to those skilled in the art. Such methods include, but are not limited to, DNA sequencing; primer extension assays, including allele-specific nucleotide incorporation assays and allele-specific primer extension assays (e.g., allele-specific PCR, allele-specific ligation chain reaction (LCR), and gap-LCR); allele-specific oligonucleotide hybridization assays (e.g., oligonucleotide ligation assays); cleavage protection assays in which protection from cleavage agents is used to detect mismatched bases in nucleic acid duplexes; analysis of MutS protein binding; electrophoretic analysis comparing the mobility of variant and wild type nucleic acid molecules; denaturing-gradient gel electrophoresis (DGGE, as in, e.g., Myers et al. (1985) *Nature* 313:495); analysis of RNase cleavage at mismatched base pairs; analysis of chemical or enzymatic cleavage of heteroduplex DNA; mass spectrometry (e.g., MALDI-TOF); genetic bit analysis (GBA); 5' nuclease assays (e.g., TaqMan[®]); and assays employing molecular beacons. Certain of these methods are discussed in further detail below.

Detection of variations in target nucleic acids may be accomplished by molecular cloning and sequencing of the target nucleic acids using techniques well known in the art. Alternatively, amplification techniques such as the polymerase chain reaction (PCR) can be

used to amplify target nucleic acid sequences directly from a genomic DNA preparation from tumor tissue. The nucleic acid sequence of the amplified sequences can then be determined and variations identified therefrom. Amplification techniques are well known in the art, e.g., polymerase chain reaction is described in Saiki et al., *Science* 239:487, 1988; U.S. Pat. Nos. 4,683,203 and 4,683,195.

The ligase chain reaction, which is known in the art, can also be used to amplify target nucleic acid sequences. See, e.g., Wu et al., *Genomics* 4:560-569 (1989). In addition, a technique known as allele-specific PCR can also be used to detect variations (e.g., substitutions). See, e.g., Ruano and Kidd (1989) *Nucleic Acids Research* 17:8392; McClay et al. (2002) *Analytical Biochem.* 301:200-206. In certain embodiments of this technique, an allele-specific primer is used wherein the 3' terminal nucleotide of the primer is complementary to (i.e., capable of specifically base-pairing with) a particular variation in the target nucleic acid. If the particular variation is not present, an amplification product is not observed. Amplification Refractory Mutation System (ARMS) can also be used to detect variations (e.g., substitutions). ARMS is described, e.g., in European Patent Application Publication No. 0332435, and in Newton et al., *Nucleic Acids Research*, 17:7, 1989.

Other methods useful for detecting variations (e.g., substitutions) include, but are not limited to, (1) allele-specific nucleotide incorporation assays, such as single base extension assays (see, e.g., Chen et al. (2000) *Genome Res.* 10:549-557; Fan et al. (2000) *Genome Res.* 10:853-860; Pastinen et al. (1997) *Genome Res.* 7:606-614; and Ye et al. (2001) *Hum. Mut.* 17:305-316); (2) allele-specific primer extension assays (see, e.g., Ye et al. (2001) *Hum. Mut.* 17:305-316; and Shen et al. *Genetic Engineering News*, vol. 23, Mar. 15, 2003), including allele-specific PCR; (3) 5' nuclease assays (see, e.g., De La Vega et al. (2002) *BioTechniques* 32:S48-S54 (describing the TaqMan® assay); Ranade et al. (2001) *Genome Res.* 11:1262-1268; and Shi (2001) *Clin. Chem.* 47:164-172); (4) assays employing molecular beacons (see, e.g., Tyagi et al. (1998) *Nature Biotech.* 16:49-53; and Mhlanga et al. (2001) *Methods* 25:463-71); and (5) oligonucleotide ligation assays (see, e.g., Grossman et al. (1994) *Nuc. Acids Res.* 22:4527-4534; patent application Publication No. US 2003/0119004 A1; PCT International Publication No. WO 01/92579 A2; and U.S. Pat. No. 6,027,889).

Variations may also be detected by mismatch detection methods. Mismatches are hybridized nucleic acid duplexes which are not 100% complementary. The lack of total complementarity may be due to deletions, insertions, inversions, or substitutions. One example of a mismatch detection method is the Mismatch Repair Detection (MRD) assay

described, e.g., in Faham et al., *Proc. Natl Acad. Sci. USA* 102:14717-14722 (2005) and Faham et al., *Hum. Mol. Genet.* 10:1657-1664 (2001). Another example of a mismatch cleavage technique is the RNase protection method, which is described in detail in Winter et al., *Proc. Natl. Acad. Sci. USA*, 82:7575, 1985, and Myers et al., *Science* 230:1242, 1985.

5 For example, a method of the invention may involve the use of a labeled riboprobe which is complementary to the human wild-type target nucleic acid. The riboprobe and target nucleic acid derived from the tissue sample are annealed (hybridized) together and subsequently digested with the enzyme RNase A which is able to detect some mismatches in a duplex RNA structure. If a mismatch is detected by RNase A, it cleaves at the site of the mismatch.

10 Thus, when the annealed RNA preparation is separated on an electrophoretic gel matrix, if a mismatch has been detected and cleaved by RNase A, an RNA product will be seen which is smaller than the full-length duplex RNA for the riboprobe and the mRNA or DNA. The riboprobe need not be the full length of the target nucleic acid, but can a portion of the target nucleic acid, provided it encompasses the position suspected of having a variation.

15 In a similar manner, DNA probes can be used to detect mismatches, for example through enzymatic or chemical cleavage. See, e.g., Cotton et al., *Proc. Natl. Acad. Sci. USA*, 85:4397, 1988; and Shenk et al., *Proc. Natl. Acad. Sci. USA*, 72:989, 1975. Alternatively, mismatches can be detected by shifts in the electrophoretic mobility of mismatched duplexes relative to matched duplexes. See, e.g., Cariello, *Human Genetics*, 42:726, 1988. With either
20 riboprobes or DNA probes, the target nucleic acid suspected of comprising a variation may be amplified before hybridization. Changes in target nucleic acid can also be detected using Southern hybridization, especially if the changes are gross rearrangements, such as deletions and insertions.

25 Restriction fragment length polymorphism (RFLP) probes for the target nucleic acid or surrounding marker genes can be used to detect variations, e.g., insertions or deletions. Insertions and deletions can also be detected by cloning, sequencing and amplification of a target nucleic acid. Single stranded conformation polymorphism (SSCP) analysis can also be used to detect base change variants of an allele. See, e.g. Orita et al., *Proc. Natl. Acad. Sci. USA* 86:2766-2770, 1989, and *Genomics*, 5:874-879, 1989.

30 The invention also provides a variety of compositions suitable for use in performing methods of the invention. For example, the invention provides arrays that can be used in such methods. In one embodiment, an array of the invention comprises individual or collections of nucleic acid molecules useful for detecting variations of the invention. For

instance, an array of the invention may comprise a series of discretely placed individual allele-specific oligonucleotides or sets of allele-specific oligonucleotides. Several techniques are well-known in the art for attaching nucleic acids to a solid substrate such as a glass slide. One method is to incorporate modified bases or analogs that contain a reactive moiety that is capable of attachment to a solid substrate, such as an amine group, a derivative of an amine group, or another group with a positive charge, into nucleic acid molecules that are synthesized. The synthesized product is then contacted with a solid substrate, such as a glass slide coated with an aldehyde or other reactive group. The aldehyde or other reactive group will form a covalent link with the reactive moiety on the amplified product, which will become covalently attached to the glass slide. Other methods, such as those using amino propyl silican surface chemistry are also known in the art.

A biological sample, according to any of the above methods, may be obtained using certain methods known to those skilled in the art. Biological samples may be obtained from vertebrate animals, and in particular, mammals. Tissue biopsy is often used to obtain a representative piece of tumor tissue. Alternatively, tumor cells can be obtained indirectly in the form of tissues or fluids that are known or thought to contain the tumor cells of interest. For instance, samples of lung cancer lesions may be obtained by resection, bronchoscopy, fine needle aspiration, bronchial brushings, or from sputum, pleural fluid or blood. Variations in target nucleic acids (or encoded polypeptides) may be detected from a tumor sample or from other body samples such as urine, sputum or serum. (Cancer cells are sloughed off from tumors and appear in such body samples.) By screening such body samples, a simple early diagnosis can be achieved for diseases such as cancer. In addition, the progress of therapy can be monitored more easily by testing such body samples for variations in target nucleic acids (or encoded polypeptides). Additionally, methods for enriching a tissue preparation for tumor cells are known in the art. For example, the tissue may be isolated from paraffin or cryostat sections. Cancer cells may also be separated from normal cells by flow cytometry or laser capture microdissection.

III. EXAMPLES

A. Identification of Variations in Human Tumors

Seven hundred and eight human tumor specimens were obtained from commercial sources. The tumors were subjected to pathology review to ensure sufficient tumor content (i.e., greater than 80% tumor cells). One hundred fifty-three genes were chosen for analysis based on their potential importance in cancer. PCR was used to amplify exons and some

intronic sequences from those genes using genomic DNA obtained from the tumor specimens. Amplicons were sequenced using standard Sanger sequencing, and the sequences were compared with the corresponding wild-type sequences to identify variations. The variations were compared with single nucleotide polymorphisms in the NCBI “dbSNP” database (see Sherry et al. (1999) *Genome Res.* 9:677-679) and with somatic mutations in the Catalogue of Somatic Mutations in Cancer (COSMIC) database (see Bamford et al. (2004) *British Journal of Cancer* 91:355-358) to identify the variations that were not present in those databases and were thus determined to be novel. Variations were validated (i.e., confirmed) by reamplifying and resequencing the exons from the original tumor samples. Amplicons from genomic DNA of patient matched normal samples were generated and sequenced to determine whether the variations were somatic or germline mutations. The results of the foregoing analysis are shown in Figures 1 and 2, which are described in further detail in the above Detailed Description of Embodiments.

B. Analysis of Variations

It is noted that somatic mutations were discovered in genes involved in the phosphatidylinositol 3-kinase (PI3K) signaling pathway. Those genes include but are not limited to PIK3R1, PIK3CA, and PTEN. PIK3R1 (also referred to as PI3KR), encodes p85 α , which is the regulatory subunit of PI3K. p85 α negatively regulates the protein encoded by PIK3CA (referred to as p110 α), which is the catalytic subunit of PI3K. Activating mutations in PIK3CA are known to occur frequently in colon and breast cancer. Loss of function mutations in PIK3R1 would therefore be predicted to result in activation of p110 α and tumor promotion. PTEN is a tumor suppressor gene that acts downstream of and antagonizes PI3K signaling. Loss of function mutations in PTEN would also be predicted to result in tumor promotion.

The present study identified somatic mutations in PIK3R1 in colon, pancreatic, and breast tumor specimens, as indicated in Figures 1 and 2. The positions of some of the mutations found in p85 α are graphically depicted in Figure 3. It is noted that truncation mutations in PIK3R1 have been reported at very low frequency in lymphomas, and splice site mutations in PIK3R1 have been reported at low frequency in primary colon tumors (1/60) and ovarian tumors (3/80). See Philp et al. (2001) *Cancer Res.* 61:7426-7429. However, the present findings provide evidence for mutations in the coding sequence of PIK3R1 in solid tumors (particularly colon tumors) at a frequency of greater than 6%.

The ability of p85 α mutants to bind to p110 α was assessed. Cos7 cells were transiently transfected with nucleic acid encoding N-terminally HA-tagged p85 α protein (either wild-type or mutant, as indicated in Table 2 below) and with nucleic acid encoding p110 α (either wild-type or mutant, as indicated in Table 2 below). Proteins were immunoprecipitated using HA beads, separated by SDS-PAGE, transferred to nitrocellulose, and detected using anti-HA and anti- p110 α antibodies. Binding of p85 α to p110 α is indicated as either “yes”(“Y”) or “no” (“N”) in Table 2. In the second row of Table 2, the term “p85 Dominant Negative” refers to a known dominant negative form of p85 α in which the p110 α binding domain from amino acids 479-513 is deleted. The remaining mutant forms of p85 α listed in the first column of Table 2 were discovered pursuant to this study. In the header row of Table 2, the terms “p110alpha E545K” and “p110alpha H1047R” refer to two known mutational “hot spots” in p110 α which result in constitutively active p110 α . The results show that many of the p85 α mutants discovered in this study retained the ability to bind wild type and mutant p110 α , except for mutants resulting in truncated forms of p85 α that lack the p110 α binding domain.

Table 2

Enzyme	p110alpha WT	p110alpha E545K	p110alpha H1047R
p85 WT	Y	Y	Y
p85 Dominant Negative	N	N	N
p85 R162stop	N	N	N
p85 R642stop	Y	Y	Y
p85 E666K	Y	Y	Y
p85 L449S	Y	Y	Y
p85 A682V	Y	Y	Y
p85 N285H	Y	Y	Y
p85 R348stop	N	N	N
p85 R649Q	Y	Y	Y
p85 N527K	Y	Y	Y
p85 N564D	Y	Y	Y
p85 R543I	Y	Y	Y
p85 R574I	Y	Y	Y

The ability of p85 α mutant proteins to form active complexes with p110 α was also assessed. Complexes consisting of p85 α protein (either wild-type or mutant, as indicated in Table 3 below) and wild-type p110 α were expressed in baculovirus. Activity of p110 α in the complexes was assessed using a fluorescence polarization assay with phosphoinositide as the substrate. The assay was conducted in the absence or presence of a phosphotyrosine peptide (referred to as “peptide” in Table 3 below). That peptide corresponds to a phosphotyrosine-containing region of Insulin Receptor Substrate-1 that binds to the SH2 region of p85 α and

enhances the activity of the wild-type p85 α /p110 α complex. See Miled et al., *Science*, 317:239-242 (2007). The p85 α mutants tested in Table 3 have mutations in their C-terminal SH2 domains. The activity of p110 α in the complexes is shown in Table 3. The activities were normalized to the value obtained for p110 α in the wild-type complex in the absence of peptide. The results show that one of the p85 α mutants (“p85 N564D”) resulted in a complex with increased p110 α activity in the absence of peptide. Two of the p85 α mutants (“p85 R649Q” and “p85 N527K”) resulted in complexes with decreased p110 α activity in the absence of peptide. One of the p85 α mutants (“p85 E666K”) resulted in a complex with p110 α activity comparable to that seen in the wild type complex. Both wild-type and mutant complexes showed increased p110 α activity in the presence of peptide.

Table 3

Enzyme	No peptide	Peptide (1uM)
p85 WT	1	2.77
p85 N564D	1.71	2.47
p85 E666K	0.92	2.54
p85 R649Q	0.45	1.7
p85 N527K	0.75	1.92

Somatic mutations were also discovered in PIK3CA and PTEN, as indicated in Figures 1 and 2. Some of the mutations in PTEN were found in the same tumor specimens as the mutations in PIK3R1. See Figure 3. Thus, the PI3K pathway may provide multiple targets for tumor diagnosis and therapy.

Additionally, analysis of the frequency of mutations in B-raf, KRAS, PIK3R1, PIK3CA, ERBB3, and ERBB4 reveals that those mutations are predicted to be “driver” mutations, i.e., mutations that play a causative role in tumorigenesis or tumor progression, with statistical significance as follows:

Table 4

Gene	P-value
B-raf	0
KRAS	0
PIK3R1	0.003
PIK3CA	0
ERBB3	0.035
ERBB4	0.003

The frequency of somatic mutations in various genes was also analyzed across different types of cancer. Genes having somatic mutations at a frequency of $\geq 5\%$ for a particular cancer (≥ 10 samples) are depicted in Figure 4. Consistent with the above analysis, arrows show high mutation frequency for PIK3R1, ERBB3, and ERBB4 in colorectal cancer.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, the descriptions and examples should not be construed as limiting the scope of the invention. The disclosures of all patent and scientific literatures cited herein are expressly incorporated in their entirety by reference.

In the claims which follow and in the preceding description of the invention, except where the context requires otherwise due to express language or necessary implication, the word "comprise" or variations such as "comprises" or "comprising" is used in an inclusive sense, i.e. to specify the presence of the stated features but not to preclude the presence or addition of further features in various embodiments of the invention.

It is to be understood that, if any prior art publication is referred to herein, such reference does not constitute an admission that the publication forms a part of the common general knowledge in the art, in Australia or any other country.

WHAT IS CLAIMED IS:

1. A method for predicting whether a tumor will respond to a therapeutic agent that targets a protein in the PI3K pathway, the method comprising detecting in the tumor (i) a nucleotide substitution in a coding sequence of a PIK3R1 polynucleotide or (ii) an amino acid substitution in a PIK3R1 polypeptide, which nucleotide or amino acid substitution results in activation of a PIK3CA polypeptide, wherein the presence of the substitution indicates that the tumor will respond to the therapeutic agent.
2. The method of claim 1, wherein the tumor is a solid tumor.
3. The method of claim 1 or claim 2, wherein the tumor is a colon tumor.
4. The method of any one of claims 1 to 3, wherein the tumor comprises a nucleotide substitution in a coding sequence of a PIK3R1 polynucleotide.
5. The method of claim 4, wherein the nucleotide substitution is at 1732A.
6. The method of any one of claims 1 to 3, wherein the tumor comprises an amino acid substitution in a PIK3R1 polypeptide.
7. The method of claim 6, wherein the amino acid variation is in an SH2 domain of a PIK3R1 polypeptide.
8. The method of claim 7, wherein the amino acid variation is at 564N.
9. The method of claim 8, wherein the amino acid variation is 564N>D.
10. The method of any one of claims 1 to 9, wherein the therapeutic agent targets a PIK3CA polypeptide.
11. A method of treating a tumor comprising an amino acid substitution in a PIK3R1 polypeptide, wherein the amino acid substitution results in activation of a PIK3CA polypeptide, the method comprising detecting the amino acid substitution and administering to a mammal having the tumor an effective amount of a pharmaceutical formulation comprising an antagonist of PI3K signaling.
12. The method of claim 11, wherein the tumor is a solid tumor.
13. The method of claim 11 or claim 12, wherein the tumor is a colon tumor.

14. The method of any one of claims 11 to 13, wherein the amino acid substitution results from a nucleotide substitution in a coding sequence of a PIK3R1 polynucleotide.
15. The method of any one of claims 11 to 14, wherein the amino acid substitution is in an SH2 domain of a PIK3R1 polypeptide.
16. The method of claim 15, wherein the amino acid substitution is at 564N.
17. The method of claim 16, wherein the amino acid substitution is 564N>D.
18. The method of any one of claims 11 to 17, wherein the antagonist is an antagonist of a PIK3CA polypeptide.
19. Use of an antagonist of PI3K signaling in the manufacture of a medicament for treating a tumor comprising an amino acid substitution in a PIK3R1 polypeptide, wherein treating comprises detecting the amino acid substitution, and wherein the amino acid substitution results in activation of a PIK3CA polypeptide.
20. The method of claim 1 or claim 11, or the use of claim 19, substantially as hereinbefore described with reference to the examples and figures.

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FIGURE 1

VARIANT ID	UNQ ID	DNA ID	GENE	GENE DESCRIPTION (HUGO)	NT_CHGE	AA_CHGE
1049	2295	103509	AKT-1	v-akt murine thymoma viral oncogene homolog 1	HETSUB.1165G>C	323D>H
11228	2295	103509	AKT-1	v-akt murine thymoma viral oncogene homolog 1	HETSUB.484C>T	96R>W
34129	2295	103509	AKT-1	v-akt murine thymoma viral oncogene homolog 1	HETSUB.765G>T	189K>N
48337	2295	103509	AKT-1	v-akt murine thymoma viral oncogene homolog 1	HOMSUB.765G>T	189K>N
21270	6167	226506	AKT2	v-akt murine thymoma viral oncogene homolog 2	HETSUB.505G>T	101R>L
24683	6167	226506	AKT2	v-akt murine thymoma viral oncogene homolog 2	HETSUB.471G>T	90V>L
48080	6520	188261	ALK	anaplastic lymphoma kinase (Ki-1)	HETSUB.2369C>A	486F>L
52468	6520	188261	ALK	anaplastic lymphoma kinase (Ki-1)	HETSUB.2664G>A	585A>T
52471	6520	188261	ALK	anaplastic lymphoma kinase (Ki-1)	HETSUB.5371C>T	1487S>L
62942	6520	188261	ALK	anaplastic lymphoma kinase (Ki-1)	HETSUB.2563G>A	551R>Q
1744	2290	226502	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	HETSUB.1487G>T	429D>Y
1825	2290	226502	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	HETSUB.1605G>A	468G>E
21222	2290	226502	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	HOMSUB.1686A>G	495Y>C
39239	2290	226502	ARAF	v-raf murine sarcoma 3611 viral oncogene homolog	HETSUB.1686A>G	495Y>C
42019	4200	349269	AXIN1	axin 1	HETSUB.970G>T	314G>O
47109	4200	349269	AXIN1	axin 1	HETSUB.875G>A	282G>D

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FIGURE 1 (CONTINUED)

47753	4200	349269	AXIN1	axin 1	HETSUB.659A>C	210K>T
57801	4200	349269	AXIN1	axin 1	HETSUB.1234C>A	402R>S
61414	4200	349269	AXIN1	axin 1	HETSUB.2548G>C	840G>R
47301	10494	351940	AXIN2	axin 2 (conductin, axil)	HETSUB.2598G>T	837G>C
47604	10494	351940	AXIN2	axin 2 (conductin, axil)	HETSUB.449G>T	120M>I
58101	10494	351940	AXIN2	axin 2 (conductin, axil)	HETSUB.2526G>T	813A>S
58308	10494	351940	AXIN2	axin 2 (conductin, axil)	HETSUB.862C>T	258T>M
62903	10494	351940	AXIN2	axin 2 (conductin, axil)	HETSUB.487C>T	133A>V
47966	452	208152	AXL	AXL receptor tyrosine kinase	HETSUB.1913T>C	637L>P
48190	452	208152	AXL	AXL receptor tyrosine kinase	HETSUB.1831C>T	610R>O
63193	6156	513210	BAX	BCL2-associated X protein	HETSUB.583C>A	172L>I
19629	2707	326808	BCL-XL	BCL2-like 1	HETSUB.619G>T	85A>S
50324	2152	401383	B-raf	v-raf murine sarcoma viral oncogene homolog B1	HETSUB.1516G>T	485L>F
53270	2152	401383	B-raf	v-raf murine sarcoma viral oncogene homolog B1	HETSUB.1358G>T	433E>O
59665	2152	401383	B-raf	oncogene homolog B1	HETSUB.2074A>G	671R>R
60390	2152	401383	B-raf	v-raf murine sarcoma viral oncogene homolog B1	HETSUB.1792C>T	577L>L
61456	2152	401383	B-raf	oncogene homolog B1	HETSUB.1215A>G	385D>G
3465	9979	516878	CBL	oncogene homolog B1	HETSUB.1145+2T>G	INTRONIC
1188	14620	516881	CBLB	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	HETSUB.3089C>T	923H>Y
60761	22478	326714	CBLC	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	HETINS.1296C>CCA	419Q>FS

FIGURE 1 (CONTINUED)

20454	1983	513190	CDKN2A (isoform 2)	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	HETSUB.349G>C	46R>P
33648	1983	513227	CDKN2A (isoform 1)	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	HETSUB.488G>C	151G>R
40455	1983	513190	CDKN2A (isoform 2)	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	HETSUB.371G>A	53M>I
42941	1983	513190	CDKN2A (isoform 2)	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	HETSUB.362G>C	50Q>H
60943	1983	513190	CDKN2A (isoform 2)	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	HETSUB.511C>A	100A>D
39399	8258	533136	CIAS1 (isoform 2)	cold autoinflammatory syndrome 1	HETSUB.1215C>G	157R>G
42354	8258	347968	CIAS1 (isoform 1)	cold autoinflammatory syndrome 1	HETSUB.2152T>A	469L>H
42552	8258	347968	CIAS1 (isoform 1)	cold autoinflammatory syndrome 1	HETSUB.2124C>A	460H>N
48256	8258	347968	CIAS1 (isoform 1)	cold autoinflammatory syndrome 1	HETSUB.1801C>T	352P>L
56750	8258	347968	CIAS1 (isoform 1)	cold autoinflammatory syndrome 1	HETSUB.1422G>T	226G>W
58209	8258	347968	CIAS1 (isoform 1)	cold autoinflammatory syndrome 1	HETSUB.2829G>T	695E>O
58530	8258	347968	CIAS1 (isoform 1)	cold autoinflammatory syndrome 1	HETSUB.1795C>A	350T>K
61627	8258	347968	CIAS1 (isoform 1)	cold autoinflammatory syndrome 1	HETSUB.2730G>A	662D>N

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FIGURE 1 (CONTINUED)

61648	8258	347968	CIAS1 (isoform 1)	cold autoimmune syndrome 1	HETSUB.2476T>G	577V>G
61663	8258	347968	CIAS1 (isoform 1)	cold autoimmune syndrome 1	HETSUB.2653A>T	636E>V
20439	42	398842	cMet	met proto-oncogene (hepatocyte growth factor receptor)	HETSUB.264G>T	26C>F
45237	42	398842	cMet	met proto-oncogene (hepatocyte growth factor receptor)	HETSUB.503A>G	106N>D
47993	42	398842	cMet	met proto-oncogene (hepatocyte growth factor receptor)	HETSUB.763C>A	192F>L
48958	42	398842	cMet	met proto-oncogene (hepatocyte growth factor receptor)	HETSUB.2184A>G	666Y>C
49423	42	398842	cMet	met proto-oncogene (hepatocyte growth factor receptor)	HETSUB.2208T>G	674L>O
49952	42	398842	cMet	met proto-oncogene (hepatocyte growth factor receptor)	HETSUB.3695C>T	1170R>O
50550	42	398842	cMet	met proto-oncogene (hepatocyte growth factor receptor)	HETSUB.3683C>T	1166R>O
57867	42	398842	cMet	met proto-oncogene (hepatocyte growth factor receptor)	HETSUB.1757C>T	524Q>O
61708	42	398842	cMet	met proto-oncogene (hepatocyte growth factor receptor)	HETSUB.3378A>G	1064Q>R

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FIGURE 1 (CONTINUED)

63708	42	398842	cMet	met proto-oncogene (hepatocyte growth factor receptor)	HETSUB.1218G>T	344G>V
48913	1975	226176	CXCR4	chemokine (C-X-C motif) receptor 4	HETSUB.596C>G	170P>X
49180	1975	226176	CXCR4	chemokine (C-X-C motif) receptor 4	HETSUB.1034G>A	316A>T
42025	1794	208132	DDR2	discoidin domain receptor family, member 2	HETSUB.2538A>C	763K>T
43879	1794	208132	DDR2	discoidin domain receptor family, member 2	HETSUB.1581G>T	444S>I
47978	1794	208132	DDR2	discoidin domain receptor family, member 2	HETSUB.534A>G	95H>R
48035	1794	208132	DDR2	discoidin domain receptor family, member 2	HETSUB.2098G>T	616K>N
58143	1794	208132	DDR2	discoidin domain receptor family, member 2	HETSUB.2558G>T	770V>L
24752	28426	513229	DUBA2	OTU domain containing 6A	HETSUB.591T>A	186L>Q
25271	28426	513229	DUBA2	OTU domain containing 6A	HETSUB.482G>A	150G>S
31451	28426	513229	DUBA2	OTU domain containing 6A	HETSUB.356C>A	108R>S
32342	28426	513229	DUBA2	OTU domain containing 6A	HETSUB.182C>G	50R>G
60791	28426	513229	DUBA2	OTU domain containing 6A	HETSUB.387C>T	118S>L
41814	2395	354686	EDG1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	HETSUB.897G>T	282C>F
47493	2395	354686	EDG1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	HETSUB.809G>T	253A>S
48130	9424	216539	EGFL11	EGF-like-domain, multiple 11	HETSUB.633C>A	79P>H
49336	9424	216539	EGFL11	EGF-like-domain, multiple 11	HETSUB.942T>G	182F>C
49363	9424	216539	EGFL11	EGF-like-domain, multiple 11	HETSUB.1145+2T>C	INTRONIC

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FIGURE 1 (CONTINUED)

49432	9424	216539	EGFL11	EGF-like-domain, multiple 11	HETSUB.810C>A	138S>Y
57447	9424	216539	EGFL11	EGF-like-domain, multiple 11	HETSUB.753C>A	119T>K
57642	9424	216539	EGFL11	EGF-like-domain, multiple 11	HETSUB.1113C>A	239A>E
57648	9424	216539	EGFL11	EGF-like-domain, multiple 11	HETSUB.882G>T	162G>V
61381	9424	216539	EGFL11	EGF-like-domain, multiple 11	HETSUB.645A>C	83Q>P
503	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	HOMSUB.906C>T	220S>S
3561	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	HOMDEL.2481GGAATTA AGAGAAGC> 745KELREA>K	
8278	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	HETSUB.906C>T	220S>S
18069	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	HETSUB.2745G>T	833L>F
22617	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	HETSUB.3791A>T	1182K>M
25259	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	HETSUB.2516A>T	757K>M

FIGURE 1 (CONTINUED)

39041	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETDEL.2481GGAAATTA AGAGAAGC>	745KELREA>K
39042	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETDEL.2483AATTAAG AGAAGCAACATC>	746>FS
41329	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.691C>T	149R>W
43418	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.593C>T	116S>F
45939	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.1525C>T	427R>C
46170	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.2257C>T	671R>C
46653	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.2007C>T	587D>D

FIGURE 1 (CONTINUED)

46815	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.1067C>T	274T>M
48406	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HOMDEL.2523C>	759>FS
48769	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.748G>A	168V>I
48832	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.740G>A	165R>Q
54515	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.856G>A	204E>K
56867	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.2790G>A	848P>P
56978	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.984C>T	246S>S

FIGURE 1 (CONTINUED)

62480	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETSUB.2605C>A	787Q>K
68160	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETDEL.2498CATCTCC GAAAGCCCAACAAGGAA A> E >I 751TSPKANIK	
71325	1033	401352	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v- erb-b) oncogene homolog, avian)	HETINS.2554G>GCCAG CGTGG	770D>ASVD
14413	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.503G>T	104V>L
21276	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.2333G>A	714V>M
43376	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.1801G>A	536L>L
46092	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.1166G>A	325G>R
46128	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.1043G>A	284G>R
46155	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.977C>T	262P>S

FIGURE 1 (CONTINUED)

46722	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.770C>T	193R>O
46737	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.1077T>C	295V>A
46818	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.4096G>A	1301Q>Q
48772	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.888C>T	232A>V
48823	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.3683A>G	1164T>A
48847	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.372T>A	60M>K
54581	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.1489C>T	432I>I
59575	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.1667G>C	492D>H
62615	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.978C>A	262P>H
62669	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.2619A>G	809Q>R

FIGURE 1 (CONTINUED)

63244	974	513202	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	HETSUB.2730G>T	846S>I
518	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.779G>C	249C>S
998	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.2488C>A	819L>M
22644	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.1885C>T	618H>Y
22674	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.299T>C	89V>A
22677	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.301G>A	90A>T
23115	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.2181T>G	716T>T
41302	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.1183A>G	384I>V
45987	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.3781C>T	1250R>W
46068	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.1414A>G	461T>A

FIGURE 1 (CONTINUED)

46215	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.1292T>G	420L>R
46257	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.3547G>T	1172V>F
46287	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.1516A>C	495N>H
46581	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.92T>C	20V>A
46617	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.1495C>T	488R>W
46686	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.2253A>C	740E>D
46725	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.3935A>G	1301Y>C
46773	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.535C>T	168R>W
46821	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.486G>T	151Q>H
48430	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.2565G>T	844L>F

FIGURE 1 (CONTINUED)

48433	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETDEL.2566G>	845>FS
48883	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.2653G>T	874E>O
48889	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.2670A>C	879G>G
53759	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.2822C>A	930P>H
53933	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.325C>A	98P>T
53936	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.657G>T	208L>F
54383	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.3682G>A	1217G>R
54494	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.1949C>T	639T>M
54527	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.822C>A	263P>P
54584	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.3591C>T	1186P>P

FIGURE 1 (CONTINUED)

56996	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.2470G>A	813D>N
60368	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.3167G>T	1045R>M
62305	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.1291C>T	420L>L
62317	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.3200A>T	1056Y>F
63370	2758	115980	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	HETSUB.3850C>T	1273R>W
40143 6736	1477 527	342173 344519	ETBR FGFR1	endothelin receptor type B fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	HETDEL.1114T> HETSUB.2094G>T	293>FS 456M>I
51801	527	344519	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	HETSUB.2750G>A	675R>Q
65700	527	344519	FGFR1	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	HETDEL.3060C>	778>FS

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FIGURE 1 (CONTINUED)

25094	942	513191	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	HETSUB.2285G>A	584E>K
25295	942	513191	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	HETSUB.2265-47G>C	INTRONIC
25298	942	513191	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	HETSUB.2265-23G>A	INTRONIC
41110	942	513191	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	HETSUB.2239T>G	568N>K

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FIGURE 1 (CONTINUED)

51435	942	513191	FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	HETSUB.2123G>A	530A>T
43654	1186	513192	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	HETSUB.752G>A	238R>Q
59653	1186	513192	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	HETSUB.2151C>G	704F>L
59726	1186	513192	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	HETSUB.2174G>A	712R>H
66719	1186	513192	FGFR3	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	HETSUB.1134G>T	365E>D
49258	1646	513203	FGFR4	fibroblast growth factor receptor 4	HETSUB.2321-1G>T	INTRONIC
50030	1646	513203	FGFR4	fibroblast growth factor receptor 4	HETSUB.2158G>T	664R>L
35617	13642	513212	FRAP1	FK506 binding protein 12- rapamycin associated protein 1	HETSUB.6682C>G	2201L>L
35620	13642	513212	FRAP1	FK506 binding protein 12- rapamycin associated protein 1	HETSUB.6687G>T	2203G>V
47061	16212	331202	GPR73	G protein-coupled receptor 73	HETSUB.875C>T	292A>V
47214	16212	331202	GPR73	G protein-coupled receptor 73	HETSUB.919C>T	307R>C
47550	16212	331202	GPR73	G protein-coupled receptor 73	HETSUB.835C>T	279R>C
48187	16212	331202	GPR73	G protein-coupled receptor 73	HETSUB.637G>A	213E>K

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FIGURE 1 (CONTINUED)

58254	16212	331202	GPR73	G protein-coupled receptor 73	HETSUB.517C>T	173R>W
61498	16212	331202	GPR73	G protein-coupled receptor 73	HETSUB.592G>A	198A>T
8909	615	401384	Her2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	HETSUB.2271G>A	678R>Q
46206	615	401384	Her2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	HETSUB.3404G>A	1056G>S
46596	615	401384	Her2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	HETSUB.2501T>A	755L>M
56924	615	401384	Her2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	HETSUB.861G>A	208S>N
59047	615	401384	Her2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	HETSUB.3963C>T	1242T>M
64241	615	401384	Her2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	HETSUB.2844T>G	869L>R
16877	902	329563	IGF1-R	insulin-like growth factor 1 receptor	HETSUB.3640G>A	1199G>R
53381	902	329563	IGF1-R	insulin-like growth factor 1 receptor	HETSUB.2971G>T	976V>L

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FIGURE 1 (CONTINUED)

59230	902	329563	IGF1-R	insulin-like growth factor 1 receptor	HETSUB.4021G>A	1326E>K
66898	3144	227470	JAG1	jagged 1 (Alagille syndrome)	HETDEL.502GG>	30>FS
63696	8891	327520	JAG2	jagged 2	HETSUB.616T>C	71V>A
42407	7982	328574	JAK2	Janus kinase 2 (a protein tyrosine kinase)	HETSUB.2478C>T	662H>Y
48119	7982	328574	JAK2	Janus kinase 2 (a protein tyrosine kinase)	HETSUB.1868G>T	458E>D
48226	7982	328574	JAK2	Janus kinase 2 (a protein tyrosine kinase)	HETSUB.1516T>C	341V>A
61840	7982	328574	JAK2	Janus kinase 2 (a protein tyrosine kinase)	HETSUB.2818C>T	775P>L
62456	7982	328574	JAK2	Janus kinase 2 (a protein tyrosine kinase)	HETSUB.3832G>A	1113R>H
62735	7982	328574	JAK2	Janus kinase 2 (a protein tyrosine kinase)	HETSUB.3076G>A	861G>E
42835	2105	513213	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	HETSUB.252T>A	24I>N
56131	3150	513205	MAP2K1	mitogen-activated protein kinase kinase 1	HETDEL.375GGAGA>	101>FS
54898	11655	396729	MELK	maternal embryonic leucine zipper kinase	HETSUB.1067A>T	310Y>F
54916	11655	396729	MELK	maternal embryonic leucine zipper kinase	HETSUB.406C>T	90P>S
55173	11655	396729	MELK	maternal embryonic leucine zipper kinase	HETSUB.311T>C	58I>T
55383	11655	396729	MELK	maternal embryonic leucine zipper kinase	HETSUB.1003G>T	289E>O
66421	11655	396729	MELK	maternal embryonic leucine zipper kinase	HETSUB.673T>G	179L>V
44002	9143	352688	Notch2	Notch homolog 2 (Drosophila)	HETSUB.5153G>A	1633V>I

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FIGURE 1 (CONTINUED)

47589	9143	352688	Notch2	Notch homolog 2 (Drosophila)	HETSUB.4848G>T	1531G>V
52914	9143	352688	Notch2	Notch homolog 2 (Drosophila)	HETSUB.6312G>T	2019R>L
63840	9143	352688	Notch2	Notch homolog 2 (Drosophila)	HETSUB.6777G>A	2174G>E
47340	3628	328482	NOTCH3	Notch homolog 3 (Drosophila)	HETSUB.4529G>A	1484C>Y
49231	3628	328482	NOTCH3	Notch homolog 3 (Drosophila)	HETSUB.3940C>T	1288R>W
52510	3628	328482	NOTCH3	Notch homolog 3 (Drosophila)	HETSUB.4787G>A	1570R>H
52902	3628	328482	NOTCH3	Notch homolog 3 (Drosophila)	HETSUB.4859C>T	1594S>L
62513	3628	328482	NOTCH3	Notch homolog 3 (Drosophila)	HETSUB.6698G>A	2207R>Q
47322	485	225514	NRP1	neuropilin 1	HETSUB.355C>A	119L>I
47643	485	225514	NRP1	neuropilin 1	HETSUB.1955T>G	652F>C
47900	485	225514	NRP1	neuropilin 1	HETSUB.1388G>A	463R>H
48017	485	225514	NRP1	neuropilin 1	HETSUB.2350G>A	784E>K
48026	485	225514	NRP1	neuropilin 1	HETSUB.668A>G	223H>R
48268	485	225514	NRP1	neuropilin 1	HETSUB.703C>T	235R>O
61336	485	225514	NRP1	neuropilin 1	HETSUB.2188G>T	730G>W
63891	485	225514	NRP1	neuropilin 1	HETSUB.407T>C	136I>T
66091	485	225514	NRP1	neuropilin 1	HETSUB.1730G>C	577R>T
44988	1000	513189	NTC1	Notch homolog 1, translocation-associated (Drosophila)	HETSUB.6616T>G	2206S>A
49114	1000	513189	NTC1	Notch homolog 1, translocation-associated (Drosophila)	HETSUB.3908G>A	1303R>H
57882	1000	513189	NTC1	Notch homolog 1, translocation-associated (Drosophila)	HETSUB.6760C>G	2254P>A
57918	1000	513189	NTC1	Notch homolog 1, translocation-associated (Drosophila)	HETSUB.7379A>G	2460Q>R
58713	1000	513189	NTC1	Notch homolog 1, translocation-associated (Drosophila)	HETSUB.4568A>T	1523Q>L
66106	1000	513189	NTC1	Notch homolog 1, translocation-associated (Drosophila)	HETSUB.7117C>T	2373R>W
52351	1364	226140	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	HETSUB.2012T>C	671M>T

FIGURE 1 (CONTINUED)

52357	1364	226140	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	HETSUB.1876C>A	626Q>K
52908	1364	226140	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	HETSUB.1463G>A	488G>D
52920	1364	226140	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	HETSUB.1472T>C	491I>T
61207	1364	226140	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	HETSUB.1721G>T	574R>L
61990	1364	226140	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	HETSUB.653A>T	218E>V
62729	1364	226140	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	HETSUB.2231G>T	744R>L
58317	1365	226141	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	HETSUB.2695G>T	782V>L
62561	1365	226141	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	HETSUB.2467T>G	706Y>D
62627	1365	226141	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	HETSUB.2350C>A	667L>M
19623	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.1828G>T	556E>O
19635	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.1367-1G>A	INTRONIC
42588	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.2497-1G>A	INTRONIC
42699	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.1879-2A>T	INTRONIC
42938	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.2004C>G	614I>M
46920	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.1023G>T	287E>D

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FIGURE 1 (CONTINUED)

48110	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.428G>A	89R>H
49517	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.2401T>G	747F>V
51192	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.1967A>G	602K>R
51450	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.2650G>T	830A>S
56023	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.1396G>A	412E>K
56795	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.513C>A	117S>R
57158	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.2497-1G>T	INTRONIC
58980	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.253G>T	31A>S
60140	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.1700A>G	513N>S
60311	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.1642C>A	494L>M
62459	1366	520002	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	HETSUB.636G>C	158E>D
44095	16971	338340	OTUD1	OTU domain containing 1	HETSUB.1300T>A	434Y>N
48113	16971	338340	OTUD1	OTU domain containing 1	HETSUB.228G>T	76M>I
49144	16971	338340	OTUD1	OTU domain containing 1	HETSUB.833A>C	278K>T
20093	18800	519636	PAK6	p21(CDKN1A)-activated kinase 6	HETSUB.1403G>T	328S>I
50778	1436	513204	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	HETSUB.2674C>T	773A>V
50916	1436	513204	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	HETSUB.2839C>T	828A>V

FIGURE 1 (CONTINUED)

55440	1436	513204	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	HETSUB.2427G>A	691D>N
57266	1436	513204	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	HETSUB.2295G>T	647A>S
59089	1436	513204	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	HETSUB.2164-2A>T	INTRONIC
62978	1436	513204	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	HETSUB.2905A>T	850D>V
32048	15838	393324	PDK1	pyruvate dehydrogenase kinase, isoenzyme 1	HETSUB.792-2A>C	INTRONIC
33706	15838	393324	PDK1	pyruvate dehydrogenase kinase, isoenzyme 1	HETSUB.1238G>T	380G>C
42747	4924	513220	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	HETSUB.1568C>G	471P>A
50685	4924	513220	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	HETSUB.1937A>G	594K>E
51456	4924	513220	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	HETSUB.2692G>A	845V>V
51750	4924	513220	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	HETSUB.3115G>T	986K>N
51810	4924	513220	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	HETSUB.269C>A	38R>S
55527	4924	513220	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	HETSUB.3061C>T	968A>A
55858	4924	513220	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	HETSUB.2333G>A	726E>K
63813	4924	513220	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	HETSUB.192G>A	12G>D
66964	4924	513220	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	HETSUB.2754T>G	866L>W

FIGURE 1 (CONTINUED)

47187	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.895A>C	285N>H
48068	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.1084C>T	348R>O
49877	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.1763G>T	574R>I
50039	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.1623T>G	527N>K
50042	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.1732A>G	564N>D
50486	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.1988G>A	649R>Q
50694	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.1966C>T	642R>O
51309	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.2038G>A	666E>K
51612	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.2087C>T	682A>V
52429	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.526C>T	162R>O
56185	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETDEL.1182AATC>	380>FS
56188	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.1388T>C	449L>S
66584	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETSUB.1670G>T	543R>I
71322	5003	516883	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	HETINS.2047C>CTAAAG C	669H>LKH
67250	3473	590779	PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	HETSUB.1546G>A	345R>Q

FIGURE 1 (CONTINUED)

