

METHODS AND COMPOSITIONS FOR PREDICTING RESPONSE TO ERIBULIN

RELATED APPLICATIONS

5 This application claims priority to U.S. Provisional Application No. 61/454426, filed March 18, 2011, the entire contents of which are hereby incorporated by reference herein.

BACKGROUND OF THE INVENTION

10 Cancer is a term used to describe a wide variety of diseases that are each characterized by the uncontrolled growth of a particular type of cell. It begins in a tissue containing such a cell and, if the cancer has not spread to any additional tissues at the time of diagnosis, may be treated by, for example, surgery, radiation, or another type of localized therapy. However, when there is evidence that cancer has metastasized from its tissue of origin, different approaches to treatment are typically used. Indeed, because it
15 is not possible to determine the extent of metastasis, systemic approaches to therapy are usually undertaken when any evidence of spread is detected. These approaches involve the administration of chemotherapeutic drugs that interfere with the growth of rapidly dividing cells, such as cancer cells.

 Halichondrin B is a structurally complex, macrocyclic compound that was
20 originally isolated from the marine sponge *Halichondria okadai*, and subsequently was found in *Axinella sp.*, *Phakellia carteri*, and *Lissodendoryx sp.* A total synthesis of halichondrin B was published in 1992 (Aicher *et al.*, *J. Am. Chem. Soc.* 114:3162-3164, 1992). Halichondrin B has been shown to inhibit tubulin polymerization, microtubule assembly, beta-tubulin crosslinking, GTP and vinblastine binding to tubulin, and
25 tubulin-dependent GTP hydrolysis *in vitro*. This molecule has also been shown to have anti-cancer properties *in vitro* and *in vivo*. Halichondrin B analogs having anti-cancer activities are described in U.S. Pat. No. 6,214,865 B1.

 In particular, eribulin mesylate, a Halichondrin B analog, has been developed as an anticancer drug. Recently, eribulin mesylate was approved for the treatment of
30 patients with metastatic breast cancer who have previously received at least two chemotherapeutic regimens for the treatment of metastatic disease, wherein prior therapy may have included an anthracycline and/or a taxane in either the adjuvant or metastatic setting. The ability to predict in advance of treatment whether a cancer patient is likely to be responsive to an anti-cancer agent can guide selection of appropriate treatment, and
35 is beneficial to patients. Accordingly, there is a need for methods for and compositions

useful in, assessing or predicting responsiveness to eribulin in patients having cancer and, in particular, breast cancer.

SUMMARY OF THE INVENTION

5 The invention is based, at least in part, on the observation that a low level of expression, *e.g.*, the absence of expression, of the biomarkers identified herein is indicative of responsiveness to eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate). Specifically, the absence of expression or a low level of expression of these biomarkers, including, for example, one or more of
10 those biomarkers set forth in Table 1, in a subject is indicative that the subject will be responsive to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate).

 Accordingly, in one aspect, the present invention provides a method for determining whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer, by
15 assaying a sample derived from the subject to determine the level of expression in the sample of a biomarker selected from the group of biomarkers listed in Table 1, wherein a low level of expression of the biomarker is indicative that eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), will be effective
20 in treating the subject having breast cancer. In another aspect, the present invention provides a method for determining whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer, by determining the level of expression of a biomarker selected from the group of biomarkers listed in Table 1 in a sample derived from the
25 subject, wherein a low level of expression of the biomarker is indicative that eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), will be effective in treating the subject having breast cancer. In a further aspect, the present invention provides a method for predicting whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to
30 treat a subject having breast cancer, by determining the level of expression of a biomarker selected from the group of biomarkers listed in Table 1 in a sample derived from the subject, and predicting that eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), will be effective in treating a subject having breast cancer when there is a low level of expression of the biomarker in the
35 sample. In one embodiment of the foregoing aspects of the invention, the methods may further include obtaining a sample from a subject.

In yet another aspect, the present invention provides a method for determining the sensitivity of a breast tumor, for example, derived from a subject having breast cancer, to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), by determining the level of expression of a biomarker selected from the group of biomarkers listed in Table 1 in the tumor, wherein a low level of expression of the biomarker in the tumor indicates that the tumor is sensitive to treatment with eribulin, or an analog thereof. In yet another aspect, the present invention provides a method for determining the sensitivity of a breast tumor, for example, derived from a subject having breast cancer, to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), by determining the level of expression of a biomarker selected from the group of biomarkers listed in Table 1 in the tumor, and identifying the tumor as being sensitive to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), when the biomarker is expressed in the tumor at a low level.

In further aspects of the invention, methods are provided for treating a subject having breast cancer. The methods include identifying a subject having breast cancer in which a biomarker selected from the group of biomarkers listed in Table 1 is expressed at a low level, and administering a therapeutically effective amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), to the subject. In yet a further aspect, the present invention provides methods of treating a subject having breast cancer, by assaying a sample derived from the subject to determine the level of expression in the sample of a biomarker selected from the group of biomarkers listed in Table 1, and administering a therapeutically effective amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), to the subject when a low level of expression of the biomarker is detected in the sample. In one embodiment of the foregoing aspects of the invention, the methods may further include obtaining a sample from a subject.

In further aspects of the invention, methods are provided for treating a subject having breast cancer that is sensitive to eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof. The methods include identifying a subject having breast cancer that is sensitive to eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, (*e.g.*, a breast cancer in which a biomarker selected from the group of biomarkers listed in Table 1 is expressed at a low level), and administering a therapeutically effective amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), to the subject. In yet a further aspect, the present invention provides methods of treating a subject having breast cancer that is sensitive to eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, by

assaying a sample derived from the subject to determine the level of expression in the sample of a biomarker selected from the group of biomarkers listed in Table 1, and administering a therapeutically effective amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), to the subject when a
5 low level of expression of the biomarker is detected in the sample. In one embodiment of the foregoing aspects of the invention, the methods may further include obtaining a sample from a subject.

In various embodiments, the subject has not been previously treated with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin
10 mesylate). Alternatively, the subject has been previously treated with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof. In certain embodiments, the breast cancer is an Estrogen Receptor (ER) negative breast cancer and/or a Progesterone Receptor (PR) negative breast cancer and/or a Her-2 negative breast cancer.

In various embodiments, the level of expression of at least 2, at least 3, at least 4
15 or at least 5 biomarkers selected from the group of biomarkers listed in Table 1 is determined.

In particular embodiments, a predictive gene signature comprising a sub-combination of 2 or more biomarkers selected from the group of biomarkers listed in Table 1 is used. In various embodiments, the level of expression of at least 2, at least 3,
20 at least 4 or at least 5 biomarkers selected from the group of biomarkers listed in Table 1 is determined. For example, the predictive gene signature may include at least 2 biomarkers, *e.g.*, DYSF and EDIL3; GNAT1 and ERGIC3; KRT24 and PAPLN; MANSC1 and PDGFB; PCDH1 and PDGFB; or PHOSPHO2 and PSENEN. In another embodiment, the predictive gene signature may include at least 3 biomarkers, *e.g.*,
25 COL7A1, YTHDF1 and ZIC5; CKLF, IL10 and TUBB6; CDC20, CFL1 and TMEM79; HYAL2, NCBP1 and SNX11; or CEP152, NCBP1 and SATB1. In another embodiment, the predictive gene signature may include at least 4 biomarkers, *e.g.*, APBB2, CCL26, PSENEN and SATB1; ANG, JAM3, KLHL17 and PAPLN; ITFG3, MAD2L1BP, NMU and PDGFB; SPTA1, TYROBP, SNX11 and PSENEN; GRAMD4,
30 GNAT1, TMIGD2 and YTHDF1; or GRAMD4, HYAL2, PHOSPHO2 and TUBB6. In another embodiment, the predictive gene signature may include at least 5 biomarkers, *e.g.*, CCL26, CDC20, ERGIC3, EDIL3 and PCDH1; DYSF, NMU, PHOSPHO2, PSENEN and SNX11; APBB2, CKLF, CYP4F3, TUBB6 and YTHDF1; or CEP152, MAD2L1BP, SPTA1, TMEM79 and ZIC5.