67382	13736	590780	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4, p150	HETSUB.2544G>A	655E>K
67451	13736	590780	PIK3R4	phosphoinositide-3-kinase, regulatory subunit 4, p150	HETSUB.3721C>T	1047T>M
67331	9122	227999	PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5, p101	HETSUB.102G>A	12R>H
34015	3368	513214	PLK1	polo-like kinase 1 (Drosophila)	HETSUB.1544C>G	497I>M
46956	3338	227487	PRKCB1	protein kinase C, beta 1	HETSUB.1964C>T	610R>C
47232	3338	227487	PRKCB1	protein kinase C, beta 1	HETSUB.1147G>A	337M>I
47421	3338	227487	PRKCB1	protein kinase C, beta 1	HETSUB.2106T>G	657F>C
47652	3338	227487	PRKCB1	protein kinase C, beta 1	HETSUB.522G>A	129G>E
48092	3338	227487	PRKCB1	protein kinase C, beta 1	HETSUB.1453G>T	439K>N
48259	3338	227487	PRKCB1	protein kinase C, beta 1	HETSUB.1086C>T	317P>L
61462	3338	227487	PRKCB1	protein kinase C, beta 1	HETSUB.1649C>A	505P>T
55155	5024	548660	PRKCI	protein kinase C, iota	HETSUB.1582G>T	441R>M
55401	5024	548660	PRKCI	protein kinase C, iota	HETSUB.1425G>A	389G>S
55410	5024	548660	PRKCI	protein kinase C, iota	HETSUB.807C>T	183R>W
56522	5024	548660	PRKCI	protein kinase C, iota	HETSUB.1671C>T	471R>C
20448	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.1764G>T	526G>O
43144	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.1108C>T	307T>I
44713	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.297G>C	37G>R
50060	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.2553G>T	789D>Y
51702	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.1790+1G>A	INTRONIC
52327	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.3382T>G	1065V>G
55494	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.1099G>A	304C>Y
55557	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.785G>T	199L>F
55861	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.1062A>T	292M>L
56116	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.801A>T	205K>O
57936	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.285C>G	33R>G
66641	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.4448T>A	1420C>O
66842	622	513193	PTCH	patched homolog (Drosophila)	HETSUB.4269G>A	1361V>M

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FIGURE 1 (CONTINUED)

38084	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETDEL.1828A>	266>FS
39546	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETDEL.1539A>	170>FS
50580	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETSUB.1725C>T	232R>O
50700	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETSUB.1115T>G	28I>M
50703	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETSUB.1122A>C	31N>H
52999	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETSUB.1039C>A	3A>D
55476	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETSUB.1207C>T	59S>L
60284	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETSUB.1240+1G>A	INTRONIC
62314	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETSUB.1809C>T	260Q>O
66596	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETDEL.1130TGCTATG GG>	33I/AMG>I

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FIGURE 1 (CONTINUED)

66602	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETSUB.2036C>A	335Y>O
66608	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETSUB.2030C>T	333N>N
66611	2113	393189	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	HETSUB.1976A>G	315L>L
4353	2172	226395	RB1	retinoblastoma 1 (including osteosarcoma)	HETSUB.308T>G	57F>C
4377	2172	226395	RB1	retinoblastoma 1 (including osteosarcoma)	HETSUB.2658+1G>A	INTRONIC
16796	2172	226395	RB1	retinoblastoma 1 (including osteosarcoma)	HETSUB.1834-1G>A	INTRONIC
39300	18517	518966	Rem2		HOMDEL.374AGCCCCT GCTCA>	96AAPAQ>A
39768	18517	518966	Rem2		HETDEL.374AGCCCCTG CTC>	96>FS
49348	1020	513223	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	HETSUB.1753C>T	525R>W
49808	1020	513223	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	HETSUB.2122G>A	648V>I
50366	1020	513223	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	HETSUB.3056G>A	959R>Q

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FIGURE 1 (CONTINUED)

53324	1020	513223	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	HETSUB.2461A>T	761K>O
57074	1020	513223	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	HETSUB.2864T>C	895L>S
57972	1020	513223	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	HETSUB.1874G>T	565C>F
59035	1020	513223	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	HETSUB.2969C>T	930T>M
61201	1020	513223	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	HETSUB.1823G>A	548G>D
62750	1020	513223	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	HETSUB.2007C>A	609C>O
63699	1020	513223	RET	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	HETSUB.2522A>T	781Q>L
19605	1514	83169	RON	ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease) macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	HETSUB.3368A>T	1114K>O

FIGURE 1 (CONTINUED)

50420	1514	83169	RON	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	HETSUB.3771G>A	1248R>H
66566	1514	83169	RON	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	HETDEL.2762G>	912>FS
56158	3359	513219	SMAD2	SMAD, mothers against DPP homolog 2 (Drosophila)	HETSUB.1627C>T	460S>L
20571	10842	396295	Stk6	serine/threonine kinase 6	HETSUB.1004G>T	216G>O
43237	650	144601	SUFU	suppressor of fused homolog (Drosophila)	HETSUB.452C>T	102N>X
57071	650	144601	SUFU	suppressor of fused homolog (Drosophila)	HETSUB.501G>C	119E>Q
57110	650	144601	SUFU	suppressor of fused homolog (Drosophila)	HETSUB.1245G>A	367E>K
34775	918	225645	TGFB1	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)	HETSUB.1274G>A	400D>N
48340	918	225645	TGFB1	transforming growth factor, beta receptor I (activin A receptor type II-like kinase, 53kDa)	HETSUB.782T>C	236S>P
48535	1362	88656	TGFB2	transforming growth factor, beta receptor II (70/80kDa)	HETDEL.718A>	128>FS
1828	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.1171-1G>T	INTRONIC
4480	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.861G>T	204E>O
6188	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.923G>T	224E>D
6593	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.786C>T	179H>Y

FIGURE 1 (CONTINUED)

6605	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.631C>A	127S>Y
9510	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.348-2A>G	INTRONIC
21243	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.1047G>T	266G>O
21252	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.1093A>T	281D>V
22224	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.1171-2A>G	INTRONIC
34021	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.627-2A>G	INTRONIC
34054	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.646A>T	132K>M
34078	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.825C>T	192Q>O
34081	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.841T>A	197V>E
34123	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.923+1G>T	INTRONIC
40894	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETINS.899G>GGG	217V>FS
40900	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETDEL.913AGCCGCCCT >	221>FS
40915	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETINS.1030C>CCC	260S>FS
40942	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETDEL.1111A>	287>FS
40954	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETDEL.1178C>	309>FS

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FIGURE 1 (CONTINUED)

40966	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETDEL.1294T>	348>FS
40981	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETDEL.538C>	96>FS
40990	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETINS.621T>TTG	124C>FS
41023	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETINS.707G>GGC	153P>FS
41047	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETDEL.497G>	82>FS
41059	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETINS.760C>CCG	170T>FS
65679	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.987A>G	246M>V
68057	2060	226297	TP53	tumor protein p53 (Li-Fraumeni syndrome)	HETSUB.569C>G	106S>R
44439	18339	345840	USP21	ubiquitin specific protease 21	HETSUB.1187G>A	154R>H
47472	18339	345840	USP21	ubiquitin specific protease 21	HETSUB.1508G>A	261R>Q
52917	18339	345840	USP21	ubiquitin specific protease 21	HETSUB.1234C>T	170R>O
57318	18339	345840	USP21	ubiquitin specific protease 21	HETSUB.1744C>T	340R>W
64414	18339	345840	USP21	ubiquitin specific protease 21	HETSUB.835-2A>G	INTRONIC
45826	11424	547924	USP24	ubiquitin specific protease 24	HETSUB.4991G>C	1420L>F
45763	17211	547823	USP25	ubiquitin specific protease 25	HETSUB.610-2A>G	INTRONIC
44782	17145	401357	USP28	ubiquitin specific protease 28	HETSUB.928G>T	310E>O
47058	22165	373482	USP35	ubiquitin specific protease 35	HETSUB.1087G>A	178S>N
51994	22165	373482	USP35	ubiquitin specific protease 35	HETSUB.1737C>T	395P>S
61276	22165	373482	USP35	ubiquitin specific protease 35	HETSUB.2572C>T	673A>V
62068	22165	373482	USP35	ubiquitin specific protease 35	HETSUB.1495C>T	314P>L
16805	1025	188418	VEGFR2	kinase insert domain receptor (a type III receptor tyrosine kinase)	HETSUB.3205A>T	968S>C

FIGURE 1 (CONTINUED)

33675	1025	188418	VEGFR2	kinase insert domain receptor (a type III receptor tyrosine kinase)	HETSUB.2615C>T	771T>M
34093	1025	188418	VEGFR2	kinase insert domain receptor (a type III receptor tyrosine kinase)	HETSUB.2681A>G	793N>S
39732	1025	188418	VEGFR2	kinase insert domain receptor (a type III receptor tyrosine kinase)	HETSUB.3496G>C	1065A>P
47112	1025	188418	VEGFR2	kinase insert domain receptor (a type III receptor tyrosine kinase)	HETSUB.3877C>T	1192L>F
55762	1025	188418	VEGFR2	kinase insert domain receptor (a type III receptor tyrosine kinase)	HETSUB.2749C>T	816H>Y
59032	1025	188418	VEGFR2	kinase insert domain receptor (a type III receptor tyrosine kinase)	HETSUB.2635T>G	778F>V
60047	1025	188418	VEGFR2	kinase insert domain receptor (a type III receptor tyrosine kinase)	HETSUB.2838T>G	845F>L

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FIGURE 2

VARIANT ID	GENE	EFFECT	LOCATION	DOMAIN	TISSUE	TUMOR TYPE
1049	AKT-1	Nonsyn.	Coding	Pkinase, Pkinase_Tyr	Breast	Breast Cancer, Non-matched normal
11228	AKT-1	Nonsyn.	Coding	PH	Colon	Colorectal Cancer
34129	AKT-1	Nonsyn.	Coding	Pkinase,	Lung	Non-Small Cell Lung Cancer
48337	AKT-1	Nonsyn.	Coding	Pkinase_Tyr	Breast, Colon	Breast Cancer, Colorectal Cancer
21270	AKT2	Nonsyn.	Coding	PH	Lung	Non-Small Cell Lung Cancer
24683	AKT2	Nonsyn.	Coding	PH	Lung	Non-Small Cell Lung Cancer
48080	ALK	Nonsyn.	Coding	MAM	Colon	Colorectal Cancer
52468	ALK	Nonsyn.	Coding	MAM	Colon	Colorectal Cancer
52471	ALK	Nonsyn.	Coding		Colon	Colorectal Cancer
62942	ALK	Nonsyn.	Coding	MAM	Cecum	Colorectal Cancer
1744	ARAF	Nonsyn.	Coding	Pkinase,	Lung	Small Cell Lung Cancer
1825	ARAF	Nonsyn.	Coding	Pkinase_Tyr	Lung	Small Cell Lung Cancer
21222	ARAF	Nonsyn.	Coding	Pkinase,	Lung	Non-Small Cell Lung Cancer
39239	ARAF	Nonsyn.	Coding	Pkinase_Tyr	Lung	Normal
42019	AXIN1	Nonsense	Coding	Pkinase_Tyr	Liver	Hepatocellular Carcinoma
47109	AXIN1	Nonsyn.	Coding		Colon	Colorectal Cancer
47753	AXIN1	Nonsyn.	Coding		Colon	Colorectal Cancer
57801	AXIN1	Nonsyn.	Coding		Stomach	Gastric Cancer
61414	AXIN1	Nonsyn.	Coding	DIX	Lung	Non-Small Cell Lung Cancer
47301	AXIN2	Nonsyn.	Coding	DIX	Colon	Colorectal Cancer
47604	AXIN2	Nonsyn.	Coding	RGS	Colon	Colorectal Cancer
58101	AXIN2	Nonsyn.	Coding	DIX	Lung	Non-Small Cell Lung Cancer
58308	AXIN2	Nonsyn.	Coding		Stomach	Gastric Cancer

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FIGURE 2 (CONTINUED)

62903	AXIN2	Nonsyn.	Coding	RGS	Lung	Non-Small Cell Lung Cancer
47966	AXL	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
48190	AXL	Nonsense	Coding	Pkinase_Tyr, Pkinase	Colon Ascending	Colorectal Cancer
63193	BAX	Nonsyn.	Coding		Kidney	Renal Cell Carcinoma
19629	BCL-XL	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
50324	B-raf	Nonsyn.	Coding	Pkinase, Pkinase_Tyr	Colon Ascending	Colorectal Cancer
53270	B-raf	Nonsense	Coding		Lung	Non-Small Cell Lung Cancer
59665	B-raf	Syn.	Coding	Pkinase, Pkinase_Tyr	Lung	Non-Small Cell Lung Cancer
60390	B-raf	Syn.	Coding	Pkinase, Pkinase_Tyr	Lung	Non-Small Cell Lung Cancer
61456	B-raf	Nonsyn.	Coding		Stomach	Gastric Cancer
3465	CBL		Splice Site		Breast	Breast Cancer
1188	CBLB	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
60761	CBLC		Coding		Breast, Lung, Ovary	Breast Cancer, Non-Small Cell Lung Cancer, Ovarian Cancer, Small Cell Lung Cancer
20454	CDKN2A	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
33648	CDKN2A	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
40455	CDKN2A	Nonsyn.	Coding		Breast	Breast Cancer
42941	CDKN2A	Nonsyn.	Coding		Liver	Hepatocellular Carcinoma
60943	CDKN2A	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
39399	CIAS1	Nonsyn.	Coding		Lung	Small Cell Lung Cancer
42354	CIAS1	Nonsyn.	Coding		Lung	Small Cell Lung Cancer
42552	CIAS1	Nonsyn.	Coding		Lung	Small Cell Lung Cancer
48256	CIAS1	Nonsyn.	Coding	NACHT	Colon	Colorectal Cancer
56750	CIAS1	Nonsyn.	Coding	NACHT	Lung	Non-Small Cell Lung Cancer

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FIGURE 2 (CONTINUED)

58209	CIAS1	Nonsense	Coding	NACHT	Lung	Non-Small Cell Lung Cancer
58530	CIAS1	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
61627	CIAS1	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
61648	CIAS1	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
61663	CIAS1	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
20439	cMet	Nonsyn.	Coding	sema	Lung	Non-Small Cell Lung Cancer
45237	cMet	Nonsyn.	Coding	sema	Liver	Non-Small Cell Lung Cancer
47993	cMet	Nonsyn.	Coding	TIG	Colon	Hepatocellular Carcinoma
48958	cMet	Nonsyn.	Coding	TIG	Colon	Colorectal Cancer
49423	cMet	Nonsense	Coding	Pkinase_Tyr,	Colon	Colorectal Cancer
49952	cMet	Nonsense	Coding	Pkinase	Colon	Colorectal Cancer
50550	cMet	Nonsense	Coding	Pkinase_Tyr,	Colon	Colorectal Cancer
				Pkinase		
57867	cMet	Nonsense	Coding	psi	Skin	Melanoma
61708	cMet	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
63708	cMet	Nonsyn.	Coding	sema	Lung	Non-Small Cell Lung Cancer
48913	CXCR4	Nonsyn.	Coding	7tm_1	Skin	Melanoma
49180	CXCR4	Nonsyn.	Coding		Colon	Colorectal Cancer
42025	DDR2	Nonsyn.	Coding	Pkinase,	Stomach	Gastric Cancer
				Pkinase_Tyr		
43879	DDR2	Nonsyn.	Coding		Stomach	Gastric Cancer
47978	DDR2	Nonsyn.	Coding	F5_F8_type_C	Stomach	Gastric Cancer
48035	DDR2	Nonsyn.	Coding	Pkinase,	Colon	Colorectal Cancer
				Pkinase_Tyr		
58143	DDR2	Nonsyn.	Coding	Pkinase,	Lung	Non-Small Cell Lung Cancer
				Pkinase_Tyr		
24752	DUBA2	Nonsyn.	Coding	OTU	Lung	Non-Small Cell Lung Cancer
25271	DUBA2	Nonsyn.	Coding	OTU	Lung	Non-Small Cell Lung Cancer
31451	DUBA2	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
32342	DUBA2	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer

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FIGURE 2 (CONTINUED)

60791	DUBA2	Nonsyn.	Coding			Non-Small Cell Lung Cancer
41814	EDG1	Nonsyn.	Coding	7tm_1	Lung	Small Cell Lung Cancer
47493	EDG1	Nonsyn.	Coding	7tm_1	Colon	Colorectal Cancer
48130	EGFL11	Nonsyn.	Coding		Colon	Colorectal Cancer
49336	EGFL11	Nonsyn.	Coding	EGF	Colon	Colorectal Cancer
49363	EGFL11		Splice Site		Colon	Colorectal Cancer
49432	EGFL11	Nonsyn.	Coding		Colon	Colorectal Cancer
57447	EGFL11	Nonsyn.	Coding		Colon	Colorectal Cancer
57642	EGFL11	Nonsyn.	Coding		Lung	Small Cell Lung Cancer
57648	EGFL11	Nonsyn.	Coding	EGF	Lung	Non-Small Cell Lung Cancer
61381	EGFL11	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
503	EGFR	Syn.	Coding	Furin-like	Lung, Ovary	Non-Small Cell Lung Cancer, Ovarian Cancer
3561	EGFR		Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
8278	EGFR	Syn.	Coding	Furin-like	Liver, Lung	Hepatocellular Carcinoma, Non-Small Cell Lung Cancer
18069	EGFR	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
22617	EGFR	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
25259	EGFR	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
39041	EGFR		Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
39042	EGFR		Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
41329	EGFR	Nonsyn.	Coding	Recep_L_domain	Liver	Hepatocellular Carcinoma
43418	EGFR	Nonsyn.	Coding	Recep_L_domain	Skin	Melanoma
45939	EGFR	Nonsyn.	Coding	Recep_L_domain	Colon	Colorectal Cancer
46170	EGFR	Nonsyn.	Coding		Colon	Colorectal Cancer
46653	EGFR	Syn.	Coding		Colon	Colorectal Cancer

FIGURE 2 (CONTINUED)

46815	EGFR	Nonsyn.	Coding	Furin-like	Colon	Colorectal Cancer
48406	EGFR		Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
48769	EGFR	Nonsyn.	Coding	Recep_L_domain	Colon	Colorectal Cancer
48832	EGFR	Nonsyn.	Coding	Recep_L_domain	Colon	Colorectal Cancer
54515	EGFR	Nonsyn.	Coding	Furin-like	Lung	Non-Small Cell Lung Cancer
56867	EGFR	Syn.	Coding	Pkinase_Tyr, Pkinase	Stomach	Gastric Cancer
56978	EGFR	Syn.	Coding	Furin-like	Kidney	Renal Cell Carcinoma
62480	EGFR	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
68160	EGFR		Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
71325	EGFR		Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
14413	ERBB3	Nonsyn.	Coding	Recep_L_domain	Colon	Colorectal Cancer
21276	ERBB3	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
43376	ERBB3	Syn.	Coding		Ovary	Ovarian Cancer
46092	ERBB3	Nonsyn.	Coding	Furin-like	Colon	Colorectal Cancer
46128	ERBB3	Nonsyn.	Coding	Furin-like	Colon, Rectum	Colorectal Cancer
46155	ERBB3	Nonsyn.	Coding	Furin-like	Colon	Colorectal Cancer
46722	ERBB3	Nonsense	Coding	Furin-like	Colon	Colorectal Cancer
46737	ERBB3	Nonsyn.	Coding	Furin-like	Colon	Colorectal Cancer
46818	ERBB3	Syn.	Coding		Colon	Colorectal Cancer
48772	ERBB3	Nonsyn.	Coding	Furin-like	Stomach	Gastric Cancer
48823	ERBB3	Nonsyn.	Coding		Colon	Colorectal Cancer
48847	ERBB3	Nonsyn.	Coding	Recep_L_domain	Colon	Colorectal Cancer
54581	ERBB3	Syn.	Coding	Recep_L_domain	Stomach	Gastric Cancer
59575	ERBB3	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
62615	ERBB3	Nonsyn.	Coding	Furin-like	Stomach	Gastric Cancer

FIGURE 2 (CONTINUED)

62669	ERBB3	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Stomach	Gastric Cancer
63244	ERBB3	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Cecum	Colorectal Cancer
518	ERBB4	Nonsyn.	Coding	Furin-like	Lung	Small Cell Lung Cancer
998	ERBB4	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Small Cell Lung Cancer
22644	ERBB4	Nonsyn.	Coding	Recep_L_domain	Lung	Non-Small Cell Lung Cancer
22674	ERBB4	Nonsyn.	Coding	Recep_L_domain	Lung	Non-Small Cell Lung Cancer
22677	ERBB4	Nonsyn.	Coding	Recep_L_domain	Lung	Non-Small Cell Lung Cancer
23115	ERBB4	Syn.	Coding	Recep_L_domain	Esophagus	Esophageal Cancer
41302	ERBB4	Nonsyn.	Coding	Recep_L_domain	Kidney	Renal Cell Carcinoma
45987	ERBB4	Nonsyn.	Coding	Recep_L_domain	Colon	Colorectal Cancer
46068	ERBB4	Nonsyn.	Coding	Recep_L_domain	Colon	Colorectal Cancer
46215	ERBB4	Nonsyn.	Coding	Recep_L_domain	Colon	Colorectal Cancer
46257	ERBB4	Nonsyn.	Coding	Recep_L_domain	Colon, Kidney, Lung, Ovary, Skin	Colorectal Cancer, Melanoma, Non-Small Cell Lung Cancer, Ovarian Cancer, Renal Cell Carcinoma
46287	ERBB4	Nonsyn.	Coding		Colon	Colorectal Cancer
46581	ERBB4	Nonsyn.	Coding		Stomach	Gastric Cancer
46617	ERBB4	Nonsyn.	Coding		Colon	Colorectal Cancer
46686	ERBB4	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
46725	ERBB4	Nonsyn.	Coding		Colon	Colorectal Cancer
46773	ERBB4	Nonsyn.	Coding		Colon	Colorectal Cancer
46821	ERBB4	Nonsyn.	Coding	Recep_L_domain	Colon	Colorectal Cancer
48430	ERBB4	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer

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FIGURE 2 (CONTINUED)

48433	ERBB4	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
48883	ERBB4	Nonsense	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
48889	ERBB4	Syn.	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
53759	ERBB4	Nonsyn.	Pkinase_Tyr	Skin	Melanoma
53933	ERBB4	Nonsyn.	Recep_L_domain	Lung	Non-Small Cell Lung Cancer
53936	ERBB4	Nonsyn.	Furin-like	Lung	Non-Small Cell Lung Cancer
54383	ERBB4	Nonsyn.		Skin	Melanoma
54494	ERBB4	Nonsyn.		Stomach	Gastric Cancer
54527	ERBB4	Syn.	Furin-like	Lung	Non-Small Cell Lung Cancer
54584	ERBB4	Syn.		Skin	Melanoma
56996	ERBB4	Nonsyn.	Pkinase_Tyr, Pkinase	Skin	Melanoma
60368	ERBB4	Nonsyn.		Lung	Non-Small Cell Lung Cancer
62305	ERBB4	Syn.	Recep_L_domain	Lung	Non-Small Cell Lung Cancer
62317	ERBB4	Nonsyn.		Lung	Non-Small Cell Lung Cancer
63370	ERBB4	Nonsyn.		Cecum	Colorectal Cancer
40143	ETBR			Colon, Stomach	Colorectal Cancer, Gastric Cancer
6736	FGFR1	Nonsyn.		Kidney, Lung	Non-Small Cell Lung Cancer, Renal Cell Carcinoma
51801	FGFR1	Nonsyn.	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
65700	FGFR1			Colon	Colorectal Cancer
25094	FGFR2	Nonsyn.	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
25295	FGFR2	Intronic		Lung	Non-Small Cell Lung Cancer
25298	FGFR2	Intronic		Lung	Non-Small Cell Lung Cancer

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FIGURE 2 (CONTINUED)

41110	FGFR2	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Breast	Breast Cancer
51435	FGFR2	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Skin, Stomach	Gastric Cancer, Melanoma
43654	FGFR3	Nonsyn.	Coding	I-set	Lung	Small Cell Lung Cancer
59653	FGFR3	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
59726	FGFR3	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Stomach	Gastric Cancer
66719	FGFR3	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
49258	FGFR4		Splice Site		Stomach	Gastric Cancer
50030	FGFR4	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
35617	FRAP1	Syn.	Coding	PI3_PI4_kinase	Lung	Non-Small Cell Lung Cancer
35620	FRAP1	Nonsyn.	Coding	PI3_PI4_kinase	Lung	Non-Small Cell Lung Cancer
47061	GPR73	Nonsyn.	Coding	7tm_1	Colon	Colorectal Cancer
47214	GPR73	Nonsyn.	Coding	7tm_1	Colon	Colorectal Cancer
47550	GPR73	Nonsyn.	Coding	7tm_1	Colon, Stomach	Colorectal Cancer, Gastric Cancer
48187	GPR73	Nonsyn.	Coding	7tm_1	Colon	Colorectal Cancer
58254	GPR73	Nonsyn.	Coding	7tm_1	Ovary	Ovarian Cancer
61498	GPR73	Nonsyn.	Coding	7tm_1	Stomach	Gastric Cancer
8909	Her2	Nonsyn.	Coding		Breast, Colon	Breast Cancer, Colorectal Cancer
46206	Her2	Nonsyn.	Coding		Colon	Colorectal Cancer
46596	Her2	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
56924	Her2	Nonsyn.	Coding	Furin-like	Lung	Non-Small Cell Lung Cancer
59047	Her2	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
64241	Her2	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Stomach	Gastric Cancer

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FIGURE 2 (CONTINUED)

16877	IGF1-R	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
53381	IGF1-R	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
59230	IGF1-R	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
66898	JAG1		Coding		Stomach	Gastric Cancer
63696	JAG2	Nonsyn.	Coding	MNHL	Stomach	Gastric Cancer
42407	JAK2	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Ovary	Ovarian Cancer
48119	JAK2	Nonsyn.	Coding	SH2	Colon	Colorectal Cancer
48226	JAK2	Nonsyn.	Coding		Stomach	Gastric Cancer
61840	JAK2	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
62456	JAK2	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
62735	JAK2	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
42835	KRAS	Nonsyn.	Coding	Ras	Ovary	Ovarian Cancer
56131	MAP2K1		Coding	Pkinase	Lung	Non-Small Cell Lung Cancer
54898	MELK	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
54916	MELK	Nonsyn.	Coding	Pkinase, Pkinase_Tyr	Lung	Non-Small Cell Lung Cancer
55173	MELK	Nonsyn.	Coding	Pkinase, Pkinase_Tyr	Colon	Colorectal Cancer
55383	MELK	Nonsense	Coding	Pkinase_Tyr	Colon	Colorectal Cancer
66421	MELK	Nonsyn.	Coding	Pkinase, Pkinase_Tyr	Stomach	Gastric Cancer
44002	Notch2	Nonsyn.	Coding		Lung	Small Cell Lung Cancer
47589	Notch2	Nonsyn.	Coding		Colon	Colorectal Cancer
52914	Notch2	Nonsyn.	Coding		Colon	Colorectal Cancer
63840	Notch2	Nonsyn.	Coding		Kidney	Renal Cell Carcinoma
47340	NOTCH3	Nonsyn.	Coding		Colon	Colorectal Cancer

FIGURE 2 (CONTINUED)

49231	NOTCH3	Nonsyn.	Coding		Colon	Colorectal Cancer
52510	NOTCH3	Nonsyn.	Coding		Colon	Colorectal Cancer
52902	NOTCH3	Nonsyn.	Coding		Colon	Colorectal Cancer
62513	NOTCH3	Nonsyn.	Coding		Stomach	Gastric Cancer
47322	NRP1	Nonsyn.	Coding	CUB	Colon	Colorectal Cancer
47643	NRP1	Nonsyn.	Coding	MAM	Colon	Colorectal Cancer
47900	NRP1	Nonsyn.	Coding	F5_F8_type_C	Colon	Colorectal Cancer
48017	NRP1	Nonsyn.	Coding	MAM	Colon	Colorectal Cancer
48026	NRP1	Nonsyn.	Coding	CUB	Colon	Colorectal Cancer
48268	NRP1	Nonsense	Coding	CUB	Colon	Colorectal Cancer
61336	NRP1	Nonsyn.	Coding	MAM	Lung	Non-Small Cell Lung Cancer
63891	NRP1	Nonsyn.	Coding	CUB	Rectum	Colorectal Cancer
66091	NRP1	Nonsyn.	Coding	F5_F8_type_C	Liver	Hepatocellular Carcinoma
44988	NTC1	Nonsyn.	Coding		Kidney	Renal Cell Carcinoma
49114	NTC1	Nonsyn.	Coding	EGF	Stomach	Gastric Cancer
57882	NTC1	Nonsyn.	Coding		Ovary	Ovarian Cancer
57918	NTC1	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
58713	NTC1	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
66106	NTC1	Nonsyn.	Coding		Colon	Colorectal Cancer
52351	NTRK1	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
52357	NTRK1	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
52908	NTRK1	Nonsyn.	Coding		Colon	Colorectal Cancer
52920	NTRK1	Nonsyn.	Coding		Colon	Colorectal Cancer
61207	NTRK1	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
61990	NTRK1	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
62729	NTRK1	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer

FIGURE 2 (CONTINUED)

58317	NTRK2	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
62561	NTRK2	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
62627	NTRK2	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Kidney	Renal Cell Carcinoma
19623	NTRK3	Nonsense	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
19635	NTRK3	Nonsyn.	Splice Site	Pkinase_Tyr, Pkinase I-set	Lung	Non-Small Cell Lung Cancer
42588	NTRK3		Splice Site		Skin	Melanoma
42699	NTRK3		Splice Site		Skin	Melanoma
42938	NTRK3	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Small Cell Lung Cancer
46920	NTRK3	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
48110	NTRK3	Nonsyn.	Coding		Colon	Colorectal Cancer
49517	NTRK3	Nonsyn.	Coding		Colon	Colorectal Cancer
51192	NTRK3	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
51450	NTRK3	Nonsyn.	Coding	LRRNT	Colon	Colorectal Cancer
56023	NTRK3	Nonsyn.	Coding		Skin	Melanoma
56795	NTRK3	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
57158	NTRK3	Nonsyn.	Splice Site		Lung	Non-Small Cell Lung Cancer
58980	NTRK3	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
60140	NTRK3	Nonsyn.	Coding		Kidney	Renal Cell Carcinoma
60311	NTRK3	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
62459	NTRK3	Nonsyn.	Coding		Kidney	Renal Cell Carcinoma
44095	OTUD1	Nonsyn.	Coding		Lung	Small Cell Lung Cancer
48113	OTUD1	Nonsyn.	Coding		Colon	Colorectal Cancer
49144	OTUD1	Nonsyn.	Coding		Colon	Colorectal Cancer
20093	PAK6	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer

FIGURE 2 (CONTINUED)

50778	PDGFRB	Nonsyn.	Coding	Pkinase_Tyr	Colon	Colorectal Cancer
50916	PDGFRB	Nonsyn.	Coding	Pkinase_Tyr,	Colon	Colorectal Cancer
				Pkinase		
55440	PDGFRB	Nonsyn.	Coding	Pkinase_Tyr,	Skin	Melanoma
				Pkinase		
57266	PDGFRB	Nonsyn.	Coding	Pkinase_Tyr,	Lung	Small Cell Lung Cancer
				Pkinase		
59089	PDGFRB		Splice Site		Kidney	Renal Cell Carcinoma
62978	PDGFRB	Nonsyn.	Coding	Pkinase_Tyr,	Kidney	Renal Cell Carcinoma
				Pkinase		
32048	PDK1		Splice Site		Lung	Non-Small Cell Lung Cancer
33706	PDK1	Nonsyn.	Coding	HATPase_c	Lung	Non-Small Cell Lung Cancer
42747	PIK3CA	Nonsyn.	Coding	PI3K_C2	Breast	Breast Cancer
50685	PIK3CA	Nonsyn.	Coding	PI3Ka	Colon	Colorectal Cancer
51456	PIK3CA	Syn.	Coding	PI3_P14_kinase	Colon	Colorectal Cancer
51750	PIK3CA	Nonsyn.	Coding	PI3_P14_kinase	Colon	Colorectal Cancer
51810	PIK3CA	Nonsyn.	Coding	PI3K_p85B	Stomach	Gastric Cancer
55527	PIK3CA	Syn.	Coding	PI3_P14_kinase	Skin	Melanoma
55858	PIK3CA	Nonsyn.	Coding		Colon Sigmoid,	Colorectal Cancer
					Rectum	
63813	PIK3CA	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
66964	PIK3CA	Nonsyn.	Coding	PI3_P14_kinase	Stomach	Gastric Cancer
47187	PIK3R1	Nonsyn.	Coding		Colon	Colorectal Cancer
48068	PIK3R1	Nonsense	Coding		Colon	Colorectal Cancer
49877	PIK3R1	Nonsyn.	Coding		Colon	Colorectal Cancer
50039	PIK3R1	Nonsyn.	Coding		Colon	Colorectal Cancer
50042	PIK3R1	Nonsyn.	Coding		Colon	Colorectal Cancer
50486	PIK3R1	Nonsyn.	Coding		Colon	Colorectal Cancer
50694	PIK3R1	Nonsense	Coding		Colon	Colorectal Cancer
51309	PIK3R1	Nonsyn.	Coding		Colon	Colorectal Cancer
51612	PIK3R1	Nonsyn.	Coding		Colon	Colorectal Cancer

FIGURE 2 (CONTINUED)

52429	PIK3R1	Nonsense	Coding	SH2	Colon	Colorectal Cancer
56185	PIK3R1	Nonsyn.	Coding		Pancreas	Pancreatic Cancer
56188	PIK3R1	Nonsyn.	Coding		Breast	Breast Cancer
66584	PIK3R1	Nonsyn.	Coding		Colon	Colorectal Cancer
71322	PIK3R1	Nonsyn.	Coding		Colon	Colorectal Cancer
67250	PIK3R2	Nonsyn.	Coding		Colon	Colorectal Cancer
67382	PIK3R4	Nonsyn.	Coding		Stomach	Gastric Cancer
67451	PIK3R4	Nonsyn.	Coding		Ovary	Ovarian Cancer
67331	PIK3R5	Nonsyn.	Coding		Stomach	Gastric Cancer
34015	PLK1	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
46956	PRKCB1	Nonsyn.	Coding		Colon	Colorectal Cancer
47232	PRKCB1	Nonsyn.	Coding		Skin	Melanoma
47421	PRKCB1	Nonsyn.	Coding	Pkinase_C	Colon	Colorectal Cancer
47652	PRKCB1	Nonsyn.	Coding	C1_1	Skin	Melanoma
48092	PRKCB1	Nonsyn.	Coding	Pkinase,	Colon	Colorectal Cancer
				Pkinase_Tyr		
48259	PRKCB1	Nonsyn.	Coding		Colon	Colorectal Cancer
61462	PRKCB1	Nonsyn.	Coding	Pkinase,	Lung	Non-Small Cell Lung Cancer
				Pkinase_Tyr		
55155	PRKCI	Nonsyn.	Coding	Pkinase,	Stomach	Gastric Cancer
				Pkinase_Tyr		
55401	PRKCI	Nonsyn.	Coding	Pkinase,	Colon	Colorectal Cancer
				Pkinase_Tyr		
55410	PRKCI	Nonsyn.	Coding	Pkinase,	Colon	Colorectal Cancer
56522	PRKCI	Nonsyn.	Coding	C1_1	Ovary	Ovarian Cancer
				Pkinase,		
				Pkinase_Tyr		
				Patched		
20448	PTCH	Nonsense	Coding		Lung	Non-Small Cell Lung Cancer
43144	PTCH	Nonsyn.	Coding		Ovary	Ovarian Cancer
44713	PTCH	Nonsyn.	Coding		Breast, Lung	Breast Cancer, Non-Small Cell Lung Cancer
50060	PTCH	Nonsyn.	Coding		Colon	Colorectal Cancer

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FIGURE 2 (CONTINUED)

51702	PTCH		Splice Site		Colon	Colorectal Cancer
52327	PTCH	Nonsyn.	Coding		Colon	Colorectal Cancer
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55557	PTCH	Nonsyn.	Coding		Liver	Hepatocellular Carcinoma
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56116	PTCH	Nonsense	Coding		Lung	Non-Small Cell Lung Cancer
57936	PTCH	Nonsyn.	Coding		Stomach	Gastric Cancer
66641	PTCH	Nonsense	Coding		Skin	Melanoma
66842	PTCH	Nonsyn.	Coding		Colon	Colorectal Cancer
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39546	PTEN		Coding		Lung	Non-Small Cell Lung Cancer
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55476	PTEN	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
60284	PTEN		Splice Site		Stomach	Gastric Cancer
62314	PTEN	Nonsense	Coding		Skin	Melanoma
66596	PTEN		Coding		Stomach	Gastric Cancer
66602	PTEN	Nonsense	Coding		Colon	Colorectal Cancer
66608	PTEN	Syn.	Coding		Skin	Melanoma
66611	PTEN	Syn.	Coding		Skin	Melanoma
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4377	RB1		Splice Site		Lung	Non-Small Cell Lung Cancer
16796	RB1		Splice Site		Lung	Non-Small Cell Lung Cancer
39300	Rem2		Coding		Lung	Non-Small Cell Lung Cancer
39768	Rem2		Coding		Lung	Non-Small Cell Lung Cancer
49348	RET	Nonsyn.	Coding		Colon	Colorectal Cancer
49808	RET	Nonsyn.	Coding		Colon	Colorectal Cancer
50366	RET	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer

FIGURE 2 (CONTINUED)

53324	RET	Nonsense	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
57074	RET	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
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61201	RET	Nonsyn.	Coding		Ovary	Ovarian Cancer
62750	RET	Nonsense	Coding		Lung	Non-Small Cell Lung Cancer
63699	RET	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
19605	RON	Nonsense	Coding	Pkinase_Tyr, Pkinase	Lung	Non-Small Cell Lung Cancer
50420	RON	Nonsyn.	Coding	Pkinase_Tyr, Pkinase	Colon	Colorectal Cancer
66566	RON		Coding		Colon	Colorectal Cancer
56158	SMAD2	Nonsyn.	Coding		Lung	Non-Small Cell Lung Cancer
20571	Stk6	Nonsense	Coding	Pkinase, Pkinase_Tyr	Lung	Non-Small Cell Lung Cancer
43237	SUFU	Nonsyn.	Coding	SUFU	Colon, Skin	Colorectal Cancer, Melanoma
57071	SUFU	Nonsyn.	Coding	SUFU	Stomach	Gastric Cancer
57110	SUFU	Nonsyn.	Coding	SUFU	Lung	Non-Small Cell Lung Cancer
34775	TGFB1	Nonsyn.	Coding	Pkinase	Lung	Non-Small Cell Lung Cancer
48340	TGFB1	Nonsyn.	Coding	Pkinase, Pkinase_Tyr	Lung	Non-Small Cell Lung Cancer

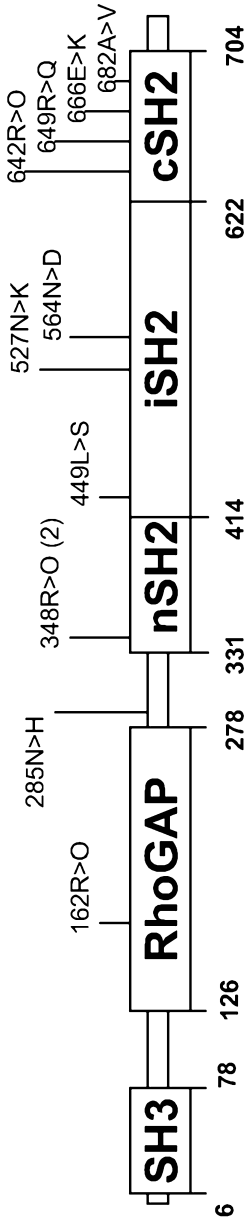
FIGURE 2 (CONTINUED)

48535	TGFB2		Coding		Breast, Colon, Kidney, Lung, Lung, Lymph Node, Lymph Node, Ovary, Urinary Bladder	Bladder Cancer, Breast Cancer, Colorectal Cancer, Non-Small Cell Lung Cancer, Ovarian Cancer, Renal Cell Carcinoma, Small Cell Lung Cancer
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4480	TP53	Nonsense	Coding	P53	Breast, Ovary	Breast Cancer, Ovarian Cancer
6188	TP53	Nonsyn.	Coding	P53	Lung	Non-Small Cell Lung Cancer
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9510	TP53		Splice Site		Lung	Non-Small Cell Lung Cancer
21243	TP53	Nonsense	Coding	P53	Lung	Non-Small Cell Lung Cancer
21252	TP53	Nonsyn.	Coding	P53	Lung	Non-Small Cell Lung Cancer
22224	TP53		Splice Site		Lung	Non-Small Cell Lung Cancer
34021	TP53		Splice Site		Lung	Non-Small Cell Lung Cancer
34054	TP53	Nonsyn.	Coding	P53	Lung	Non-Small Cell Lung Cancer
34078	TP53	Nonsense	Coding	P53	Lung	Non-Small Cell Lung Cancer
34081	TP53	Nonsyn.	Coding	P53	Lung	Non-Small Cell Lung Cancer
34123	TP53		Splice Site		Lung	Non-Small Cell Lung Cancer
40894	TP53		Coding	P53	Breast	Breast Cancer
40900	TP53		Coding	P53	Lung	Non-Small Cell Lung Cancer
40915	TP53		Coding	P53	Lung	Non-Small Cell Lung Cancer
40942	TP53		Coding	P53	Lung	Non-Small Cell Lung Cancer
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40966	TP53		Coding	P53_tetramer	Lung	Non-Small Cell Lung Cancer
40981	TP53		Coding	P53	Breast	Breast Cancer
40990	TP53		Coding	P53	Breast	Breast Cancer
41023	TP53		Coding	P53	Breast	Breast Cancer

FIGURE 2 (CONTINUED)

41047	TP53	Coding	Lung	Non-Small Cell Lung Cancer
41059	TP53	Coding	Lung	Non-Small Cell Lung Cancer
65679	TP53	Nonsyn.	Lung	Non-Small Cell Lung Cancer
68057	TP53	Nonsyn.	Lung	Small Cell Lung Cancer
44439	USP21	Nonsyn.	Lung	Small Cell Lung Cancer
47472	USP21	Nonsyn.	Colon	Colorectal Cancer
52917	USP21	Nonsense	Colon	Colorectal Cancer
57318	USP21	Nonsyn.	Kidney	Renal Cell Carcinoma
64414	USP21	Splice Site	Cecum	Colorectal Cancer
45826	USP24	Coding	Lung	Non-Small Cell Lung Cancer
45763	USP25	Splice Site	Lung	Non-Small Cell Lung Cancer
44782	USP28	Coding	Lung	Non-Small Cell Lung Cancer
47058	USP35	Coding	Colon	Colorectal Cancer
51994	USP35	Coding	Pancreas	Pancreatic Cancer
61276	USP35	Coding	Kidney	Renal Cell Carcinoma
62068	USP35	Coding	Stomach	Gastric Cancer
16805	VEGFR2	Coding	Lung	Non-Small Cell Lung Cancer
33675	VEGFR2	Coding	Kidney, Lung	Non-Small Cell Lung Cancer, Renal Cell Carcinoma
34093	VEGFR2	Coding	Lung	Non-Small Cell Lung Cancer
39732	VEGFR2	Coding	Breast	Breast Cancer
47112	VEGFR2	Coding	Skin	Melanoma
55762	VEGFR2	Coding	Lung	Small Cell Lung Cancer
59032	VEGFR2	Coding	Stomach	Gastric Cancer
60047	VEGFR2	Coding	Stomach	Gastric Cancer
		Pkinase_Tyr, Pkinase		
		Pkinase_Tyr, Pkinase		
		Pkinase_Tyr, Pkinase		

Somatic mutations in PIK3R1



Sample	p85 α (PIK3R1)	PTEN
Colon 1	HETSUB.285N>H, 527N>K, 564N>D	HETSUB.31N>H, 28I>M
Colon 2	HETSUB.162R>O, 666E>K	HETSUB.232R>O
Colon 3	HETSUB.642R>O	
Colon 4	HETSUB.348R>O	
Colon 5	HETSUB.348R>O, 574R>I	
Colon 6	HETSUB.682A>V	
Colon 7	HETSUB.649R>Q	
Breast	HETSUB.449L>S	

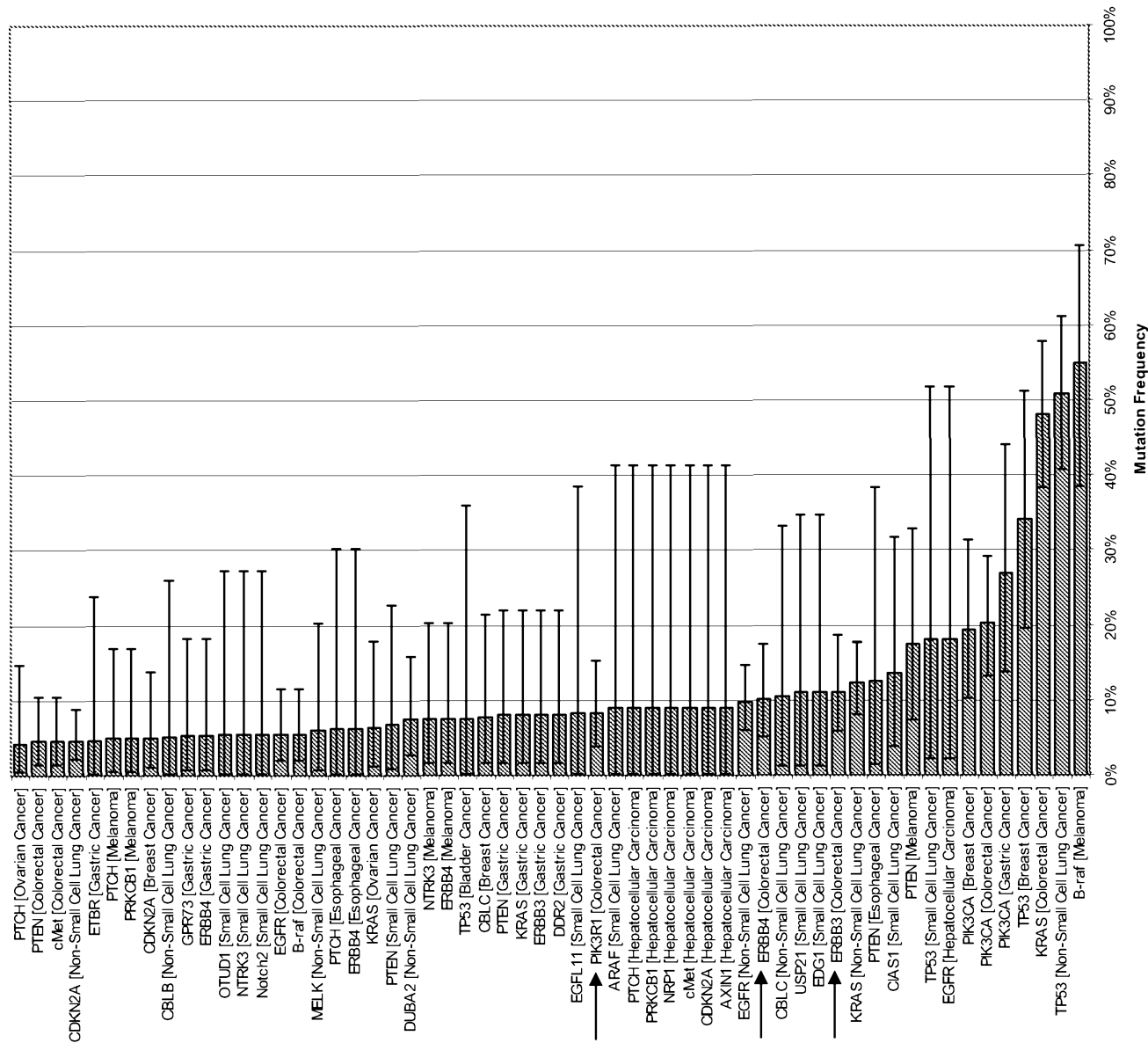
- 6.4% (7/108) of colorectal cancers have p85 α mutation
- 1.6% (1/62) of breast cancers have p85 α mutation

FIGURE 4

50/50

Gene-level Somatic
Mutation Frequencies
Across Diseases
($\geq 5\%$)

Mutation Frequency: % of samples
mutated
Diseases: ≥ 10 samples



2007329740 06 May 2009

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2007329740 06 May 2009

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Asp Gln Thr Leu Pro Pro Leu Asn Asn Phe Ser Val Ala Glu Cys
50 55 60

Gln Leu Met Lys Thr Glu Arg Pro Arg Pro Asn Thr Phe Val Ile
65 70 75

Arg Cys Leu Gln Trp Thr Thr Val Ile Glu Arg Thr Phe His Val
80 85 90

Asp Ser Pro Asp Glu Arg Glu Glu Trp Met Arg Ala Ile Gln Met
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Val Ala Asn Ser Leu Lys Gln Arg Ala Pro Gly Glu Asp Pro Met
110 115 120

Asp Tyr Lys Cys Gly Ser Pro Ser Asp Ser Ser Thr Thr Glu Glu
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Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys
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170 175 180

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His Thr Val Thr Glu Ser Arg Val Leu Gln Asn Thr Arg His Pro
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Ser	Leu	Glu	Ser	Pro	Thr	Asn	Met	Pro	Ser	Pro	Ser	Pro	Asp	Tyr
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Phe	Thr	Trp	Asn	Leu	Thr	Trp	Ile	Met	Lys	Asp	Ser	Phe	Pro	Phe
				245					250					255
Leu	Ser	His	Arg	Ser	Arg	Tyr	Gly	Leu	Glu	Cys	Ser	Phe	Asp	Phe
				260					265					270
Pro	Cys	Glu	Leu	Glu	Tyr	Ser	Pro	Pro	Leu	His	Asp	Leu	Arg	Asn
				275					280					285
Gln	Ser	Trp	Ser	Trp	Arg	Arg	Ile	Pro	Ser	Glu	Glu	Ala	Ser	Gln
				290					295					300
Met	Asp	Leu	Leu	Asp	Gly	Pro	Gly	Ala	Glu	Arg	Ser	Lys	Glu	Met
				305					310					315
Pro	Arg	Gly	Ser	Phe	Leu	Leu	Leu	Asn	Thr	Ser	Ala	Asp	Ser	Lys
				320					325					330
His	Thr	Ile	Leu	Ser	Pro	Trp	Met	Arg	Ser	Ser	Ser	Glu	His	Cys
				335					340					345
Thr	Leu	Ala	Val	Ser	Val	His	Arg	His	Leu	Gln	Pro	Ser	Gly	Arg
				350					355					360
Tyr	Ile	Ala	Gln	Leu	Leu	Pro	His	Asn	Glu	Ala	Ala	Arg	Glu	Ile
				365					370					375
Leu	Leu	Met	Pro	Thr	Pro	Gly	Lys	His	Gly	Trp	Thr	Val	Leu	Gln
				380					385					390
Gly	Arg	Ile	Gly	Arg	Pro	Asp	Asn	Pro	Phe	Arg	Val	Ala	Leu	Glu
				395					400					405
Tyr	Ile	Ser	Ser	Gly	Asn	Arg	Ser	Leu	Ser	Ala	Val	Asp	Phe	Phe
				410					415					420

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

1100		1105		1110
Val Pro Arg Lys Asn Ile Thr Leu Ile Arg Gly Leu Gly His Gly	1115	1120		1125
Ala Phe Gly Glu Val Tyr Glu Gly Gln Val Ser Gly Met Pro Asn	1130	1135		1140
Asp Pro Ser Pro Leu Gln Val Ala Val Lys Thr Leu Pro Glu Val	1145	1150		1155
Cys Ser Glu Gln Asp Glu Leu Asp Phe Leu Met Glu Ala Leu Ile	1160	1165		1170
Ile Ser Lys Phe Asn His Gln Asn Ile Val Arg Cys Ile Gly Val	1175	1180		1185
Ser Leu Gln Ser Leu Pro Arg Phe Ile Leu Leu Glu Leu Met Ala	1190	1195		1200
Gly Gly Asp Leu Lys Ser Phe Leu Arg Glu Thr Arg Pro Arg Pro	1205	1210		1215
Ser Gln Pro Ser Ser Leu Ala Met Leu Asp Leu Leu His Val Ala	1220	1225		1230
Arg Asp Ile Ala Cys Gly Cys Gln Tyr Leu Glu Glu Asn His Phe	1235	1240		1245
Ile His Arg Asp Ile Ala Ala Arg Asn Cys Leu Leu Thr Cys Pro	1250	1255		1260
Gly Pro Gly Arg Val Ala Lys Ile Gly Asp Phe Gly Met Ala Arg	1265	1270		1275
Asp Ile Tyr Arg Ala Ser Tyr Tyr Arg Lys Gly Gly Cys Ala Met	1280	1285		1290
Leu Pro Val Lys Trp Met Pro Pro Glu Ala Phe Met Glu Gly Ile	1295	1300		1305
Phe Thr Ser Lys Thr Asp Thr Trp Ser Phe Gly Val Leu Leu Trp	1310	1315		1320
Glu Ile Phe Ser Leu Gly Tyr Met Pro Tyr Pro Ser Lys Ser Asn	1325	1330		1335
Gln Glu Val Leu Glu Phe Val Thr Ser Gly Gly Arg Met Asp Pro	1340	1345		1350
Pro Lys Asn Cys Pro Gly Pro Val Tyr Arg Ile Met Thr Gln Cys	1355	1360		1365
Trp Gln His Gln Pro Glu Asp Arg Pro Asn Phe Ala Ile Ile Leu	1370	1375		1380
Glu Arg Ile Glu Tyr Cys Thr Gln Asp Pro Asp Val Ile Asn Thr	1385	1390		1395
Ala Leu Pro Ile Glu Tyr Gly Pro Leu Val Glu Glu Glu Glu Lys	1400	1405		1410
Val Pro Val Arg Pro Lys Asp Pro Glu Gly Val Pro Pro Leu Leu	1415	1420		1425
Val Ser Gln Gln Ala Lys Arg Glu Glu Glu Arg Ser Pro Ala Ala	1430	1435		1440

P2490R1SEQ.txt

Pro Pro Pro Leu Pro Thr Thr Ser Ser Gly Lys Ala Ala Lys Lys
 1445 1450 1455
 Pro Thr Ala Ala Glu Val Ser Val Arg Val Pro Arg Gly Pro Ala
 1460 1465 1470
 Val Glu Gly Gly His Val Asn Met Ala Phe Ser Gln Ser Asn Pro
 1475 1480 1485
 Pro Ser Glu Leu His Arg Val His Gly Ser Arg Asn Lys Pro Thr
 1490 1495 1500
 Ser Leu Trp Asn Pro Thr Tyr Gly Ser Trp Phe Thr Glu Lys Pro
 1505 1510 1515
 Thr Lys Lys Asn Asn Pro Ile Ala Lys Lys Glu Pro His Glu Arg
 1520 1525 1530
 Gly Asn Leu Gly Leu Glu Gly Ser Cys Thr Val Pro Pro Asn Val
 1535 1540 1545
 Ala Thr Gly Arg Leu Pro Gly Ala Ser Leu Leu Leu Glu Pro Ser
 1550 1555 1560
 Ser Leu Thr Ala Asn Met Lys Glu Val Pro Leu Phe Arg Leu Arg
 1565 1570 1575
 His Phe Pro Cys Gly Asn Val Asn Tyr Gly Tyr Gln Gln Gln Gly
 1580 1585 1590
 Leu Pro Leu Glu Ala Ala Thr Ala Pro Gly Ala Gly His Tyr Glu
 1595 1600 1605
 Asp Thr Ile Leu Lys Ser Lys Asn Ser Met Asn Gln Pro Gly Pro
 1610 1615 1620

<210> 82
 <211> 606
 <212> PRT
 <213> Homo sapiens

<400> 82
 Met Glu Pro Pro Arg Gly Pro Pro Ala Asn Gly Ala Glu Pro Ser
 1 5 10 15
 Arg Ala Val Gly Thr Val Lys Val Tyr Leu Pro Asn Lys Gln Arg
 20 25 30
 Thr Val Val Thr Val Arg Asp Gly Met Ser Val Tyr Asp Ser Leu
 35 40 45
 Asp Lys Ala Leu Lys Val Arg Gly Leu Asn Gln Asp Cys Cys Val
 50 55 60
 Val Tyr Arg Leu Ile Lys Gly Arg Lys Thr Val Thr Ala Trp Asp
 65 70 75
 Thr Ala Ile Ala Pro Leu Asp Gly Glu Glu Leu Ile Val Glu Val
 80 85 90
 Leu Glu Asp Val Pro Leu Thr Met His Asn Phe Val Arg Lys Thr
 95 100 105
 Phe Phe Ser Leu Ala Phe Cys Asp Phe Cys Leu Lys Phe Leu Phe
 110 115 120
 His Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Gln His
 125 130 135

P2490R1SEQ.txt

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

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	470		475		480
Gln Asp Pro Asn	Pro 485	Tyr Ser Phe Gln	Ser 490	Asp Val Tyr Ala	Tyr 495
Gly Val Val Leu	Tyr 500	Glu Leu Met Thr	Gly 505	Ser Leu Pro Tyr	Ser 510
His Ile Gly Cys	Arg 515	Asp Gln Ile Ile	Phe 520	Met Val Gly Arg	Gly 525
Tyr Leu Ser Pro	Asp 530	Leu Ser Lys Ile	Ser 535	Ser Asn Cys Pro	Lys 540
Ala Met Arg Arg	Leu 545	Leu Ser Asp Cys	Leu 550	Lys Phe Gln Arg	Glu 555
Glu Arg Pro Leu	Phe 560	Pro Gln Ile Leu	Ala 565	Thr Ile Glu Leu	Leu 570
Gln Arg Ser Leu	Pro 575	Lys Ile Glu Arg	Ser 580	Ala Ser Glu Pro	Ser 585
Leu His Arg Thr	Gln 590	Ala Asp Glu Leu	Pro 595	Ala Cys Leu Leu	Ser 600
Ala Ala Arg Leu	Val 605	Pro			

<210> 83
 <211> 911
 <212> PRT
 <213> Homo sapiens

<400> 83
 Met Gly Pro Asp Arg Ala Ala Pro Leu Arg Glu Pro Gly Pro Gly
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 Ser Arg His His Arg Ala Arg Asp Arg Leu Ile His Phe Gly Ala
 20 25 30
 Val Ser Thr Asp Val Leu Gly Cys Ser Ala His Cys Ser Leu Thr
 35 40 45
 Gln Ser Pro Lys Met Asn Ile Gln Glu Gln Gly Phe Pro Leu Asp
 50 55 60
 Leu Gly Ala Ser Phe Thr Glu Asp Ala Pro Arg Pro Pro Val Pro
 65 70 75
 Gly Glu Glu Gly Glu Leu Val Ser Thr Asp Pro Arg Pro Ala Ser
 80 85 90
 Tyr Ser Phe Cys Ser Gly Lys Gly Val Gly Ile Lys Gly Glu Thr
 95 100 105
 Ser Thr Ala Thr Pro Arg Arg Ser Asp Leu Asp Leu Gly Tyr Glu
 110 115 120
 Pro Glu Gly Ser Ala Ser Pro Thr Pro Pro Tyr Leu Lys Trp Ala
 125 130 135
 Glu Ser Leu His Ser Leu Leu Asp Asp Gln Asp Gly Ile Ser Leu
 140 145 150
 Phe Arg Thr Phe Leu Lys Gln Glu Gly Cys Ala Asp Leu Leu Asp
 155 160 165

P2490R1SEQ.txt

Phe	Trp	Phe	Ala	Cys	Thr	Gly	Phe	Arg	Lys	Leu	Glu	Pro	Cys	Asp
				170					175					180
Ser	Asn	Glu	Glu	Lys	Arg	Leu	Lys	Leu	Ala	Arg	Ala	Ile	Tyr	Arg
				185					190					195
Lys	Tyr	Ile	Leu	Asp	Asn	Asn	Gly	Ile	Val	Ser	Arg	Gln	Thr	Lys
				200					205					210
Pro	Ala	Thr	Lys	Ser	Phe	Ile	Lys	Gly	Cys	Ile	Met	Lys	Gln	Leu
				215					220					225
Ile	Asp	Pro	Ala	Met	Phe	Asp	Gln	Ala	Gln	Thr	Glu	Ile	Gln	Ala
				230					235					240
Thr	Met	Glu	Glu	Asn	Thr	Tyr	Pro	Ser	Phe	Leu	Lys	Ser	Asp	Ile
				245					250					255
Tyr	Leu	Glu	Tyr	Thr	Arg	Thr	Gly	Ser	Glu	Ser	Pro	Lys	Val	Cys
				260					265					270
Ser	Asp	Gln	Ser	Ser	Gly	Ser	Gly	Thr	Gly	Lys	Gly	Ile	Ser	Gly
				275					280					285
Tyr	Leu	Pro	Thr	Leu	Asn	Glu	Asp	Glu	Glu	Trp	Lys	Cys	Asp	Gln
				290					295					300
Asp	Met	Asp	Glu	Asp	Asp	Gly	Arg	Asp	Ala	Ala	Pro	Pro	Gly	Arg
				305					310					315
Leu	Pro	Gln	Lys	Leu	Leu	Leu	Glu	Thr	Ala	Ala	Pro	Arg	Val	Ser
				320					325					330
Ser	Ser	Arg	Arg	Tyr	Ser	Glu	Gly	Arg	Glu	Phe	Arg	Tyr	Gly	Ser
				335					340					345
Trp	Arg	Glu	Pro	Val	Asn	Pro	Tyr	Tyr	Val	Asn	Ala	Gly	Tyr	Ala
				350					355					360
Leu	Ala	Pro	Ala	Thr	Ser	Ala	Asn	Asp	Ser	Glu	Gln	Gln	Ser	Leu
				365					370					375
Ser	Ser	Asp	Ala	Asp	Thr	Leu	Ser	Leu	Thr	Asp	Ser	Ser	Val	Asp
				380					385					390
Gly	Ile	Pro	Pro	Tyr	Arg	Ile	Arg	Lys	Gln	His	Arg	Arg	Glu	Met
				395					400					405
Gln	Glu	Ser	Val	Gln	Val	Asn	Gly	Arg	Val	Pro	Leu	Pro	His	Ile
				410					415					420
Pro	Arg	Thr	Tyr	Arg	Val	Pro	Lys	Glu	Val	Arg	Val	Glu	Pro	Gln
				425					430					435
Lys	Phe	Ala	Glu	Glu	Leu	Ile	His	Arg	Leu	Glu	Ala	Val	Gln	Arg
				440					445					450
Thr	Arg	Glu	Ala	Glu	Glu	Lys	Leu	Glu	Glu	Arg	Leu	Lys	Arg	Val
				455					460					465
Arg	Met	Glu	Glu	Glu	Gly	Glu	Asp	Gly	Asp	Pro	Ser	Ser	Gly	Pro
				470					475					480
Pro	Gly	Pro	Cys	His	Lys	Leu	Pro	Pro	Ala	Pro	Ala	Trp	His	His
				485					490					495
Phe	Pro	Pro	Arg	Cys	Val	Asp	Met	Gly	Cys	Ala	Gly	Leu	Arg	Asp
				500					505					510

P2490R1SEQ.txt

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

P2490R1SEQ.txt

	845		850		855
Leu Gly Gln Phe	Lys 860	Glu Leu Leu Thr	Lys 865	Lys Gly Ser Tyr	Arg 870
Tyr Tyr Phe Lys	Lys 875	Val Ser Asp Glu	Phe 880	Asp Cys Gly Val	Val 885
Phe Glu Glu Val	Arg 890	Glu Asp Glu Ala	Val 895	Leu Pro Val Phe	Glu 900
Glu Lys Ile Ile	Gly 905	Lys Val Glu Lys	Val 910	Asp	

<210> 84
 <211> 843
 <212> PRT
 <213> Homo sapiens

<400> 84

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Thr Glu Pro Gly Leu Ala Leu Pro Ala Arg Glu Gly Gly Ala Pro
 590 595 600
 Gly Gly Ala Gly Ala Leu Gln Leu Pro Arg Glu Glu Gly Asp Arg
 605 610 615
 Ser Gln Asp Val Trp Gln Trp Met Leu Glu Ser Glu Arg Gln Ser
 620 625 630
 Lys Pro Lys Pro His Ser Ala Gln Ser Thr Lys Lys Ala Tyr Pro
 635 640 645
 Leu Glu Ser Ala Arg Ser Ser Pro Gly Glu Arg Ala Ser Arg His
 650 655 660
 His Leu Trp Gly Gly Asn Ser Gly His Pro Arg Thr Thr Pro Arg
 665 670 675
 Ala His Leu Phe Thr Gln Asp Pro Ala Met Pro Pro Leu Thr Pro
 680 685 690
 Pro Asn Thr Leu Ala Gln Leu Glu Glu Ala Cys Arg Arg Leu Ala
 695 700 705
 Glu Val Ser Lys Pro Pro Lys Gln Arg Cys Cys Val Ala Ser Gln
 710 715 720
 Gln Arg Asp Arg Asn His Ser Ala Thr Val Gln Thr Gly Ala Thr
 725 730 735
 Pro Phe Ser Asn Pro Ser Leu Ala Pro Glu Asp His Lys Glu Pro
 740 745 750
 Lys Lys Leu Ala Gly Val His Ala Leu Gln Ala Ser Glu Leu Val
 755 760 765
 Val Thr Tyr Phe Phe Cys Gly Glu Glu Ile Pro Tyr Arg Arg Met
 770 775 780
 Leu Lys Ala Gln Ser Leu Thr Leu Gly His Phe Lys Glu Gln Leu
 785 790 795
 Ser Lys Lys Gly Asn Tyr Arg Tyr Tyr Phe Lys Lys Ala Ser Asp
 800 805 810
 Glu Phe Ala Cys Gly Ala Val Phe Glu Glu Ile Trp Glu Asp Glu
 815 820 825
 Thr Val Leu Pro Met Tyr Glu Gly Arg Ile Leu Gly Lys Val Glu
 830 835 840

Arg Ile Asp

<210> 85
 <211> 894
 <212> PRT
 <213> Homo sapiens

<400> 85
 Met Ala Trp Arg Cys Pro Arg Met Gly Arg Val Pro Leu Ala Trp
 1 5 10 15

Cys Leu Ala Leu Cys Gly Trp Ala Cys Met Ala Pro Arg Gly Thr
 20 25 30

Gln Ala Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn Ile Thr

P2490R1SEQ.txt

	35		40		45
Gly	Ala	Arg	Gly	Leu	Thr
	50			55	
Gln	Gly	Glu	Pro	Pro	Glu
	65			70	
Leu	Glu	Leu	Ala	Asp	Ser
	80			85	
Asp	Glu	Gln	Asp	Asp	Trp
	95			100	
Ser	Leu	Gln	Leu	Ser	Asp
	110			115	
Leu	Gly	His	Gln	Thr	Phe
	125			130	
Glu	Gly	Leu	Pro	Tyr	Phe
	140			145	
Ala	Ala	Asn	Thr	Pro	Phe
	155			160	
Pro	Glu	Pro	Val	Asp	Leu
	170			175	
Ala	Thr	Ala	Pro	Gly	His
	185			190	
Gly	Leu	Asn	Lys	Thr	Ser
	200			205	
Lys	Gly	Val	Thr	Thr	Ser
	215			220	
Gln	Gln	Pro	Arg	Asn	Leu
	230			235	
Leu	Glu	Val	Ala	Trp	Thr
	245			250	
Thr	His	Cys	Thr	Leu	Gln
	260			265	
Ile	Gln	Ala	Gly	Glu	Pro
	275			280	
Gln	Ala	Ser	Val	Pro	Pro
	290			295	
Pro	His	Thr	Pro	Tyr	His
	305			310	
Gly	Pro	Ser	Ser	Trp	Thr
	320			325	
Gly	Val	Pro	Leu	Gly	Pro
	335			340	
Gly	Ser	Gln	Ala	Phe	Val
	350			355	
Gln	Gly	Thr	Leu	Leu	Gly
	365			370	

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ser Phe
 725 730 735
 Gly Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr Pro Tyr
 740 745 750
 Pro Gly Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln Gly
 755 760 765
 Asn Arg Leu Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala
 770 775 780
 Leu Met Ser Arg Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser
 785 790 795
 Phe Thr Glu Leu Arg Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu
 800 805 810
 Pro Pro Ala Gln Glu Pro Asp Glu Ile Leu Tyr Val Asn Met Asp
 815 820 825
 Glu Gly Gly Gly Tyr Pro Glu Pro Pro Gly Ala Ala Gly Gly Ala
 830 835 840
 Asp Pro Pro Thr Gln Pro Asp Pro Lys Asp Ser Cys Ser Cys Leu
 845 850 855
 Thr Ala Ala Glu Val His Pro Ala Gly Arg Tyr Val Leu Cys Pro
 860 865 870
 Ser Thr Thr Pro Ser Pro Ala Gln Pro Ala Asp Arg Gly Ser Pro
 875 880 885
 Ala Ala Pro Gly Gln Glu Asp Gly Ala
 890

<210> 86
 <211> 218
 <212> PRT
 <213> Homo sapiens

<400> 86
 Met Asp Gly Ser Gly Glu Gln Pro Arg Gly Gly Gly Pro Thr Ser
 1 5 10 15
 Ser Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe
 20 25 30
 Ile Gln Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu
 35 40 45
 Ala Leu Asp Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser
 50 55 60
 Glu Cys Leu Lys Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu
 65 70 75
 Leu Gln Arg Met Ile Ala Ala Val Asp Thr Asp Ser Pro Arg Glu
 80 85 90
 Val Phe Phe Arg Val Ala Ala Asp Met Phe Ser Asp Gly Asn Phe
 95 100 105
 Asn Trp Gly Arg Val Val Ala Leu Phe Tyr Phe Ala Ser Lys Leu
 110 115 120
 Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr
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P2490R1SEQ.txt

125		130	135
Ile Met Gly Trp Thr	Leu Asp Phe Leu Arg Glu Arg Leu Leu Gly		
140	145		150
Trp Ile Gln Asp Gln	Gly Gly Trp Val Arg Leu Leu Lys Pro Pro		
155	160		165
His Pro His His Arg	Ala Leu Thr Thr Ala Pro Ala Pro Pro Ser		
170	175		180
Leu Pro Pro Ala Thr	Pro Leu Gly Pro Trp Ala Phe Trp Ser Arg		
185	190		195
Ser Gln Trp Cys Pro	Leu Pro Ile Phe Arg Ser Ser Asp Val Val		
200	205		210
Tyr Asn Ala Phe Ser	Leu Arg Val		
215			

<210> 87
 <211> 233
 <212> PRT
 <213> Homo sapiens

<400> 87
 Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe Leu Ser Tyr
 1 5 10 15
 Lys Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser Asp Val
 20 25 30
 Glu Glu Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu Met
 35 40 45
 Glu Thr Pro Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala
 50 55 60
 Asp Ser Pro Ala Val Asn Gly Ala Thr Gly His Ser Ser Ser Leu
 65 70 75
 Asp Ala Arg Glu Val Ile Pro Met Ala Ala Val Lys Gln Ala Leu
 80 85 90
 Arg Glu Ala Gly Asp Glu Phe Glu Leu Arg Tyr Arg Arg Ala Phe
 95 100 105
 Ser Asp Leu Thr Ser Gln Leu His Ile Thr Pro Gly Thr Ala Tyr
 110 115 120
 Gln Ser Phe Glu Gln Val Val Asn Glu Leu Phe Arg Asp Gly Val
 125 130 135
 Asn Trp Gly Arg Ile Val Ala Phe Phe Ser Phe Gly Gly Ala Leu
 140 145 150
 Cys Val Glu Ser Val Asp Lys Glu Met Gln Val Leu Val Ser Arg
 155 160 165
 Ile Ala Ala Trp Met Ala Thr Tyr Leu Asn Asp His Leu Glu Pro
 170 175 180
 Trp Ile Gln Glu Asn Gly Gly Trp Asp Thr Phe Val Glu Leu Tyr
 185 190 195
 Gly Asn Asn Ala Ala Ala Glu Ser Arg Lys Gly Gln Glu Arg Phe
 200 205 210

P2490R1SEQ.txt

Asn Arg Trp Phe Leu Thr Gly Met Thr Val Ala Gly Val Val Leu
215 220 225

Leu Gly Ser Leu Phe Ser Arg Lys
230

<210> 88
<211> 766
<212> PRT
<213> Homo sapiens

<400> 88
Met Ala Ala Leu Ser Gly Gly Gly Gly Gly Gly Ala Glu Pro Gly
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Gln Ala Leu Phe Asn Gly Asp Met Glu Pro Glu Ala Gly Ala Gly
20 25 30
Ala Gly Ala Ala Ala Ser Ser Ala Ala Asp Pro Ala Ile Pro Glu
35 40 45
Glu Val Trp Asn Ile Lys Gln Met Ile Lys Leu Thr Gln Glu His
50 55 60
Ile Glu Ala Leu Leu Asp Lys Phe Gly Gly Glu His Asn Pro Pro
65 70 75
Ser Ile Tyr Leu Glu Ala Tyr Glu Glu Tyr Thr Ser Lys Leu Asp
80 85 90
Ala Leu Gln Gln Arg Glu Gln Gln Leu Leu Glu Ser Leu Gly Asn
95 100 105
Gly Thr Asp Phe Ser Val Ser Ser Ser Ala Ser Met Asp Thr Val
110 115 120
Thr Ser Ser Ser Ser Ser Ser Leu Ser Val Leu Pro Ser Ser Leu
125 130 135
Ser Val Phe Gln Asn Pro Thr Asp Val Ala Arg Ser Asn Pro Lys
140 145 150
Ser Pro Gln Lys Pro Ile Val Arg Val Phe Leu Pro Asn Lys Gln
155 160 165
Arg Thr Val Val Pro Ala Arg Cys Gly Val Thr Val Arg Asp Ser
170 175 180
Leu Lys Lys Ala Leu Met Met Arg Gly Leu Ile Pro Glu Cys Cys
185 190 195
Ala Val Tyr Arg Ile Gln Asp Gly Glu Lys Lys Pro Ile Gly Trp
200 205 210
Asp Thr Asp Ile Ser Trp Leu Thr Gly Glu Glu Leu His Val Glu
215 220 225
Val Leu Glu Asn Val Pro Leu Thr Thr His Asn Phe Val Arg Lys
230 235 240
Thr Phe Phe Thr Leu Ala Phe Cys Asp Phe Cys Arg Lys Leu Leu
245 250 255
Phe Gln Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Gln
260 265 270
Arg Cys Ser Thr Glu Val Pro Leu Met Cys Val Asn Tyr Asp Gln
275 280 285

P2490R1SEQ.txt

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

P2490R1SEQ.txt

	620		625		630
Asn Pro Tyr Ser	Phe Gln Ser Asp Val	Tyr Ala Phe Gly Ile	Val		
	635	640		645	
Leu Tyr Glu Leu	Met Thr Gly Gln Leu	Pro Tyr Ser Asn Ile	Asn		
	650	655	660		
Asn Arg Asp Gln	Ile Ile Phe Met Val	Gly Arg Gly Tyr Leu	Ser		
	665	670	675		
Pro Asp Leu Ser	Lys Val Arg Ser Asn	Cys Pro Lys Ala Met	Lys		
	680	685	690		
Arg Leu Met Ala	Glu Cys Leu Lys Lys	Lys Arg Asp Glu Arg	Pro		
	695	700	705		
Leu Phe Pro Gln	Ile Leu Ala Ser Ile	Glu Leu Leu Ala Arg	Ser		
	710	715	720		
Leu Pro Lys Ile	His Arg Ser Ala Ser	Glu Pro Ser Leu Asn	Arg		
	725	730	735		
Ala Gly Phe Gln	Thr Glu Asp Phe Ser	Leu Tyr Ala Cys Ala	Ser		
	740	745	750		
Pro Lys Thr Pro	Ile Gln Ala Gly Gly	Tyr Gly Ala Phe Pro	Val		
	755	760	765		

His

<210> 89
 <211> 906
 <212> PRT
 <213> Homo sapiens

<400> 89
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 20 25 30
 Asp Ala Phe Gln Pro His His His His His His His Leu Ser Pro
 35 40 45
 His Pro Pro Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp
 50 55 60
 Lys Leu Met Asp Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu
 65 70 75
 Ala Leu Lys Asn Ser Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp
 80 85 90
 Thr Tyr Gln His Leu Arg Thr Ile Leu Ser Arg Tyr Glu Gly Lys
 95 100 105
 Met Glu Thr Leu Gly Glu Asn Glu Tyr Phe Arg Val Phe Met Glu
 110 115 120
 Asn Leu Met Lys Lys Thr Lys Gln Thr Ile Ser Leu Phe Lys Glu
 125 130 135
 Gly Lys Glu Arg Met Tyr Glu Glu Asn Ser Gln Pro Arg Arg Asn
 140 145 150

P2490R1SEQ.txt

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

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P2490R1SEQ.txt

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

P2490R1SEQ.txt

830		835		840
Gln Gln Gly Ser Gly	Pro Ala Ala Ser	Ala Ala Thr Ala Ser	Pro	
845		850		855
Gln Leu Ser Ser Glu	Ile Glu Asn Leu Met	Ser Gln Gly Tyr Ser		
860		865		870
Tyr Gln Asp Ile Gln	Lys Ala Leu Val Ile	Ala Gln Asn Asn Ile		
875		880		885
Glu Met Ala Lys Asn	Ile Leu Arg Glu Phe	Val Ser Ile Ser Ser		
890		895		900

Pro Ala His Val Ala Thr
905

<210> 90
<211> 982
<212> PRT
<213> Homo sapiens

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

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P2490R1SEQ.txt

	905		910		915
Glu Ile His His	Arg 920	Lys Pro His Gly	Pro 925	Glu Ala Ala Leu	Glu 930
Asn Val Asp Ala	Lys 935	Ile Ala Lys Leu	Met 940	Gly Glu Gly Tyr	Ala 945
Phe Glu Glu Val	Lys 950	Arg Ala Leu Glu	Ile 955	Ala Gln Asn Asn	Val 960
Glu Val Ala Arg	Ser 965	Ile Leu Arg Glu	Phe 970	Ala Phe Pro Pro	Pro 975
Val Ser Pro Arg	Leu 980	Asn Leu			

<210> 91
 <211> 474
 <212> PRT
 <213> Homo sapiens

<400> 91

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

P2490R1SEQ.txt

Lys Asn Trp Gln Leu Leu Ala Val Thr His Pro Gly Tyr Met Ala
230 235 240

Phe Leu Thr Tyr Asp Glu Val Gln Glu Arg Leu Gln Ala Cys Arg
245 250 255

Asp Lys Pro Gly Ser Tyr Ile Phe Arg Pro Ser Cys Thr Arg Leu
260 265 270

Gly Gln Trp Ala Ile Gly Tyr Val Ser Ser Asp Gly Ser Ile Leu
275 280 285

Gln Thr Ile Pro Ala Asn Lys Pro Leu Ser Gln Val Leu Leu Glu
290 295 300

Gly Gln Lys Asp Gly Phe Tyr Leu Tyr Pro Asp Gly Lys Thr His
305 310 315

Asn Pro Asp Leu Thr Glu Leu Gly Gln Ala Glu Pro Gln Gln Arg
320 325 330

Ile His Val Ser Glu Glu Gln Leu Gln Leu Tyr Trp Ala Met Asp
335 340 345

Ser Thr Phe Glu Leu Cys Lys Ile Cys Ala Glu Ser Asn Lys Asp
350 355 360

Val Lys Ile Glu Pro Cys Gly His Leu Leu Cys Ser Cys Cys Leu
365 370 375

Ala Ala Trp Gln His Ser Asp Ser Gln Thr Cys Pro Phe Cys Arg
380 385 390

Cys Glu Ile Lys Gly Trp Glu Ala Val Ser Ile Tyr Gln Phe Tyr
395 400 405

Gly Gln Ala Thr Ala Glu Asp Ser Gly Asn Ser Ser Asp Gln Glu
410 415 420

Gly Arg Glu Leu Glu Leu Gly Gln Val Pro Leu Ser Ala Pro Pro
425 430 435

Leu Pro Pro Arg Pro Asp Leu Pro Pro Arg Lys Pro Arg Asn Ala
440 445 450

Gln Pro Lys Val Arg Leu Leu Lys Gly Asn Ser Pro Pro Ala Ala
455 460 465

Leu Gly Pro Gln Asp Pro Ala Pro Ala
470

<210> 92
<211> 173
<212> PRT
<213> Homo sapiens

<400> 92
Met Gly Arg Gly Arg Cys Val Gly Pro Ser Leu Gln Leu Arg Gly
1 5 10 15

Gln Glu Trp Arg Cys Ser Pro Leu Val Pro Lys Gly Gly Ala Ala
20 25 30

Ala Ala Glu Leu Gly Pro Gly Gly Gly Glu Asn Met Val Arg Arg
35 40 45

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

P2490R1SEQ.txt

Val Arg Val Phe Val Val His Ile Pro Arg Leu Thr Gly Glu Trp
65 70 75
Ala Ala Pro Gly Ala Pro Ala Ala Val Ala Leu Val Leu Met Leu
80 85 90
Leu Arg Ser Gln Arg Leu Gly Gln Gln Pro Leu Pro Arg Arg Pro
95 100 105
Gly His Asp Asp Gly Gln Arg Pro Ser Gly Gly Ala Ala Ala Ala
110 115 120
Pro Arg Arg Gly Ala Gln Leu Arg Arg Pro Arg His Ser His Pro
125 130 135
Thr Arg Ala Arg Arg Cys Pro Gly Gly Leu Pro Gly His Ala Gly
140 145 150
Gly Ala Ala Pro Gly Arg Gly Ala Ala Gly Arg Ala Arg Cys Leu
155 160 165
Gly Pro Ser Ala Arg Gly Pro Gly
170

<210> 93
<211> 156
<212> PRT
<213> Homo sapiens

<400> 93
Met Glu Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp
1 5 10 15
Leu Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala
20 25 30
Leu Leu Glu Ala Gly Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly
35 40 45
Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala
50 55 60
Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro
65 70 75
Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe
80 85 90
Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp
95 100 105
Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Glu
110 115 120
Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala Ala Gly
125 130 135
Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu Gly
140 145 150
Pro Ser Asp Ile Pro Asp
155

<210> 94
<211> 1036
<212> PRT
<213> Homo sapiens

P2490R1SEQ.txt

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<400> 94
Met 1 Lys Met Ala Ser 5 Thr Arg Cys Lys Leu 10 Ala Arg Tyr Leu Glu 15
Asp Leu Glu Asp Val 20 Asp Leu Lys Lys Phe 25 Lys Met His Leu Glu 30
Asp Tyr Pro Pro Gln 35 Lys Gly Cys Ile Pro 40 Leu Pro Arg Gly Gln 45
Thr Glu Lys Ala Asp 50 His Val Asp Leu Ala 55 Thr Leu Met Ile Asp 60
Phe Asn Gly Glu Glu 65 Lys Ala Trp Ala Met 70 Ala Val Trp Ile Phe 75
Ala Ala Ile Asn Arg 80 Arg Asp Leu Tyr Glu 85 Lys Ala Lys Arg Asp 90
Glu Pro Lys Trp Gly 95 Ser Asp Asn Ala Arg 100 Val Ser Asn Pro Thr 105
Val Ile Cys Gln Glu 110 Asp Ser Ile Glu Glu 115 Glu Trp Met Gly Leu 120
Leu Glu Tyr Leu Ser 125 Arg Ile Ser Ile Cys 130 Lys Met Lys Lys Asp 135
Tyr Arg Lys Lys Tyr 140 Arg Lys Tyr Val Arg 145 Ser Arg Phe Gln Cys 150
Ile Glu Asp Arg Asn 155 Ala Arg Leu Gly Glu 160 Ser Val Ser Leu Asn 165
Lys Arg Tyr Thr Arg 170 Leu Arg Leu Ile Lys 175 Glu His Arg Ser Gln 180
Gln Glu Arg Glu Gln 185 Glu Leu Leu Ala Ile 190 Gly Lys Thr Lys Thr 195
Cys Glu Ser Pro Val 200 Ser Pro Ile Lys Met 205 Glu Leu Leu Phe Asp 210
Pro Asp Asp Glu His 215 Ser Glu Pro Val His 220 Thr Val Val Phe Gln 225
Gly Ala Ala Gly Ile 230 Gly Lys Thr Ile Leu 235 Ala Arg Lys Met Met 240
Leu Asp Trp Ala Ser 245 Gly Thr Leu Tyr Gln 250 Asp Arg Phe Asp Tyr 255
Leu Phe Tyr Ile His 260 Cys Arg Glu Val Ser 265 Leu Val Thr Gln Arg 270
Ser Leu Gly Asp Leu 275 Ile Met Ser Cys Cys 280 Pro Asp Pro Asn Pro 285
Pro Ile His Lys Ile 290 Val Arg Lys Pro Ser 295 Arg Ile Leu Phe Leu 300
Met Asp Gly Phe Asp 305 Glu Leu Gln Gly Ala 310 Phe Asp Glu His Ile 315
Gly Pro Leu Cys Thr 320 Asp Trp Gln Lys Ala 325 Glu Arg Gly Asp Ile 330

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P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

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P2490R1SEQ.txt

1010		1015		1020
Leu Gln Glu Glu Lys	Pro Glu Leu Thr Val	Val Phe Glu Pro Ser		
1025	1030	1035		

Trp

<210> 95

<211> 1036

<212> PRT

<213> Homo sapiens

<400> 95

Met	Lys	Met	Ala	Ser	Thr	Arg	Cys	Lys	Leu	Ala	Arg	Tyr	Leu	Glu
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Asp	Leu	Glu	Asp	Val	Asp	Leu	Lys	Lys	Phe	Lys	Met	His	Leu	Glu
				20					25					30

Asp	Tyr	Pro	Pro	Gln	Lys	Gly	Cys	Ile	Pro	Leu	Pro	Arg	Gly	Gln
				35					40					45

Thr	Glu	Lys	Ala	Asp	His	Val	Asp	Leu	Ala	Thr	Leu	Met	Ile	Asp
				50					55					60

Phe	Asn	Gly	Glu	Glu	Lys	Ala	Trp	Ala	Met	Ala	Val	Trp	Ile	Phe
				65					70					75

Ala	Ala	Ile	Asn	Arg	Arg	Asp	Leu	Tyr	Glu	Lys	Ala	Lys	Arg	Asp
				80					85					90

Glu	Pro	Lys	Trp	Gly	Ser	Asp	Asn	Ala	Arg	Val	Ser	Asn	Pro	Thr
				95					100					105

Val	Ile	Cys	Gln	Glu	Asp	Ser	Ile	Glu	Glu	Glu	Trp	Met	Gly	Leu
				110					115					120

Leu	Glu	Tyr	Leu	Ser	Arg	Ile	Ser	Ile	Cys	Lys	Met	Lys	Lys	Asp
				125					130					135

Tyr	Arg	Lys	Lys	Tyr	Arg	Lys	Tyr	Val	Arg	Ser	Arg	Phe	Gln	Cys
				140					145					150

Ile	Glu	Asp	Arg	Asn	Ala	Arg	Leu	Gly	Glu	Ser	Val	Ser	Leu	Asn
				155					160					165

Lys	Arg	Tyr	Thr	Arg	Leu	Arg	Leu	Ile	Lys	Glu	His	Arg	Ser	Gln
				170					175					180

Gln	Glu	Arg	Glu	Gln	Glu	Leu	Leu	Ala	Ile	Gly	Lys	Thr	Lys	Thr
				185					190					195

Cys	Glu	Ser	Pro	Val	Ser	Pro	Ile	Lys	Met	Glu	Leu	Leu	Phe	Asp
				200					205					210

Pro	Asp	Asp	Glu	His	Ser	Glu	Pro	Val	His	Thr	Val	Val	Phe	Gln
				215					220					225

Gly	Ala	Ala	Gly	Ile	Gly	Lys	Thr	Ile	Leu	Ala	Arg	Lys	Met	Met
				230					235					240

Leu	Asp	Trp	Ala	Ser	Gly	Thr	Leu	Tyr	Gln	Asp	Arg	Phe	Asp	Tyr
				245					250					255

Leu	Phe	Tyr	Ile	His	Cys	Arg	Glu	Val	Ser	Leu	Val	Thr	Gln	Arg
				260					265					270