35 In particular embodiments, the predictive gene signature may include 2 or more of biomarkers ABI3, ANG, APBB2, CCL26, CDC20, CEP152, CFL1, CKLF, COL7A1,

CYP4F3, DYSE, GNAT1, GRAMD4, HYAL2, IL10, ITFG3, JAM3, KLHL17, KRT24, MAD2L1BP, MANSC1, MOBKL1B, NCBP1, NMU, PCDH1, PHOSPHO2, SPTA1, TMIGD2, TYROBP, ZIC5, ERGIC3, PDGFB, PSENEN, SATB1, SNX11, TMEM79 and YTHDF1, *e.g.*, ABI3 and ANG; APBB2 and CCL26; GNAT1 and GRAMD4; IL10 and ITFG3; MACSC1 and MOBKL1B; NMU and PCDH1; or TYROBP and ZIC5. In other embodiments, the predictive gene signature includes at least 3 of the previously recited biomarkers, *e.g.*, ABI3, ANG and APBB2; CCL26, CKLF and COL7A1; DYSE, GNAT1 and HYAL2; JAM3, KLHL17 and KRT24; NCBP1, NMU and PCDH1; SPTA1, TMIGD2 and TYROBP; or ZIC5, MAD2L1BP and CDC20. In other

embodiments, the predictive gene signature includes at least 4 of the previously recited biomarkers, *e.g.*, ABI3, ANG, APBB2 and CCL26; CEP152, CFL1, CKLF and COL7A1; KRT24, MANSC1, MOBKL1B and SPTA1; TYROBP, TMIGD2, PHOSPHO2 and NMU; ABI3, GNAT1, KLHL17 and SPTA1; or CEP152, HYAL2, PCDH1 and TMIGD2. In yet further embodiments, the predictive gene signature includes at least 5 of the previously recited biomarkers, *e.g.*, CKLF, COL7A1, GRAMD4, JAM3 and PCDH1; APBB2, CEP152, DYSE, IL10 and TYROBP; CYP4F3, HYAL2, ITFG3, KLHL17 and KRT24; NCBP1, SPTA1, TMIGD2, IL10 and JAM3; or CCL26, PHOSPHO2, SPTA1, TMIGD2 and ZIC5.

In other embodiments, the predictive gene signature may include 2 or more of biomarkers ERGIC3, PDGFB, PSENEN, SATB1, SNX11, TMEM79 or YTHDF1, or any sub-combination thereof, *e.g.*, ERGIC3 and PDGFB; ERGIC3 and PSENEN; ERGIC3 and SATB1; ERGIC3 and SNX11; ERGIC3 and TMEM79; ERGIC3 and YTHDF1; PDGFB and PSENEN; PDGFB and SATB1; PDGFB and SNX11; PDGFB and TMEM79; PDGFB and YTHDF1; PSENEN and SATB1; PSENEN and SNX11; PSENEN and TMEM79; PSENEN and YTHDF1; SATB1 and SNX11; SATB1 and TMEM79; SATB1 and YTHDF1; SNX11 and TMEM79; SNX11 and YTHDF1; or TMEM79 and YTHDF1. In other embodiments, the predictive gene signature includes at least 3 biomarkers, for example, ERGIC3, PDGFB and PSENEN; SATB1, SNX11 and TMEM79; SNX11, TMEM79 and YTHDF1; or ERGIC3, PDGFB and SATB1. In further embodiments, the predictive gene signature includes at least 4 biomarkers, for example, ERGIC3, PDGFB, PSENEN and SATB1; SNX11, TMEM79, YTHDF1 and ERGIC3; or ERGIC3, PDGFB, PSENEN and YTHDF1. In further embodiments, the predictive gene signature includes at least 5 biomarkers, for example, ERGIC3, PDGFB, PSENEN, SATB1 and SNX11; ERGIC3, PDGFB, PSENEN, SATB1 and TMEM79; or PSENEN, SATB1, SNX11, TMEM79 and YTHDF1. In yet further embodiments, the predictive gene signature includes at least 6 biomarkers, for example, ERGIC3, PDGFB, PSENEN, SATB1, SNX11 and TMEM79; PDGFB, PSENEN, SATB1, SNX11,

TMEM79 and YTHDF1; or ERGIC3, PSENEN, SATB1, SNX11, TMEM79 and YTHDF1. In yet another embodiment, the predictive gene signature includes 7 biomarkers, for example, ERGIC3, PDGFB, PSENEN, SATB1, SNX11, TMEM79 and YTHDF1.

5 In various embodiments, the biomarker is not one or more of SPTA1, PAPLN, PCDH1, TMIGD2 and/or KRT24. In a particular embodiment, the biomarker is not SPTA1, PAPLN, PCDH1, TMIGD2 and KRT24. In one embodiment, the biomarker is not SPTA1. In another embodiment, the biomarker is not PAPLN. In another embodiment, the biomarker is not PCDH1. In another embodiment, the biomarker is not
10 TMIGD2. In yet another embodiment, the biomarker is not KRT24.