P2490R1SEQ.txt

Ser	Leu	Gly	Asp	Leu	Ile	Met	Ser	Cys	Cys	Pro	Asp	Pro	Asn	Pro	275	280	285
Pro	Ile	His	Lys	Ile	Val	Arg	Lys	Pro	Ser	Arg	Ile	Leu	Phe	Leu	290	295	300
Met	Asp	Gly	Phe	Asp	Glu	Leu	Gln	Gly	Ala	Phe	Asp	Glu	His	Ile	305	310	315
Gly	Pro	Leu	Cys	Thr	Asp	Trp	Gln	Lys	Ala	Glu	Arg	Gly	Asp	Ile	320	325	330
Leu	Leu	Ser	Ser	Leu	Ile	Arg	Lys	Lys	Leu	Leu	Pro	Glu	Ala	Ser	335	340	345
Leu	Leu	Ile	Thr	Thr	Arg	Pro	Val	Ala	Leu	Glu	Lys	Leu	Gln	His	350	355	360
Leu	Leu	Asp	His	Pro	Arg	His	Val	Glu	Ile	Leu	Gly	Phe	Ser	Glu	365	370	375
Ala	Lys	Arg	Lys	Glu	Tyr	Phe	Phe	Lys	Tyr	Phe	Ser	Asp	Glu	Ala	380	385	390
Gln	Ala	Arg	Ala	Ala	Phe	Ser	Leu	Ile	Gln	Glu	Asn	Glu	Val	Leu	395	400	405
Phe	Thr	Met	Cys	Phe	Ile	Pro	Leu	Val	Cys	Trp	Ile	Val	Cys	Thr	410	415	420
Gly	Leu	Lys	Gln	Gln	Met	Glu	Ser	Gly	Lys	Ser	Leu	Ala	Gln	Thr	425	430	435
Ser	Lys	Thr	Thr	Thr	Ala	Val	Tyr	Val	Phe	Phe	Leu	Ser	Ser	Leu	440	445	450
Leu	Gln	Pro	Arg	Gly	Gly	Ser	Gln	Glu	His	Gly	Leu	Cys	Ala	His	455	460	465
Leu	Trp	Gly	Leu	Cys	Ser	Leu	Ala	Ala	Asp	Gly	Ile	Trp	Asn	Gln	470	475	480
Lys	Ile	Leu	Phe	Glu	Glu	Ser	Asp	Leu	Arg	Asn	His	Gly	Leu	Gln	485	490	495
Lys	Ala	Asp	Val	Ser	Ala	Phe	Leu	Arg	Met	Asn	Leu	Phe	Gln	Lys	500	505	510
Glu	Val	Asp	Cys	Glu	Lys	Phe	Tyr	Ser	Phe	Ile	His	Met	Thr	Phe	515	520	525
Gln	Glu	Phe	Phe	Ala	Ala	Met	Tyr	Tyr	Leu	Leu	Glu	Glu	Glu	Lys	530	535	540
Glu	Gly	Arg	Thr	Asn	Val	Pro	Gly	Ser	Arg	Leu	Lys	Leu	Pro	Ser	545	550	555
Arg	Asp	Val	Thr	Val	Leu	Leu	Glu	Asn	Tyr	Gly	Lys	Phe	Glu	Lys	560	565	570
Gly	Tyr	Leu	Ile	Phe	Val	Val	Arg	Phe	Leu	Phe	Gly	Leu	Val	Asn	575	580	585
Gln	Glu	Arg	Thr	Ser	Tyr	Leu	Glu	Lys	Lys	Leu	Ser	Cys	Lys	Ile	590	595	600
Ser	Gln	Gln	Ile	Arg	Leu	Glu	Leu	Leu	Lys	Trp	Ile	Glu	Val	Lys	605	610	615

P2490R1SEQ.txt

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

P2490R1SEQ.txt

	950		955		960
Leu Ser Thr Leu	Leu Thr Ser Ser Gln Ser Leu Arg Lys Leu Ser				
	965		970		975
Leu Gly Asn Asn Asp	Leu Gly Asp Leu Gly Val Met Met Phe Cys				
	980		985		990
Glu Val Leu Lys Gln	Gln Ser Cys Leu Leu Gln Asn Leu Gly Leu				
	995		1000		1005
Ser Glu Met Tyr Phe	Asn Tyr Glu Thr Lys Ser Ala Leu Glu Thr				
	1010		1015		1020
Leu Gln Glu Glu Lys	Pro Glu Leu Thr Val Val Phe Glu Pro Ser				
	1025		1030		1035

Trp

<210> 96
 <211> 1390
 <212> PRT
 <213> Homo sapiens

<400> 96
 Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Leu
 1 5 10 15
 Phe Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu
 20 25 30
 Ala Lys Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn
 35 40 45
 Phe Thr Ala Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His
 50 55 60
 His Ile Phe Leu Gly Ala Thr Asn Tyr Ile Tyr Val Leu Asn Glu
 65 70 75
 Glu Asp Leu Gln Lys Val Ala Glu Tyr Lys Thr Gly Pro Val Leu
 80 85 90
 Glu His Pro Asp Cys Phe Pro Cys Gln Asp Cys Ser Ser Lys Ala
 95 100 105
 Asn Leu Ser Gly Gly Val Trp Lys Asp Asn Ile Asn Met Ala Leu
 110 115 120
 Val Val Asp Thr Tyr Tyr Asp Asp Gln Leu Ile Ser Cys Gly Ser
 125 130 135
 Val Asn Arg Gly Thr Cys Gln Arg His Val Phe Pro His Asn His
 140 145 150
 Thr Ala Asp Ile Gln Ser Glu Val His Cys Ile Phe Ser Pro Gln
 155 160 165
 Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val Val Ser Ala Leu
 170 175 180
 Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe Ile Asn Phe
 185 190 195
 Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp His Pro
 200 205 210

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Asp Lys Glu Tyr Tyr Ser Val His Asn Lys Thr Gly Ala Lys Leu
1235 1240 1245
Pro Val Lys Trp Met Ala Leu Glu Ser Leu Gln Thr Gln Lys Phe
1250 1255 1260
Thr Thr Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
1265 1270 1275
Leu Met Thr Arg Gly Ala Pro Pro Tyr Pro Asp Val Asn Thr Phe
1280 1285 1290
Asp Ile Thr Val Tyr Leu Leu Gln Gly Arg Arg Leu Leu Gln Pro
1295 1300 1305
Glu Tyr Cys Pro Asp Pro Leu Tyr Glu Val Met Leu Lys Cys Trp
1310 1315 1320
His Pro Lys Ala Glu Met Arg Pro Ser Phe Ser Glu Leu Val Ser
1325 1330 1335
Arg Ile Ser Ala Ile Phe Ser Thr Phe Ile Gly Glu His Tyr Val
1340 1345 1350
His Val Asn Ala Thr Tyr Val Asn Val Lys Cys Val Ala Pro Tyr
1355 1360 1365
Pro Ser Leu Leu Ser Ser Glu Asp Asn Ala Asp Asp Glu Val Asp
1370 1375 1380
Thr Arg Pro Ala Ser Phe Trp Glu Thr Ser
1385 1390

<210> 97
<211> 352
<212> PRT
<213> Homo sapiens

<400> 97
Met Glu Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu
1 5 10 15
Met Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg
20 25 30
Glu Glu Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile Tyr
35 40 45
Ser Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile
50 55 60
Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys
65 70 75
Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr
80 85 90
Leu Pro Phe Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly
95 100 105
Asn Phe Leu Cys Lys Ala Val His Val Ile Tyr Thr Val Asn Leu
110 115 120
Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr
125 130 135
Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu
140 145 150

P2490R1SEQ.txt

Leu Ala Glu Lys Val Val Tyr Val Gly Val Trp Ile Pro Ala Leu
155 160 165
Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn Val Ser Glu Ala
170 175 180
Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn Asp Leu Trp
185 190 195
Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu Ile Leu
200 205 210
Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser Lys
215 220 225
Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
230 235 240
Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr
245 250 255
Tyr Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile
260 265 270
Lys Gln Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser
275 280 285
Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile
290 295 300
Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His
305 310 315
Ala Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser
320 325 330
Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu
335 340 345
Ser Ser Ser Phe His Ser Ser
350

<210> 98
<211> 855
<212> PRT
<213> Homo sapiens

<400> 98
Met Ile Leu Ile Pro Arg Met Leu Leu Val Leu Phe Leu Leu Leu
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Pro Ile Leu Ser Ser Ala Lys Ala Gln Val Asn Pro Ala Ile Cys
20 25 30
Arg Tyr Pro Leu Gly Met Ser Gly Gly Gln Ile Pro Asp Glu Asp
35 40 45
Ile Thr Ala Ser Ser Gln Trp Ser Glu Ser Thr Ala Ala Lys Tyr
50 55 60
Gly Arg Leu Asp Ser Glu Glu Gly Asp Gly Ala Trp Cys Pro Glu
65 70 75
Ile Pro Val Glu Pro Asp Asp Leu Lys Glu Phe Leu Gln Ile Asp
80 85 90
Leu His Thr Leu His Phe Ile Thr Leu Val Gly Thr Gln Gly Arg
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P2490R1SEQ.txt														
95					100					105				
His	Ala	Gly	Gly	His	Gly	Ile	Glu	Phe	Ala	Pro	Met	Tyr	Lys	Ile
				110					115					120
Asn	Tyr	Ser	Arg	Asp	Gly	Thr	Arg	Trp	Ile	Ser	Trp	Arg	Asn	Arg
				125					130					135
His	Gly	Lys	Gln	Val	Leu	Asp	Gly	Asn	Ser	Asn	Pro	Tyr	Asp	Ile
				140					145					150
Phe	Leu	Lys	Asp	Leu	Glu	Pro	Pro	Ile	Val	Ala	Arg	Phe	Val	Arg
				155					160					165
Phe	Ile	Pro	Val	Thr	Asp	His	Ser	Met	Asn	Val	Cys	Met	Arg	Val
				170					175					180
Glu	Leu	Tyr	Gly	Cys	Val	Trp	Leu	Asp	Gly	Leu	Val	Ser	Tyr	Asn
				185					190					195
Ala	Pro	Ala	Gly	Gln	Gln	Phe	Val	Leu	Pro	Gly	Gly	Ser	Ile	Ile
				200					205					210
Tyr	Leu	Asn	Asp	Ser	Val	Tyr	Asp	Gly	Ala	Val	Gly	Tyr	Ser	Met
				215					220					225
Thr	Glu	Gly	Leu	Gly	Gln	Leu	Thr	Asp	Gly	Val	Ser	Gly	Leu	Asp
				230					235					240
Asp	Phe	Thr	Gln	Thr	His	Glu	Tyr	His	Val	Trp	Pro	Gly	Tyr	Asp
				245					250					255
Tyr	Val	Gly	Trp	Arg	Asn	Glu	Ser	Ala	Thr	Asn	Gly	Tyr	Ile	Glu
				260					265					270
Ile	Met	Phe	Glu	Phe	Asp	Arg	Ile	Arg	Asn	Phe	Thr	Thr	Met	Lys
				275					280					285
Val	His	Cys	Asn	Asn	Met	Phe	Ala	Lys	Gly	Val	Lys	Ile	Phe	Lys
				290					295					300
Glu	Val	Gln	Cys	Tyr	Phe	Arg	Ser	Glu	Ala	Ser	Glu	Trp	Glu	Pro
				305					310					315
Asn	Ala	Ile	Ser	Phe	Pro	Leu	Val	Leu	Asp	Asp	Val	Asn	Pro	Ser
				320					325					330
Ala	Arg	Phe	Val	Thr	Val	Pro	Leu	His	His	Arg	Met	Ala	Ser	Ala
				335					340					345
Ile	Lys	Cys	Gln	Tyr	His	Phe	Ala	Asp	Thr	Trp	Met	Met	Phe	Ser
				350					355					360
Glu	Ile	Thr	Phe	Gln	Ser	Asp	Ala	Ala	Met	Tyr	Asn	Asn	Ser	Glu
				365					370					375
Ala	Leu	Pro	Thr	Ser	Pro	Met	Ala	Pro	Thr	Thr	Tyr	Asp	Pro	Met
				380					385					390
Leu	Lys	Val	Asp	Asp	Ser	Asn	Thr	Arg	Ile	Leu	Ile	Gly	Cys	Leu
				395					400					405
Val	Ala	Ile	Ile	Phe	Ile	Leu	Leu	Ala	Ile	Ile	Val	Ile	Ile	Leu
				410					415					420
Trp	Arg	Gln	Phe	Trp	Gln	Lys	Met	Leu	Glu	Lys	Ala	Ser	Arg	Arg
				425					430					435

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Phe Thr Phe Cys Gln Glu Gln Pro Tyr Ser Gln Leu Ser Asp Glu
785 790 795
Gln Val Ile Glu Asn Thr Gly Glu Phe Phe Arg Asp Gln Gly Arg
800 805 810
Gln Thr Tyr Leu Pro Gln Pro Ala Ile Cys Pro Asp Ser Val Tyr
815 820 825
Lys Leu Met Leu Ser Cys Trp Arg Arg Asp Thr Lys Asn Arg Pro
830 835 840
Ser Phe Gln Glu Ile His Leu Leu Leu Leu Gln Gln Gly Asp Glu
845 850 855

<210> 99
<211> 288
<212> PRT
<213> Homo sapiens

<400> 99
Met Asp Asp Pro Lys Ser Glu Gln Gln Arg Ile Leu Arg Arg His
1 5 10 15
Gln Arg Glu Arg Gln Glu Leu Gln Ala Gln Ile Arg Ser Leu Lys
20 25 30
Asn Ser Val Pro Lys Thr Asp Lys Thr Lys Arg Lys Gln Leu Leu
35 40 45
Gln Asp Val Ala Arg Met Glu Ala Glu Met Ala Gln Lys His Arg
50 55 60
Gln Glu Leu Glu Lys Phe Gln Asp Asp Ser Ser Ile Glu Ser Val
65 70 75
Val Glu Asp Leu Ala Lys Met Asn Leu Glu Asn Arg Pro Pro Arg
80 85 90
Ser Ser Lys Ala His Arg Lys Arg Glu Arg Met Glu Ser Glu Glu
95 100 105
Arg Glu Arg Gln Glu Ser Ile Phe Gln Ala Glu Met Ser Glu His
110 115 120
Leu Ala Gly Phe Lys Arg Glu Glu Glu Glu Lys Leu Ala Ala Ile
125 130 135
Leu Gly Ala Arg Gly Leu Glu Met Lys Ala Ile Pro Ala Asp Gly
140 145 150
His Cys Met Tyr Arg Ala Ile Gln Asp Gln Leu Val Phe Ser Val
155 160 165
Ser Val Glu Met Leu Arg Cys Arg Thr Ala Ser Tyr Met Lys Lys
170 175 180
His Val Asp Glu Phe Leu Pro Phe Phe Ser Asn Pro Glu Thr Ser
185 190 195
Asp Ser Phe Gly Tyr Asp Asp Phe Met Ile Tyr Cys Asp Asn Ile
200 205 210
Val Arg Thr Thr Ala Trp Gly Gly Gln Leu Glu Leu Arg Ala Leu
215 220 225
Ser His Val Leu Lys Thr Pro Ile Glu Val Ile Gln Ala Asp Ser
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P2490R1SEQ.txt

230		235		240
Pro Thr Leu Ile	Ile Gly Glu Glu Tyr Val Lys Lys Pro Ile			Ile
	245	250		255
Leu Val Tyr Leu	Arg Tyr Ala Tyr Ser Leu Gly Glu His Tyr			Asn
	260	265		270
Ser Val Thr Pro	Leu Glu Ala Gly Ala Ala Gly Gly Val Leu			Pro
	275	280		285
Arg Leu Leu				
<210> 100				
<211> 382				
<212> PRT				
<213> Homo sapiens				
<400> 100				
Met Gly Pro Thr Ser	Val Pro Leu Val Lys Ala His Arg Ser			Ser
1	5	10		15
Val Ser Asp Tyr	Val Asn Tyr Asp Ile Ile Val Arg His Tyr			Asn
	20	25		30
Tyr Thr Gly Lys	Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser			Ile
	35	40		45
Lys Leu Thr Ser	Val Val Phe Ile Leu Ile Cys Cys Phe Ile			Ile
	50	55		60
Leu Glu Asn Ile	Phe Val Leu Leu Thr Ile Trp Lys Thr Lys			Lys
	65	70		75
Phe His Arg Pro	Met Tyr Tyr Phe Ile Gly Asn Leu Ala Leu			Ser
	80	85		90
Asp Leu Leu Ala	Gly Val Ala Tyr Thr Ala Asn Leu Leu Leu			Ser
	95	100		105
Gly Ala Thr Thr	Tyr Lys Leu Thr Pro Ala Gln Trp Phe Leu			Arg
	110	115		120
Glu Gly Ser Met	Phe Val Ala Leu Ser Ala Ser Val Phe Ser			Leu
	125	130		135
Leu Ala Ile Ala	Ile Glu Arg Tyr Ile Thr Met Leu Lys Met			Lys
	140	145		150
Leu His Asn Gly	Ser Asn Asn Phe Arg Leu Phe Leu Leu Ile			Ser
	155	160		165
Ala Cys Trp Val	Ile Ser Leu Ile Leu Gly Gly Leu Pro Ile			Met
	170	175		180
Gly Trp Asn Cys	Ile Ser Ala Leu Ser Ser Cys Ser Thr Val			Leu
	185	190		195
Pro Leu Tyr His	Lys His Tyr Ile Leu Phe Cys Thr Thr Val			Phe
	200	205		210
Thr Leu Leu Leu	Leu Ser Ile Val Ile Leu Tyr Cys Arg Ile			Tyr
	215	220		225
Ser Leu Val Arg	Thr Arg Ser Arg Arg Leu Thr Phe Arg Lys			Asn
	230	235		240

P2490R1SEQ.txt

Ile Ser Lys Ala Ser Arg Ser Ser Glu Lys Ser Leu Ala Leu Leu
 245 250 255
 Lys Thr Val Ile Ile Val Leu Ser Val Phe Ile Ala Cys Trp Ala
 260 265 270
 Pro Leu Phe Ile Leu Leu Leu Leu Asp Val Gly Cys Lys Val Lys
 275 280 285
 Thr Cys Asp Ile Leu Phe Arg Ala Glu Tyr Phe Leu Val Leu Ala
 290 295 300
 Val Leu Asn Ser Gly Thr Asn Pro Ile Ile Tyr Thr Leu Thr Asn
 305 310 315
 Lys Glu Met Arg Arg Ala Phe Ile Arg Ile Met Ser Cys Cys Lys
 320 325 330
 Cys Pro Ser Gly Asp Ser Ala Gly Lys Phe Lys Arg Pro Ile Ile
 335 340 345
 Ala Gly Met Glu Phe Ser Arg Ser Lys Ser Asp Asn Ser Ser His
 350 355 360
 Pro Gln Lys Asp Glu Gly Asp Asn Pro Glu Thr Ile Met Ser Ser
 365 370 375
 Gly Asn Val Asn Ser Ser Ser
 380

<210> 101
 <211> 594
 <212> PRT
 <213> Homo sapiens

<400> 101
 Met Thr Asp Lys Ser Ile Val Ile Leu Ser Leu Met Val Phe His
 1 5 10 15
 Ser Ser Phe Ile Asn Gly Lys Thr Cys Arg Arg Gln Leu Val Glu
 20 25 30
 Glu Trp His Pro Gln Pro Ser Ser Tyr Val Val Asn Trp Thr Leu
 35 40 45
 Thr Glu Asn Ile Cys Leu Asp Phe Tyr Arg Asp Cys Trp Phe Leu
 50 55 60
 Gly Val Asn Thr Lys Ile Asp Thr Ser Gly Asn Gln Ala Val Pro
 65 70 75
 Gln Ile Cys Pro Leu Gln Ile Gln Leu Gly Asp Ile Leu Val Ile
 80 85 90
 Ser Ser Glu Pro Ser Leu Gln Phe Pro Glu Ile Asn Leu Met Asn
 95 100 105
 Val Ser Glu Thr Ser Phe Val Gly Cys Val Gln Asn Thr Thr Thr
 110 115 120
 Glu Asp Gln Leu Leu Phe Gly Cys Arg Leu Lys Gly Met His Thr
 125 130 135
 Val Asn Ser Lys Trp Leu Ser Val Gly Thr His Tyr Phe Ile Thr
 140 145 150
 Val Met Ala Ser Gly Pro Ser Pro Cys Pro Leu Gly Leu Arg Leu
 155 160 165

P2490R1SEQ.txt

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

P2490R1SEQ.txt

500	505	510
Ala Thr Tyr Val	Asn Asp Pro Glu Asp Asn Asn Ser Ser Cys Trp	
515	520	525
Phe Pro His Glu	Gly Thr Lys Glu Ile Cys Ala Asn Gly Cys Ser	
530	535	540
Cys Leu Ser Glu	Glu Asp Ser Gln Glu Tyr Arg Tyr Leu Cys Phe	
545	550	555
Leu Arg Trp Ala	Gly Asn Met Tyr Leu Glu Asn Thr Thr Asp Asp	
560	565	570
Gln Glu Asn Glu	Cys Gln His Glu Ala Val Cys Lys Asp Glu Ile	
575	580	585
Asn Arg Pro Arg	Tyr Leu Cys Ile Ile	
590		

<210> 102
 <211> 1210
 <212> PRT
 <213> Homo sapiens

<400> 102
 Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu
 1 5 10 15
 Ala Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val
 20 25 30
 Cys Gln Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu
 35 40 45
 Asp His Phe Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val
 50 55 60
 Val Leu Gly Asn Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp
 65 70 75
 Leu Ser Phe Leu Lys Thr Ile Gln Glu Val Ala Gly Tyr Val Leu
 80 85 90
 Ile Ala Leu Asn Thr Val Glu Arg Ile Pro Leu Glu Asn Leu Gln
 95 100 105
 Ile Ile Arg Gly Asn Met Tyr Tyr Glu Asn Ser Tyr Ala Leu Ala
 110 115 120
 Val Leu Ser Asn Tyr Asp Ala Asn Lys Thr Gly Leu Lys Glu Leu
 125 130 135
 Pro Met Arg Asn Leu Gln Glu Ile Leu His Gly Ala Val Arg Phe
 140 145 150
 Ser Asn Asn Pro Ala Leu Cys Asn Val Glu Ser Ile Gln Trp Arg
 155 160 165
 Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met Ser Met Asp Phe
 170 175 180
 Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro Ser Cys Pro
 185 190 195
 Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln Lys Leu
 200 205 210

P2490R1SEQ.txt

```

Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg Gly
215 220 225

Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg
245 250 255

Asp Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr
260 265 270

Asn Pro Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr
275 280 285

Ser Phe Gly Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val
290 295 300

Val Thr Asp His Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser
305 310 315

Tyr Glu Met Glu Glu Asp Gly Val Arg Lys Cys Lys Lys Cys Glu
320 325 330

Gly Pro Cys Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
335 340 345

Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys
350 355 360

Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
365 370 375

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln
380 385 390

Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu
395 400 405

Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe
410 415 420

Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln
425 430 435

Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu
440 445 450

Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly
455 460 465

Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly
485 490 495

Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys
500 505 510

Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
515 520 525

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn
530 535 540

Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys
545 550 555

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P2490R1SEQ.txt

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

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P2490R1SEQ.txt

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

<210> 103
 <211> 1342
 <212> PRT

P2490R1SEQ.txt

<213> Homo sapiens

<400> 103

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

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P2490R1SEQ.txt

Cys Glu Gly Thr Gly Ser Gly Ser Arg Phe Gln Thr Val Asp Ser
 335 340 345
 Ser Asn Ile Asp Gly Phe Val Asn Cys Thr Lys Ile Leu Gly Asn
 350 355 360
 Leu Asp Phe Leu Ile Thr Gly Leu Asn Gly Asp Pro Trp His Lys
 365 370 375
 Ile Pro Ala Leu Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val
 380 385 390
 Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln Ser Trp Pro Pro His
 395 400 405
 Met His Asn Phe Ser Val Phe Ser Asn Leu Thr Thr Ile Gly Gly
 410 415 420
 Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile Met Lys Asn
 425 430 435
 Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu Ile Ser
 440 445 450
 Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr His
 455 460 465
 His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu
 470 475 480
 Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala
 485 490 495
 Glu Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp
 500 505 510
 Gly Pro Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg
 515 520 525
 Gly Gly Val Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro
 530 535 540
 Arg Glu Phe Ala His Glu Ala Glu Cys Phe Ser Cys His Pro Glu
 545 550 555
 Cys Gln Pro Met Glu Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser
 560 565 570
 Asp Thr Cys Ala Gln Cys Ala His Phe Arg Asp Gly Pro His Cys
 575 580 585
 Val Ser Ser Cys Pro His Gly Val Leu Gly Ala Lys Gly Pro Ile
 590 595 600
 Tyr Lys Tyr Pro Asp Val Gln Asn Glu Cys Arg Pro Cys His Glu
 605 610 615
 Asn Cys Thr Gln Gly Cys Lys Gly Pro Glu Leu Gln Asp Cys Leu
 620 625 630
 Gly Gln Thr Leu Val Leu Ile Gly Lys Thr His Leu Thr Met Ala
 635 640 645
 Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe Met Met Leu Gly
 650 655 660
 Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln Asn Lys Arg
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P2490R1SEQ.txt

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

P2490R1SEQ.txt

Glu Pro Glu Leu Asp 1010 Leu Asp Leu Asp Leu Glu Ala Glu Glu Asp 1020
 Asn Leu Ala Thr Thr 1025 Thr Leu Gly Ser Ala Leu Ser Leu Pro Val 1035
 Gly Thr Leu Asn Arg 1040 Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro 1050
 Ser Ser Gly Tyr Met 1055 Pro Met Asn Gln Gly Asn Leu Gly Glu Ser 1065
 Cys Gln Glu Ser Ala 1070 Val Ser Gly Ser Ser Glu Arg Cys Pro Arg 1080
 Pro Val Ser Leu His 1085 Pro Met Pro Arg Gly Cys Leu Ala Ser Glu 1095
 Ser Ser Glu Gly His 1100 Val Thr Gly Ser Glu Ala Glu Leu Gln Glu 1110
 Lys Val Ser Met Cys 1115 Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg 1125
 Pro Arg Gly Asp Ser 1130 Ala Tyr His Ser Gln Arg His Ser Leu Leu 1140
 Thr Pro Val Thr Pro 1145 Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp 1155
 Val Asn Gly Tyr Val 1160 Met Pro Asp Thr His Leu Lys Gly Thr Pro 1170
 Ser Ser Arg Glu Gly 1175 Thr Leu Ser Ser Val Gly Leu Ser Ser Val 1185
 Leu Gly Thr Glu Glu 1190 Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met 1200
 Asn Arg Arg Arg Arg 1205 His Ser Pro Pro His Pro Pro Arg Pro Ser 1215
 Ser Leu Glu Glu Leu 1220 Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp 1230
 Leu Ser Ala Ser Leu 1235 Gly Ser Thr Gln Ser Cys Pro Leu His Pro 1245
 Val Pro Ile Met Pro 1250 Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr 1260
 Glu Tyr Met Asn Arg 1265 Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp 1275
 Tyr Ala Ala Met Gly 1280 Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu 1290
 Glu Met Arg Ala Phe 1295 Gln Gly Pro Gly His Gln Ala Pro His Val 1305
 His Tyr Ala Arg Leu 1310 Lys Thr Leu Arg Ser Leu Glu Ala Thr Asp 1320
 Ser Ala Phe Asp Asn 1325 Pro Asp Tyr Trp His Ser Arg Leu Phe Pro 1335
 Lys Ala Asn Ala Gln Arg Thr 1340

P2490R1SEQ.txt

<210> 104
 <211> 1308
 <212> PRT
 <213> Homo sapiens

<400> 104

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

```

P2490R1SEQ.txt														
305					310					315				
Glu	Glu	Asn	Gly	Ile	Lys	Met	Cys	Lys	Pro	Cys	Thr	Asp	Ile	Cys
				320					325					330
Pro	Lys	Ala	Cys	Asp	Gly	Ile	Gly	Thr	Gly	Ser	Leu	Met	Ser	Ala
				335					340					345
Gln	Thr	Val	Asp	Ser	Ser	Asn	Ile	Asp	Lys	Phe	Ile	Asn	Cys	Thr
				350					355					360
Lys	Ile	Asn	Gly	Asn	Leu	Ile	Phe	Leu	Val	Thr	Gly	Ile	His	Gly
				365					370					375
Asp	Pro	Tyr	Asn	Ala	Ile	Glu	Ala	Ile	Asp	Pro	Glu	Lys	Leu	Asn
				380					385					390
Val	Phe	Arg	Thr	Val	Arg	Glu	Ile	Thr	Gly	Phe	Leu	Asn	Ile	Gln
				395					400					405
Ser	Trp	Pro	Pro	Asn	Met	Thr	Asp	Phe	Ser	Val	Phe	Ser	Asn	Leu
				410					415					420
Val	Thr	Ile	Gly	Gly	Arg	Val	Leu	Tyr	Ser	Gly	Leu	Ser	Leu	Leu
				425					430					435
Ile	Leu	Lys	Gln	Gln	Gly	Ile	Thr	Ser	Leu	Gln	Phe	Gln	Ser	Leu
				440					445					450
Lys	Glu	Ile	Ser	Ala	Gly	Asn	Ile	Tyr	Ile	Thr	Asp	Asn	Ser	Asn
				455					460					465
Leu	Cys	Tyr	Tyr	His	Thr	Ile	Asn	Trp	Thr	Thr	Leu	Phe	Ser	Thr
				470					475					480
Ile	Asn	Gln	Arg	Ile	Val	Ile	Arg	Asp	Asn	Arg	Lys	Ala	Glu	Asn
				485					490					495
Cys	Thr	Ala	Glu	Gly	Met	Val	Cys	Asn	His	Leu	Cys	Ser	Ser	Asp
				500					505					510
Gly	Cys	Trp	Gly	Pro	Gly	Pro	Asp	Gln	Cys	Leu	Ser	Cys	Arg	Arg
				515					520					525
Phe	Ser	Arg	Gly	Arg	Ile	Cys	Ile	Glu	Ser	Cys	Asn	Leu	Tyr	Asp
				530					535					540
Gly	Glu	Phe	Arg	Glu	Phe	Glu	Asn	Gly	Ser	Ile	Cys	Val	Glu	Cys
				545					550					555
Asp	Pro	Gln	Cys	Glu	Lys	Met	Glu	Asp	Gly	Leu	Leu	Thr	Cys	His
				560					565					570
Gly	Pro	Gly	Pro	Asp	Asn	Cys	Thr	Lys	Cys	Ser	His	Phe	Lys	Asp
				575					580					585
Gly	Pro	Asn	Cys	Val	Glu	Lys	Cys	Pro	Asp	Gly	Leu	Gln	Gly	Ala
				590					595					600
Asn	Ser	Phe	Ile	Phe	Lys	Tyr	Ala	Asp	Pro	Asp	Arg	Glu	Cys	His
				605					610					615
Pro	Cys	His	Pro	Asn	Cys	Thr	Gln	Gly	Cys	Asn	Gly	Pro	Thr	Ser
				620					625					630
His	Asp	Cys	Ile	Tyr	Tyr	Pro	Trp	Thr	Gly	His	Ser	Thr	Leu	Pro
				635					640					645

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

<211> 442
<212> PRT
<213> Homo sapiens

<400> 105

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

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P2490R1SEQ.txt

Lys Gln Arg Arg Glu Val Ala Lys Thr Val Phe Cys Leu Val Leu
 320 325 330
 Val Phe Ala Leu Cys Trp Leu Pro Leu His Leu Ser Arg Ile Leu
 335 340 345
 Lys Leu Thr Leu Tyr Asn Gln Asn Asp Pro Asn Arg Cys Glu Leu
 350 355 360
 Leu Ser Phe Leu Leu Val Leu Asp Tyr Ile Gly Ile Asn Met Ala
 365 370 375
 Ser Leu Asn Ser Cys Ile Asn Pro Ile Ala Leu Tyr Leu Val Ser
 380 385 390
 Lys Arg Phe Lys Asn Cys Phe Lys Ser Cys Leu Cys Cys Trp Cys
 395 400 405
 Gln Ser Phe Glu Glu Lys Gln Ser Leu Glu Glu Lys Gln Ser Cys
 410 415 420
 Leu Lys Phe Lys Ala Asn Asp His Gly Tyr Asp Asn Phe Arg Ser
 425 430 435
 Ser Asn Lys Tyr Ser Ser Ser
 440