 In particular embodiments, the predictive gene signature may include 2 or more of biomarkers ABI3, ANG, APBB2, CCL26, CDC20, CEP152, CFL1, CKLF, COL7A1, CYP4F3, DYSF, GNAT1, GRAMD4, HYAL2, IL10, ITFG3, JAM3, KLHL17, MAD2L1BP, MANSC1, MOBKL1B, NCBP1, NMU, PHOSPHO2, TYROBP, ZIC5,
15 ERGIC3, PDGFB, PSENEN, SATB1, SNX11, TMEM79, YTHDF1, EDIL3 and TUBB6, *e.g.*, ABI3 and ANG; GRAMD4 and HYAL2; NMU and PHOSPHO2; ZIC5 and PSENEN; or SNX11 and MOBKL1B. In other embodiments, the predictive gene signature includes at least 3 of the previously recited biomarkers, *e.g.*, APBB2, CDC20 and CKLF; COL7A1, DYSF and GNAT1; NCBP1, SATB1 and EDIL3; PSENEN,
20 DYSF and GNAT1; MANSC1, ZIC5 and CFL1; or CKLF, GRAMD4 and NMU. In other embodiments, the predictive gene signature includes at least 4 of the previously recited biomarkers, *e.g.*, ANG, CCL26, CEP152 and JAM3; APBB2, CYP4F3, ITFG3 and TYROBP; CYP4F3, MANSC1, PDGFB and YTHDF1; TUBB6, DYSF, PHOSPHO2 and CDC20; or CKLF, KLHL17, HYAL2 and ZIC5. In yet further
25 embodiments, the predictive gene signature includes at least 5 of the previously recited biomarkers, *e.g.*, IL10, CEP152, COL7A1, TYROBP and ERGIC3; TMEM79, SNX11, PSENEN, GNAT1 and GRAMD4; JAM3, SNX11, KLHL17, MOBKL1B and ERGIC3; or NMU, PHOSPHO2, PDGFB, CFL1 and ANG.

 In various methods and or kits of the invention, the biomarker is not ABI3, is not
30 ANG, is not APBB2, is not CCL26, is not CDC20, is not CEP152, is not CFL1, is not CKLF, is not COL7A1, is not CYP4F3, is not DYSF, is not GNAT1, is not GRAMD4, is not HYAL2, is not IL10, is not ITFG3, is not JAM3, is not KLHL17, is not KRT24, is not MAD2L1BP, is not MANSC1, is not MOBKL1B, is not NCBP1, is not NMU, is not PCDH1, is not PHOSPHO2, is not SPTA1, is not TMIGD2, is not TYROBP, is not
35 ZIC5, is not ERGIC3, is not PDGFB, is not PSENEN, is not SATB1, is not SNX11, is not TMEM79, is not EDIL3, is not PAPLN, is not TUBB6 and/or is not YTHDF1.

In certain embodiments, the biomarker is not expressed at a detectable level. In another embodiment, the biomarker is expressed at a low level as compared to a control. Expression can be determined directly or indirectly by any suitable method. In certain embodiments, the level of expression of the biomarker is determined at the nucleic acid level using any suitable method. For example, the level of expression of the biomarker can be determined by detecting cDNA, mRNA or DNA. In particular embodiments, the level of expression of the biomarker is determined by using a technique selected from the group consisting of polymerase chain reaction (PCR) amplification reaction, reverse-transcriptase PCR analysis, quantitative reverse-transcriptase PCR analysis, Northern blot analysis, RNAase protection assay, digital RNA detection/ quantitation (*e.g.*, nanoString) and combinations or sub-combinations thereof.

In certain embodiments, the level of expression of the biomarker can be determined by detecting miRNA. Specifically, mRNA expression can be assessed indirectly by assessing levels of miRNA, wherein an elevated level of an miRNA which controls the expression of an mRNA is indicative of a low level of expression of the mRNA encoding the biomarker.