<210> 106

<211> 822

<212> PRT

<213> Homo sapiens

<400> 106

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

P2490R1SEQ.txt

```

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

```

P2490R1SEQ.txt

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

<210> 107
 <211> 840
 <212> PRT
 <213> Homo sapiens
 <400> 107

P2490R1SEQ.txt

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

```

P2490R1SEQ.txt

Leu Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr
 350 355 360
 Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp
 365 370 375
 Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala
 380 385 390
 Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe
 395 400 405
 Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met Lys
 410 415 420
 Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His
 425 430 435
 Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
 440 445 450
 Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg
 455 460 465
 Ile Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala
 470 475 480
 Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe
 485 490 495
 Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys
 500 505 510
 Phe Gly Gln Val Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp
 515 520 525
 Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu Lys Asp
 530 535 540
 Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu
 545 550 555
 Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu
 560 565 570
 Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr
 575 580 585
 Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Arg Ala Arg Arg Pro
 590 595 600
 Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg Val Pro Glu Glu
 605 610 615
 Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr Gln Leu Ala
 620 625 630
 Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His Arg Asp
 635 640 645
 Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met Lys
 650 655 660
 Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr
 665 670 675
 Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
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P2490R1SEQ.txt

	680	685	690
Pro Glu Ala Leu	Phe Asp Arg Val Tyr	Thr His Gln Ser Asp	Val
	695	700	705
Trp Ser Phe Gly	Val Leu Met Trp Glu	Ile Phe Thr Leu Gly	Gly
	710	715	720
Ser Pro Tyr Pro	Gly Ile Pro Val Glu	Glu Leu Phe Lys Leu	Leu
	725	730	735
Lys Glu Gly His	Arg Met Asp Lys Pro	Ala Asn Cys Thr Asn	Glu
	740	745	750
Leu Tyr Met Met	Met Arg Asp Cys Trp	His Ala Val Pro Ser	Gln
	755	760	765
Arg Pro Thr Phe	Lys Gln Leu Val Glu	Asp Leu Asp Arg Ile	Leu
	770	775	780
Thr Leu Thr Thr	Asn Glu Glu Tyr Leu	Asp Leu Ser Gln Pro	Leu
	785	790	795
Glu Gln Tyr Ser	Pro Ser Tyr Pro Asp	Thr Arg Ser Ser Cys	Ser
	800	805	810
Ser Gly Asp Asp	Ser Val Phe Ser Pro	Asp Pro Met Pro Tyr	Glu
	815	820	825
Pro Cys Leu Pro	Gln Tyr Pro His Ile	Asn Gly Ser Val Lys	Thr
	830	835	840

<210> 108
 <211> 806
 <212> PRT
 <213> Homo sapiens

<400> 108
 Met Gly Ala Pro Ala Cys Ala Leu Ala Leu Cys Val Ala Val Ala
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 Ile Val Ala Gly Ala Ser Ser Glu Ser Leu Gly Thr Glu Gln Arg
 20 25 30
 Val Val Gly Arg Ala Ala Glu Val Pro Gly Pro Glu Pro Gly Gln
 35 40 45
 Gln Glu Gln Leu Val Phe Gly Ser Gly Asp Ala Val Glu Leu Ser
 50 55 60
 Cys Pro Pro Pro Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val
 65 70 75
 Lys Asp Gly Thr Gly Leu Val Pro Ser Glu Arg Val Leu Val Gly
 80 85 90
 Pro Gln Arg Leu Gln Val Leu Asn Ala Ser His Glu Asp Ser Gly
 95 100 105
 Ala Tyr Ser Cys Arg Gln Arg Leu Thr Gln Arg Val Leu Cys His
 110 115 120
 Phe Ser Val Arg Val Thr Asp Ala Pro Ser Ser Gly Asp Asp Glu
 125 130 135
 Asp Gly Glu Asp Glu Ala Glu Asp Thr Gly Val Asp Thr Gly Ala
 140 145 150

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Lys	Asp	Arg	Ala	Ala	Lys	Pro	Val	Thr	Val	Ala	Val	Lys	Met	Leu
				500					505					510
Lys	Asp	Asp	Ala	Thr	Asp	Lys	Asp	Leu	Ser	Asp	Leu	Val	Ser	Glu
				515					520					525
Met	Glu	Met	Met	Lys	Met	Ile	Gly	Lys	His	Lys	Asn	Ile	Ile	Asn
				530					535					540
Leu	Leu	Gly	Ala	Cys	Thr	Gln	Gly	Gly	Pro	Leu	Tyr	Val	Leu	Val
				545					550					555
Glu	Tyr	Ala	Ala	Lys	Gly	Asn	Leu	Arg	Glu	Phe	Leu	Arg	Ala	Arg
				560					565					570
Arg	Pro	Pro	Gly	Leu	Asp	Tyr	Ser	Phe	Asp	Thr	Cys	Lys	Pro	Pro
				575					580					585
Glu	Glu	Gln	Leu	Thr	Phe	Lys	Asp	Leu	Val	Ser	Cys	Ala	Tyr	Gln
				590					595					600
Val	Ala	Arg	Gly	Met	Glu	Tyr	Leu	Ala	Ser	Gln	Lys	Cys	Ile	His
				605					610					615
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Thr	Glu	Asp	Asn	Val
				620					625					630
Met	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Val	His	Asn	Leu
				635					640					645
Asp	Tyr	Tyr	Lys	Lys	Thr	Thr	Asn	Gly	Arg	Leu	Pro	Val	Lys	Trp
				650					655					660
Met	Ala	Pro	Glu	Ala	Leu	Phe	Asp	Arg	Val	Tyr	Thr	His	Gln	Ser
				665					670					675
Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu	Trp	Glu	Ile	Phe	Thr	Leu
				680					685					690
Gly	Gly	Ser	Pro	Tyr	Pro	Gly	Ile	Pro	Val	Glu	Glu	Leu	Phe	Lys
				695					700					705
Leu	Leu	Lys	Glu	Gly	His	Arg	Met	Asp	Lys	Pro	Ala	Asn	Cys	Thr
				710					715					720
His	Asp	Leu	Tyr	Met	Ile	Met	Arg	Glu	Cys	Trp	His	Ala	Ala	Pro
				725					730					735
Ser	Gln	Arg	Pro	Thr	Phe	Lys	Gln	Leu	Val	Glu	Asp	Leu	Asp	Arg
				740					745					750
Val	Leu	Thr	Val	Thr	Ser	Thr	Asp	Glu	Tyr	Leu	Asp	Leu	Ser	Ala
				755					760					765
Pro	Phe	Glu	Gln	Tyr	Ser	Pro	Gly	Gly	Gln	Asp	Thr	Pro	Ser	Ser
				770					775					780
Ser	Ser	Ser	Gly	Asp	Asp	Ser	Val	Phe	Ala	His	Asp	Leu	Leu	Pro
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Pro	Ala	Pro	Pro	Ser	Ser	Gly	Gly	Ser	Arg	Thr				
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<210> 109
 <211> 802
 <212> PRT
 <213> Homo sapiens

P2490R1SEQ.txt

<400> 109

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

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P2490R1SEQ.txt

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

P2490R1SEQ.txt

Gly Ile Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
 680 685 690
 Pro Gly Ile Pro Val Glu Glu Leu Phe Ser Leu Leu Arg Glu Gly
 695 700 705
 His Arg Met Asp Arg Pro Pro His Cys Pro Pro Glu Leu Tyr Gly
 710 715 720
 Leu Met Arg Glu Cys Trp His Ala Ala Pro Ser Gln Arg Pro Thr
 725 730 735
 Phe Lys Gln Leu Val Glu Ala Leu Asp Lys Val Leu Leu Ala Val
 740 745 750
 Ser Glu Glu Tyr Leu Asp Leu Arg Leu Thr Phe Gly Pro Tyr Ser
 755 760 765
 Pro Ser Gly Gly Asp Ala Ser Ser Thr Cys Ser Ser Ser Asp Ser
 770 775 780
 Val Phe Ser His Asp Pro Leu Pro Leu Gly Ser Ser Ser Phe Pro
 785 790 795
 Phe Gly Ser Gly Val Gln Thr
 800

<210> 110
 <211> 2549
 <212> PRT
 <213> Homo sapiens

<400> 110
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 Ser Ser Asn Val Ser Val Leu Gln Gln Phe Ala Ser Gly Leu Lys
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 35 40 45
 His Tyr Val Thr Met Glu Leu Arg Glu Met Ser Gln Glu Glu Ser
 50 55 60
 Thr Arg Phe Tyr Asp Gln Leu Asn His His Ile Phe Glu Leu Val
 65 70 75
 Ser Ser Ser Asp Ala Asn Glu Arg Lys Gly Gly Ile Leu Ala Ile
 80 85 90
 Ala Ser Leu Ile Gly Val Glu Gly Gly Asn Ala Thr Arg Ile Gly
 95 100 105
 Arg Phe Ala Asn Tyr Leu Arg Asn Leu Leu Pro Ser Asn Asp Pro
 110 115 120
 Val Val Met Glu Met Ala Ser Lys Ala Ile Gly Arg Leu Ala Met
 125 130 135
 Ala Gly Asp Thr Phe Thr Ala Glu Tyr Val Glu Phe Glu Val Lys
 140 145 150
 Arg Ala Leu Glu Trp Leu Gly Ala Asp Arg Asn Glu Gly Arg Arg
 155 160 165
 His Ala Ala Val Leu Val Leu Arg Glu Leu Ala Ile Ser Val Pro

P2490R1SEQ.txt														
170					175					180				
Thr	Phe	Phe	Phe	Gln	Gln	Val	Gln	Pro	Phe	Phe	Asp	Asn	Ile	Phe
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Val	Ala	Val	Trp	Asp	Pro	Lys	Gln	Ala	Ile	Arg	Glu	Gly	Ala	Val
				200					205					210
Ala	Ala	Leu	Arg	Ala	Cys	Leu	Ile	Leu	Thr	Thr	Gln	Arg	Glu	Pro
				215					220					225
Lys	Glu	Met	Gln	Lys	Pro	Gln	Trp	Tyr	Arg	His	Thr	Phe	Glu	Glu
				230					235					240
Ala	Glu	Lys	Gly	Phe	Asp	Glu	Thr	Leu	Ala	Lys	Glu	Lys	Gly	Met
				245					250					255
Asn	Arg	Asp	Asp	Arg	Ile	His	Gly	Ala	Leu	Leu	Ile	Leu	Asn	Glu
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Leu	Val	Arg	Ile	Ser	Ser	Met	Glu	Gly	Glu	Arg	Leu	Arg	Glu	Glu
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Met	Glu	Glu	Ile	Thr	Gln	Gln	Gln	Leu	Val	His	Asp	Lys	Tyr	Cys
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Lys	Asp	Leu	Met	Gly	Phe	Gly	Thr	Lys	Pro	Arg	His	Ile	Thr	Pro
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Phe	Thr	Ser	Phe	Gln	Ala	Val	Gln	Pro	Gln	Gln	Ser	Asn	Ala	Leu
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Val	Gly	Leu	Leu	Gly	Tyr	Ser	Ser	His	Gln	Gly	Leu	Met	Gly	Phe
				335					340					345
Gly	Thr	Ser	Pro	Ser	Pro	Ala	Lys	Ser	Thr	Leu	Val	Glu	Ser	Arg
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Cys	Cys	Arg	Asp	Leu	Met	Glu	Glu	Lys	Phe	Asp	Gln	Val	Cys	Gln
				365					370					375
Trp	Val	Leu	Lys	Cys	Arg	Asn	Ser	Lys	Asn	Ser	Leu	Ile	Gln	Met
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Thr	Ile	Leu	Asn	Leu	Leu	Pro	Arg	Leu	Ala	Ala	Phe	Arg	Pro	Ser
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Ala	Phe	Thr	Asp	Thr	Gln	Tyr	Leu	Gln	Asp	Thr	Met	Asn	His	Val
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Leu	Ser	Cys	Val	Lys	Lys	Glu	Lys	Glu	Arg	Thr	Ala	Ala	Phe	Gln
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Ala	Leu	Gly	Leu	Leu	Ser	Val	Ala	Val	Arg	Ser	Glu	Phe	Lys	Val
				440					445					450
Tyr	Leu	Pro	Arg	Val	Leu	Asp	Ile	Ile	Arg	Ala	Ala	Leu	Pro	Pro
				455					460					465
Lys	Asp	Phe	Ala	His	Lys	Arg	Gln	Lys	Ala	Met	Gln	Val	Asp	Ala
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Thr	Val	Phe	Thr	Cys	Ile	Ser	Met	Leu	Ala	Arg	Ala	Met	Gly	Pro
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P2490R1SEQ.txt

Val	Gly	Leu	Ser	Pro	Ala	Leu	Thr	Ala	Val	Leu	Tyr	Asp	Leu	Ser
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Thr	Thr	Leu	Pro	Glu	Ala	Ser	Asp	Val	Gly	Ser	Ile	Thr	Leu	Ala
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Leu	Arg	Thr	Leu	Gly	Ser	Phe	Glu	Phe	Glu	Gly	His	Ser	Leu	Thr
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Gln	Phe	Val	Arg	His	Cys	Ala	Asp	His	Phe	Leu	Asn	Ser	Glu	His
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Lys	Glu	Ile	Arg	Met	Glu	Ala	Ala	Arg	Thr	Cys	Ser	Arg	Leu	Leu
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Thr	Pro	Ser	Ile	His	Leu	Ile	Ser	Gly	His	Ala	His	Val	Val	Ser
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Gln	Thr	Ala	Val	Gln	Val	Val	Ala	Asp	Val	Leu	Ser	Lys	Leu	Leu
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Val	Val	Gly	Ile	Thr	Asp	Pro	Asp	Pro	Asp	Ile	Arg	Tyr	Cys	Val
				665					670					675
Leu	Ala	Ser	Leu	Asp	Glu	Arg	Phe	Asp	Ala	His	Leu	Ala	Gln	Ala
				680					685					690
Glu	Asn	Leu	Gln	Ala	Leu	Phe	Val	Ala	Leu	Asn	Asp	Gln	Val	Phe
				695					700					705
Glu	Ile	Arg	Glu	Leu	Ala	Ile	Cys	Thr	Val	Gly	Arg	Leu	Ser	Ser
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Met	Asn	Pro	Ala	Phe	Val	Met	Pro	Phe	Leu	Arg	Lys	Met	Leu	Ile
				725					730					735
Gln	Ile	Leu	Thr	Glu	Leu	Glu	His	Ser	Gly	Ile	Gly	Arg	Ile	Lys
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Glu	Gln	Ser	Ala	Arg	Met	Leu	Gly	His	Leu	Val	Ser	Asn	Ala	Pro
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Arg	Leu	Ile	Arg	Pro	Tyr	Met	Glu	Pro	Ile	Leu	Lys	Ala	Leu	Ile
				770					775					780
Leu	Lys	Leu	Lys	Asp	Pro	Asp	Pro	Asp	Pro	Asn	Pro	Gly	Val	Ile
				785					790					795
Asn	Asn	Val	Leu	Ala	Thr	Ile	Gly	Glu	Leu	Ala	Gln	Val	Ser	Gly
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Leu	Glu	Met	Arg	Lys	Trp	Val	Asp	Glu	Leu	Phe	Ile	Ile	Ile	Met
				815					820					825
Asp	Met	Leu	Gln	Asp	Ser	Ser	Leu	Leu	Ala	Lys	Arg	Gln	Val	Ala
				830					835					840
Leu	Trp	Thr	Leu	Gly	Gln	Leu	Val	Ala	Ser	Thr	Gly	Tyr	Val	Val
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P2490R1SEQ.txt

Glu Pro Tyr Arg Lys Tyr Pro Thr Leu Leu Glu Val Leu Leu Asn
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 Phe Leu Lys Thr Glu Gln Asn Gln Gly Thr Arg Arg Glu Ala Ile
 875 880 885
 Arg Val Leu Gly Leu Leu Gly Ala Leu Asp Pro Tyr Lys His Lys
 890 895 900
 Val Asn Ile Gly Met Ile Asp Gln Ser Arg Asp Ala Ser Ala Val
 905 910 915
 Ser Leu Ser Glu Ser Lys Ser Ser Gln Asp Ser Ser Asp Tyr Ser
 920 925 930
 Thr Ser Glu Met Leu Val Asn Met Gly Asn Leu Pro Leu Asp Glu
 935 940 945
 Phe Tyr Pro Ala Val Ser Met Val Ala Leu Met Arg Ile Phe Arg
 950 955 960
 Asp Gln Ser Leu Ser His His His Thr Met Val Val Gln Ala Ile
 965 970 975
 Thr Phe Ile Phe Lys Ser Leu Gly Leu Lys Cys Val Gln Phe Leu
 980 985 990
 Pro Gln Val Met Pro Thr Phe Leu Asn Val Ile Arg Val Cys Asp
 995 1000 1005
 Gly Ala Ile Arg Glu Phe Leu Phe Gln Gln Leu Gly Met Leu Val
 1010 1015 1020
 Ser Phe Val Lys Ser His Ile Arg Pro Tyr Met Asp Glu Ile Val
 1025 1030 1035
 Thr Leu Met Arg Glu Phe Trp Val Met Asn Thr Ser Ile Gln Ser
 1040 1045 1050
 Thr Ile Ile Leu Leu Ile Glu Gln Ile Val Val Ala Leu Gly Gly
 1055 1060 1065
 Glu Phe Lys Leu Tyr Leu Pro Gln Leu Ile Pro His Met Leu Arg
 1070 1075 1080
 Val Phe Met His Asp Asn Ser Pro Gly Arg Ile Val Ser Ile Lys
 1085 1090 1095
 Leu Leu Ala Ala Ile Gln Leu Phe Gly Ala Asn Leu Asp Asp Tyr
 1100 1105 1110
 Leu His Leu Leu Leu Pro Pro Ile Val Lys Leu Phe Asp Ala Pro
 1115 1120 1125
 Glu Ala Pro Leu Pro Ser Arg Lys Ala Ala Leu Glu Thr Val Asp
 1130 1135 1140
 Arg Leu Thr Glu Ser Leu Asp Phe Thr Asp Tyr Ala Ser Arg Ile
 1145 1150 1155
 Ile His Pro Ile Val Arg Thr Leu Asp Gln Ser Pro Glu Leu Arg
 1160 1165 1170
 Ser Thr Ala Met Asp Thr Leu Ser Ser Leu Val Phe Gln Leu Gly
 1175 1180 1185
 Lys Lys Tyr Gln Ile Phe Ile Pro Met Val Asn Lys Val Leu Val
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P2490R1SEQ.txt														
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Ile	Val	Lys	Gly	Tyr	Thr	Leu	Ala	Asp	Glu	Glu	Glu	Asp	Pro	Leu
1220					1225					1230				
Ile	Tyr	Gln	His	Arg	Met	Leu	Arg	Ser	Gly	Gln	Gly	Asp	Ala	Leu
1235					1240					1245				
Ala	Ser	Gly	Pro	Val	Glu	Thr	Gly	Pro	Met	Lys	Lys	Leu	His	Val
1250					1255					1260				
Ser	Thr	Ile	Asn	Leu	Gln	Lys	Ala	Trp	Gly	Ala	Ala	Arg	Arg	Val
1265					1270					1275				
Ser	Lys	Asp	Asp	Trp	Leu	Glu	Trp	Leu	Arg	Arg	Leu	Ser	Leu	Glu
1280					1285					1290				
Leu	Leu	Lys	Asp	Ser	Ser	Ser	Pro	Ser	Leu	Arg	Ser	Cys	Trp	Ala
1295					1300					1305				
Leu	Ala	Gln	Ala	Tyr	Asn	Pro	Met	Ala	Arg	Asp	Leu	Phe	Asn	Ala
1310					1315					1320				
Ala	Phe	Val	Ser	Cys	Trp	Ser	Glu	Leu	Asn	Glu	Asp	Gln	Gln	Asp
1325					1330					1335				
Glu	Leu	Ile	Arg	Ser	Ile	Glu	Leu	Ala	Leu	Thr	Ser	Gln	Asp	Ile
1340					1345					1350				
Ala	Glu	Val	Thr	Gln	Thr	Leu	Leu	Asn	Leu	Ala	Glu	Phe	Met	Glu
1355					1360					1365				
His	Ser	Asp	Lys	Gly	Pro	Leu	Pro	Leu	Arg	Asp	Asp	Asn	Gly	Ile
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Val	Leu	Leu	Gly	Glu	Arg	Ala	Ala	Lys	Cys	Arg	Ala	Tyr	Ala	Lys
1385					1390					1395				
Ala	Leu	His	Tyr	Lys	Glu	Leu	Glu	Phe	Gln	Lys	Gly	Pro	Thr	Pro
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Ala	Ile	Leu	Glu	Ser	Leu	Ile	Ser	Ile	Asn	Asn	Lys	Leu	Gln	Gln
1415					1420					1425				
Pro	Glu	Ala	Ala	Ala	Gly	Val	Leu	Glu	Tyr	Ala	Met	Lys	His	Phe
1430					1435					1440				
Gly	Glu	Leu	Glu	Ile	Gln	Ala	Thr	Trp	Tyr	Glu	Lys	Leu	His	Glu
1445					1450					1455				
Trp	Glu	Asp	Ala	Leu	Val	Ala	Tyr	Asp	Lys	Lys	Met	Asp	Thr	Asn
1460					1465					1470				
Lys	Asp	Asp	Pro	Glu	Leu	Met	Leu	Gly	Arg	Met	Arg	Cys	Leu	Glu
1475					1480					1485				
Ala	Leu	Gly	Glu	Trp	Gly	Gln	Leu	His	Gln	Gln	Cys	Cys	Glu	Lys
1490					1495					1500				
Trp	Thr	Leu	Val	Asn	Asp	Glu	Thr	Gln	Ala	Lys	Met	Ala	Arg	Met
1505					1510					1515				
Ala	Ala	Ala	Ala	Ala	Trp	Gly	Leu	Gly	Gln	Trp	Asp	Ser	Met	Glu
1520					1525					1530				

P2490R1SEQ.txt

Glu Tyr Thr Cys Met Ile Pro Arg Asp Thr His Asp Gly Ala Phe
1535 1540 1545

Tyr Arg Ala Val Leu Ala Leu His Gln Asp Leu Phe Ser Leu Ala
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Gln Gln Cys Ile Asp Lys Ala Arg Asp Leu Leu Asp Ala Glu Leu
1565 1570 1575

Thr Ala Met Ala Gly Glu Ser Tyr Ser Arg Ala Tyr Gly Ala Met
1580 1585 1590

Val Ser Cys His Met Leu Ser Glu Leu Glu Glu Val Ile Gln Tyr
1595 1600 1605

Lys Leu Val Pro Glu Arg Arg Glu Ile Ile Arg Gln Ile Trp Trp
1610 1615 1620

Glu Arg Leu Gln Gly Cys Gln Arg Ile Val Glu Asp Trp Gln Lys
1625 1630 1635

Ile Leu Met Val Arg Ser Leu Val Val Ser Pro His Glu Asp Met
1640 1645 1650

Arg Thr Trp Leu Lys Tyr Ala Ser Leu Cys Gly Lys Ser Gly Arg
1655 1660 1665

Leu Ala Leu Ala His Lys Thr Leu Val Leu Leu Leu Gly Val Asp
1670 1675 1680

Pro Ser Arg Gln Leu Asp His Pro Leu Pro Thr Val His Pro Gln
1685 1690 1695

Val Thr Tyr Ala Tyr Met Lys Asn Met Trp Lys Ser Ala Arg Lys
1700 1705 1710

Ile Asp Ala Phe Gln His Met Gln His Phe Val Gln Thr Met Gln
1715 1720 1725

Gln Gln Ala Gln His Ala Ile Ala Thr Glu Asp Gln Gln His Lys
1730 1735 1740

Gln Glu Leu His Lys Leu Met Ala Arg Cys Phe Leu Lys Leu Gly
1745 1750 1755

Glu Trp Gln Leu Asn Leu Gln Gly Ile Asn Glu Ser Thr Ile Pro
1760 1765 1770

Lys Val Leu Gln Tyr Tyr Ser Ala Ala Thr Glu His Asp Arg Ser
1775 1780 1785

Trp Tyr Lys Ala Trp His Ala Trp Ala Val Met Asn Phe Glu Ala
1790 1795 1800

Val Leu His Tyr Lys His Gln Asn Gln Ala Arg Asp Glu Lys Lys
1805 1810 1815

Lys Leu Arg His Ala Ser Gly Ala Asn Ile Thr Asn Ala Thr Thr
1820 1825 1830

Ala Ala Thr Thr Ala Ala Thr Ala Thr Thr Thr Ala Ser Thr Glu
1835 1840 1845

Gly Ser Asn Ser Glu Ser Glu Ala Glu Ser Thr Glu Asn Ser Pro
1850 1855 1860

Thr Pro Ser Pro Leu Gln Lys Lys Val Thr Glu Asp Leu Ser Lys
1865 1870 1875

P2490R1SEQ.txt

Thr Leu Leu Met Tyr Thr Val Pro Ala Val Gln Gly Phe Phe Arg
1880 1885 1890

Ser Ile Ser Leu Ser Arg Gly Asn Asn Leu Gln Asp Thr Leu Arg
1895 1900 1905

Val Leu Thr Leu Trp Phe Asp Tyr Gly His Trp Pro Asp Val Asn
1910 1915 1920

Glu Ala Leu Val Glu Gly Val Lys Ala Ile Gln Ile Asp Thr Trp
1925 1930 1935

Leu Gln Val Ile Pro Gln Leu Ile Ala Arg Ile Asp Thr Pro Arg
1940 1945 1950

Pro Leu Val Gly Arg Leu Ile His Gln Leu Leu Thr Asp Ile Gly
1955 1960 1965

Arg Tyr His Pro Gln Ala Leu Ile Tyr Pro Leu Thr Val Ala Ser
1970 1975 1980

Lys Ser Thr Thr Thr Ala Arg His Asn Ala Ala Asn Lys Ile Leu
1985 1990 1995

Lys Asn Met Cys Glu His Ser Asn Thr Leu Val Gln Gln Ala Met
2000 2005 2010

Met Val Ser Glu Glu Leu Ile Arg Val Ala Ile Leu Trp His Glu
2015 2020 2025

Met Trp His Glu Gly Leu Glu Glu Ala Ser Arg Leu Tyr Phe Gly
2030 2035 2040

Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu Glu Pro Leu His
2045 2050 2055

Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu Thr Ser Phe
2060 2065 2070

Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu Trp Cys
2075 2080 2085

Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln Ala
2090 2095 2100

Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser Lys Gln Leu
2105 2110 2115

Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro Lys Leu
2120 2125 2130

Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Asp
2135 2140 2145

Pro Asn Gln Pro Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu
2150 2155 2160

Gln Val Ile Thr Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met
2165 2170 2175

Gly Ser Asn Gly His Glu Phe Val Phe Leu Leu Lys Gly His Glu
2180 2185 2190

Asp Leu Arg Gln Asp Glu Arg Val Met Gln Leu Phe Gly Leu Val
2195 2200 2205

Asn Thr Leu Leu Ala Asn Asp Pro Thr Ser Leu Arg Lys Asn Leu
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Ser Ile Gln Arg Tyr	Ala Val Ile Pro Leu Ser Thr Asn Ser Gly	
2225	2230	2235
Leu Ile Gly Trp Val	Pro His Cys Asp Thr Leu His Ala Leu Ile	
2240	2245	2250
Arg Asp Tyr Arg Glu	Lys Lys Lys Ile Leu Leu Asn Ile Glu His	
2255	2260	2265
Arg Ile Met Leu Arg	Met Ala Pro Asp Tyr Asp His Leu Thr Leu	
2270	2275	2280
Met Gln Lys Val Glu	Val Phe Glu His Ala Val Asn Asn Thr Ala	
2285	2290	2295
Gly Asp Asp Leu Ala	Lys Leu Leu Trp Leu Lys Ser Pro Ser Ser	
2300	2305	2310
Glu Val Trp Phe Asp	Arg Arg Thr Asn Tyr Thr Arg Ser Leu Ala	
2315	2320	2325
Val Met Ser Met Val	Gly Tyr Ile Leu Gly Leu Gly Asp Arg His	
2330	2335	2340
Pro Ser Asn Leu Met	Leu Asp Arg Leu Ser Gly Lys Ile Leu His	
2345	2350	2355
Ile Asp Phe Gly Asp	Cys Phe Glu Val Ala Met Thr Arg Glu Lys	
2360	2365	2370
Phe Pro Glu Lys Ile	Pro Phe Arg Leu Thr Arg Met Leu Thr Asn	
2375	2380	2385
Ala Met Glu Val Thr	Gly Leu Asp Gly Asn Tyr Arg Ile Thr Cys	
2390	2395	2400
His Thr Val Met Glu	Val Leu Arg Glu His Lys Asp Ser Val Met	
2405	2410	2415
Ala Val Leu Glu Ala	Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg	
2420	2425	2430
Leu Met Asp Thr Asn	Thr Lys Gly Asn Lys Arg Ser Arg Thr Arg	
2435	2440	2445
Thr Asp Ser Tyr Ser	Ala Gly Gln Ser Val Glu Ile Leu Asp Gly	
2450	2455	2460
Val Glu Leu Gly Glu	Pro Ala His Lys Lys Thr Gly Thr Thr Val	
2465	2470	2475
Pro Glu Ser Ile His	Ser Phe Ile Gly Asp Gly Leu Val Lys Pro	
2480	2485	2490
Glu Ala Leu Asn Lys	Lys Ala Ile Gln Ile Ile Asn Arg Val Arg	
2495	2500	2505
Asp Lys Leu Thr Gly	Arg Asp Phe Ser His Asp Asp Thr Leu Asp	
2510	2515	2520
Val Pro Thr Gln Val	Glu Leu Leu Ile Lys Gln Ala Thr Ser His	
2525	2530	2535
Glu Asn Leu Cys Gln	Cys Tyr Ile Gly Trp Cys Pro Phe Trp	
2540	2545	

P2490R1SEQ.txt

<210> 111
 <211> 393
 <212> PRT
 <213> Homo sapiens

<400> 111
 Met Glu Thr Thr Met Gly Phe Met Asp Asp Asn Ala Thr Asn Thr
 1 5 10 15
 Ser Thr Ser Phe Leu Ser Val Leu Asn Pro His Gly Ala His Ala
 20 25 30
 Thr Ser Phe Pro Phe Asn Phe Ser Tyr Ser Asp Tyr Asp Met Pro
 35 40 45
 Leu Asp Glu Asp Glu Asp Val Thr Asn Ser Arg Thr Phe Phe Ala
 50 55 60
 Ala Lys Ile Val Ile Gly Met Ala Leu Val Gly Ile Met Leu Val
 65 70 75
 Cys Gly Ile Gly Asn Phe Ile Phe Ile Ala Ala Leu Val Arg Tyr
 80 85 90
 Lys Lys Leu Arg Asn Leu Thr Asn Leu Leu Ile Ala Asn Leu Ala
 95 100 105
 Ile Ser Asp Phe Leu Val Ala Ile Val Cys Cys Pro Phe Glu Met
 110 115 120
 Asp Tyr Tyr Val Val Arg Gln Leu Ser Trp Glu His Gly His Val
 125 130 135
 Leu Cys Thr Ser Val Asn Tyr Leu Arg Thr Val Ser Leu Tyr Val
 140 145 150
 Ser Thr Asn Ala Leu Leu Ala Ile Ala Ile Asp Arg Tyr Leu Ala
 155 160 165
 Ile Val His Pro Leu Arg Pro Arg Met Lys Cys Gln Thr Ala Thr
 170 175 180
 Gly Leu Ile Ala Leu Val Trp Thr Val Ser Ile Leu Ile Ala Ile
 185 190 195
 Pro Ser Ala Tyr Phe Thr Thr Glu Thr Val Leu Val Ile Val Lys
 200 205 210
 Ser Gln Glu Lys Ile Phe Cys Gly Gln Ile Trp Pro Val Asp Gln
 215 220 225
 Gln Leu Tyr Tyr Lys Ser Tyr Phe Leu Phe Ile Phe Gly Ile Glu
 230 235 240
 Phe Val Gly Pro Val Val Thr Met Thr Leu Cys Tyr Ala Arg Ile
 245 250 255
 Ser Arg Glu Leu Trp Phe Lys Ala Val Pro Gly Phe Gln Thr Glu
 260 265 270
 Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val
 275 280 285
 Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe
 290 295 300
 Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr Val Phe Val
 305 310 315

P2490R1SEQ.txt

Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Ile Val Glu Cys Ile
 320 325 330
 Ala Met Ser Asn Ser Met Ile Asn Thr Leu Cys Phe Val Thr Val
 335 340 345
 Lys Asn Asp Thr Val Lys Tyr Phe Lys Lys Ile Met Leu Leu His
 350 355 360
 Trp Lys Ala Ser Tyr Asn Gly Gly Lys Ser Ser Ala Asp Leu Asp
 365 370 375
 Leu Lys Thr Ile Gly Met Pro Ala Thr Glu Glu Val Asp Cys Ile
 380 385 390

Arg Leu Lys

<210> 112
 <211> 1255
 <212> PRT
 <213> Homo sapiens

<400> 112
 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu
 1 5 10 15
 Leu Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp
 20 25 30
 Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
 35 40 45
 Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu
 50 55 60
 Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln
 65 70 75
 Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln
 80 85 90
 Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr
 95 100 105
 Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly
 110 115 120
 Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro Gly
 125 130 135
 Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu Lys
 140 145 150
 Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp
 155 160 165
 Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn Asn Gln Leu Ala
 170 175 180
 Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys
 185 190 195
 Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu
 200 205 210
 Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys Ala
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P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu
 905 910 915
 Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala Arg Glu
 920 925 930
 Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro
 935 940 945
 Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
 950 955 960
 Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu
 965 970 975
 Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln
 980 985 990
 Asn Glu Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr
 995 1000 1005
 Arg Ser Leu Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala
 1010 1015 1020
 Glu Glu Tyr Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro
 1025 1030 1035
 Ala Pro Gly Ala Gly Gly Met Val His His Arg His Arg Ser Ser
 1040 1045 1050
 Ser Thr Arg Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro
 1055 1060 1065
 Ser Glu Glu Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly
 1070 1075 1080
 Ala Gly Ser Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala
 1085 1090 1095
 Lys Gly Leu Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln
 1100 1105 1110
 Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp
 1115 1120 1125
 Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val
 1130 1135 1140
 Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly
 1145 1150 1155
 Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro
 1160 1165 1170
 Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe
 1175 1180 1185
 Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
 1190 1195 1200
 Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro
 1205 1210 1215
 Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg
 1220 1225 1230
 Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn
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P2490R1SEQ.txt

1235	1240	1245

Pro Glu Tyr Leu Gly Leu Asp Val Pro Val
1250 1255

<210> 113
<211> 1367
<212> PRT
<213> Homo sapiens

<400> 113

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

P2490R1SEQ.txt

Leu	Ser	Ala	Glu	Ser	Ser	Asp	Ser	Glu	Gly	Phe	Val	Ile	His	Asp
				290					295					300
Gly	Glu	Cys	Met	Gln	Glu	Cys	Pro	Ser	Gly	Phe	Ile	Arg	Asn	Gly
				305					310					315
Ser	Gln	Ser	Met	Tyr	Cys	Ile	Pro	Cys	Glu	Gly	Pro	Cys	Pro	Lys
				320					325					330
Val	Cys	Glu	Glu	Glu	Lys	Lys	Thr	Lys	Thr	Ile	Asp	Ser	Val	Thr
				335					340					345
Ser	Ala	Gln	Met	Leu	Gln	Gly	Cys	Thr	Ile	Phe	Lys	Gly	Asn	Leu
				350					355					360
Leu	Ile	Asn	Ile	Arg	Arg	Gly	Asn	Asn	Ile	Ala	Ser	Glu	Leu	Glu
				365					370					375
Asn	Phe	Met	Gly	Leu	Ile	Glu	Val	Val	Thr	Gly	Tyr	Val	Lys	Ile
				380					385					390
Arg	His	Ser	His	Ala	Leu	Val	Ser	Leu	Ser	Phe	Leu	Lys	Asn	Leu
				395					400					405
Arg	Leu	Ile	Leu	Gly	Glu	Glu	Gln	Leu	Glu	Gly	Asn	Tyr	Ser	Phe
				410					415					420
Tyr	Val	Leu	Asp	Asn	Gln	Asn	Leu	Gln	Gln	Leu	Trp	Asp	Trp	Asp
				425					430					435
His	Arg	Asn	Leu	Thr	Ile	Lys	Ala	Gly	Lys	Met	Tyr	Phe	Ala	Phe
				440					445					450
Asn	Pro	Lys	Leu	Cys	Val	Ser	Glu	Ile	Tyr	Arg	Met	Glu	Glu	Val
				455					460					465
Thr	Gly	Thr	Lys	Gly	Arg	Gln	Ser	Lys	Gly	Asp	Ile	Asn	Thr	Arg
				470					475					480
Asn	Asn	Gly	Glu	Arg	Ala	Ser	Cys	Glu	Ser	Asp	Val	Leu	His	Phe
				485					490					495
Thr	Ser	Thr	Thr	Thr	Ser	Lys	Asn	Arg	Ile	Ile	Ile	Thr	Trp	His
				500					505					510
Arg	Tyr	Arg	Pro	Pro	Asp	Tyr	Arg	Asp	Leu	Ile	Ser	Phe	Thr	Val
				515					520					525
Tyr	Tyr	Lys	Glu	Ala	Pro	Phe	Lys	Asn	Val	Thr	Glu	Tyr	Asp	Gly
				530					535					540
Gln	Asp	Ala	Cys	Gly	Ser	Asn	Ser	Trp	Asn	Met	Val	Asp	Val	Asp
				545					550					555
Leu	Pro	Pro	Asn	Lys	Asp	Val	Glu	Pro	Gly	Ile	Leu	Leu	His	Gly
				560					565					570
Leu	Lys	Pro	Trp	Thr	Gln	Tyr	Ala	Val	Tyr	Val	Lys	Ala	Val	Thr
				575					580					585
Leu	Thr	Met	Val	Glu	Asn	Asp	His	Ile	Arg	Gly	Ala	Lys	Ser	Glu
				590					595					600
Ile	Leu	Tyr	Ile	Arg	Thr	Asn	Ala	Ser	Val	Pro	Ser	Ile	Pro	Leu
				605					610					615
Asp	Val	Leu	Ser	Ala	Ser	Asn	Ser	Ser	Ser	Gln	Leu	Ile	Val	Lys
				620					625					630

P2490R1SEQ.txt

Trp Asn Pro Pro Ser Leu Pro Asn Gly Asn Leu Ser Tyr Tyr Ile
 635 640 645
 Val Arg Trp Gln Arg Gln Pro Gln Asp Gly Tyr Leu Tyr Arg His
 650 655 660
 Asn Tyr Cys Ser Lys Asp Lys Ile Pro Ile Arg Lys Tyr Ala Asp
 665 670 675
 Gly Thr Ile Asp Ile Glu Glu Val Thr Glu Asn Pro Lys Thr Glu
 680 685 690
 Val Cys Gly Gly Glu Lys Gly Pro Cys Cys Ala Cys Pro Lys Thr
 695 700 705
 Glu Ala Glu Lys Gln Ala Glu Lys Glu Glu Ala Glu Tyr Arg Lys
 710 715 720
 Val Phe Glu Asn Phe Leu His Asn Ser Ile Phe Val Pro Arg Pro
 725 730 735
 Glu Arg Lys Arg Arg Asp Val Met Gln Val Ala Asn Thr Thr Met
 740 745 750
 Ser Ser Arg Ser Arg Asn Thr Thr Ala Ala Asp Thr Tyr Asn Ile
 755 760 765
 Thr Asp Pro Glu Glu Leu Glu Thr Glu Tyr Pro Phe Phe Glu Ser
 770 775 780
 Arg Val Asp Asn Lys Glu Arg Thr Val Ile Ser Asn Leu Arg Pro
 785 790 795
 Phe Thr Leu Tyr Arg Ile Asp Ile His Ser Cys Asn His Glu Ala
 800 805 810
 Glu Lys Leu Gly Cys Ser Ala Ser Asn Phe Val Phe Ala Arg Thr
 815 820 825
 Met Pro Ala Glu Gly Ala Asp Asp Ile Pro Gly Pro Val Thr Trp
 830 835 840
 Glu Pro Arg Pro Glu Asn Ser Ile Phe Leu Lys Trp Pro Glu Pro
 845 850 855
 Glu Asn Pro Asn Gly Leu Ile Leu Met Tyr Glu Ile Lys Tyr Gly
 860 865 870
 Ser Gln Val Glu Asp Gln Arg Glu Cys Val Ser Arg Gln Glu Tyr
 875 880 885
 Arg Lys Tyr Gly Gly Ala Lys Leu Asn Arg Leu Asn Pro Gly Asn
 890 895 900
 Tyr Thr Ala Arg Ile Gln Ala Thr Ser Leu Ser Gly Asn Gly Ser
 905 910 915
 Trp Thr Asp Pro Val Phe Phe Tyr Val Gln Ala Lys Thr Gly Tyr
 920 925 930
 Glu Asn Phe Ile His Leu Ile Ile Ala Leu Pro Val Ala Val Leu
 935 940 945
 Leu Ile Val Gly Gly Leu Val Ile Met Leu Tyr Val Phe His Arg
 950 955 960
 Lys Arg Asn Asn Ser Arg Leu Gly Asn Gly Val Leu Tyr Ala Ser

P2490R1SEQ.txt

965	970	975
Val Asn Pro Glu Tyr Phe Ser Ala Ala Asp Val Tyr Val Pro Asp	980	990
Glu Trp Glu Val Ala Arg Glu Lys Ile Thr Met Ser Arg Glu Leu	995	1005
Gly Gln Gly Ser Phe Gly Met Val Tyr Glu Gly Val Ala Lys Gly	1010	1020
Val Val Lys Asp Glu Pro Glu Thr Arg Val Ala Ile Lys Thr Val	1025	1035
Asn Glu Ala Ala Ser Met Arg Glu Arg Ile Glu Phe Leu Asn Glu	1040	1050
Ala Ser Val Met Lys Glu Phe Asn Cys His His Val Val Arg Leu	1055	1065
Leu Gly Val Val Ser Gln Gly Gln Pro Thr Leu Val Ile Met Glu	1070	1080
Leu Met Thr Arg Gly Asp Leu Lys Ser Tyr Leu Arg Ser Leu Arg	1085	1095
Pro Glu Met Glu Asn Asn Pro Val Leu Ala Pro Pro Ser Leu Ser	1100	1110
Lys Met Ile Gln Met Ala Gly Glu Ile Ala Asp Gly Met Ala Tyr	1115	1125
Leu Asn Ala Asn Lys Phe Val His Arg Asp Leu Ala Ala Arg Asn	1130	1140
Cys Met Val Ala Glu Asp Phe Thr Val Lys Ile Gly Asp Phe Gly	1145	1155
Met Thr Arg Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys Gly Gly	1160	1170
Lys Gly Leu Leu Pro Val Arg Trp Met Ser Pro Glu Ser Leu Lys	1175	1185
Asp Gly Val Phe Thr Thr Tyr Ser Asp Val Trp Ser Phe Gly Val	1190	1200
Val Leu Trp Glu Ile Ala Thr Leu Ala Glu Gln Pro Tyr Gln Gly	1205	1215
Leu Ser Asn Glu Gln Val Leu Arg Phe Val Met Glu Gly Gly Leu	1220	1230
Leu Asp Lys Pro Asp Asn Cys Pro Asp Met Leu Phe Glu Leu Met	1235	1245
Arg Met Cys Trp Gln Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu	1250	1260
Glu Ile Ile Ser Ser Ile Lys Glu Glu Met Glu Pro Gly Phe Arg	1265	1275
Glu Val Ser Phe Tyr Tyr Ser Glu Glu Asn Lys Leu Pro Glu Pro	1280	1290
Glu Glu Leu Asp Leu Glu Pro Glu Asn Met Glu Ser Val Pro Leu	1295	1305

P2490R1SEQ.txt

Asp Pro Ser Ala Ser Ser Ser Ser Leu Pro Leu Pro Asp Arg His
1310 1315 1320
Ser Gly His Lys Ala Glu Asn Gly Pro Gly Pro Gly Val Leu Val
1325 1330 1335
Leu Arg Ala Ser Phe Asp Glu Arg Gln Pro Tyr Ala His Met Asn
1340 1345 1350
Gly Gly Arg Lys Asn Glu Arg Ala Leu Pro Leu Pro Gln Ser Ser
1355 1360 1365

Thr Cys

<210> 114
<211> 1218
<212> PRT
<213> Homo sapiens

<400> 114

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

P2490R1SEQ.txt

Lys His Gly Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr
 245 250 255
 Gly Trp Gln Gly Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly
 260 265 270
 Cys Val His Gly Ile Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu
 275 280 285
 Thr Asn Trp Gly Gly Gln Leu Cys Asp Lys Asp Leu Asn Tyr Cys
 290 295 300
 Gly Thr His Gln Pro Cys Leu Asn Gly Gly Thr Cys Ser Asn Thr
 305 310 315
 Gly Pro Asp Lys Tyr Gln Cys Ser Cys Pro Glu Gly Tyr Ser Gly
 320 325 330
 Pro Asn Cys Glu Ile Ala Glu His Ala Cys Leu Ser Asp Pro Cys
 335 340 345
 His Asn Arg Gly Ser Cys Lys Glu Thr Ser Leu Gly Phe Glu Cys
 350 355 360
 Glu Cys Ser Pro Gly Trp Thr Gly Pro Thr Cys Ser Thr Asn Ile
 365 370 375
 Asp Asp Cys Ser Pro Asn Asn Cys Ser His Gly Gly Thr Cys Gln
 380 385 390
 Asp Leu Val Asn Gly Phe Lys Cys Val Cys Pro Pro Gln Trp Thr
 395 400 405
 Gly Lys Thr Cys Gln Leu Asp Ala Asn Glu Cys Glu Ala Lys Pro
 410 415 420
 Cys Val Asn Ala Lys Ser Cys Lys Asn Leu Ile Ala Ser Tyr Tyr
 425 430 435
 Cys Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys Asp Ile Asn
 440 445 450
 Ile Asn Asp Cys Leu Gly Gln Cys Gln Asn Asp Ala Ser Cys Arg
 455 460 465
 Asp Leu Val Asn Gly Tyr Arg Cys Ile Cys Pro Pro Gly Tyr Ala
 470 475 480
 Gly Asp His Cys Glu Arg Asp Ile Asp Glu Cys Ala Ser Asn Pro
 485 490 495
 Cys Leu Asn Gly Gly His Cys Gln Asn Glu Ile Asn Arg Phe Gln
 500 505 510
 Cys Leu Cys Pro Thr Gly Phe Ser Gly Asn Leu Cys Gln Leu Asp
 515 520 525
 Ile Asp Tyr Cys Glu Pro Asn Pro Cys Gln Asn Gly Ala Gln Cys
 530 535 540
 Tyr Asn Arg Ala Ser Asp Tyr Phe Cys Lys Cys Pro Glu Asp Tyr
 545 550 555
 Glu Gly Lys Asn Cys Ser His Leu Lys Asp His Cys Arg Thr Thr
 560 565 570
 Pro Cys Glu Val Ile Asp Ser Cys Thr Val Ala Met Ala Ser Asn
 Page 287

P2490R1SEQ.txt

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

P2490R1SEQ.txt
 ser Cys Ile Pro Ile Leu Asp Asp Gln Cys Phe Val His Pro Cys
 920 925 930
 Thr Gly Val Gly Glu Cys Arg Ser Ser Ser Leu Gln Pro Val Lys
 935 940 945
 Thr Lys Cys Thr Ser Asp Ser Tyr Tyr Gln Asp Asn Cys Ala Asn
 950 955 960
 Ile Thr Phe Thr Phe Asn Lys Glu Met Met Ser Pro Gly Leu Thr
 965 970 975
 Thr Glu His Ile Cys Ser Glu Leu Arg Asn Leu Asn Ile Leu Lys
 980 985 990
 Asn Val Ser Ala Glu Tyr Ser Ile Tyr Ile Ala Cys Glu Pro Ser
 995 1000 1005
 Pro Ser Ala Asn Asn Glu Ile His Val Ala Ile Ser Ala Glu Asp
 1010 1015 1020
 Ile Arg Asp Asp Gly Asn Pro Ile Lys Glu Ile Thr Asp Lys Ile
 1025 1030 1035
 Ile Asp Leu Val Ser Lys Arg Asp Gly Asn Ser Ser Leu Ile Ala
 1040 1045 1050
 Ala Val Ala Glu Val Arg Val Gln Arg Arg Pro Leu Lys Asn Arg
 1055 1060 1065
 Thr Asp Phe Leu Val Pro Leu Leu Ser Ser Val Leu Thr Val Ala
 1070 1075 1080
 Trp Ile Cys Cys Leu Val Thr Ala Phe Tyr Trp Cys Leu Arg Lys
 1085 1090 1095
 Arg Arg Lys Pro Gly Ser His Thr His Ser Ala Ser Glu Asp Asn
 1100 1105 1110
 Thr Thr Asn Asn Val Arg Glu Gln Leu Asn Gln Ile Lys Asn Pro
 1115 1120 1125
 Ile Glu Lys His Gly Ala Asn Thr Val Pro Ile Lys Asp Tyr Glu
 1130 1135 1140
 Asn Lys Asn Ser Lys Met Ser Lys Ile Arg Thr His Asn Ser Glu
 1145 1150 1155
 Val Glu Glu Asp Asp Met Asp Lys His Gln Gln Lys Ala Arg Phe
 1160 1165 1170
 Ala Lys Gln Pro Ala Tyr Thr Leu Val Asp Arg Glu Glu Lys Pro
 1175 1180 1185
 Pro Asn Gly Thr Pro Thr Lys His Pro Asn Trp Thr Asn Lys Gln
 1190 1195 1200
 Asp Asn Arg Asp Leu Glu Ser Ala Gln Ser Leu Asn Arg Met Glu
 1205 1210 1215
 Tyr Ile Val

<210> 115
 <211> 1238
 <212> PRT
 <213> Homo sapiens

P2490R1SEQ.txt

<400> 115

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

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P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

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P2490R1SEQ.txt

Ala Ser Ala Val Glu Val Ala Val Ser Phe Ser Pro Ala Arg Asp
 1025 1030 1035
 Leu Pro Asp Ser Ser Leu Ile Gln Gly Ala Ala His Ala Ile Val
 1040 1045 1050
 Ala Ala Ile Thr Gln Arg Gly Asn Ser Ser Leu Leu Leu Ala Val
 1055 1060 1065
 Thr Glu Val Lys Val Glu Thr Val Val Thr Gly Gly Ser Ser Thr
 1070 1075 1080
 Gly Leu Leu Val Pro Val Leu Cys Gly Ala Phe Ser Val Leu Trp
 1085 1090 1095
 Leu Ala Cys Val Val Leu Cys Val Trp Trp Thr Arg Lys Arg Arg
 1100 1105 1110
 Lys Glu Arg Glu Arg Ser Arg Leu Pro Arg Glu Glu Ser Ala Asn
 1115 1120 1125
 Asn Gln Trp Ala Pro Leu Asn Pro Ile Arg Asn Pro Ile Glu Arg
 1130 1135 1140
 Pro Gly Gly His Lys Asp Val Leu Tyr Gln Cys Lys Asn Phe Thr
 1145 1150 1155
 Pro Pro Pro Arg Arg Ala Asp Glu Ala Leu Pro Gly Pro Ala Gly
 1160 1165 1170
 His Ala Ala Val Arg Glu Asp Glu Glu Asp Glu Asp Leu Gly Arg
 1175 1180 1185
 Gly Glu Glu Asp Ser Leu Glu Ala Glu Lys Phe Leu Ser His Lys
 1190 1195 1200
 Phe Thr Lys Asp Pro Gly Arg Ser Pro Gly Arg Pro Ala His Trp
 1205 1210 1215
 Ala Ser Gly Pro Lys Val Asp Asn Arg Ala Val Arg Ser Ile Asn
 1220 1225 1230
 Glu Ala Arg Tyr Ala Gly Lys Glu
 1235

<210> 116
 <211> 1132
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Gly Met Ala Cys Leu Thr Met Thr Glu Met Glu Gly Thr Ser
 1 5 10 15
 Thr Ser Ser Ile Tyr Gln Asn Gly Asp Ile Ser Gly Asn Ala Asn
 20 25 30
 Ser Met Lys Gln Ile Asp Pro Val Leu Gln Val Tyr Leu Tyr His
 35 40 45
 Ser Leu Gly Lys Ser Glu Ala Asp Tyr Leu Thr Phe Pro Ser Gly
 50 55 60
 Glu Tyr Val Ala Glu Glu Ile Cys Ile Ala Ala Ser Lys Ala Cys
 65 70 75
 Gly Ile Thr Pro Val Tyr His Asn Met Phe Ala Leu Met Ser Glu
 Page 293

														P2490R1SEQ.txt											
														80				85				90			
Thr	Glu	Arg	Ile	Trp	Tyr	Pro	Pro	Asn	His	Val	Phe	His	Ile	Asp											
				95					100					105											
Glu	Ser	Thr	Arg	His	Asn	Val	Leu	Tyr	Arg	Ile	Arg	Phe	Tyr	Phe											
				110					115					120											
Pro	Arg	Trp	Tyr	Cys	Ser	Gly	Ser	Asn	Arg	Ala	Tyr	Arg	His	Gly											
				125					130					135											
Ile	Ser	Arg	Gly	Ala	Glu	Ala	Pro	Leu	Leu	Asp	Asp	Phe	Val	Met											
				140					145					150											
Ser	Tyr	Leu	Phe	Ala	Gln	Trp	Arg	His	Asp	Phe	Val	His	Gly	Trp											
				155					160					165											
Ile	Lys	Val	Pro	Val	Thr	His	Glu	Thr	Gln	Glu	Glu	Cys	Leu	Gly											
				170					175					180											
Met	Ala	Val	Leu	Asp	Met	Met	Arg	Ile	Ala	Lys	Glu	Asn	Asp	Gln											
				185					190					195											
Thr	Pro	Leu	Ala	Ile	Tyr	Asn	Ser	Ile	Ser	Tyr	Lys	Thr	Phe	Leu											
				200					205					210											
Pro	Lys	Cys	Ile	Arg	Ala	Lys	Ile	Gln	Asp	Tyr	His	Ile	Leu	Thr											
				215					220					225											
Arg	Lys	Arg	Ile	Arg	Tyr	Arg	Phe	Arg	Arg	Phe	Ile	Gln	Gln	Phe											
				230					235					240											
Ser	Gln	Cys	Lys	Ala	Thr	Ala	Arg	Asn	Leu	Lys	Leu	Lys	Tyr	Leu											
				245					250					255											
Ile	Asn	Leu	Glu	Thr	Leu	Gln	Ser	Ala	Phe	Tyr	Thr	Glu	Lys	Phe											
				260					265					270											
Glu	Val	Lys	Glu	Pro	Gly	Ser	Gly	Pro	Ser	Gly	Glu	Glu	Ile	Phe											
				275					280					285											
Ala	Thr	Ile	Ile	Ile	Thr	Gly	Asn	Gly	Gly	Ile	Gln	Trp	Ser	Arg											
				290					295					300											
Gly	Lys	His	Lys	Glu	Ser	Glu	Thr	Leu	Thr	Glu	Gln	Asp	Leu	Gln											
				305					310					315											
Leu	Tyr	Cys	Asp	Phe	Pro	Asn	Ile	Ile	Asp	Val	Ser	Ile	Lys	Gln											
				320					325					330											
Ala	Asn	Gln	Glu	Gly	Ser	Asn	Glu	Ser	Arg	Val	Val	Thr	Ile	His											
				335					340					345											
Lys	Gln	Asp	Gly	Lys	Asn	Leu	Glu	Ile	Glu	Leu	Ser	Ser	Leu	Arg											
				350					355					360											
Glu	Ala	Leu	Ser	Phe	Val	Ser	Leu	Ile	Asp	Gly	Tyr	Tyr	Arg	Leu											
				365					370					375											
Thr	Ala	Asp	Ala	His	His	Tyr	Leu	Cys	Lys	Glu	Val	Ala	Pro	Pro											
				380					385					390											
Ala	Val	Leu	Glu	Asn	Ile	Gln	Ser	Asn	Cys	His	Gly	Pro	Ile	Ser											
				395					400					405											
Met	Asp	Phe	Ala	Ile	Ser	Lys	Leu	Lys	Lys	Ala	Gly	Asn	Gln	Thr											
				410					415					420											

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Tyr Glu Asp Arg His Gln Leu Pro Ala Pro Lys Trp Ala Glu Leu
 770 775 780
 Ala Asn Leu Ile Asn Asn Cys Met Asp Tyr Glu Pro Asp Phe Arg
 785 790 795
 Pro Ser Phe Arg Ala Ile Ile Arg Asp Leu Asn Ser Leu Phe Thr
 800 805 810
 Pro Asp Tyr Glu Leu Leu Thr Glu Asn Asp Met Leu Pro Asn Met
 815 820 825
 Arg Ile Gly Ala Leu Gly Phe Ser Gly Ala Phe Glu Asp Arg Asp
 830 835 840
 Pro Thr Gln Phe Glu Glu Arg His Leu Lys Phe Leu Gln Gln Leu
 845 850 855
 Gly Lys Gly Asn Phe Gly Ser Val Glu Met Cys Arg Tyr Asp Pro
 860 865 870
 Leu Gln Asp Asn Thr Gly Glu Val Val Ala Val Lys Lys Leu Gln
 875 880 885
 His Ser Thr Glu Glu His Leu Arg Asp Phe Glu Arg Glu Ile Glu
 890 895 900
 Ile Leu Lys Ser Leu Gln His Asp Asn Ile Val Lys Tyr Lys Gly
 905 910 915
 Val Cys Tyr Ser Ala Gly Arg Arg Asn Leu Lys Leu Ile Met Glu
 920 925 930
 Tyr Leu Pro Tyr Gly Ser Leu Arg Asp Tyr Leu Gln Lys His Lys
 935 940 945
 Glu Arg Ile Asp His Ile Lys Leu Leu Gln Tyr Thr Ser Gln Ile
 950 955 960
 Cys Lys Gly Met Glu Tyr Leu Gly Thr Lys Arg Tyr Ile His Arg
 965 970 975
 Asp Leu Ala Thr Arg Asn Ile Leu Val Glu Asn Glu Asn Arg Val
 980 985 990
 Lys Ile Gly Asp Phe Gly Leu Thr Lys Val Leu Pro Gln Asp Lys
 995 1000 1005
 Glu Tyr Tyr Lys Val Lys Glu Pro Gly Glu Ser Pro Ile Phe Trp
 1010 1015 1020
 Tyr Ala Pro Glu Ser Leu Thr Glu Ser Lys Phe Ser Val Ala Ser
 1025 1030 1035
 Asp Val Trp Ser Phe Gly Val Val Leu Tyr Glu Leu Phe Thr Tyr
 1040 1045 1050
 Ile Glu Lys Ser Lys Ser Pro Pro Ala Glu Phe Met Arg Met Ile
 1055 1060 1065
 Gly Asn Asp Lys Gln Gly Gln Met Ile Val Phe His Leu Ile Glu
 1070 1075 1080
 Leu Leu Lys Asn Asn Gly Arg Leu Pro Arg Pro Asp Gly Cys Pro
 1085 1090 1095
 Asp Glu Ile Tyr Met Ile Met Thr Glu Cys Trp Asn Asn Asn Val
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P2490R1SEQ.txt

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1100                                     1105                                     1110
Asn Gln Arg Pro Ser Phe Arg Asp Leu Ala Leu Arg Val Asp Gln
1115                                     1120                                     1125

Ile Arg Asp Asn Met Ala Gly
1130

<210> 117
<211> 188
<212> PRT
<213> Homo sapiens

<400> 117
Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly
 1      5      10      15
Lys Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp
20      25      30
Glu Tyr Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val
35      40      45
Ile Asp Gly Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly
50      55      60
Gln Glu Glu Tyr Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly
65      70      75
Glu Gly Phe Leu Cys Val Phe Ala Ile Asn Asn Thr Lys Ser Phe
80      85      90
Glu Asp Ile His His Tyr Arg Glu Gln Ile Lys Arg Val Lys Asp
95     100     105
Ser Glu Asp Val Pro Met Val Leu Val Gly Asn Lys Cys Asp Leu
110     115     120
Pro Ser Arg Thr Val Asp Thr Lys Gln Ala Gln Asp Leu Ala Arg
125     130     135
Ser Tyr Gly Ile Pro Phe Ile Glu Thr Ser Ala Lys Thr Arg Gln
140     145     150
Gly Val Asp Asp Ala Phe Tyr Thr Leu Val Arg Glu Ile Arg Lys
155     160     165
His Lys Glu Lys Met Ser Lys Asp Gly Lys Lys Lys Lys Lys
170     175     180

Ser Lys Thr Lys Cys Val Ile Met
185

<210> 118
<211> 393
<212> PRT
<213> Homo sapiens

<400> 118
Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro
 1      5      10      15
Asp Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu
20      25      30
Glu Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln
35      40      45

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P2490R1SEQ.txt

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

P2490R1SEQ.txt

Ala Gly Val

<210> 119

<211> 651

<212> PRT

<213> Homo sapiens

<400> 119

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

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P2490R1SEQ.txt

	290		295		300
Met Glu Asp Leu	Ile Ser Leu Trp Gln	Tyr Asp His Leu Thr	Ala		
	305		310		315
Thr Tyr Leu Leu	Leu Leu Ala Lys Lys	Ala Arg Gly Lys Pro	Val		
	320		325		330
Arg Leu Arg Leu	Ser Ser Phe Ser Cys	Gly Gln Ala Ser Ala	Thr		
	335		340		345
Pro Phe Thr Asp	Ile Lys Ser Asn Asn	Trp Ser Leu Glu Asp	Val		
	350		355		360
Thr Ala Ser Asp	Lys Asn Tyr Val Ala	Gly Leu Ile Asp Tyr	Asp		
	365		370		375
Trp Cys Glu Asp	Asp Leu Ser Thr Gly	Ala Ala Thr Pro Arg	Thr		
	380		385		390
Ser Gln Phe Thr	Lys Tyr Trp Thr Glu	Ser Asn Gly Val Glu	Ser		
	395		400		405
Lys Ser Leu Thr	Pro Ala Leu Cys Arg	Thr Pro Ala Asn Lys	Leu		
	410		415		420
Lys Asn Lys Glu	Asn Val Tyr Thr Pro	Lys Ser Ala Val Lys	Asn		
	425		430		435
Glu Glu Tyr Phe	Met Phe Pro Glu Pro	Lys Thr Pro Val Asn	Lys		
	440		445		450
Asn Gln His Lys	Arg Glu Ile Leu Thr	Thr Pro Asn Arg Tyr	Thr		
	455		460		465
Thr Pro Ser Lys	Ala Arg Asn Gln Cys	Leu Lys Glu Thr Pro	Ile		
	470		475		480
Lys Ile Pro Val	Asn Ser Thr Gly Thr	Asp Lys Leu Met Thr	Gly		
	485		490		495
Val Ile Ser Pro	Glu Arg Arg Cys Arg	Ser Val Glu Leu Asp	Leu		
	500		505		510
Asn Gln Ala His	Met Glu Glu Thr Pro	Lys Arg Lys Gly Ala	Lys		
	515		520		525
Val Phe Gly Ser	Leu Glu Arg Gly Leu	Asp Lys Val Ile Thr	Val		
	530		535		540
Leu Thr Arg Ser	Lys Arg Lys Gly Ser	Ala Arg Asp Gly Pro	Arg		
	545		550		555
Arg Leu Lys Leu	His Tyr Asn Val Thr	Thr Thr Arg Leu Val	Asn		
	560		565		570
Pro Asp Gln Leu	Leu Asn Glu Ile Met	Ser Ile Leu Pro Lys	Lys		
	575		580		585
His Val Asp Phe	Val Gln Lys Gly Tyr	Thr Leu Lys Cys Gln	Thr		
	590		595		600
Gln Ser Asp Phe	Gly Lys Val Thr Met	Gln Phe Glu Leu Glu	Val		
	605		610		615
Cys Gln Leu Gln	Lys Pro Asp Val Val	Gly Ile Arg Arg Gln	Arg		
	620		625		630

P2490R1SEQ.txt

Leu Lys Gly Asp Ala Trp Val Tyr Lys Arg Leu Val Glu Asp Ile
635 640 645

Leu Ser Ser Cys Lys Val
650

<210> 120
<211> 2471
<212> PRT
<213> Homo sapiens

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

P2490R1SEQ.txt

Cys Pro Pro Gln Trp Thr Gly Gln Phe Cys Thr Glu Asp Val Asp
 290 295 300
 Glu Cys Leu Leu Gln Pro Asn Ala Cys Gln Asn Gly Gly Thr Cys
 305 310 315
 Ala Asn Arg Asn Gly Gly Tyr Gly Cys Val Cys Val Asn Gly Trp
 320 325 330
 Ser Gly Asp Asp Cys Ser Glu Asn Ile Asp Asp Cys Ala Phe Ala
 335 340 345
 Ser Cys Thr Pro Gly Ser Thr Cys Ile Asp Arg Val Ala Ser Phe
 350 355 360
 Ser Cys Met Cys Pro Glu Gly Lys Ala Gly Leu Leu Cys His Leu
 365 370 375
 Asp Asp Ala Cys Ile Ser Asn Pro Cys His Lys Gly Ala Leu Cys
 380 385 390
 Asp Thr Asn Pro Leu Asn Gly Gln Tyr Ile Cys Thr Cys Pro Gln
 395 400 405
 Gly Tyr Lys Gly Ala Asp Cys Thr Glu Asp Val Asp Glu Cys Ala
 410 415 420
 Met Ala Asn Ser Asn Pro Cys Glu His Ala Gly Lys Cys Val Asn
 425 430 435
 Thr Asp Gly Ala Phe His Cys Glu Cys Leu Lys Gly Tyr Ala Gly
 440 445 450
 Pro Arg Cys Glu Met Asp Ile Asn Glu Cys His Ser Asp Pro Cys
 455 460 465
 Gln Asn Asp Ala Thr Cys Leu Asp Lys Ile Gly Gly Phe Thr Cys
 470 475 480
 Leu Cys Met Pro Gly Phe Lys Gly Val His Cys Glu Leu Glu Ile
 485 490 495
 Asn Glu Cys Gln Ser Asn Pro Cys Val Asn Asn Gly Gln Cys Val
 500 505 510
 Asp Lys Val Asn Arg Phe Gln Cys Leu Cys Pro Pro Gly Phe Thr
 515 520 525
 Gly Pro Val Cys Gln Ile Asp Ile Asp Asp Cys Ser Ser Thr Pro
 530 535 540
 Cys Leu Asn Gly Ala Lys Cys Ile Asp His Pro Asn Gly Tyr Glu
 545 550 555
 Cys Gln Cys Ala Thr Gly Phe Thr Gly Val Leu Cys Glu Glu Asn
 560 565 570
 Ile Asp Asn Cys Asp Pro Asp Pro Cys His His Gly Gln Cys Gln
 575 580 585
 Asp Gly Ile Asp Ser Tyr Thr Cys Ile Cys Asn Pro Gly Tyr Met
 590 595 600
 Gly Ala Ile Cys Ser Asp Gln Ile Asp Glu Cys Tyr Ser Ser Pro
 605 610 615
 Cys Leu Asn Asp Gly Arg Cys Ile Asp Leu Val Asn Gly Tyr Gln
 Page 302

P2490R1SEQ.txt														
620					625					630				
Cys	Asn	Cys	Gln	Pro	Gly	Thr	Ser	Gly	Val	Asn	Cys	Glu	Ile	Asn
				635					640					645
Phe	Asp	Asp	Cys	Ala	Ser	Asn	Pro	Cys	Ile	His	Gly	Ile	Cys	Met
				650					655					660
Asp	Gly	Ile	Asn	Arg	Tyr	Ser	Cys	Val	Cys	Ser	Pro	Gly	Phe	Thr
				665					670					675
Gly	Gln	Arg	Cys	Asn	Ile	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Asn	Pro
				680					685					690
Cys	Arg	Lys	Gly	Ala	Thr	Cys	Ile	Asn	Gly	Val	Asn	Gly	Phe	Arg
				695					700					705
Cys	Ile	Cys	Pro	Glu	Gly	Pro	His	His	Pro	Ser	Cys	Tyr	Ser	Gln
				710					715					720
Val	Asn	Glu	Cys	Leu	Ser	Asn	Pro	Cys	Ile	His	Gly	Asn	Cys	Thr
				725					730					735
Gly	Gly	Leu	Ser	Gly	Tyr	Lys	Cys	Leu	Cys	Asp	Ala	Gly	Trp	Val
				740					745					750
Gly	Ile	Asn	Cys	Glu	Val	Asp	Lys	Asn	Glu	Cys	Leu	Ser	Asn	Pro
				755					760					765
Cys	Gln	Asn	Gly	Gly	Thr	Cys	Asp	Asn	Leu	Val	Asn	Gly	Tyr	Arg
				770					775					780
Cys	Thr	Cys	Lys	Lys	Gly	Phe	Lys	Gly	Tyr	Asn	Cys	Gln	Val	Asn
				785					790					795
Ile	Asp	Glu	Cys	Ala	Ser	Asn	Pro	Cys	Leu	Asn	Gln	Gly	Thr	Cys
				800					805					810
Phe	Asp	Asp	Ile	Ser	Gly	Tyr	Thr	Cys	His	Cys	Val	Leu	Pro	Tyr
				815					820					825
Thr	Gly	Lys	Asn	Cys	Gln	Thr	Val	Leu	Ala	Pro	Cys	Ser	Pro	Asn
				830					835					840
Pro	Cys	Glu	Asn	Ala	Ala	Val	Cys	Lys	Glu	Ser	Pro	Asn	Phe	Glu
				845					850					855
Ser	Tyr	Thr	Cys	Leu	Cys	Ala	Pro	Gly	Trp	Gln	Gly	Gln	Arg	Cys
				860					865					870
Thr	Ile	Asp	Ile	Asp	Glu	Cys	Ile	Ser	Lys	Pro	Cys	Met	Asn	His
				875					880					885
Gly	Leu	Cys	His	Asn	Thr	Gln	Gly	Ser	Tyr	Met	Cys	Glu	Cys	Pro
				890					895					900
Pro	Gly	Phe	Ser	Gly	Met	Asp	Cys	Glu	Glu	Asp	Ile	Asp	Asp	Cys
				905					910					915
Leu	Ala	Asn	Pro	Cys	Gln	Asn	Gly	Gly	Ser	Cys	Met	Asp	Gly	Val
				920					925					930
Asn	Thr	Phe	Ser	Cys	Leu	Cys	Leu	Pro	Gly	Phe	Thr	Gly	Asp	Lys
				935					940					945
Cys	Gln	Thr	Asp	Met	Asn	Glu	Cys	Leu	Ser	Glu	Pro	Cys	Lys	Asn
				950					955					960

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Leu His Trp Ala Ala Ala Val Asn Asn Val Glu Ala Thr Leu Leu
 1985 1990 1995
 Leu Leu Lys Asn Gly Ala Asn Arg Asp Met Gln Asp Asn Lys Glu
 2000 2005 2010
 Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly Ser Tyr Glu Ala
 2015 2020 2025
 Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp Ile Thr Asp
 2030 2035 2040
 His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg Met His
 2045 2050 2055
 His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro Ser
 2060 2065 2070
 Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser Pro Val Ile Cys
 2075 2080 2085
 Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys His Thr Pro Met Gly
 2090 2095 2100
 Lys Lys Ser Arg Arg Pro Ser Ala Lys Ser Thr Met Pro Thr Ser
 2105 2110 2115
 Leu Pro Asn Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly Ser Arg
 2120 2125 2130
 Arg Lys Lys Ser Leu Ser Glu Lys Val Gln Leu Ser Glu Ser Ser
 2135 2140 2145
 Val Thr Leu Ser Pro Val Asp Ser Leu Glu Ser Pro His Thr Tyr
 2150 2155 2160
 Val Ser Asp Thr Thr Ser Ser Pro Met Ile Thr Ser Pro Gly Ile
 2165 2170 2175
 Leu Gln Ala Ser Pro Asn Pro Met Leu Ala Thr Ala Ala Pro Pro
 2180 2185 2190
 Ala Pro Val His Ala Gln His Ala Leu Ser Phe Ser Asn Leu His
 2195 2200 2205
 Glu Met Gln Pro Leu Ala His Gly Ala Ser Thr Val Leu Pro Ser
 2210 2215 2220
 Val Ser Gln Leu Leu Ser His His His Ile Val Ser Pro Gly Ser
 2225 2230 2235
 Gly Ser Ala Gly Ser Leu Ser Arg Leu His Pro Val Pro Val Pro
 2240 2245 2250
 Ala Asp Trp Met Asn Arg Met Glu Val Asn Glu Thr Gln Tyr Asn
 2255 2260 2265
 Glu Met Phe Gly Met Val Leu Ala Pro Ala Glu Gly Thr His Pro
 2270 2275 2280
 Gly Ile Ala Pro Gln Ser Arg Pro Pro Glu Gly Lys His Ile Thr
 2285 2290 2295
 Thr Pro Arg Glu Pro Leu Pro Pro Ile Val Thr Phe Gln Leu Ile
 2300 2305 2310
 Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly Ala Pro Gln Pro Gln
 2315 2320 2325

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P2490R1SEQ.txt

Ser	Thr	Cys	Pro	Ala	Val	Ala	Gly	Leu	Pro	Thr	Met	Tyr
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Gln	Ile	Pro	Glu	Met	Ala	Arg	Leu	Pro	Ser	Val	Ala	Phe
			2345						2350			2355
Ala	Met	Met	Pro	Gln	Gln	Asp	Gly	Gln	Val	Ala	Gln	Thr
			2360						2365			2370
Pro	Ala	Tyr	His	Pro	Phe	Pro	Ala	Ser	Val	Gly	Lys	Tyr
			2375						2380			2385
Pro	Pro	Ser	Gln	His	Ser	Tyr	Ala	Ser	Ser	Asn	Ala	Ala
			2390						2395			2400
Thr	Pro	Ser	His	Ser	Gly	His	Leu	Gln	Gly	Glu	His	Pro
			2405						2410			2415
Thr	Pro	Ser	Pro	Glu	Ser	Pro	Asp	Gln	Trp	Ser	Ser	Ser
			2420						2425			2430
His	Ser	Ala	Ser	Asp	Trp	Ser	Asp	Val	Thr	Thr	Ser	Pro
			2435						2440			2445
Gly	Gly	Ala	Gly	Gly	Gly	Gln	Arg	Gly	Pro	Gly	Thr	His
			2450						2455			2460
Glu	Pro	Pro	His	Asn	Asn	Met	Gln	Val	Tyr	Ala		
			2465						2470			

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<210> 121
<211> 2321
<212> PRT
<213> Homo sapiens
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<400>	121														
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Ser	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Val	Arg	Ala	Leu	Pro	Leu	Leu	
				20					25					30	
Leu	Leu	Leu	Ala	Gly	Pro	Gly	Ala	Ala	Ala	Pro	Pro	Cys	Leu	Asp	
				35					40					45	
Gly	Ser	Pro	Cys	Ala	Asn	Gly	Gly	Arg	Cys	Thr	Gln	Leu	Pro	Ser	
				50					55					60	
Arg	Glu	Ala	Ala	Cys	Leu	Cys	Pro	Pro	Gly	Trp	Val	Gly	Glu	Arg	
				65					70					75	
Cys	Gln	Leu	Glu	Asp	Pro	Cys	His	Ser	Gly	Pro	Cys	Ala	Gly	Arg	
				80					85					90	
Gly	Val	Cys	Gln	Ser	Ser	Val	Val	Ala	Gly	Thr	Ala	Arg	Phe	Ser	
				95					100					105	
Cys	Arg	Cys	Pro	Arg	Gly	Phe	Arg	Gly	Pro	Asp	Cys	Ser	Leu	Pro	
				110					115					120	
Asp	Pro	Cys	Leu	Ser	Ser	Pro	Cys	Ala	His	Gly	Ala	Arg	Cys	Ser	
				125					130					135	
Val	Gly	Pro	Asp	Gly	Arg	Phe	Leu	Cys	Ser	Cys	Pro	Pro	Gly	Tyr	
				140					145					150	
Gln	Gly	Arg	Ser	Cys	Arg	Ser	Asp	Val	Asp	Glu	Cys	Arg	Val	Gly	

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Tyr Thr Gly Pro Ser Cys Asp Gln Asp Ile Asn Asp Cys Asp Pro
 845 850 855
 Asn Pro Cys Leu Asn Gly Gly Ser Cys Gln Asp Gly Val Gly Ser
 860 865 870
 Phe Ser Cys Ser Cys Leu Pro Gly Phe Ala Gly Pro Arg Cys Ala
 875 880 885
 Arg Asp Val Asp Glu Cys Leu Ser Asn Pro Cys Gly Pro Gly Thr
 890 895 900
 Cys Thr Asp His Val Ala Ser Phe Thr Cys Thr Cys Pro Pro Gly
 905 910 915
 Tyr Gly Gly Phe His Cys Glu Gln Asp Leu Pro Asp Cys Ser Pro
 920 925 930
 Ser Ser Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Val Asn Ser
 935 940 945
 Phe Ser Cys Leu Cys Arg Pro Gly Tyr Thr Gly Ala His Cys Gln
 950 955 960
 His Glu Ala Asp Pro Cys Leu Ser Arg Pro Cys Leu His Gly Gly
 965 970 975
 Val Cys Ser Ala Ala His Pro Gly Phe Arg Cys Thr Cys Leu Glu
 980 985 990
 Ser Phe Thr Gly Pro Gln Cys Gln Thr Leu Val Asp Trp Cys Ser
 995 1000 1005
 Arg Gln Pro Cys Gln Asn Gly Gly Arg Cys Val Gln Thr Gly Ala
 1010 1015 1020
 Tyr Cys Leu Cys Pro Pro Gly Trp Ser Gly Arg Leu Cys Asp Ile
 1025 1030 1035
 Arg Ser Leu Pro Cys Arg Glu Ala Ala Ala Gln Ile Gly Val Arg
 1040 1045 1050
 Leu Glu Gln Leu Cys Gln Ala Gly Gly Gln Cys Val Asp Glu Asp
 1055 1060 1065
 Ser Ser His Tyr Cys Val Cys Pro Glu Gly Arg Thr Gly Ser His
 1070 1075 1080
 Cys Glu Gln Glu Val Asp Pro Cys Leu Ala Gln Pro Cys Gln His
 1085 1090 1095
 Gly Gly Thr Cys Arg Gly Tyr Met Gly Gly Tyr Met Cys Glu Cys
 1100 1105 1110
 Leu Pro Gly Tyr Asn Gly Asp Asn Cys Glu Asp Asp Val Asp Glu
 1115 1120 1125
 Cys Ala Ser Gln Pro Cys Gln His Gly Gly Ser Cys Ile Asp Leu
 1130 1135 1140
 Val Ala Arg Tyr Leu Cys Ser Cys Pro Pro Gly Thr Leu Gly Val
 1145 1150 1155
 Leu Cys Glu Ile Asn Glu Asp Asp Cys Gly Pro Gly Pro Pro Leu
 1160 1165 1170
 Asp Ser Gly Pro Arg Cys Leu His Asn Gly Thr Cys Val Asp Leu
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1175		1180		1185
Val Gly Gly Phe Arg Cys Thr Cys Pro Pro Gly Tyr Thr Gly Leu				
1190		1195		1200
Arg Cys Glu Ala Asp Ile Asn Glu Cys Arg Ser Gly Ala Cys His				
1205		1210		1215
Ala Ala His Thr Arg Asp Cys Leu Gln Asp Pro Gly Gly Gly Phe				
1220		1225		1230
Arg Cys Leu Cys His Ala Gly Phe Ser Gly Pro Arg Cys Gln Thr				
1235		1240		1245
Val Leu Ser Pro Cys Glu Ser Gln Pro Cys Gln His Gly Gly Gln				
1250		1255		1260
Cys Arg Pro Ser Pro Gly Pro Gly Gly Gly Leu Thr Phe Thr Cys				
1265		1270		1275
His Cys Ala Gln Pro Phe Trp Gly Pro Arg Cys Glu Arg Val Ala				
1280		1285		1290
Arg Ser Cys Arg Glu Leu Gln Cys Pro Val Gly Val Pro Cys Gln				
1295		1300		1305
Gln Thr Pro Arg Gly Pro Arg Cys Ala Cys Pro Pro Gly Leu Ser				
1310		1315		1320
Gly Pro Ser Cys Arg Ser Phe Pro Gly Ser Pro Pro Gly Ala Ser				
1325		1330		1335
Asn Ala Ser Cys Ala Ala Ala Pro Cys Leu His Gly Gly Ser Cys				
1340		1345		1350
Arg Pro Ala Pro Leu Ala Pro Phe Phe Arg Cys Ala Cys Ala Gln				
1355		1360		1365
Gly Trp Thr Gly Pro Arg Cys Glu Ala Pro Ala Ala Ala Pro Glu				
1370		1375		1380
Val Ser Glu Glu Pro Arg Cys Pro Arg Ala Ala Cys Gln Ala Lys				
1385		1390		1395
Arg Gly Asp Gln Arg Cys Asp Arg Glu Cys Asn Ser Pro Gly Cys				
1400		1405		1410
Gly Trp Asp Gly Gly Asp Cys Ser Leu Ser Val Gly Asp Pro Trp				
1415		1420		1425
Arg Gln Cys Glu Ala Leu Gln Cys Trp Arg Leu Phe Asn Asn Ser				
1430		1435		1440
Arg Cys Asp Pro Ala Cys Ser Ser Pro Ala Cys Leu Tyr Asp Asn				
1445		1450		1455
Phe Asp Cys His Ala Gly Gly Arg Glu Arg Thr Cys Asn Pro Val				
1460		1465		1470
Tyr Glu Lys Tyr Cys Ala Asp His Phe Ala Asp Gly Arg Cys Asp				
1475		1480		1485
Gln Gly Cys Asn Thr Glu Glu Cys Gly Trp Asp Gly Leu Asp Cys				
1490		1495		1500
Ala Ser Glu Val Pro Ala Leu Leu Ala Arg Gly Val Leu Val Leu				
1505		1510		1515

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Ala Gly Ala Asp Thr Asn Ala Gln Asp His Ser Gly Arg Thr Pro
 1865 1870 1875
 Leu His Thr Ala Val Thr Ala Asp Ala Gln Gly Val Phe Gln Ile
 1880 1885 1890
 Leu Ile Arg Asn Arg Ser Thr Asp Leu Asp Ala Arg Met Ala Asp
 1895 1900 1905
 Gly Ser Thr Ala Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly
 1910 1915 1920
 Met Val Glu Glu Leu Ile Ala Ser His Ala Asp Val Asn Ala Val
 1925 1930 1935
 Asp Glu Leu Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn
 1940 1945 1950
 Asn Val Glu Ala Thr Leu Ala Leu Leu Lys Asn Gly Ala Asn Lys
 1955 1960 1965
 Asp Met Gln Asp Ser Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala
 1970 1975 1980
 Arg Glu Gly Ser Tyr Glu Ala Ala Lys Leu Leu Leu Asp His Phe
 1985 1990 1995
 Ala Asn Arg Glu Ile Thr Asp His Leu Asp Arg Leu Pro Arg Asp
 2000 2005 2010
 Val Ala Gln Glu Arg Leu His Gln Asp Ile Val Arg Leu Leu Asp
 2015 2020 2025
 Gln Pro Ser Gly Pro Arg Ser Pro Pro Gly Pro His Gly Leu Gly
 2030 2035 2040
 Pro Leu Leu Cys Pro Pro Gly Ala Phe Leu Pro Gly Leu Lys Ala
 2045 2050 2055
 Ala Gln Ser Gly Ser Lys Lys Ser Arg Arg Pro Pro Gly Lys Ala
 2060 2065 2070
 Gly Leu Gly Pro Gln Gly Pro Arg Gly Arg Gly Lys Lys Leu Thr
 2075 2080 2085
 Leu Ala Cys Pro Gly Pro Leu Ala Asp Ser Ser Val Thr Leu Ser
 2090 2095 2100
 Pro Val Asp Ser Leu Asp Ser Pro Arg Pro Phe Gly Gly Pro Pro
 2105 2110 2115
 Ala Ser Pro Gly Gly Phe Pro Leu Glu Gly Pro Tyr Ala Ala Ala
 2120 2125 2130
 Thr Ala Thr Ala Val Ser Leu Ala Gln Leu Gly Gly Pro Gly Arg
 2135 2140 2145
 Ala Gly Leu Gly Arg Gln Pro Pro Gly Gly Cys Val Leu Ser Leu
 2150 2155 2160
 Gly Leu Leu Asn Pro Val Ala Val Pro Leu Asp Trp Ala Arg Leu
 2165 2170 2175
 Pro Pro Pro Ala Pro Pro Gly Pro Ser Phe Leu Leu Pro Leu Ala
 2180 2185 2190
 Pro Gly Pro Gln Leu Leu Asn Pro Gly Thr Pro Val Ser Pro Gln

P2490R1SEQ.txt
2200

2195		2205
Glu Arg Pro Pro Pro Tyr Leu Ala Val Pro Gly His Gly Glu Glu		
2210	2215	2220
Tyr Pro Val Ala Gly Ala His Ser Ser Pro Pro Lys Ala Arg Phe		
2225	2230	2235
Leu Arg Val Pro Ser Glu His Pro Tyr Leu Thr Pro Ser Pro Glu		
2240	2245	2250
Ser Pro Glu His Trp Ala Ser Pro Ser Pro Pro Ser Leu Ser Asp		
2255	2260	2265
Trp Ser Glu Ser Thr Pro Ser Pro Ala Thr Ala Thr Gly Ala Met		
2270	2275	2280
Ala Thr Thr Thr Gly Ala Leu Pro Ala Gln Pro Leu Pro Leu Ser		
2285	2290	2295
Val Pro Ser Ser Leu Ala Gln Ala Gln Thr Gln Leu Gly Pro Gln		
2300	2305	2310
Pro Glu Val Thr Pro Lys Arg Gln Val Leu Ala		
2315	2320	

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<211> 923
<212> PRT
<213> Homo sapiens

<400> 122
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Leu Ala Pro Ala Gly Ala Phe Arg Asn Asp Glu Cys Gly Asp Thr
20 25 30
Ile Lys Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro
35 40 45
His Ser Tyr His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala
50 55 60
Pro Asp Pro Tyr Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe
65 70 75
Asp Leu Glu Asp Arg Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe
80 85 90
Asp Gly Glu Asn Glu Asn Gly His Phe Arg Gly Lys Phe Cys Gly
95 100 105
Lys Ile Ala Pro Pro Pro Val Val Ser Ser Gly Pro Phe Leu Phe
110 115 120
Ile Lys Phe Val Ser Asp Tyr Glu Thr His Gly Ala Gly Phe Ser
125 130 135
Ile Arg Tyr Glu Ile Phe Lys Arg Gly Pro Glu Cys Ser Gln Asn
140 145 150
Tyr Thr Thr Pro Ser Gly Val Ile Lys Ser Pro Gly Phe Pro Glu
155 160 165
Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile Val Phe Ala Pro
170 175 180

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

860		865		870
Leu Gly Ala Val	Cys Gly Val Val Leu Tyr Cys Ala Cys Trp His			
	875		880	885
Asn Gly Met Ser	Glu Arg Asn Leu Ser Ala Leu Glu Asn Tyr Asn			
	890		895	900
Phe Glu Leu Val	Asp Gly Val Lys Leu Lys Lys Asp Lys Leu Asn			
	905		910	915
Thr Gln Ser Thr	Tyr Ser Glu Ala			
	920			

<210> 123
 <211> 2556
 <212> PRT
 <213> Homo sapiens

<400> 123

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

920	925	930
Phe Cys Asp Cys Leu Pro Gly Phe Arg Gly Thr Phe Cys Glu Glu	935	940
Asp Ile Asn Glu Cys Ala Ser Asp Pro Cys Arg Asn Gly Ala Asn	950	955
Cys Thr Asp Cys Val Asp Ser Tyr Thr Cys Thr Cys Pro Ala Gly	965	970
Phe Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu	980	985
Ser Ser Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser	995	1000
Phe Thr Cys Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln	1010	1015
His Asp Val Asn Glu Cys Asp Ser Gln Pro Cys Leu His Gly Gly	1025	1030
Thr Cys Gln Asp Gly Cys Gly Ser Tyr Arg Cys Thr Cys Pro Gln	1040	1045
Gly Tyr Thr Gly Pro Asn Cys Gln Asn Leu Val His Trp Cys Asp	1055	1060
Ser Ser Pro Cys Lys Asn Gly Gly Lys Cys Trp Gln Thr His Thr	1070	1075
Gln Tyr Arg Cys Glu Cys Pro Ser Gly Trp Thr Gly Leu Tyr Cys	1085	1090
Asp Val Pro Ser Val Ser Cys Glu Val Ala Ala Gln Arg Gln Gly	1100	1105
Val Asp Val Ala Arg Leu Cys Gln His Gly Gly Leu Cys Val Asp	1115	1120
Ala Gly Asn Thr His His Cys Arg Cys Gln Ala Gly Tyr Thr Gly	1130	1135
Ser Tyr Cys Glu Asp Leu Val Asp Glu Cys Ser Pro Ser Pro Cys	1145	1150
Gln Asn Gly Ala Thr Cys Thr Asp Tyr Leu Gly Gly Tyr Ser Cys	1160	1165
Lys Cys Val Ala Gly Tyr His Gly Val Asn Cys Ser Glu Glu Ile	1175	1180
Asp Glu Cys Leu Ser His Pro Cys Gln Asn Gly Gly Thr Cys Leu	1190	1195
Asp Leu Pro Asn Thr Tyr Lys Cys Ser Cys Pro Arg Gly Thr Gln	1205	1210
Gly Val His Cys Glu Ile Asn Val Asp Asp Cys Asn Pro Pro Val	1220	1225
Asp Pro Val Ser Arg Ser Pro Lys Cys Phe Asn Asn Gly Thr Cys	1235	1240
Val Asp Gln Val Gly Gly Tyr Ser Cys Thr Cys Pro Pro Gly Phe	1250	1255
		1260

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Val Phe Lys Arg Asp Ala His Gly Gln Gln Met Ile Phe Pro Tyr
 1610 1615 1620
 Tyr Gly Arg Glu Glu Glu Leu Arg Lys His Pro Ile Lys Arg Ala
 1625 1630 1635
 Ala Glu Gly Trp Ala Ala Pro Asp Ala Leu Leu Gly Gln Val Lys
 1640 1645 1650
 Ala Ser Leu Leu Pro Gly Gly Ser Glu Gly Gly Arg Arg Arg Arg
 1655 1660 1665
 Glu Leu Asp Pro Met Asp Val Arg Gly Ser Ile Val Tyr Leu Glu
 1670 1675 1680
 Ile Asp Asn Arg Gln Cys Val Gln Ala Ser Ser Gln Cys Phe Gln
 1685 1690 1695
 Ser Ala Thr Asp Val Ala Ala Phe Leu Gly Ala Leu Ala Ser Leu
 1700 1705 1710
 Gly Ser Leu Asn Ile Pro Tyr Lys Ile Glu Ala Val Gln Ser Glu
 1715 1720 1725
 Thr Val Glu Pro Pro Pro Pro Ala Gln Leu His Phe Met Tyr Val
 1730 1735 1740
 Ala Ala Ala Ala Phe Val Leu Leu Phe Phe Val Gly Cys Gly Val
 1745 1750 1755
 Leu Leu Ser Arg Lys Arg Arg Arg Gln His Gly Gln Leu Trp Phe
 1760 1765 1770
 Pro Glu Gly Phe Lys Val Ser Glu Ala Ser Lys Lys Lys Arg Arg
 1775 1780 1785
 Glu Pro Leu Gly Glu Asp Ser Val Gly Leu Lys Pro Leu Lys Asn
 1790 1795 1800
 Ala Ser Asp Gly Ala Leu Met Asp Asp Asn Gln Asn Glu Trp Gly
 1805 1810 1815
 Asp Glu Asp Leu Glu Thr Lys Lys Phe Arg Phe Glu Glu Pro Val
 1820 1825 1830
 Val Leu Pro Asp Leu Asp Asp Gln Thr Asp His Arg Gln Trp Thr
 1835 1840 1845
 Gln Gln His Leu Asp Ala Ala Asp Leu Arg Met Ser Ala Met Ala
 1850 1855 1860
 Pro Thr Pro Pro Gln Gly Glu Val Asp Ala Asp Cys Met Asp Val
 1865 1870 1875
 Asn Val Arg Gly Pro Asp Gly Phe Thr Pro Leu Met Ile Ala Ser
 1880 1885 1890
 Cys Ser Gly Gly Gly Leu Glu Thr Gly Asn Ser Glu Glu Glu Glu
 1895 1900 1905
 Asp Ala Pro Ala Val Ile Ser Asp Phe Ile Tyr Gln Gly Ala Ser
 1910 1915 1920
 Leu His Asn Gln Thr Asp Arg Thr Gly Glu Thr Ala Leu His Leu
 1925 1930 1935
 Ala Ala Arg Tyr Ser Arg Ser Asp Ala Ala Lys Arg Leu Leu Glu
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P2490R1SEQ.txt

1940	1945	1950
Ala Ser Ala Asp Ala	Asn Ile Gln Asp Asn Met Gly Arg Thr Pro	
1955	1960	1965
Leu His Ala Ala Val	Ser Ala Asp Ala Gln Gly Val Phe Gln Ile	
1970	1975	1980
Leu Ile Arg Asn Arg	Ala Thr Asp Leu Asp Ala Arg Met His Asp	
1985	1990	1995
Gly Thr Thr Pro Leu	Ile Leu Ala Ala Arg Leu Ala Val Glu Gly	
2000	2005	2010
Met Leu Glu Asp Leu	Ile Asn Ser His Ala Asp Val Asn Ala Val	
2015	2020	2025
Asp Asp Leu Gly Lys	Ser Ala Leu His Trp Ala Ala Ala Val Asn	
2030	2035	2040
Asn Val Asp Ala Ala	Val Val Leu Leu Lys Asn Gly Ala Asn Lys	
2045	2050	2055
Asp Met Gln Asn Asn	Arg Glu Glu Thr Pro Leu Phe Leu Ala Ala	
2060	2065	2070
Arg Glu Gly Ser Tyr	Glu Thr Ala Lys Val Leu Leu Asp His Phe	
2075	2080	2085
Ala Asn Arg Asp Ile	Thr Asp His Met Asp Arg Leu Pro Arg Asp	
2090	2095	2100
Ile Ala Gln Glu Arg	Met His His Asp Ile Val Arg Leu Leu Asp	
2105	2110	2115
Glu Tyr Asn Leu Val	Arg Ser Pro Gln Leu His Gly Ala Pro Leu	
2120	2125	2130
Gly Gly Thr Pro Thr	Leu Ser Pro Pro Leu Cys Ser Pro Asn Gly	
2135	2140	2145
Tyr Leu Gly Ser Leu	Lys Pro Gly Val Gln Gly Lys Lys Val Arg	
2150	2155	2160
Lys Pro Ser Ser Lys	Gly Leu Ala Cys Gly Ser Lys Glu Ala Lys	
2165	2170	2175
Asp Leu Lys Ala Arg	Arg Lys Lys Ser Gln Asp Gly Lys Gly Cys	
2180	2185	2190
Leu Leu Asp Ser Ser	Gly Met Leu Ser Pro Val Asp Ser Leu Glu	
2195	2200	2205
Ser Pro His Gly Tyr	Leu Ser Asp Val Ala Ser Pro Pro Leu Leu	
2210	2215	2220
Pro Ser Pro Phe Gln	Gln Ser Pro Ser Val Pro Leu Asn His Leu	
2225	2230	2235
Pro Gly Met Pro Asp	Thr His Leu Gly Ile Gly His Leu Asn Val	
2240	2245	2250
Ala Ala Lys Pro Glu	Met Ala Ala Leu Gly Gly Gly Gly Arg Leu	
2255	2260	2265
Ala Phe Glu Thr Gly	Pro Pro Arg Leu Ser His Leu Pro Val Ala	
2270	2275	2280

P2490R1SEQ.txt

Ser Gly Thr Ser Thr Val Leu Gly Ser Ser Ser Gly Gly Ala Leu
2285 2290 2295
Asn Phe Thr Val Gly Gly Ser Thr Ser Leu Asn Gly Gln Cys Glu
2300 2305 2310
Trp Leu Ser Arg Leu Gln Ser Gly Met Val Pro Asn Gln Tyr Asn
2315 2320 2325
Pro Leu Arg Gly Ser Val Ala Pro Gly Pro Leu Ser Thr Gln Ala
2330 2335 2340
Pro Ser Leu Gln His Gly Met Val Gly Pro Leu His Ser Ser Leu
2345 2350 2355
Ala Ala Ser Ala Leu Ser Gln Met Met Ser Tyr Gln Gly Leu Pro
2360 2365 2370
Ser Thr Arg Leu Ala Thr Gln Pro His Leu Val Gln Thr Gln Gln
2375 2380 2385
Val Gln Pro Gln Asn Leu Gln Met Gln Gln Gln Asn Leu Gln Pro
2390 2395 2400
Ala Asn Ile Gln Gln Gln Gln Ser Leu Gln Pro Pro Pro Pro Pro
2405 2410 2415
Pro Gln Pro His Leu Gly Val Ser Ser Ala Ala Ser Gly His Leu
2420 2425 2430
Gly Arg Ser Phe Leu Ser Gly Glu Pro Ser Gln Ala Asp Val Gln
2435 2440 2445
Pro Leu Gly Pro Ser Ser Leu Ala Val His Thr Ile Leu Pro Gln
2450 2455 2460
Glu Ser Pro Ala Leu Pro Thr Ser Leu Pro Ser Ser Leu Val Pro
2465 2470 2475
Pro Val Thr Ala Ala Gln Phe Leu Thr Pro Pro Ser Gln His Ser
2480 2485 2490
Tyr Ser Ser Pro Val Asp Asn Thr Pro Ser His Gln Leu Gln Val
2495 2500 2505
Pro Glu His Pro Phe Leu Thr Pro Ser Pro Glu Ser Pro Asp Gln