In other embodiments, the level of expression of the biomarker is determined at the protein level using any suitable method. For example, the presence or level of the protein can be detected using an antibody or antigen binding fragment thereof, which specifically binds to the protein. In particular embodiments, the antibody or antigen binding fragment thereof is selected from the group consisting of a murine antibody, a human antibody, a humanized antibody, a bispecific antibody, a chimeric antibody, a Fab, Fab', F(ab')₂, ScFv, SMIP, affibody, avimer, versabody, nanobody, and a domain antibody, or an antigen binding fragment of any of the foregoing. In particular embodiments, the antibody or antigen binding portion thereof is labeled, for example, with a label selected from the group consisting of a radio-label, a biotin-label, a chromophore-label, a fluorophore-label, and an enzyme-label. In certain embodiments, the level of expression of the biomarker is determined by using a technique selected from the group consisting of an immunoassay, a western blot analysis, a radioimmunoassay, immunofluorimetry, immunoprecipitation, equilibrium dialysis, immunodiffusion, electrochemiluminescence immunoassay (ECLIA), ELISA assay, immunopolymerase chain reaction and combinations or sub-combinations thereof. In particular embodiments, the immunoassay is a solution-based immunoassay selected from the group consisting of electrochemiluminescence, chemiluminescence, fluorogenic chemiluminescence, fluorescence polarization, and time-resolved fluorescence. In other embodiments, the immunoassay is a sandwich immunoassay selected from the group consisting of electrochemiluminescence, chemiluminescence,

and fluorogenic chemiluminescence. Other assays which rely on agents capable of detecting the protein, such as those relying upon a suitable binding partner or enzymatic activity, can also be used (*e.g.*, use of a ligand to detect a receptor molecule).

Samples can be obtained from a subject by any suitable method, and may
5 optionally have undergone further processing step(s) (*e.g.*, freezing, fractionation, fixation, guanidine treatment, etc). Any suitable sample derived from a subject can be used, such as any tissue (*e.g.*, biopsy), cell, or fluid, as well as any component thereof, such as a fraction or extract. In various embodiments, the sample is a fluid obtained from the subject, or a component of such a fluid. For example, the fluid can be blood,
10 plasma, serum, sputum, lymph, cystic fluid, nipple aspirate, urine, or fluid collected from a biopsy (*e.g.*, lump biopsy). In other embodiments, the sample is a tissue or component thereof obtained from the subject. For example, the tissue can be tissue obtained from a biopsy (*e.g.*, lump biopsy), breast tissue, connective tissue, and/or lymphatic tissue. In a particular embodiment, the tissue is breast tissue, or a component
15 thereof (*e.g.*, cells collected from the breast tissue). In a particular embodiment, the component of the breast tissue are breast tissue cells. In another embodiment, the component of the breast tissue are circulating breast tumor cells.

In one embodiment, the subject is a human.

In another aspect, the present invention provides a kit for predicting whether
20 eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer, including reagents for determining the level of expression of a biomarker selected from the group of biomarkers listed in Table 1; and instructions for use of the kit to predict whether
25 eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer. For example, the reagent for determining the level of expression of the biomarker can be a probe for identifying a null mutation in the biomarker. The reagent for determining the level of expression of the biomarker can be a probe for amplifying and/or detecting the biomarker. In yet
30 another embodiment, the reagent for determining the level of expression of the biomarker can be an antibody, for example, an antibody specific for the product of the expression of the wild type or null mutant version of the biomarker.

In a particular embodiment, the kit further includes reagents for obtaining a biological sample from a subject. In another embodiment, the kit includes a control sample.

35 In another aspect, the present invention provides methods for determining whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*,

eribulin mesylate), may be used to treat a subject having breast cancer by determining and/or identifying whether the subject carries at least one gene, selected from the group of biomarkers set forth in Table 1, which contains a null mutation. In another aspect, the present invention provides methods for predicting whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer by assaying a sample derived from the subject to determine whether the subject carries at least one gene, selected from the group of biomarkers set forth in Table 1, which contains a null mutation. In a further aspect, the present invention provides methods for determining the sensitivity of a breast tumor to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof by determining and/or identifying whether said tumor is characterized by at least one gene, selected from the group of biomarkers set forth in Table 1, which contains a null mutation. In yet another aspect, the present invention is directed to methods for treating a subject having breast cancer with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof by identifying whether at least one gene, selected from the group of biomarkers set forth in Table 1, which contains a null mutation and administering a therapeutically effective amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate) to the subject.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 depicts the high throughput siRNA screening methods in Breast Cancer Cell Lines performed as described in Example 1.

Figure 2 depicts the identification and selection of certain genes for further consideration as biomarkers of efficacy of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof.

Figure 3 depicts the confirmation assays performed as described in Example 1.