2510 2515 2520
Trp Ser Ser Ser Ser Pro His Ser Asn Val Ser Asp Trp Ser Glu
2525 2530 2535
Gly Val Ser Ser Pro Pro Thr Ser Met Gln Ser Gln Ile Ala Arg
2540 2545 2550
Ile Pro Glu Ala Phe Lys
2555

<210> 124
<211> 796
<212> PRT
<213> Homo sapiens

<400> 124
Met Leu Arg Gly Gly Arg Arg Gly Gln Leu Gly Trp His Ser Trp
1 5 10 15
Ala Ala Gly Pro Gly Ser Leu Leu Ala Trp Leu Ile Leu Ala Ser
20 25 30

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Thr	Glu	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Val	Leu	Trp	Glu	Ile
				710					715					720
Phe	Thr	Tyr	Gly	Lys	Gln	Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Thr	Glu
				725					730					735
Ala	Ile	Asp	Cys	Ile	Thr	Gln	Gly	Arg	Glu	Leu	Glu	Arg	Pro	Arg
				740					745					750
Ala	Cys	Pro	Pro	Glu	Val	Tyr	Ala	Ile	Met	Arg	Gly	Cys	Trp	Gln
				755					760					765
Arg	Glu	Pro	Gln	Gln	Arg	His	Ser	Ile	Lys	Asp	Val	His	Ala	Arg
				770					775					780
Leu	Gln	Ala	Leu	Ala	Gln	Ala	Pro	Pro	Val	Tyr	Leu	Asp	Val	Leu
				785					790					795

Gly

<210> 125
 <211> 822
 <212> PRT
 <213> Homo sapiens

<400> 125

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

P2490R1SEQ.txt

Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro Val
 215 220 225
 Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met
 230 235 240
 Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile
 245 250 255
 Ser Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn
 260 265 270
 Leu Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe
 275 280 285
 Ala Pro Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His
 290 295 300
 Trp Cys Ile Pro Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu
 305 310 315
 Gln Trp Phe Tyr Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile
 320 325 330
 Cys Thr Lys Ile His Val Thr Asn His Thr Glu Tyr His Gly Cys
 335 340 345
 Leu Gln Leu Asp Asn Pro Thr His Met Asn Asn Gly Asp Tyr Thr
 350 355 360
 Leu Ile Ala Lys Asn Glu Tyr Gly Lys Asp Glu Lys Gln Ile Ser
 365 370 375
 Ala His Phe Met Gly Trp Pro Gly Ile Asp Asp Gly Ala Asn Pro
 380 385 390
 Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr Gly Thr Ala Ala Asn
 395 400 405
 Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu Ile Pro Ser Thr
 410 415 420
 Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser Val Tyr Ala
 425 430 435
 Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val Met
 440 445 450
 Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys
 455 460 465
 Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro
 470 475 480
 Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu
 485 490 495
 Gly Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val
 500 505 510
 Ile Glu Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys
 515 520 525
 Pro Asp Thr Phe Val Gln His Ile Lys Arg His Asn Ile Val Leu
 530 535 540
 Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala
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P2490R1SEQ.txt

	545		550		555
Glu Cys Tyr Asn	Leu Cys Pro Glu Gln	Asp Lys Ile Leu Val	Ala		
	560		565		570
Val Lys Thr Leu	Lys Asp Ala Ser Asp	Asn Ala Arg Lys Asp	Phe		
	575		580		585
His Arg Glu Ala	Glu Leu Leu Thr Asn	Leu Gln His Glu His	Ile		
	590		595		600
Val Lys Phe Tyr	Gly Val Cys Val Glu	Gly Asp Pro Leu Ile	Met		
	605		610		615
Val Phe Glu Tyr	Met Lys His Gly Asp	Leu Asn Lys Phe Leu	Arg		
	620		625		630
Ala His Gly Pro	Asp Ala Val Leu Met	Ala Glu Gly Asn Pro	Pro		
	635		640		645
Thr Glu Leu Thr	Gln Ser Gln Met Leu	His Ile Ala Gln Gln	Ile		
	650		655		660
Ala Ala Gly Met	Val Tyr Leu Ala Ser	Gln His Phe Val His	Arg		
	665		670		675
Asp Leu Ala Thr	Arg Asn Cys Leu Val	Gly Glu Asn Leu Leu	Val		
	680		685		690
Lys Ile Gly Asp	Phe Gly Met Ser Arg	Asp Val Tyr Ser Thr	Asp		
	695		700		705
Tyr Tyr Arg Val	Gly Gly His Thr Met	Leu Pro Ile Arg Trp	Met		
	710		715		720
Pro Pro Glu Ser	Ile Met Tyr Arg Lys	Phe Thr Thr Glu Ser	Asp		
	725		730		735
Val Trp Ser Leu	Gly Val Val Leu Trp	Glu Ile Phe Thr Tyr	Gly		
	740		745		750
Lys Gln Pro Trp	Tyr Gln Leu Ser Asn	Asn Glu Val Ile Glu	Cys		
	755		760		765
Ile Thr Gln Gly	Arg Val Leu Gln Arg	Pro Arg Thr Cys Pro	Gln		
	770		775		780
Glu Val Tyr Glu	Leu Met Leu Gly Cys	Trp Gln Arg Glu Pro	His		
	785		790		795
Met Arg Lys Asn	Ile Lys Gly Ile His	Thr Leu Leu Gln Asn	Leu		
	800		805		810
Ala Lys Ala Ser	Pro Val Tyr Leu Asp	Ile Leu Gly			
	815		820		

<210> 126
 <211> 839
 <212> PRT
 <213> Homo sapiens

<400> 126
 Met Asp Val Ser Leu Cys Pro Ala Lys Cys Ser Phe Trp Arg Ile
 1 5 10 15
 Phe Leu Leu Gly Ser Val Trp Leu Asp Tyr Val Gly Ser Val Leu
 20 25 30

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

710		715		720
Cys Ile Trp Cys	Glu Val Gly Gly His	Thr Met Leu Pro Ile	Arg	
	725	730	735	
Trp Met Pro Pro	Glu Ser Ile Met Tyr	Arg Lys Phe Thr Thr	Glu	
	740	745	750	
Ser Asp Val Trp	Ser Phe Gly Val Ile	Leu Trp Glu Ile Phe	Thr	
	755	760	765	
Tyr Gly Lys Gln	Pro Trp Phe Gln Leu	Ser Asn Thr Glu Val	Ile	
	770	775	780	
Glu Cys Ile Thr	Gln Gly Arg Val Leu	Glu Arg Pro Arg Val	Cys	
	785	790	795	
Pro Lys Glu Val	Tyr Asp Val Met Leu	Gly Cys Trp Gln Arg	Glu	
	800	805	810	
Pro Gln Gln Arg	Leu Asn Ile Lys Glu	Ile Tyr Lys Ile Leu	His	
	815	820	825	
Ala Leu Gly Lys	Ala Thr Pro Ile Tyr	Leu Asp Ile Leu Gly		
	830	835		

<210> 127
 <211> 470
 <212> PRT
 <213> Homo sapiens

<400> 127

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

P2490R1SEQ.txt

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

<210> 128
 <211> 681
 <212> PRT
 <213> Homo sapiens

<400> 128
 Met Phe Arg Lys Lys Lys Lys Arg Pro Glu Ile Ser Ala Pro
 1 5 10 15

P2490R1SEQ.txt

Gln Asn Phe Gln His Arg Val His Thr Ser Phe Asp Pro Lys Glu
 20 25 30
 Gly Lys Phe Val Gly Leu Pro Pro Gln Trp Gln Asn Ile Leu Asp
 35 40 45
 Thr Leu Arg Arg Pro Lys Pro Val Val Asp Pro Ser Arg Ile Thr
 50 55 60
 Arg Val Gln Leu Gln Pro Met Lys Thr Val Val Arg Gly Ser Ala
 65 70 75
 Met Pro Val Asp Gly Tyr Ile Ser Gly Leu Leu Asn Asp Ile Gln
 80 85 90
 Lys Leu Ser Val Ile Ser Ser Asn Thr Leu Arg Gly Arg Ser Pro
 95 100 105
 Thr Ser Arg Arg Arg Ala Gln Ser Leu Gly Leu Leu Gly Asp Glu
 110 115 120
 His Trp Ala Thr Asp Pro Asp Met Tyr Leu Gln Ser Pro Gln Ser
 125 130 135
 Glu Arg Thr Asp Pro His Gly Leu Tyr Leu Ser Cys Asn Gly Gly
 140 145 150
 Thr Pro Ala Gly His Lys Gln Met Pro Trp Pro Glu Pro Gln Ser
 155 160 165
 Pro Arg Val Leu Pro Asn Gly Leu Ala Ala Lys Ala Gln Ser Leu
 170 175 180
 Gly Pro Ala Glu Phe Gln Gly Ala Ser Gln Arg Cys Leu Gln Leu
 185 190 195
 Gly Ala Cys Leu Gln Ser Ser Pro Pro Gly Ala Ser Pro Pro Thr
 200 205 210
 Gly Thr Asn Arg His Gly Met Lys Ala Ala Lys His Gly Ser Glu
 215 220 225
 Glu Ala Arg Pro Gln Ser Cys Leu Val Gly Ser Ala Thr Gly Arg
 230 235 240
 Pro Gly Gly Glu Gly Ser Pro Ser Pro Lys Thr Arg Glu Ser Ser
 245 250 255
 Leu Lys Arg Arg Leu Phe Arg Ser Met Phe Leu Ser Thr Ala Ala
 260 265 270
 Thr Ala Pro Pro Ser Ser Ser Lys Pro Gly Pro Pro Pro Gln Ser
 275 280 285
 Lys Pro Asn Ser Ser Phe Arg Pro Pro Gln Lys Asp Asn Pro Pro
 290 295 300
 Ser Leu Val Ala Lys Ala Gln Ser Leu Pro Ser Asp Gln Pro Val
 305 310 315
 Gly Thr Phe Ser Pro Leu Thr Thr Ser Asp Thr Ser Ser Pro Gln
 320 325 330
 Lys Ser Leu Arg Thr Ala Pro Ala Thr Gly Gln Leu Pro Gly Arg
 335 340 345
 Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp His Ala Gln Ile Ser
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P2490R1SEQ.txt														
350					355					360				
Thr	Ser	Asn	Leu	Tyr	Leu	Pro	Gln	Asp	Pro	Thr	Val	Ala	Lys	Gly
				365					370					375
Ala	Leu	Ala	Gly	Glu	Asp	Thr	Gly	Val	Val	Thr	His	Glu	Gln	Phe
				380					385					390
Lys	Ala	Ala	Leu	Arg	Met	Val	Val	Asp	Gln	Gly	Asp	Pro	Arg	Leu
				395					400					405
Leu	Leu	Asp	Ser	Tyr	Val	Lys	Ile	Gly	Glu	Gly	Ser	Thr	Gly	Ile
				410					415					420
Val	Cys	Leu	Ala	Arg	Glu	Lys	His	Ser	Gly	Arg	Gln	Val	Ala	Val
				425					430					435
Lys	Met	Met	Asp	Leu	Arg	Lys	Gln	Gln	Arg	Arg	Glu	Leu	Leu	Phe
				440					445					450
Asn	Glu	Val	Val	Ile	Met	Arg	Asp	Tyr	Gln	His	Phe	Asn	Val	Val
				455					460					465
Glu	Met	Tyr	Lys	Ser	Tyr	Leu	Val	Gly	Glu	Glu	Leu	Trp	Val	Leu
				470					475					480
Met	Glu	Phe	Leu	Gln	Gly	Gly	Ala	Leu	Thr	Asp	Ile	Val	Ser	Gln
				485					490					495
Val	Arg	Leu	Asn	Glu	Glu	Gln	Ile	Ala	Thr	Val	Cys	Glu	Ala	Val
				500					505					510
Leu	Gln	Ala	Leu	Ala	Tyr	Leu	His	Ala	Gln	Gly	Val	Ile	His	Arg
				515					520					525
Asp	Ile	Lys	Ser	Asp	Ser	Ile	Leu	Leu	Thr	Leu	Asp	Gly	Arg	Val
				530					535					540
Lys	Leu	Ser	Asp	Phe	Gly	Phe	Cys	Ala	Gln	Ile	Ser	Lys	Asp	Val
				545					550					555
Pro	Lys	Arg	Lys	Ser	Leu	Val	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro
				560					565					570
Glu	Val	Ile	Ser	Arg	Ser	Leu	Tyr	Ala	Thr	Glu	Val	Asp	Ile	Trp
				575					580					585
Ser	Leu	Gly	Ile	Met	Val	Ile	Glu	Met	Val	Asp	Gly	Glu	Pro	Pro
				590					595					600
Tyr	Phe	Ser	Asp	Ser	Pro	Val	Gln	Ala	Met	Lys	Arg	Leu	Arg	Asp
				605					610					615
Ser	Pro	Pro	Pro	Lys	Leu	Lys	Asn	Ser	His	Lys	Val	Ser	Pro	Val
				620					625					630
Leu	Arg	Asp	Phe	Leu	Glu	Arg	Met	Leu	Val	Arg	Asp	Pro	Gln	Glu
				635					640					645
Arg	Ala	Thr	Ala	Gln	Glu	Leu	Leu	Asp	His	Pro	Phe	Leu	Leu	Gln
				650					655					660
Thr	Gly	Leu	Pro	Glu	Cys	Leu	Val	Pro	Leu	Ile	Gln	Leu	Tyr	Arg
				665					670					675
Lys	Gln	Thr	Ser	Thr	Cys									
				680										

P2490R1SEQ.txt

<210> 129
 <211> 1106
 <212> PRT
 <213> Homo sapiens

<400> 129
 Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu
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 Leu Leu Leu Leu Ser Leu Leu Leu Leu Leu Glu Pro Gln Ile Ser
 20 25 30
 Gln Gly Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn
 35 40 45
 Val Ser Ser Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val
 50 55 60
 Val Trp Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys
 65 70 75
 Ala Gln Asp Gly Thr Phe Ser Ser Val Leu Thr Leu Thr Asn Leu
 80 85 90
 Thr Gly Leu Asp Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser
 95 100 105
 Arg Gly Leu Glu Thr Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val
 110 115 120
 Pro Asp Pro Thr Val Gly Phe Leu Pro Asn Asp Ala Glu Glu Leu
 125 130 135
 Phe Ile Phe Leu Thr Glu Ile Thr Glu Ile Thr Ile Pro Cys Arg
 140 145 150
 Val Thr Asp Pro Gln Leu Val Val Thr Leu His Glu Lys Lys Gly
 155 160 165
 Asp Val Ala Leu Pro Val Pro Tyr Asp His Gln Arg Gly Phe Ser
 170 175 180
 Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr Thr Ile Gly
 185 190 195
 Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val Tyr Arg Leu Gln
 200 205 210
 Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln Thr Val Val
 215 220 225
 Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile Gly Asn
 230 235 240
 Glu Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly
 245 250 255
 Arg Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr
 260 265 270
 His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp
 275 280 285
 Ser Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His
 290 295 300
 Gln Asp Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr
 305 310 315

P2490R1SEQ.txt

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

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P2490R1SEQ.txt

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

P2490R1SEQ.txt

Arg Leu Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser
 995 1000 1005
 Ser Val Leu Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp
 1010 1015 1020
 Tyr Ile Ile Pro Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu
 1025 1030 1035
 Gly Pro Leu Glu Gly Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn
 1040 1045 1050
 Glu Val Asn Thr Ser Ser Thr Ile Ser Cys Asp Ser Pro Leu Glu
 1055 1060 1065
 Pro Gln Asp Glu Pro Glu Pro Glu Pro Gln Leu Glu Leu Gln Val
 1070 1075 1080
 Glu Pro Glu Pro Glu Leu Glu Gln Leu Pro Asp Ser Gly Cys Pro
 1085 1090 1095
 Ala Pro Arg Ala Glu Ala Glu Asp Ser Phe Leu
 1100 1105

<210> 130
 <211> 436
 <212> PRT
 <213> Homo sapiens

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

P2490R1SEQ.txt

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

Ala

<210> 131
 <211> 1068
 <212> PRT
 <213> Homo sapiens

<400> 131
 Met Pro Pro Arg Pro Ser Ser Gly Glu Leu Trp Gly Ile His Leu
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 Met Pro Pro Arg Ile Leu Val Glu Cys Leu Leu Pro Asn Gly Met
 20 25 30
 Ile Val Thr Leu Glu Cys Leu Arg Glu Ala Thr Leu Ile Thr Ile
 35 40 45
 Lys His Glu Leu Phe Lys Glu Ala Arg Lys Tyr Pro Leu His Gln
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P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

<210> 132
<211> 724
<212> PRT
<213> Homo sapiens

<400> 132

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

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P2490R1SEQ.txt

Arg	Gln	Pro	Ala	Pro	Ala	Leu	Pro	Pro	Lys	Pro	Pro	Lys	Pro	Thr
				305					310					315
Thr	Val	Ala	Asn	Asn	Gly	Met	Asn	Asn	Asn	Met	Ser	Leu	Gln	Asp
				320					325					330
Ala	Glu	Trp	Tyr	Trp	Gly	Asp	Ile	Ser	Arg	Glu	Glu	Val	Asn	Glu
				335					340					345
Lys	Leu	Arg	Asp	Thr	Ala	Asp	Gly	Thr	Phe	Leu	Val	Arg	Asp	Ala
				350					355					360
Ser	Thr	Lys	Met	His	Gly	Asp	Tyr	Thr	Leu	Thr	Leu	Arg	Lys	Gly
				365					370					375
Gly	Asn	Asn	Lys	Leu	Ile	Lys	Ile	Phe	His	Arg	Asp	Gly	Lys	Tyr
				380					385					390
Gly	Phe	Ser	Asp	Pro	Leu	Thr	Phe	Ser	Ser	Val	Val	Glu	Leu	Ile
				395					400					405
Asn	His	Tyr	Arg	Asn	Glu	Ser	Leu	Ala	Gln	Tyr	Asn	Pro	Lys	Leu
				410					415					420
Asp	Val	Lys	Leu	Leu	Tyr	Pro	Val	Ser	Lys	Tyr	Gln	Gln	Asp	Gln
				425					430					435
Val	Val	Lys	Glu	Asp	Asn	Ile	Glu	Ala	Val	Gly	Lys	Lys	Leu	His
				440					445					450
Glu	Tyr	Asn	Thr	Gln	Phe	Gln	Glu	Lys	Ser	Arg	Glu	Tyr	Asp	Arg
				455					460					465
Leu	Tyr	Glu	Glu	Tyr	Thr	Arg	Thr	Ser	Gln	Glu	Ile	Gln	Met	Lys
				470					475					480
Arg	Thr	Ala	Ile	Glu	Ala	Phe	Asn	Glu	Thr	Ile	Lys	Ile	Phe	Glu
				485					490					495
Glu	Gln	Cys	Gln	Thr	Gln	Glu	Arg	Tyr	Ser	Lys	Glu	Tyr	Ile	Glu
				500					505					510
Lys	Phe	Lys	Arg	Glu	Gly	Asn	Glu	Lys	Glu	Ile	Gln	Arg	Ile	Met
				515					520					525
His	Asn	Tyr	Asp	Lys	Leu	Lys	Ser	Arg	Ile	Ser	Glu	Ile	Ile	Asp
				530					535					540
Ser	Arg	Arg	Arg	Leu	Glu	Glu	Asp	Leu	Lys	Lys	Gln	Ala	Ala	Glu
				545					550					555
Tyr	Arg	Glu	Ile	Asp	Lys	Arg	Met	Asn	Ser	Ile	Lys	Pro	Asp	Leu
				560					565					570
Ile	Gln	Leu	Arg	Lys	Thr	Arg	Asp	Gln	Tyr	Leu	Met	Trp	Leu	Thr
				575					580					585
Gln	Lys	Gly	Val	Arg	Gln	Lys	Lys	Leu	Asn	Glu	Trp	Leu	Gly	Asn
				590					595					600
Glu	Asn	Thr	Glu	Asp	Gln	Tyr	Ser	Leu	Val	Glu	Asp	Asp	Glu	Asp
				605					610					615
Leu	Pro	His	His	Asp	Glu	Lys	Thr	Trp	Asn	Val	Gly	Ser	Ser	Asn
				620					625					630
Arg	Asn	Lys	Ala	Glu	Asn	Leu	Leu	Arg	Gly	Lys	Arg	Asp	Gly	Thr
				635					640					645

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P2490R1SEQ.txt

Phe Leu Val Arg Glu Ser Ser Lys Gln Gly Cys Tyr Ala Cys Ser
650 655 660
Val Val Val Asp Gly Glu Val Lys His Cys Val Ile Asn Lys Thr
665 670 675
Ala Thr Gly Tyr Gly Phe Ala Glu Pro Tyr Asn Leu Tyr Ser Ser
680 685 690
Leu Lys Glu Leu Val Leu His Tyr Gln His Thr Ser Leu Val Gln
695 700 705
His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr Pro Val Tyr Ala
710 715 720
Gln Gln Arg Arg

<210> 133
<211> 728
<212> PRT
<213> Homo sapiens

<400> 133
Met Ala Gly Pro Glu Gly Phe Gln Tyr Arg Ala Leu Tyr Pro Phe
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Arg Arg Glu Arg Pro Glu Asp Leu Glu Leu Leu Pro Gly Asp Val
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Leu Val Val Ser Arg Ala Ala Leu Gln Ala Leu Gly Val Ala Glu
35 40 45
Gly Gly Glu Arg Cys Pro Gln Ser Val Gly Trp Met Pro Gly Leu
50 55 60
Asn Glu Arg Thr Arg Gln Arg Gly Asp Phe Pro Gly Thr Tyr Val
65 70 75
Glu Phe Leu Gly Pro Val Ala Leu Ala Arg Pro Gly Pro Arg Pro
80 85 90
Arg Gly Pro Arg Pro Leu Pro Ala Arg Pro Arg Asp Gly Ala Pro
95 100 105
Glu Pro Gly Leu Thr Leu Pro Asp Leu Pro Glu Gln Phe Ser Pro
110 115 120
Pro Asp Val Ala Pro Pro Leu Leu Val Lys Leu Val Glu Ala Ile
125 130 135
Glu Arg Thr Gly Leu Asp Ser Glu Ser His Tyr Arg Pro Glu Leu
140 145 150
Pro Ala Pro Arg Thr Asp Trp Ser Leu Ser Asp Val Asp Gln Trp
155 160 165
Asp Thr Ala Ala Leu Ala Asp Gly Ile Lys Ser Phe Leu Leu Ala
170 175 180
Leu Pro Ala Pro Leu Val Thr Pro Glu Ala Ser Ala Glu Ala Arg
185 190 195
Arg Ala Leu Arg Glu Ala Ala Gly Pro Val Gly Pro Ala Leu Glu
200 205 210
Pro Pro Thr Leu Pro Leu His Arg Ala Leu Thr Leu Arg Phe Leu
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P2490R1SEQ.txt

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

P2490R1SEQ.txt

Ile	Asp	Lys	Arg	Met	Asn	Ser	Leu	Lys	Pro	Asp	Leu	Met	Gln	Leu
				560					565					570
Arg	Lys	Ile	Arg	Asp	Gln	Tyr	Leu	Val	Trp	Leu	Thr	Gln	Lys	Gly
				575					580					585
Ala	Arg	Gln	Lys	Lys	Ile	Asn	Glu	Trp	Leu	Gly	Ile	Lys	Asn	Glu
				590					595					600
Thr	Glu	Asp	Gln	Tyr	Ala	Leu	Met	Glu	Asp	Glu	Asp	Asp	Leu	Pro
				605					610					615
His	His	Glu	Glu	Arg	Thr	Trp	Tyr	Val	Gly	Lys	Ile	Asn	Arg	Thr
				620					625					630
Gln	Ala	Glu	Glu	Met	Leu	Ser	Gly	Lys	Arg	Asp	Gly	Thr	Phe	Leu
				635					640					645
Ile	Arg	Glu	Ser	Ser	Gln	Arg	Gly	Cys	Tyr	Ala	Cys	Ser	Val	Val
				650					655					660
Val	Asp	Gly	Asp	Thr	Lys	His	Cys	Val	Ile	Tyr	Arg	Thr	Ala	Thr
				665					670					675
Gly	Phe	Gly	Phe	Ala	Glu	Pro	Tyr	Asn	Leu	Tyr	Gly	Ser	Leu	Lys
				680					685					690
Glu	Leu	Val	Leu	His	Tyr	Gln	His	Ala	Ser	Leu	Val	Gln	His	Asn
				695					700					705
Asp	Ala	Leu	Thr	Val	Thr	Leu	Ala	His	Pro	Val	Arg	Ala	Pro	Gly
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Pro	Gly	Pro	Pro	Pro	Ala	Ala	Arg							
				725										

<210> 134
 <211> 1358
 <212> PRT
 <213> Homo sapiens

<400> 134
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20 25 30
Ser Leu Gly Ser Thr Arg Phe Phe Lys Val Ala Arg Ala Lys His
35 40 45
Arg Glu Gly Leu Val Val Val Lys Val Phe Ala Ile Gln Asp Pro
50 55 60
Thr Leu Pro Leu Thr Ser Tyr Lys Gln Glu Leu Glu Glu Leu Lys
65 70 75
Ile Arg Leu Asn Ser Ala Gln Asn Cys Leu Pro Phe Gln Lys Ala
80 85 90
Ser Glu Lys Ala Ser Glu Lys Ala Ala Met Leu Phe Arg Gln Tyr
95 100 105
Val Arg Asp Asn Leu Tyr Asp Arg Ile Ser Thr Arg Pro Phe Leu
110 115 120
Asn Asn Ile Glu Lys Arg Trp Ile Ala Phe Gln Ile Leu Thr Ala
125 130 135

P2490R1SEQ.txt

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

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P2490R1SEQ.txt														
470					475					480				
Ala	Tyr	Ala	Glu	Asn	Ile	Ala	Leu	Leu	Ala	Glu	Thr	Ala	Leu	Arg
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Phe	Leu	Glu	Leu	Val	Gln	Leu	Lys	Asn	Leu	Asn	Met	Glu	Asn	Asp
				500					505					510
Pro	Asn	Asn	Glu	Glu	Ile	Asp	Glu	Val	Thr	His	Pro	Asn	Gly	Asn
				515					520					525
Tyr	Asp	Thr	Glu	Leu	Gln	Ala	Leu	His	Glu	Met	Val	Gln	Gln	Lys
				530					535					540
Val	Val	Thr	Leu	Leu	Ser	Asp	Pro	Glu	Asn	Ile	Val	Lys	Gln	Thr
				545					550					555
Leu	Met	Glu	Asn	Gly	Ile	Thr	Arg	Leu	Cys	Val	Phe	Phe	Gly	Arg
				560					565					570
Gln	Lys	Ala	Asn	Asp	Val	Leu	Leu	Ser	His	Met	Ile	Thr	Phe	Leu
				575					580					585
Asn	Asp	Lys	Asn	Asp	Trp	His	Leu	Arg	Gly	Ala	Phe	Phe	Asp	Ser
				590					595					600
Ile	Val	Gly	Val	Ala	Ala	Tyr	Val	Gly	Trp	Gln	Ser	Ser	Ser	Ile
				605					610					615
Leu	Lys	Pro	Leu	Leu	Gln	Gln	Gly	Leu	Ser	Asp	Ala	Glu	Glu	Phe
				620					625					630
Val	Ile	Val	Lys	Ala	Leu	Tyr	Ala	Leu	Thr	Cys	Met	Cys	Gln	Leu
				635					640					645
Gly	Leu	Leu	Gln	Lys	Pro	His	Val	Tyr	Glu	Phe	Ala	Ser	Asp	Ile
				650					655					660
Ala	Pro	Phe	Leu	Cys	His	Pro	Asn	Leu	Trp	Ile	Arg	Tyr	Gly	Ala
				665					670					675
Val	Gly	Phe	Ile	Thr	Val	Val	Ala	Arg	Gln	Ile	Ser	Thr	Ala	Asp
				680					685					690
Val	Tyr	Cys	Lys	Leu	Met	Pro	Tyr	Leu	Asp	Pro	Tyr	Ile	Thr	Gln
				695					700					705
Pro	Ile	Ile	Gln	Ile	Glu	Arg	Lys	Leu	Val	Leu	Leu	Ser	Val	Leu
				710					715					720
Lys	Glu	Pro	Val	Ser	Arg	Ser	Ile	Phe	Asp	Tyr	Ala	Leu	Arg	Ser
				725					730					735
Lys	Asp	Ile	Thr	Ser	Leu	Phe	Arg	His	Leu	His	Met	Arg	Gln	Lys
				740					745					750
Lys	Arg	Asn	Gly	Ser	Leu	Pro	Asp	Cys	Pro	Pro	Pro	Glu	Asp	Pro
				755					760					765
Ala	Ile	Ala	Gln	Leu	Leu	Lys	Lys	Leu	Leu	Ser	Gln	Gly	Met	Thr
				770					775					780
Glu	Glu	Glu	Glu	Asp	Lys	Leu	Leu	Ala	Leu	Lys	Asp	Phe	Met	Met
				785					790					795
Lys	Ser	Asn	Lys	Ala	Lys	Ala	Asn	Ile	Val	Asp	Gln	Ser	His	Leu
				800					805					810

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Leu Cys Ile Gly Thr Ser Ser Gly Thr Met Ala Cys Trp Asp Met
1160 1165 1170
Arg Phe Gln Leu Pro Ile Ser Ser His Cys His Pro Ser Arg Ala
1175 1180 1185
Arg Ile Arg Arg Leu Ser Met His Pro Leu Tyr Gln Ser Trp Val
1190 1195 1200
Ile Ala Ala Val Gln Gly Asn Asn Glu Val Ser Met Trp Asp Met
1205 1210 1215
Glu Thr Gly Asp Arg Arg Phe Thr Leu Trp Ala Ser Ser Ala Pro
1220 1225 1230
Pro Leu Ser Glu Leu Gln Pro Ser Pro His Ser Val His Gly Ile
1235 1240 1245
Tyr Cys Ser Pro Ala Asp Gly Asn Pro Ile Leu Leu Thr Ala Gly
1250 1255 1260
Ser Asp Met Lys Ile Arg Phe Trp Asp Leu Ala Tyr Pro Glu Arg
1265 1270 1275
Ser Tyr Val Val Ala Gly Ser Thr Ser Ser Pro Ser Val Ser Tyr
1280 1285 1290
Tyr Arg Lys Ile Ile Glu Gly Thr Glu Val Val Gln Glu Ile Gln
1295 1300 1305
Asn Lys Gln Lys Val Gly Pro Ser Asp Asp Thr Pro Arg Arg Gly
1310 1315 1320
Pro Glu Ser Leu Pro Val Gly His His Asp Ile Ile Thr Asp Val
1325 1330 1335
Ala Thr Phe Gln Thr Thr Gln Gly Phe Ile Val Thr Ala Ser Arg
1340 1345 1350
Asp Gly Ile Val Lys Val Trp Lys
1355

<210> 135
<211> 880
<212> PRT
<213> Homo sapiens

<400> 135
Met Gln Pro Gly Ala Thr Thr Cys Thr Glu Asp Arg Ile Gln His
1 5 10 15
Ala Leu Glu Arg Cys Leu His Gly Leu Ser Leu Ser Arg Arg Ser
20 25 30
Thr Ser Trp Ser Ala Gly Leu Cys Leu Asn Cys Trp Ser Leu Gln
35 40 45
Glu Leu Val Ser Arg Asp Pro Gly His Phe Leu Ile Leu Leu Glu
50 55 60
Gln Ile Leu Gln Lys Thr Arg Glu Val Gln Glu Lys Gly Thr Tyr
65 70 75
Asp Leu Leu Thr Pro Leu Ala Leu Leu Phe Tyr Ser Thr Val Leu
80 85 90
Cys Thr Pro His Phe Pro Pro Asp Ser Asp Leu Leu Leu Lys Ala
Page 353

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Val Lys Arg Gln Asn Ser Lys Ser Lys Lys Gly Phe Asn Gln Ile
785 790 795
Ser Thr Ser Gln Ile Lys Val Asp Lys Val Gln Ile Ile Gly Ser
800 805 810
Asn Ser Cys Pro Phe Ala Val Cys Leu Asp Gln Asp Glu Arg Lys
815 820 825
Ile Leu Gln Ser Val Val Arg Cys Glu Val Ser Pro Cys Tyr Lys
830 835 840
Pro Glu Lys Ser Asp Leu Ser Ser Pro Pro Gln Thr Pro Pro Asp
845 850 855
Leu Pro Ala Gln Ala Ala Pro Asp Leu Cys Ser Leu Leu Cys Leu
860 865 870
Pro Ile Met Thr Phe Ser Gly Ala Leu Pro
875 880

<210> 136

<211> 603

<212> PRT

<213> Homo sapiens

<400> 136

Met Ser Ala Ala Val Thr Ala Gly Lys Leu Ala Arg Ala Pro Ala
1 5 10 15
Asp Pro Gly Lys Ala Gly Val Pro Gly Val Ala Ala Pro Gly Ala
20 25 30
Pro Ala Ala Ala Pro Pro Ala Lys Glu Ile Pro Glu Val Leu Val
35 40 45
Asp Pro Arg Ser Arg Arg Arg Tyr Val Arg Gly Arg Phe Leu Gly
50 55 60
Lys Gly Gly Phe Ala Lys Cys Phe Glu Ile Ser Asp Ala Asp Thr
65 70 75
Lys Glu Val Phe Ala Gly Lys Ile Val Pro Lys Ser Leu Leu Leu
80 85 90
Lys Pro His Gln Arg Glu Lys Met Ser Met Glu Ile Ser Ile His
95 100 105
Arg Ser Leu Ala His Gln His Val Val Gly Phe His Gly Phe Phe
110 115 120
Glu Asp Asn Asp Phe Val Phe Val Val Leu Glu Leu Cys Arg Arg
125 130 135
Arg Ser Leu Leu Glu Leu His Lys Arg Arg Lys Ala Leu Thr Glu
140 145 150
Pro Glu Ala Arg Tyr Tyr Leu Arg Gln Ile Val Leu Gly Cys Gln
155 160 165
Tyr Leu His Arg Asn Arg Val Ile His Arg Asp Leu Lys Leu Gly
170 175 180
Asn Leu Phe Leu Asn Glu Asp Leu Glu Val Lys Ile Gly Asp Phe
185 190 195
Gly Leu Ala Thr Lys Val Glu Tyr Asp Gly Glu Arg Lys Lys Thr
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										P2490R1SEQ.txt									
200										205					210				
Leu	Cys	Gly	Thr	Pro	Asn	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Ser	Lys					
				215					220					225					
Lys	Gly	His	Ser	Phe	Glu	Val	Asp	Val	Trp	Ser	Ile	Gly	Cys	Ile					
				230					235					240					
Met	Tyr	Thr	Leu	Leu	Val	Gly	Lys	Pro	Pro	Phe	Glu	Thr	Ser	Cys					
				245					250					255					
Leu	Lys	Glu	Thr	Tyr	Leu	Arg	Ile	Lys	Lys	Asn	Glu	Tyr	Ser	Ile					
				260					265					270					
Pro	Lys	His	Ile	Asn	Pro	Val	Ala	Ala	Ser	Leu	Ile	Gln	Lys	Met					
				275					280					285					
Leu	Gln	Thr	Asp	Pro	Thr	Ala	Arg	Pro	Thr	Ile	Asn	Glu	Leu	Leu					
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Asn	Asp	Glu	Phe	Phe	Thr	Ser	Gly	Tyr	Ile	Pro	Ala	Arg	Leu	Pro					
				305					310					315					
Ile	Thr	Cys	Leu	Thr	Ile	Pro	Pro	Arg	Phe	Ser	Ile	Ala	Pro	Ser					
				320					325					330					
Ser	Leu	Asp	Pro	Ser	Asn	Arg	Lys	Pro	Leu	Thr	Val	Leu	Asn	Lys					
				335					340					345					
Gly	Leu	Glu	Asn	Pro	Leu	Pro	Glu	Arg	Pro	Arg	Glu	Lys	Glu	Glu					
				350					355					360					
Pro	Val	Val	Arg	Glu	Thr	Gly	Glu	Val	Val	Asp	Cys	His	Leu	Ser					
				365					370					375					
Asp	Met	Leu	Gln	Gln	Leu	His	Ser	Val	Asn	Ala	Ser	Lys	Pro	Ser					
				380					385					390					
Glu	Arg	Gly	Leu	Val	Arg	Gln	Glu	Glu	Ala	Glu	Asp	Pro	Ala	Cys					
				395					400					405					
Ile	Pro	Ile	Phe	Trp	Val	Ser	Lys	Trp	Val	Asp	Tyr	Ser	Asp	Lys					
				410					415					420					
Tyr	Gly	Leu	Gly	Tyr	Gln	Leu	Cys	Asp	Asn	Ser	Val	Gly	Val	Leu					
				425					430					435					
Phe	Asn	Asp	Ser	Thr	Arg	Leu	Ile	Leu	Tyr	Asn	Asp	Gly	Asp	Ser					
				440					445					450					
Leu	Gln	Tyr	Ile	Glu	Arg	Asp	Gly	Thr	Glu	Ser	Tyr	Leu	Thr	Val					
				455					460					465					
Ser	Ser	His	Pro	Asn	Ser	Leu	Met	Lys	Lys	Ile	Thr	Leu	Leu	Lys					
				470					475					480					
Tyr	Phe	Arg	Asn	Tyr	Met	Ser	Glu	His	Leu	Leu	Lys	Ala	Gly	Ala					
				485					490					495					
Asn	Ile	Thr	Pro	Arg	Glu	Gly	Asp	Glu	Leu	Ala	Arg	Leu	Pro	Tyr					
				500					505					510					
Leu	Arg	Thr	Trp	Phe	Arg	Thr	Arg	Ser	Ala	Ile	Ile	Leu	His	Leu					
				515					520					525					
Ser	Asn	Gly	Ser	Val	Gln	Ile	Asn	Phe	Phe	Gln	Asp	His	Thr	Lys					
				530					535					540					

P2490R1SEQ.txt

Leu Ile Leu Cys Pro Leu Met Ala Ala Val Thr Tyr Ile Asp Glu
545 550 555
Lys Arg Asp Phe Arg Thr Tyr Arg Leu Ser Leu Leu Glu Glu Tyr
560 565 570
Gly Cys Cys Lys Glu Leu Ala Ser Arg Leu Arg Tyr Ala Arg Thr
575 580 585
Met Val Asp Lys Leu Leu Ser Ser Arg Ser Ala Ser Asn Arg Leu
590 595 600
Lys Ala Ser

<210> 137
<211> 671
<212> PRT
<213> Homo sapiens

<400> 137
Met Ala Asp Pro Ala Ala Gly Pro Pro Pro Ser Glu Gly Glu Glu
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Ser Thr Val Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn
20 25 30
Val His Glu Val Lys Asn His Lys Phe Thr Ala Arg Phe Phe Lys
35 40 45
Gln Pro Thr Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe
50 55 60
Gly Lys Gln Gly Phe Gln Cys Gln Val Cys Cys Phe Val Val His
65 70 75
Lys Arg Cys His Glu Phe Val Thr Phe Ser Cys Pro Gly Ala Asp
80 85 90
Lys Gly Pro Ala Ser Asp Asp Pro Arg Ser Lys His Lys Phe Lys
95 100 105
Ile His Thr Tyr Ser Ser Pro Thr Phe Cys Asp His Cys Gly Ser
110 115 120
Leu Leu Tyr Gly Leu Ile His Gln Gly Met Lys Cys Asp Thr Cys
125 130 135
Met Met Asn Val His Lys Arg Cys Val Met Asn Val Pro Ser Leu
140 145 150
Cys Gly Thr Asp His Thr Glu Arg Arg Gly Arg Ile Tyr Ile Gln
155 160 165
Ala His Ile Asp Arg Asp Val Leu Ile Val Leu Val Arg Asp Ala
170 175 180
Lys Asn Leu Val Pro Met Asp Pro Asn Gly Leu Ser Asp Pro Tyr
185 190 195
Val Lys Leu Lys Leu Ile Pro Asp Pro Lys Ser Glu Ser Lys Gln
200 205 210
Lys Thr Lys Thr Ile Lys Cys Ser Leu Asn Pro Glu Trp Asn Glu
215 220 225
Thr Phe Arg Phe Gln Leu Lys Glu Ser Asp Lys Asp Arg Arg Leu
230 235 240

P2490R1SEQ.txt

Ser Val Glu Ile Trp Asp Trp Asp Leu Thr Ser Arg Asn Asp Phe
 245 250 255
 Met Gly Ser Leu Ser Phe Gly Ile Ser Glu Leu Gln Lys Ala Ser
 260 265 270
 Val Asp Gly Trp Phe Lys Leu Leu Ser Gln Glu Glu Gly Glu Tyr
 275 280 285
 Phe Asn Val Pro Val Pro Pro Glu Gly Ser Glu Ala Asn Glu Glu
 290 295 300
 Leu Arg Gln Lys Phe Glu Arg Ala Lys Ile Ser Gln Gly Thr Lys
 305 310 315
 Val Pro Glu Glu Lys Thr Thr Asn Thr Val Ser Lys Phe Asp Asn
 320 325 330
 Asn Gly Asn Arg Asp Arg Met Lys Leu Thr Asp Phe Asn Phe Leu
 335 340 345
 Met Val Leu Gly Lys Gly Ser Phe Gly Lys Val Met Leu Ser Glu
 350 355 360
 Arg Lys Gly Thr Asp Glu Leu Tyr Ala Val Lys Ile Leu Lys Lys
 365 370 375
 Asp Val Val Ile Gln Asp Asp Asp Val Glu Cys Thr Met Val Glu
 380 385 390
 Lys Arg Val Leu Ala Leu Pro Gly Lys Pro Pro Phe Leu Thr Gln
 395 400 405
 Leu His Ser Cys Phe Gln Thr Met Asp Arg Leu Tyr Phe Val Met
 410 415 420
 Glu Tyr Val Asn Gly Gly Asp Leu Met Tyr His Ile Gln Gln Val
 425 430 435
 Gly Arg Phe Lys Glu Pro His Ala Val Phe Tyr Ala Ala Glu Ile
 440 445 450
 Ala Ile Gly Leu Phe Phe Leu Gln Ser Lys Gly Ile Ile Tyr Arg
 455 460 465
 Asp Leu Lys Leu Asp Asn Val Met Leu Asp Ser Glu Gly His Ile
 470 475 480
 Lys Ile Ala Asp Phe Gly Met Cys Lys Glu Asn Ile Trp Asp Gly
 485 490 495
 Val Thr Thr Lys Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro
 500 505 510
 Glu Ile Ile Ala Tyr Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp
 515 520 525
 Ala Phe Gly Val Leu Leu Tyr Glu Met Leu Ala Gly Gln Ala Pro
 530 535 540
 Phe Glu Gly Glu Asp Glu Asp Glu Leu Phe Gln Ser Ile Met Glu
 545 550 555
 His Asn Val Ala Tyr Pro Lys Ser Met Ser Lys Glu Ala Val Ala
 560 565 570
 Ile Cys Lys Gly Leu Met Thr Lys His Pro Gly Lys Arg Leu Gly
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	575		580		585
Cys Gly Pro Glu	Gly 590	Glu Arg Asp Ile	Lys 595	Glu His Ala Phe	Phe 600
Arg Tyr Ile Asp	Trp 605	Glu Lys Leu Glu	Arg 610	Lys Glu Ile Gln	Pro 615
Pro Tyr Lys Pro	Lys 620	Ala Arg Asp Lys	Arg 625	Asp Thr Ser Asn	Phe 630
Asp Lys Glu Phe	Thr 635	Arg Gln Pro Val	Glu 640	Leu Thr Pro Thr	Asp 645
Lys Leu Phe Ile	Met 650	Asn Leu Asp Gln	Asn 655	Glu Phe Ala Gly	Phe 660
Ser Tyr Thr Asn	Pro 665	Glu Phe Val Ile	Asn 670	Val	

<210> 138
 <211> 587
 <212> PRT
 <213> Homo sapiens

<400> 138
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 Gln Val Arg Val Lys Ala Tyr Tyr Arg Gly Asp Ile Met Ile Thr
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 His Phe Glu Pro Ser Ile Ser Phe Glu Gly Leu Cys Asn Glu Val
 35 40 45
 Arg Asp Met Cys Ser Phe Asp Asn Glu Gln Leu Phe Thr Met Lys
 50 55 60
 Trp Ile Asp Glu Glu Gly Asp Pro Cys Thr Val Ser Ser Gln Leu
 65 70 75
 Glu Leu Glu Glu Ala Phe Arg Leu Tyr Glu Leu Asn Lys Asp Ser
 80 85 90
 Glu Leu Leu Ile His Val Phe Pro Cys Val Pro Glu Arg Pro Gly
 95 100 105
 Met Pro Cys Pro Gly Glu Asp Lys Ser Ile Tyr Arg Arg Gly Ala
 110 115 120
 Arg Arg Trp Arg Lys Leu Tyr Cys Ala Asn Gly His Thr Phe Gln
 125 130 135
 Ala Lys Arg Phe Asn Arg Arg Ala His Cys Ala Ile Cys Thr Asp
 140 145 150
 Arg Ile Trp Gly Leu Gly Arg Gln Gly Tyr Lys Cys Ile Asn Cys
 155 160 165
 Lys Leu Leu Val His Lys Lys Cys His Lys Leu Val Thr Ile Glu
 170 175 180
 Cys Gly Arg His Ser Leu Pro Gln Glu Pro Val Met Pro Met Asp
 185 190 195
 Gln Ser Ser Met His Ser Asp His Ala Gln Thr Val Ile Pro Tyr
 200 205 210

P2490R1SEQ.txt

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

P2490R1SEQ.txt

Pro Asp Asp Asp Asp Ile Val Arg Lys Ile Asp Gln Ser Glu Phe
560 565 570

Glu Gly Phe Glu Tyr Ile Asn Pro Leu Leu Met Ser Ala Glu Glu
575 580 585

Cys Val

<210> 139
<211> 1447
<212> PRT
<213> Homo sapiens

<400> 139
Met Ala Ser Ala Gly Asn Ala Ala Glu Pro Gln Asp Arg Gly Gly
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Gly Gly Ser Gly Cys Ile Gly Ala Pro Gly Arg Pro Ala Gly Gly
20 25 30

Gly Arg Arg Arg Arg Thr Gly Gly Leu Arg Arg Ala Ala Ala Pro
35 40 45

Asp Arg Asp Tyr Leu His Arg Pro Ser Tyr Cys Asp Ala Ala Phe
50 55 60

Ala Leu Glu Gln Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala
65 70 75

Pro Leu Trp Leu Arg Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu
80 85 90

Gly Cys Tyr Ile Gln Lys Asn Cys Gly Lys Phe Leu Val Val Gly
95 100 105

Leu Leu Ile Phe Gly Ala Phe Ala Val Gly Leu Lys Ala Ala Asn
110 115 120

Leu Glu Thr Asn Val Glu Glu Leu Trp Val Glu Val Gly Gly Arg
125 130 135

Val Ser Arg Glu Leu Asn Tyr Thr Arg Gln Lys Ile Gly Glu Glu
140 145 150

Ala Met Phe Asn Pro Gln Leu Met Ile Gln Thr Pro Lys Glu Glu
155 160 165

Gly Ala Asn Val Leu Thr Thr Glu Ala Leu Leu Gln His Leu Asp
170 175 180

Ser Ala Leu Gln Ala Ser Arg Val His Val Tyr Met Tyr Asn Arg
185 190 195

Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser Gly Glu Leu Ile
200 205 210

Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr Leu Tyr Pro
215 220 225

Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ala Lys
230 235 240

Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu Arg
245 250 255

Trp Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys
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P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

1280		1290
Gly Ser Leu Pro Pro	Gly Arg Gln Gly Gln Gln Pro Arg Arg Asp	
1295	1300	1305
Pro Pro Arg Glu Gly	Leu Trp Pro Pro Leu Tyr Arg Pro Arg Arg	
1310	1315	1320
Asp Ala Phe Glu Ile	Ser Thr Glu Gly His Ser Gly Pro Ser Asn	
1325	1330	1335
Arg Ala Arg Trp Gly	Pro Arg Gly Ala Arg Ser His Asn Pro Arg	
1340	1345	1350
Asn Pro Ala Ser Thr	Ala Met Gly Ser Ser Val Pro Gly Tyr Cys	
1355	1360	1365
Gln Pro Ile Thr Thr	Val Thr Ala Ser Ala Ser Val Thr Val Ala	
1370	1375	1380
Val His Pro Pro Pro	Val Pro Gly Pro Gly Arg Asn Pro Arg Gly	
1385	1390	1395
Gly Leu Cys Pro Gly	Tyr Pro Glu Thr Asp His Gly Leu Phe Glu	
1400	1405	1410
Asp Pro His Val Pro	Phe His Val Arg Cys Glu Arg Arg Asp Ser	
1415	1420	1425
Lys Val Glu Val Ile	Glu Leu Gln Asp Val Glu Cys Glu Glu Arg	
1430	1435	1440
Pro Arg Gly Ser Ser	Ser Asn	
1445		

<210> 140
<211> 402
<212> PRT
<213> Homo sapiens

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

P2490R1SEQ.txt

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

<210> 141

<211> 928

<212> PRT

<213> Homo sapiens

<400> 141

Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala
1 5 10 15

Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu
20 25 30

Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val
35 40 45

P2490R1SEQ.txt

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

P2490R1SEQ.txt														
380					385					390				
Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn
				395					400					405
Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys
				410					415					420
Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	Ala	Val	Gly
				425					430					435
Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	Gly	Val
				440					445					450
Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	Glu
				455					460					465
Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn
				470					475					480
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met
				485					490					495
Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr
				500					505					510
Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala
				515					520					525
Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly
				530					535					540
Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His
				545					550					555
Arg	Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe
				560					565					570
Asp	Leu	Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His
				575					580					585
Leu	Glu	Ser	Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His
				590					595					600
Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	Pro	Val	Arg	Ser	Pro	Lys	Lys
				605					610					615
Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	Thr	Ala	Asn	Ala	Glu	Thr
				620					625					630
Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	Pro	Leu	Lys	Ser	Thr
				635					640					645
Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	Leu	Ala	Tyr	Leu
				650					655					660
Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	His	Pro	Glu
				665					670					675
Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	Gln	Asn
				680					685					690
Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	Met
				695					700					705
Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys
				710					715					720

P2490R1SEQ.txt

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val
725 730 735

Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp
740 745 750

Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys
755 760 765

Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser
770 775 780

Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser
785 790 795

Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys
800 805 810

Ser Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met
815 820 825

Thr Pro Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly
830 835 840

Thr Ser Glu Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser
845 850 855

Asp Arg Val Leu Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys
860 865 870

Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala
875 880 885

Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys Phe Gln Gln Lys
890 895 900

Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln Lys Gln Lys
905 910 915

Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
920 925

<210> 142
<211> 330
<212> PRT
<213> Homo sapiens

<400> 142
Met Asp Thr Glu Thr Thr Ala Leu Cys Pro Ser Gly Ser Arg Arg
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Ala Ser Pro Pro Gly Thr Pro Thr Pro Glu Ala Asp Ala Thr Leu
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Leu Lys Lys Ser Glu Lys Leu Leu Ala Glu Leu Asp Arg Ser Gly
35 40 45

Leu Pro Ser Ala Pro Gly Ala Pro Arg Arg Arg Gly Ser Met Pro
50 55 60

Val Pro Tyr Lys His Gln Leu Arg Arg Ala Gln Ala Val Asp Glu
65 70 75

Leu Asp Trp Pro Pro Gln Ala Ser Ser Ser Gly Ser Ser Asp Ser
80 85 90

Leu Gly Ser Gly Glu Ala Ala Pro Ala Gln Lys Asp Gly Ile Phe
95 100 105

P2490R1SEQ.txt

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

<210> 143

<211> 1072

<212> PRT

<213> Homo sapiens

<400> 143

Met Ala Lys Ala Thr Ser Gly Ala Ala Gly Leu Arg Leu Leu Leu
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 Leu Leu Leu Leu Pro Leu Leu Gly Lys Val Ala Leu Gly Leu Tyr
 20 25 30
 Phe Ser Arg Asp Ala Tyr Trp Glu Lys Leu Tyr Val Asp Gln Ala
 35 40 45
 Ala Gly Thr Pro Leu Leu Tyr Val His Ala Leu Arg Asp Ala Pro
 50 55 60
 Glu Glu Val Pro Ser Phe Arg Leu Gly Gln His Leu Tyr Gly Thr
 65 70 75
 Tyr Arg Thr Arg Leu His Glu Asn Asn Trp Ile Cys Ile Gln Glu
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														P2490R1SEQ.txt			
														80	85	90	
Asp	Thr	Gly	Leu	Leu	Tyr	Leu	Asn	Arg	Ser	Leu	Asp	His	Ser	Ser			
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Trp	Glu	Lys	Leu	Ser	Val	Arg	Asn	Arg	Gly	Phe	Pro	Leu	Leu	Thr			
				110					115					120			
Val	Tyr	Leu	Lys	Val	Phe	Leu	Ser	Pro	Thr	Ser	Leu	Arg	Glu	Gly			
				125					130					135			
Glu	Cys	Gln	Trp	Pro	Gly	Cys	Ala	Arg	Val	Tyr	Phe	Ser	Phe	Phe			
				140					145					150			
Asn	Thr	Ser	Phe	Pro	Ala	Cys	Ser	Ser	Leu	Lys	Pro	Arg	Glu	Leu			
				155					160					165			
Cys	Phe	Pro	Glu	Thr	Arg	Pro	Ser	Phe	Arg	Ile	Arg	Glu	Asn	Arg			
				170					175					180			
Pro	Pro	Gly	Thr	Phe	His	Gln	Phe	Arg	Leu	Leu	Pro	Val	Gln	Phe			
				185					190					195			
Leu	Cys	Pro	Asn	Ile	Ser	Val	Ala	Tyr	Arg	Leu	Leu	Glu	Gly	Glu			
				200					205					210			
Gly	Leu	Pro	Phe	Arg	Cys	Ala	Pro	Asp	Ser	Leu	Glu	Val	Ser	Thr			
				215					220					225			
Arg	Trp	Ala	Leu	Asp	Arg	Glu	Gln	Arg	Glu	Lys	Tyr	Glu	Leu	Val			
				230					235					240			
Ala	Val	Cys	Thr	Val	His	Ala	Gly	Ala	Arg	Glu	Glu	Val	Val	Met			
				245					250					255			
Val	Pro	Phe	Pro	Val	Thr	Val	Tyr	Asp	Glu	Asp	Asp	Ser	Ala	Pro			
				260					265					270			
Thr	Phe	Pro	Ala	Gly	Val	Asp	Thr	Ala	Ser	Ala	Val	Val	Glu	Phe			
				275					280					285			
Lys	Arg	Lys	Glu	Asp	Thr	Val	Val	Ala	Thr	Leu	Arg	Val	Phe	Asp			
				290					295					300			
Ala	Asp	Val	Val	Pro	Ala	Ser	Gly	Glu	Leu	Val	Arg	Arg	Tyr	Thr			
				305					310					315			
Ser	Thr	Leu	Leu	Pro	Gly	Asp	Thr	Trp	Ala	Gln	Gln	Thr	Phe	Arg			
				320					325					330			
Val	Glu	His	Trp	Pro	Asn	Glu	Thr	Ser	Val	Gln	Ala	Asn	Gly	Ser			
				335					340					345			
Phe	Val	Arg	Ala	Thr	Val	His	Asp	Tyr	Arg	Leu	Val	Leu	Asn	Arg			
				350					355					360			
Asn	Leu	Ser	Ile	Ser	Glu	Asn	Arg	Thr	Met	Gln	Leu	Ala	Val	Leu			
				365					370					375			
Val	Asn	Asp	Ser	Asp	Phe	Gln	Gly	Pro	Gly	Ala	Gly	Val	Leu	Leu			
				380					385					390			
Leu	His	Phe	Asn	Val	Ser	Val	Leu	Pro	Val	Ser	Leu	His	Leu	Pro			
				395					400					405			
Ser	Thr	Tyr	Ser	Leu	Ser	Val	Ser	Arg	Arg	Ala	Arg	Arg	Phe	Ala			
				410					415					420			

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

<210> 144
 <211> 1400
 <212> PRT
 <213> Homo sapiens

P2490R1SEQ.txt

<400> 144

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

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P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

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P2490R1SEQ.txt

1010	1015	1020
Leu Ala Leu Pro Ala	Ile Asp Gly Leu Asp Ser Thr Thr Cys Val	
1025	1030	1035
His Gly Ala Ser Phe	Ser Asp Ser Glu Asp Glu Ser Cys Val Pro	
1040	1045	1050
Leu Leu Arg Lys Glu	Ser Ile Gln Leu Arg Asp Leu Asp Ser Ala	
1055	1060	1065
Leu Leu Ala Glu Val	Lys Asp Val Leu Ile Pro His Glu Arg Val	
1070	1075	1080
Val Thr His Ser Asp	Arg Val Ile Gly Lys Gly His Phe Gly Val	
1085	1090	1095
Val Tyr His Gly Glu	Tyr Ile Asp Gln Ala Gln Asn Arg Ile Gln	
1100	1105	1110
Cys Ala Ile Lys Ser	Leu Ser Arg Ile Thr Glu Met Gln Gln Val	
1115	1120	1125
Glu Ala Phe Leu Arg	Glu Gly Leu Leu Met Arg Gly Leu Asn His	
1130	1135	1140
Pro Asn Val Leu Ala	Leu Ile Gly Ile Met Leu Pro Pro Glu Gly	
1145	1150	1155
Leu Pro His Val Leu	Leu Pro Tyr Met Cys His Gly Asp Leu Leu	
1160	1165	1170
Gln Phe Ile Arg Ser	Pro Gln Arg Asn Pro Thr Val Lys Asp Leu	
1175	1180	1185
Ile Ser Phe Gly Leu	Gln Val Ala Arg Gly Met Glu Tyr Leu Ala	
1190	1195	1200
Glu Gln Lys Phe Val	His Arg Asp Leu Ala Ala Arg Asn Cys Met	
1205	1210	1215
Leu Asp Glu Ser Phe	Thr Val Lys Val Ala Asp Phe Gly Leu Ala	
1220	1225	1230
Arg Asp Ile Leu Asp	Arg Glu Tyr Tyr Ser Val Gln Gln His Arg	
1235	1240	1245
His Ala Arg Leu Pro	Val Lys Trp Met Ala Leu Glu Ser Leu Gln	
1250	1255	1260
Thr Tyr Arg Phe Thr	Thr Lys Ser Asp Val Trp Ser Phe Gly Val	
1265	1270	1275
Leu Leu Trp Glu Leu	Leu Thr Arg Gly Ala Pro Pro Tyr Arg His	
1280	1285	1290
Ile Asp Pro Phe Asp	Leu Thr His Phe Leu Ala Gln Gly Arg Arg	
1295	1300	1305
Leu Pro Gln Pro Glu	Tyr Cys Pro Asp Ser Leu Tyr Gln Val Met	
1310	1315	1320
Gln Gln Cys Trp Glu	Ala Asp Pro Ala Val Arg Pro Thr Phe Arg	
1325	1330	1335
Val Leu Val Gly Glu	Val Glu Gln Ile Val Ser Ala Leu Leu Gly	
1340	1345	1350

P2490R1SEQ.txt

Asp His Tyr Val Gln Leu Pro Ala Thr Tyr Met Asn Leu Gly Pro
 1355 1360 1365
 Ser Thr Ser His Glu Met Asn Val Arg Pro Glu Gln Pro Gln Phe
 1370 1375 1380
 Ser Pro Met Pro Gly Asn Val Arg Arg Pro Arg Pro Leu Ser Glu
 1385 1390 1395
 Pro Pro Arg Pro Thr
 1400

<210> 145
 <211> 467
 <212> PRT
 <213> Homo sapiens

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

P2490R1SEQ.txt

Pro Val Asn His Ser Leu Asp Leu Gln Pro Val Thr Tyr Ser Glu
260 265 270

Pro Ala Phe Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg
275 280 285

Val Gly Glu Thr Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp
290 295 300

Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu
305 310 315

Leu Ser Asn Val Asn Arg Asn Ala Thr Val Glu Met Thr Arg Arg
320 325 330

His Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly Gly Glu Val
335 340 345

Phe Ala Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln Ser Pro
350 355 360

Asn Cys Asn Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys Lys
365 370 375

Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe
380 385 390

Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly Phe Glu Ala Val
395 400 405

Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser Phe Val Lys
410 415 420

Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser Thr Pro
425 430 435

Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu Asp
440 445 450

Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser
455 460 465

Met Ser

<210> 146
<211> 403
<212> PRT
<213> Homo sapiens

<400> 146
Met Asp Arg Ser Lys Glu Asn Cys Ile Ser Gly Pro Val Lys Ala
1 5 10 15

Thr Ala Pro Val Gly Gly Pro Lys Arg Val Leu Val Thr Gln Gln
20 25 30

Phe Pro Cys Gln Asn Pro Leu Pro Val Asn Ser Gly Gln Ala Gln
35 40 45

Arg Val Leu Cys Pro Ser Asn Ser Ser Gln Arg Ile Pro Leu Gln
50 55 60

Ala Gln Lys Leu Val Ser Ser His Lys Pro Val Gln Asn Gln Lys
65 70 75

Gln Lys Gln Leu Gln Ala Thr Ser Val Pro His Pro Val Ser Arg

P2490R1SEQ.txt

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

<210> 147
 <211> 484
 <212> PRT

P2490R1SEQ.txt

<213> Homo sapiens

<400> 147

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

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P2490R1SEQ.txt

Arg Gln Asn Gly Leu Ala His Asp Arg Ala Pro Ser Arg Lys Asp
 335 340 345
 Ser Leu Glu Ser Asp Ser Ser Thr Ala Ile Ile Pro His Glu Leu
 350 355 360
 Ile Arg Thr Arg Gln Leu Glu Ser Val His Leu Lys Phe Asn Gln
 365 370 375
 Glu Ser Gly Ala Leu Ile Pro Leu Cys Leu Arg Gly Arg Leu Leu
 380 385 390
 His Gly Arg His Phe Thr Tyr Lys Ser Ile Thr Gly Asp Met Ala
 395 400 405
 Ile Thr Phe Val Ser Thr Gly Val Glu Gly Ala Phe Ala Thr Glu
 410 415 420
 Glu His Pro Tyr Ala Ala His Gly Pro Trp Leu Gln Ile Leu Leu
 425 430 435
 Thr Glu Glu Phe Val Glu Lys Met Leu Glu Asp Leu Glu Asp Leu
 440 445 450
 Thr Ser Pro Glu Glu Phe Lys Leu Pro Lys Glu Tyr Ser Trp Pro
 455 460 465
 Glu Lys Lys Leu Lys Val Ser Ile Leu Pro Asp Val Val Phe Asp
 470 475 480

Ser Pro Leu His

<210> 148
 <211> 503
 <212> PRT
 <213> Homo sapiens

<400> 148
 Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg Leu Leu Leu Leu
 1 5 10 15
 Val Leu Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Leu Leu Pro Gly
 20 25 30
 Ala Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys Asp Asn
 35 40 45
 Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr Glu
 50 55 60
 Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile
 65 70 75
 Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser
 80 85 90
 Lys Thr Gly Ser Val Thr Thr Thr Tyr Cys Cys Asn Gln Asp His
 95 100 105
 Cys Asn Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly
 110 115 120
 Leu Gly Pro Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys
 125 130 135
 Phe Val Cys Ile Ser Leu Met Leu Met Val Tyr Ile Cys His Asn
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P2490R1SEQ.txt

140		145		150
Arg Thr Val Ile	His 155	His Arg Val Pro	Asn 160	Glu Glu Asp Pro Ser 165
Leu Asp Arg Pro	Phe 170	Ile Ser Glu Gly	Thr 175	Thr Leu Lys Asp Leu 180
Ile Tyr Asp Met	Thr 185	Thr Ser Gly Ser	Gly 190	Ser Gly Leu Pro Leu 195
Leu Val Gln Arg	Thr 200	Ile Ala Arg Thr	Ile 205	Val Leu Gln Glu Ser 210
Ile Gly Lys Gly	Arg 215	Phe Gly Glu Val	Trp 220	Arg Gly Lys Trp Arg 225
Gly Glu Glu Val	Ala 230	Val Lys Ile Phe	Ser 235	Ser Arg Glu Glu Arg 240
Ser Trp Phe Arg	Glu 245	Ala Glu Ile Tyr	Gln 250	Thr Val Met Leu Arg 255
His Glu Asn Ile	Leu 260	Gly Phe Ile Ala	Ala 265	Asp Asn Lys Asp Asn 270
Gly Thr Trp Thr	Gln 275	Leu Trp Leu Val	Ser 280	Asp Tyr His Glu His 285
Gly Ser Leu Phe	Asp 290	Tyr Leu Asn Arg	Tyr 295	Thr Val Thr Val Glu 300
Gly Met Ile Lys	Leu 305	Ala Leu Ser Thr	Ala 310	Ser Gly Leu Ala His 315
Leu His Met Glu	Ile 320	Val Gly Thr Gln	Gly 325	Lys Pro Ala Ile Ala 330
His Arg Asp Leu	Lys 335	Ser Lys Asn Ile	Leu 340	Val Lys Lys Asn Gly 345
Thr Cys Cys Ile	Ala 350	Asp Leu Gly Leu	Ala 355	Val Arg His Asp Ser 360
Ala Thr Asp Thr	Ile 365	Asp Ile Ala Pro	Asn 370	His Arg Val Gly Thr 375
Lys Arg Tyr Met	Ala 380	Pro Glu Val Leu	Asp 385	Asp Ser Ile Asn Met 390
Lys His Phe Glu	Ser 395	Phe Lys Arg Ala	Asp 400	Ile Tyr Ala Met Gly 405
Leu Val Phe Trp	Glu 410	Ile Ala Arg Arg	Cys 415	Ser Ile Gly Gly Ile 420
His Glu Asp Tyr	Gln 425	Leu Pro Tyr Tyr	Asp 430	Leu Val Pro Ser Asp 435
Pro Ser Val Glu	Glu 440	Met Arg Lys Val	Val 445	Cys Glu Gln Lys Leu 450
Arg Pro Asn Ile	Pro 455	Asn Arg Trp Gln	Ser 460	Cys Glu Ala Leu Arg 465
Val Met Ala Lys	Ile 470	Met Arg Glu Cys	Trp 475	Tyr Ala Asn Gly Ala 480

P2490R1SEQ.txt

Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu
485 490 495

ser Gln Gln Glu Gly Ile Lys Met
500

<210> 149
<211> 567
<212> PRT
<213> Homo sapiens

<400> 149
Met Gly Arg Gly Leu Leu Arg Gly Leu Trp Pro Leu His Ile Val
1 5 10 15
Leu Trp Thr Arg Ile Ala Ser Thr Ile Pro Pro His Val Gln Lys
20 25 30
Ser Val Asn Asn Asp Met Ile Val Thr Asp Asn Asn Gly Ala Val
35 40 45
Lys Phe Pro Gln Leu Cys Lys Phe Cys Asp Val Arg Phe Ser Thr
50 55 60
Cys Asp Asn Gln Lys Ser Cys Met Ser Asn Cys Ser Ile Thr Ser
65 70 75
Ile Cys Glu Lys Pro Gln Glu Val Cys Val Ala Val Trp Arg Lys
80 85 90
Asn Asp Glu Asn Ile Thr Leu Glu Thr Val Cys His Asp Pro Lys
95 100 105
Leu Pro Tyr His Asp Phe Ile Leu Glu Asp Ala Ala Ser Pro Lys
110 115 120
Cys Ile Met Lys Glu Lys Lys Lys Pro Gly Glu Thr Phe Phe Met
125 130 135
Cys Ser Cys Ser Ser Asp Glu Cys Asn Asp Asn Ile Ile Phe Ser
140 145 150
Glu Glu Tyr Asn Thr Ser Asn Pro Asp Leu Leu Leu Val Ile Phe
155 160 165
Gln Val Thr Gly Ile Ser Leu Leu Pro Pro Leu Gly Val Ala Ile
170 175 180
Ser Val Ile Ile Ile Phe Tyr Cys Tyr Arg Val Asn Arg Gln Gln
185 190 195
Lys Leu Ser Ser Thr Trp Glu Thr Gly Lys Thr Arg Lys Leu Met
200 205 210
Glu Phe Ser Glu His Cys Ala Ile Ile Leu Glu Asp Asp Arg Ser
215 220 225
Asp Ile Ser Ser Thr Cys Ala Asn Asn Ile Asn His Asn Thr Glu
230 235 240
Leu Leu Pro Ile Glu Leu Asp Thr Leu Val Gly Lys Gly Arg Phe
245 250 255
Ala Glu Val Tyr Lys Ala Lys Leu Lys Gln Asn Thr Ser Glu Gln
260 265 270
Phe Glu Thr Val Ala Val Lys Ile Phe Pro Tyr Glu Glu Tyr Ala
275 280 285

P2490R1SEQ.txt

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

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 <212> PRT
 <213> Homo sapiens

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 1 5 10 15

P2490R1SEQ.txt

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	35			Met	Asp
Ser	Pro	Asp	Asp	Ile	Glu
	50			55	
Asp	Glu	Ala	Pro	Arg	Met
	65			70	
Ala	Pro	Ala	Ala	Pro	Thr
	80			85	
Trp	Pro	Leu	Ser	Ser	Val
	95			100	
Ser	Tyr	Gly	Phe	Arg	Leu
	110			115	
Ser	Val	Thr	Cys	Thr	Tyr
	125			130	
Gln	Leu	Ala	Lys	Thr	Cys
	140			145	
Pro	Pro	Pro	Gly	Thr	Arg
	155			160	
Ser	Gln	His	Met	Thr	Glu
	170			175	
Arg	Cys	Ser	Asp	Ser	Asp
	185			190	
Arg	Val	Glu	Gly	Asn	Leu
	200			205	
Thr	Phe	Arg	His	Ser	Val
	215			220	
Gly	Ser	Asp	Cys	Thr	Thr
	230			235	
Ser	Cys	Met	Gly	Gly	Met
	245			250	
Thr	Leu	Glu	Asp	Ser	Ser
	260			265	
Glu	Val	Arg	Val	Cys	Ala
	275			280	
Glu	Glu	Asn	Leu	Arg	Lys
	290			295	
Pro	Gly	Ser	Thr	Lys	Arg
	305			310	
Pro	Gln	Pro	Lys	Lys	Pro
	320			325	
Gln	Ile	Arg	Gly	Arg	Glu
	335			340	
Glu	Ala	Leu	Glu	Leu	Lys
	350			355	

P2490R1SEQ.txt

Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys Lys Gly Gln
365 370 375

Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys Thr Glu Gly Pro
380 385 390

Asp Ser Asp

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<211> 381
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<400> 151

Met Ile Ser Ala Arg Ser Ser Glu Pro Phe Tyr Ser Asp Asp Lys
1 5 10 15

Met Ala His His Thr Leu Leu Leu Gly Ser Gly His Val Gly Leu
20 25 30

Arg Asn Leu Gly Asn Thr Cys Phe Leu Asn Ala Val Leu Gln Cys
35 40 45

Leu Ser Ser Thr Arg Pro Leu Arg Asp Phe Cys Leu Arg Arg Asp
50 55 60

Phe Arg Gln Glu Val Pro Gly Gly Gly Arg Ala Gln Glu Leu Thr
65 70 75

Glu Ala Phe Ala Asp Val Ile Gly Ala Leu Trp His Leu Asp Ser
80 85 90

Cys Glu Ala Val Asn Pro Thr Arg Phe Arg Ala Val Phe Gln Lys
95 100 105

Tyr Val Pro Ser Phe Ser Gly Tyr Ser Gln Gln Asp Ala Gln Glu
110 115 120

Phe Leu Lys Leu Leu Met Glu Arg Leu His Leu Glu Ile Asn Arg
125 130 135

Arg Gly Arg Arg Ala Pro Pro Ile Leu Ala Asn Gly Pro Val Pro
140 145 150

Ser Pro Pro Arg Arg Gly Gly Ala Leu Leu Glu Glu Pro Glu Leu
155 160 165

Ser Asp Asp Asp Arg Ala Asn Leu Met Trp Lys Arg Tyr Leu Glu
170 175 180

Arg Glu Asp Ser Lys Ile Val Asp Leu Phe Val Gly Gln Leu Lys
185 190 195

Ser Cys Leu Lys Cys Gln Ala Cys Gly Tyr Arg Ser Thr Thr Phe
200 205 210

Glu Val Phe Cys Asp Leu Ser Leu Pro Ile Pro Lys Lys Gly Phe
215 220 225

Ala Gly Gly Lys Val Phe Leu Arg Asp Cys Phe Asn Leu Phe Thr
230 235 240

Lys Glu Glu Glu Leu Glu Ser Glu Asn Ala Pro Val Cys Asp Arg
245 250 255

Cys Arg Gln Lys Thr Arg Ser Thr Lys Lys Leu Thr Val Gln Arg
260 265 270

P2490R1SEQ.txt

Phe Pro Arg Ile Leu Val Leu His Leu Asn Arg Phe Ser Ala Ser
 275 280 285
 Arg Gly Ser Ile Lys Lys Ser Ser Val Gly Val Asp Phe Pro Leu
 290 295 300
 Gln Arg Leu Ser Leu Gly Asp Phe Ala Ser Asp Lys Ala Gly Ser
 305 310 315
 Pro Val Tyr Gln Leu Tyr Ala Leu Cys Asn His Ser Gly Ser Val
 320 325 330
 His Tyr Gly His Tyr Thr Ala Leu Cys Arg Cys Gln Thr Gly Trp
 335 340 345
 His Val Tyr Asn Asp Ser Arg Val Ser Pro Val Ser Glu Asn Gln
 350 355 360
 Val Ala Ser Ser Glu Gly Tyr Val Leu Phe Tyr Gln Leu Met Gln
 365 370 375
 Glu Pro Pro Arg Cys Leu
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 <213> Homo sapiens

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 20 25 30
 Pro Arg Ile Thr Leu Arg Val Arg Lys Leu Leu Leu Leu Ile Pro
 35 40 45
 Thr Asp Pro Ala Ile Gln Glu Ala Leu Asp Gln Leu Asp Ser Leu
 50 55 60
 Gly Arg Lys Lys Thr Leu Leu Ser Glu Ser Ser Ser Gln Ser Ser
 65 70 75
 Lys Ser Pro Ser Leu Ser Ser Lys Gln Gln His Gln Pro Ser Ala
 80 85 90
 Ser Ser Ile Leu Glu Ser Leu Phe Arg Ser Phe Ala Pro Gly Met
 95 100 105
 Ser Thr Phe Arg Val Leu Tyr Asn Leu Glu Val Leu Ser Ser Lys
 110 115 120
 Leu Met Pro Thr Ala Asp Asp Asp Met Ala Arg Ser Cys Ala Lys
 125 130 135
 Ser Phe Cys Glu Asn Phe Leu Lys Ala Gly Gly Leu Ser Leu Val
 140 145 150
 Val Asn Val Met Gln Arg Asp Ser Ile Pro Ser Glu Val Asp Tyr
 155 160 165
 Glu Thr Arg Gln Gly Val Tyr Ser Ile Cys Leu Gln Leu Ala Arg
 170 175 180
 Phe Leu Leu Val Gly Gln Thr Met Pro Thr Leu Leu Asp Glu Asp
 Page 389

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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Ser Val Asp Gln Gly Gly Gly Gly Ser Pro Arg Lys Lys Val Ala
      875      880      885
Leu Thr Glu Asn Tyr Glu Leu Val Gly Val Ile Val His Ser Gly
      890      895      900
Gln Ala His Ala Gly His Tyr Tyr Ser Phe Ile Lys Asp Arg Arg
      905      910      915
Gly Cys Gly Lys Gly Lys Trp Tyr Lys Phe Asn Asp Thr Val Ile
      920      925      930
Glu Glu Phe Asp Leu Asn Asp Glu Thr Leu Glu Tyr Glu Cys Phe
      935      940      945
Gly Gly Glu Tyr Arg Pro Lys Val Tyr Asp Gln Thr Asn Pro Tyr
      950      955      960
Thr Asp Val Arg Arg Arg Tyr Trp Asn Ala Tyr Met Leu Phe Tyr
      965      970      975
Gln Arg Val Ser Asp Gln Asn Ser Pro Val Leu Pro Lys Lys Ser
      980      985      990
Arg Val Ser Val Val Arg Gln Glu Ala Glu Asp Leu Ser Leu Ser
      995      1000      1005
Ala Pro Ser Ser Pro Glu Ile Ser Pro Gln Ser Ser Pro Arg Pro
      1010      1015      1020
His Arg Pro Asn Asn Asp Arg Leu Ser Ile Leu Thr Lys Leu Val
      1025      1030      1035
Lys Lys Gly Glu Lys Lys Gly Leu Phe Val Glu Lys Met Pro Ala
      1040      1045      1050
Arg Ile Tyr Gln Met Val Arg Asp Glu Asn Leu Lys Phe Met Lys
      1055      1060      1065
Asn Arg Asp Val Tyr Ser Ser Asp Tyr Phe Ser Phe Val Leu Ser
      1070      1075      1080
Leu Ala Ser Leu Asn Ala Thr Lys Leu Lys His Pro Tyr Tyr Pro
      1085      1090      1095
Cys Met Ala Lys Val Ser Leu Gln Leu Ala Ile Gln Phe Leu Phe
      1100      1105      1110
Gln Thr Tyr Leu Arg Thr Lys Lys Lys Leu Arg Val Asp Thr Glu
      1115      1120      1125
Glu Trp Ile Ala Thr Ile Glu Ala Leu Leu Ser Lys Ser Phe Asp
      1130      1135      1140
Ala Cys Gln Trp Leu Val Glu Tyr Phe Ile Ser Ser Glu Gly Arg
      1145      1150      1155
Glu Leu Ile Lys Ile Phe Leu Leu Glu Cys Asn Val Arg Glu Val
      1160      1165      1170
Arg Val Ala Val Ala Thr Ile Leu Glu Lys Thr Leu Asp Ser Ala
      1175      1180      1185
Leu Phe Tyr Gln Asp Lys Leu Lys Ser Leu His Gln Leu Leu Glu
      1190      1195      1200
Val Leu Leu Ala Leu Leu Asp Lys Asp Val Pro Glu Asn Cys Lys
      Page 392

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P2490R1SEQ.txt

1205	1210	1215
Asn Cys Ala Gln Tyr Phe Phe Leu Phe Asn Thr Phe Val Gln Lys		
1220	1225	1230
Gln Gly Ile Arg Ala Gly Asp Leu Leu Leu Arg His Ser Ala Leu		
1235	1240	1245
Arg His Met Ile Ser Phe Leu Leu Gly Ala Ser Arg Gln Asn Asn		
1250	1255	1260
Gln Ile Arg Arg Trp Ser Ser Ala Gln Ala Arg Glu Phe Gly Asn		
1265	1270	1275
Leu His Asn Thr Val Ala Leu Leu Val Leu His Ser Asp Val Ser		
1280	1285	1290
Ser Gln Arg Asn Val Ala Pro Gly Ile Phe Lys Gln Arg Pro Pro		
1295	1300	1305
Ile Ser Ile Ala Pro Ser Ser Pro Leu Leu Pro Leu His Glu Glu		
1310	1315	1320
Val Glu Ala Leu Leu Phe Met Ser Glu Gly Lys Pro Tyr Leu Leu		
1325	1330	1335
Glu Val Met Phe Ala Leu Arg Glu Leu Thr Gly Ser Leu Leu Ala		
1340	1345	1350
Leu Ile Glu Met Val Val Tyr Cys Cys Phe Cys Asn Glu His Phe		
1355	1360	1365
Ser Phe Thr Met Leu His Phe Ile Lys Asn Gln Leu Glu Thr Ala		
1370	1375	1380
Pro Pro His Glu Leu Lys Asn Thr Phe Gln Leu Leu His Glu Ile		
1385	1390	1395
Leu Val Ile Glu Asp Pro Ile Gln Val Glu Arg Val Lys Phe Val		
1400	1405	1410
Phe Glu Thr Glu Asn Gly Leu Leu Ala Leu Met His His Ser Asn		
1415	1420	1425
His Val Asp Ser Ser Arg Cys Tyr Gln Cys Val Lys Phe Leu Val		
1430	1435	1440
Thr Leu Ala Gln Lys Cys Pro Ala Ala Lys Glu Tyr Phe Lys Glu		
1445	1450	1455
Asn Ser His His Trp Ser Trp Ala Val Gln Trp Leu Gln Lys Lys		
1460	1465	1470
Met Ser Glu His Tyr Trp Thr Pro Gln Ser Asn Val Ser Asn Glu		
1475	1480	1485
Thr Ser Thr Gly Lys Thr Phe Gln Arg Thr Ile Ser Ala Gln Asp		
1490	1495	1500
Thr Leu Ala Tyr Ala Thr Ala Leu Leu Asn Glu Lys Glu Gln Ser		
1505	1510	1515
Gly Ser Ser Asn Gly Ser Glu Ser Ser Pro Ala Asn Glu Asn Gly		
1520	1525	1530
Asp Arg His Leu Gln Gln Gly Ser Glu Ser Pro Met Met Ile Gly		
1535	1540	1545

P2490R1SEQ.txt

Glu Leu Arg Ser Asp Leu Asp Asp Val Asp Pro
1550 1555

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<211> 1055
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<213> Homo sapiens

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

P2490R1SEQ.txt

Gly Arg Phe Leu Ala Val Gly Val Leu Glu Gly Lys Lys Phe Glu
 305 310 315
 Asn Thr Glu Met Phe Gly Gln Tyr Pro Leu Gln Val Asn Gly Phe
 320 325 330
 Lys Asp Leu His Glu Cys Leu Glu Ala Ala Met Ile Glu Gly Glu
 335 340 345
 Ile Glu Ser Leu His Ser Glu Asn Ser Gly Lys Ser Gly Gln Glu
 350 355 360
 His Trp Phe Thr Glu Leu Pro Pro Val Leu Thr Phe Glu Leu Ser
 365 370 375
 Arg Phe Glu Phe Asn Gln Ala Leu Gly Arg Pro Glu Lys Ile His
 380 385 390
 Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr Leu Asp Arg Tyr Met
 395 400 405
 His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg Glu Glu Ile Lys
 410 415 420
 Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg Leu Glu Arg
 425 430 435
 Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu Val Asp
 440 445 450
 Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val Cys
 455 460 465
 Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly
 470 475 480
 Ser Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly
 485 490 495
 Ala Leu Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala
 500 505 510
 Ala Ile Ser Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser
 515 520 525
 Arg Ile Pro Pro Asp Leu Pro Met His Pro Ala Pro Arg His Ile
 530 535 540
 Thr Glu Glu Glu Leu Ser Val Leu Glu Ser Cys Leu His Arg Trp
 545 550 555
 Arg Thr Glu Ile Glu Asn Asp Thr Arg Asp Leu Gln Glu Ser Ile
 560 565 570
 Ser Arg Ile His Arg Thr Ile Glu Leu Met Tyr Ser Asp Lys Ser
 575 580 585
 Met Ile Gln Val Pro Tyr Arg Leu His Ala Val Leu Val His Glu
 590 595 600
 Gly Gln Ala Asn Ala Gly His Tyr Trp Ala Tyr Ile Phe Asp His
 605 610 615
 Arg Glu Ser Arg Trp Met Lys Tyr Asn Asp Ile Ala Val Thr Lys
 620 625 630
 Ser Ser Trp Glu Glu Leu Val Arg Asp Ser Phe Gly Gly Tyr Arg
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P2490R1SEQ.txt

Asn	Ala	Ser	Ala	Tyr	Cys	Leu	Met	Tyr	Ile	Asn	Asp	Lys	Ala	Gln	635	640	645
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Val	Gly	Ile	Glu	Thr	Leu	Pro	Pro	Asp	Leu	Arg	Asp	Phe	Val	Glu			
				680					685					690			
Glu	Asp	Asn	Gln	Arg	Phe	Glu	Lys	Glu	Leu	Glu	Glu	Trp	Asp	Ala			
				695					700					705			
Gln	Leu	Ala	Gln	Lys	Ala	Leu	Gln	Glu	Lys	Leu	Leu	Ala	Ser	Gln			
				710					715					720			
Lys	Leu	Arg	Glu	Ser	Glu	Thr	Ser	Val	Thr	Thr	Ala	Gln	Ala	Ala			
				725					730					735			
Gly	Asp	Pro	Glu	Tyr	Leu	Glu	Gln	Pro	Ser	Arg	Ser	Asp	Phe	Ser			
				740					745					750			
Lys	His	Leu	Lys	Glu	Glu	Thr	Ile	Gln	Ile	Ile	Thr	Lys	Ala	Ser			
				755					760					765			
His	Glu	His	Glu	Asp	Lys	Ser	Pro	Glu	Thr	Val	Leu	Gln	Ser	Ala			
				770					775					780			
Ile	Lys	Leu	Glu	Tyr	Ala	Arg	Leu	Val	Lys	Leu	Ala	Gln	Glu	Asp			
				785					790					795			
Thr	Pro	Pro	Glu	Thr	Asp	Tyr	Arg	Leu	His	His	Val	Val	Val	Tyr			
				800					805					810			
Phe	Ile	Gln	Asn	Gln	Ala	Pro	Lys	Lys	Ile	Ile	Glu	Lys	Thr	Leu			
				815					820					825			
Leu	Glu	Gln	Phe	Gly	Asp	Arg	Asn	Leu	Ser	Phe	Asp	Glu	Arg	Cys			
				830					835					840			
His	Asn	Ile	Met	Lys	Val	Ala	Gln	Ala	Lys	Leu	Glu	Met	Ile	Lys			
				845					850					855			
Pro	Glu	Glu	Val	Asn	Leu	Glu	Glu	Tyr	Glu	Glu	Trp	His	Gln	Asp			
				860					865					870			
Tyr	Arg	Lys	Phe	Arg	Glu	Thr	Thr	Met	Tyr	Leu	Ile	Ile	Gly	Leu			
				875					880					885			
Glu	Asn	Phe	Gln	Arg	Glu	Ser	Tyr	Ile	Asp	Ser	Leu	Leu	Phe	Leu			
				890					895					900			
Ile	Cys	Ala	Tyr	Gln	Asn	Asn	Lys	Glu	Leu	Leu	Ser	Lys	Gly	Leu			
				905					910					915			
Tyr	Arg	Gly	His	Asp	Glu	Glu	Leu	Ile	Ser	His	Tyr	Arg	Arg	Glu			
				920					925					930			
Cys	Leu	Leu	Lys	Leu	Asn	Glu	Gln	Ala	Ala	Glu	Leu	Phe	Glu	Ser			
				935					940					945			
Gly	Glu	Asp	Arg	Glu	Val	Asn	Asn	Gly	Leu	Ile	Ile	Met	Asn	Glu			
				950					955					960			
Phe	Ile	Val	Pro	Phe	Leu	Pro	Leu	Leu	Leu	Val	Asp	Glu	Met	Glu			
				965					970					975			

P2490R1SEQ.txt

Glu Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg Trp Cys
980 985 990
Ser Tyr Leu Gly Gln Glu Met Glu Pro His Leu Gln Glu Lys Leu
995 1000 1005
Thr Asp Phe Leu Pro Lys Leu Leu Asp Cys Ser Met Glu Ile Lys
1010 1015 1020
Ser Phe His Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr His Glu
1025 1030 1035
Leu Cys Glu Arg Phe Ala Arg Ile Met Leu Ser Leu Ser Arg Thr
1040 1045 1050
Pro Ala Asp Gly Arg
1055

<210> 154
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<213> Homo sapiens

<400> 154
Glu Thr Gly Asp Pro Arg Leu Gly Ala Ser Ala Met Thr Ala Glu
1 5 10 15
Leu Gln Gln Asp Asp Ala Ala Gly Ala Ala Asp Gly His Gly Ser
20 25 30
Ser Cys Gln Met Leu Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile
35 40 45
Gln Asp Pro Ser Phe Leu His Glu Ala Leu Lys Ala Ser Asn Gly
50 55 60
Asp Ile Thr Gln Ala Val Ser Leu Leu Thr Asp Glu Arg Val Lys
65 70 75
Glu Pro Ser Gln Asp Thr Val Ala Thr Glu Pro Ser Glu Val Glu
80 85 90
Gly Ser Ala Ala Asn Lys Glu Val Leu Ala Lys Val Ile Asp Leu
95 100 105
Thr His Asp Asn Lys Asp Asp Leu Gln Ala Ala Ile Ala Leu Ser
110 115 120
Leu Leu Glu Ser Pro Lys Ile Gln Ala Asp Gly Arg Asp Leu Asn
125 130 135
Arg Met His Glu Ala Thr Ser Ala Glu Thr Lys Arg Ser Lys Arg
140 145 150
Lys Arg Cys Glu Val Trp Gly Glu Asn Pro Asn Pro Asn Asp Trp
155 160 165
Arg Arg Val Asp Gly Trp Pro Val Gly Leu Lys Asn Val Gly Asn
170 175 180
Thr Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Gln Leu Pro
185 190 195
Glu Phe Arg Arg Leu Val Leu Ser Tyr Ser Leu Pro Gln Asn Val
200 205 210
Leu Glu Asn Cys Arg Ser His Thr Glu Lys Arg Asn Ile Met Phe
215 220 225

P2490R1SEQ.txt

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

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P2490R1SEQ.txt

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

P2490R1SEQ.txt

Glu Asp Tyr Ser Leu Phe Arg Lys Val Ser Val Tyr Leu Leu Thr
905 915

Gly Leu Glu Leu Tyr Gln Lys Gly Lys Tyr Gln Glu Ala Leu Ser
920 930

Tyr Leu Val Tyr Ala Tyr Gln Ser Asn Ala Ala Leu Leu Met Lys
935 945

Gly Pro Arg Arg Gly Val Lys Glu Ser Val Ile Ala Leu Tyr Arg
950 960

Arg Lys Cys Leu Leu Glu Leu Asn Ala Lys Ala Ala Ser Leu Phe
965 975

Glu Thr Asn Asp Asp His Ser Val Thr Glu Gly Ile Asn Val Met
980 990

Asn Glu Leu Ile Ile Pro Cys Ile His Leu Ile Ile Asn Asn Asp
995 1005

Ile Ser Lys Asp Asp Leu Asp Ala Ile Glu Val Met Arg Asn His
1010 1020

Trp Cys Ser Tyr Leu Gly Gln Asp Ile Ala Glu Asn Leu Gln Leu
1025 1035

Cys Leu Gly Glu Phe Leu Pro Arg Leu Leu Asp Pro Ser Ala Glu
1040 1050

Ile Ile Val Leu Lys Glu Pro Pro Thr Ile Arg Pro Asn Ser Pro
1055 1065

Tyr Asp Leu Cys Ser Arg Phe Ala Ala Val Met Glu Ser Ile Gln
1070 1080

Gly Val Ser Thr Val Thr Val Lys
1085

<210> 155

<211> 773

<212> PRT

<213> Homo sapiens

<400> 155

Pro Leu Gly Cys Pro His Pro Ser Ile Leu Gly Val Pro Cys Pro
1 5 10 15

Cys Val Thr Val Thr Pro Leu Thr Arg Met Ile Asp Trp Val Ser
20 25 30

Trp Pro Leu Gly Lys Asn Ile Asp Lys Trp Ile Ile Ala Leu Leu
35 40 45

Lys Gly Leu Ala Ala Val Lys Lys Phe Ser Ile Leu Ile Glu Val
50 55 60

Ser Leu Thr Lys Ile Glu Lys Val Phe Ser Lys Leu Leu Tyr Pro
65 70 75

Ile Val Arg Gly Ala Ala Leu Ser Val Leu Lys Tyr Met Leu Leu
80 85 90

Thr Phe Gln His Ser His Glu Ala Phe His Leu Leu Leu Pro His
95 100 105

Ile Pro Pro Met Val Ala Ser Leu Val Lys Glu Asp Ser Asn Ser
110 115 120

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

<210> 156
 <211> 1356
 <212> PRT

P2490R1SEQ.txt

<213> Homo sapiens

<400> 156

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

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P2490R1SEQ.txt

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

P2490R1SEQ.txt

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

P2490R1SEQ.txt

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Ile Cys Tyr Ser Phe Gln Val Ala Lys Gly Met Glu Phe Leu Ala
1010 1015 1020
Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu
1025 1030 1035
Leu Ser Glu Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu Ala
1040 1045 1050
Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala
1055 1060 1065
Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg
1070 1075 1080
Val Tyr Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu
1085 1090 1095
Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys
1100 1105 1110
Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met
1115 1120 1125
Arg Ala Pro Asp Tyr Thr Thr Pro Glu Met Tyr Gln Thr Met Leu
1130 1135 1140
Asp Cys Trp His Gly Glu Pro Ser Gln Arg Pro Thr Phe Ser Glu
1145 1150 1155
Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala Gln Gln
1160 1165 1170
Asp Gly Lys Asp Tyr Ile Val Leu Pro Ile Ser Glu Thr Leu Ser
1175 1180 1185
Met Glu Glu Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser
1190 1195 1200
Cys Met Glu Glu Glu Glu Val Cys Asp Pro Lys Phe His Tyr Asp
1205 1210 1215
Asn Thr Ala Gly Ile Ser Gln Tyr Leu Gln Asn Ser Lys Arg Lys
1220 1225 1230
Ser Arg Pro Val Ser Val Lys Thr Phe Glu Asp Ile Pro Leu Glu
1235 1240 1245
Glu Pro Glu Val Lys Val Ile Pro Asp Asp Asn Gln Thr Asp Ser
1250 1255 1260
Gly Met Val Leu Ala Ser Glu Glu Leu Lys Thr Leu Glu Asp Arg
1265 1270 1275
Thr Lys Leu Ser Pro Ser Phe Gly Gly Met Val Pro Ser Lys Ser
1280 1285 1290
Arg Glu Ser Val Ala Ser Glu Gly Ser Asn Gln Thr Ser Gly Tyr
1295 1300 1305
Gln Ser Gly Tyr His Ser Asp Asp Thr Asp Thr Thr Val Tyr Ser
1310 1315 1320
Ser Glu Glu Ala Glu Leu Leu Lys Leu Ile Glu Ile Gly Val Gln
1325 1330 1335
Thr Gly Ser Thr Ala Gln Ile Leu Gln Pro Asp Ser Gly Thr Thr
1340 1345 1350

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P2490R1SEQ.txt

Leu Ser Ser Pro Pro Val
1355