Figure 4 depicts the results of the QuantiTect SYBR Assays to determine the relative quantities of cDNAs after treatment with siRNA as set forth in Example 1.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides methods for determining whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer, methods for predicting whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin

mesylate), may be used to treat a subject having breast cancer, methods for determining the sensitivity of a breast tumor to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), and methods of treating a subject having breast cancer. Generally, the methods involve determining the level of expression of at least one biomarker as set forth in Table 1 in a sample derived from the subject, wherein a low level of expression of the biomarker is an indication that eribulin, or an analog thereof may be used to treat breast cancer and/or that the breast tumor is sensitive to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate).

The invention is based, at least in part, on the observation that a low level of expression, *e.g.*, the absence of expression, of the biomarkers identified herein is indicative of responsiveness to eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate). As shown herein, siRNA techniques were employed to “knock down” expression of certain genes and assess the sensitivity of the resulting knock down cells to eribulin mesylate. Based on the findings from these studies, low levels of expression of each of the genes set forth in Table 1 was identified as being associated with the sensitivity of breast cancer cells to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate).

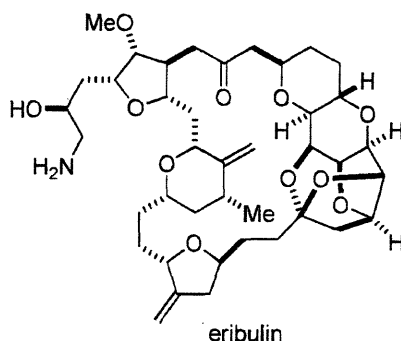
Unless otherwise defined herein, scientific and technical terms used in connection with the present invention shall have the meanings that are commonly understood by those of ordinary skill in the art. The meaning and scope of the terms should be clear, however, in the event of any latent ambiguity, definitions provided herein take precedent over any dictionary or extrinsic definition. Further, unless otherwise required by context, singular terms, for example, those characterized by “a” or “an”, shall include pluralities, *e.g.*, one or more biomarkers. In this application, the use of “or” means “and/or”, unless stated otherwise. Furthermore, the use of the term “including,” as well as other forms of the term, such as “includes” and “included”, is not limiting. Also, terms such as “element” or “component” encompass both elements and components comprising one unit and elements and components that comprise more than one unit unless specifically stated otherwise.

The phrase “determining whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer” refers to assessing the likelihood that treatment of a subject with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate) will be effective (*e.g.*, provide a therapeutic benefit to the subject) or will not be effective in the subject. Assessment of the likelihood that treatment will or will not be effective typically can be performed before treatment with

eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), has begun or before treatment is resumed. Alternatively or in combination, assessment of the likelihood of efficacious treatment can be performed during treatment, for example, to determine whether treatment should be continued or discontinued. For example, such an assessment can be performed (a) by determining the level of expression of a biomarker, for example, a biomarker selected from the group of biomarkers listed in Table 1, in a sample derived from said subject, wherein a low level of expression of the biomarker indicates that eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, may be used to treat said subject having breast cancer, or (b) by assaying a sample derived from said subject to determine the level of expression in said sample of a biomarker, for example, a biomarker selected from the group of biomarkers listed in Table 1, wherein a low level of expression of the biomarker indicates that eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, may be used to treat said subject having breast cancer.

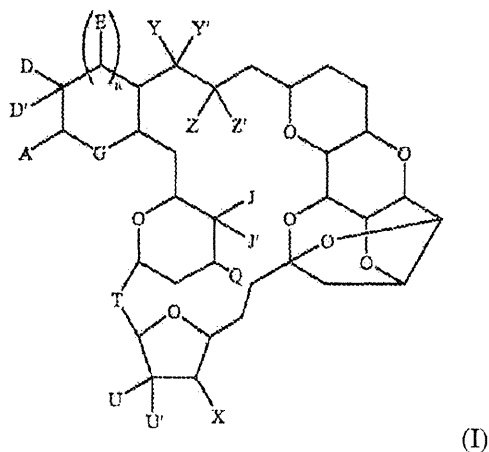
The phrase “determining the sensitivity of a breast tumor to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof”, as used herein, is intended to refer to assessing the susceptibility of a breast tumor, *e.g.*, breast cancer cells, to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate). Sensitivity of a tumor can include the ability of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), to kill tumor cells, to inhibit the spread and/or metastasis of tumor cells, and/or to inhibit the growth of tumor cells completely or partially (*e.g.*, slow down the growth of tumor cells by at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, or 95%). The assessment can be performed (i) before treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), is begun; (ii) before treatment is resumed in the subject; and/or during treatment, for example, to determine whether treatment should be continued or discontinued. For example, such a determination can be performed (a) by determining the level of expression of a biomarker, *e.g.*, a biomarker selected from the group of biomarkers listed in Table 1, in said tumor, wherein a low level of expression of the biomarker in said tumor indicates that said tumor is sensitive to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, or (b) by determining the level of expression of a biomarker *e.g.*, a biomarker selected from the group of biomarkers listed in Table 1, in said tumor, and identifying said tumor as being sensitive to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, when said biomarker is expressed in said tumor at a low level.

The term “eribulin” as used herein refers to the art-recognized fully synthetic macrocyclic ketone analog of halichondrin B. As set forth in U.S. Patent No. 6,214,865, the entire contents of which are incorporated herein by reference, eribulin has the following structure



and can be generated using techniques as described therein or as described in Kim DS et al. (November 2009) *J. Am. Chem. Soc.* 131 (43): 15636–41, the entire contents of which are incorporated herein by reference. Eribulin is also known as ER-086526 and is identified by CAS number 253128-41-5. Eribulin mesylate is also known as E7389.

As used herein, the term “eribulin analog” includes compounds in which one or more atoms or functional groups of eribulin have been replaced with different atoms or functional groups. For example, eribulin analogs include compounds having the following formula (I), which also encompasses eribulin:



In formula (I), A is a C₁₋₆ saturated or C₂₋₆ unsaturated hydrocarbon skeleton, the skeleton being unsubstituted or having between 1 and 13 substituents, preferably between 1 and 10 substituents, *e.g.*, at least one substituent selected from cyano, halo,

azido, Q₁, and oxo. Each Q₁ is independently selected from OR₁, SR₁, SO₂ R₁, OSO₂ R₁, NR₂ R₁, NR₂ (CO)R₁, NR₂ (CO)(CO)R₁, NR₄ (CO)NR₂ R₁, NR₂ (CO)OR₁, (CO)OR₁, O(CO)R₁, (CO)NR₂ R₁, and O(CO)NR₂ R₁. The number of substituents can be, for example, from 1 to 6, from 1 to 8, from 2 to 5, or from 1 to 4. Throughout the disclosure, numerical ranges are understood to be inclusive.

Each of R₁, R₂, R₄, R₅, and R₆ is independently selected from H, C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ hydroxyalkyl, C₁₋₆ aminoalkyl, C₆₋₁₀ aryl, C₆₋₁₀ haloaryl (*e.g.*, p-fluorophenyl or p-chlorophenyl), C₆₋₁₀ hydroxyaryl, C₁₋₄ alkoxy-C₆ aryl (*e.g.*, C₁₋₃ alkoxy-C₆ aryl, p-methoxyphenyl, 3,4,5-trimethoxyphenyl, p-ethoxyphenyl, or 3,5-diethoxyphenyl), C₆₋₁₀ aryl-C₁₋₆ alkyl (*e.g.*, benzyl or phenethyl), C₁₋₆ alkyl-C₆₋₁₀ aryl, C₆₋₁₀ haloaryl-C₁₋₆ alkyl, C₁₋₆ alkyl-C₆₋₁₀ haloaryl, (C₁₋₃ alkoxy-C₆ aryl)-C₁₋₃ alkyl, C₂₋₉ heterocyclic radical, C₂₋₉ heterocyclic radical-C₁₋₆ alkyl, C₂₋₉ heteroaryl, and C₂₋₉ heteroaryl-C₁₋₆ alkyl. There may be more than one R₁, for example, if A is substituted with two different alkoxy (OR₁) groups such as butoxy and 2-aminoethoxy.

Examples of A include 2,3-dihydroxypropyl, 2-hydroxyethyl, 3-hydroxy-4-perfluorobutyl, 2,4,5-trihydroxypentyl, 3-amino-2-hydroxypropyl, 1,2-dihydroxyethyl, 2,3-dihydroxy-4-perfluorobutyl, 3-cyano-2-hydroxypropyl, 2-amino-1-hydroxy ethyl, 3-azido-2-hydroxypropyl, 3,3-difluoro-2,4-dihydroxybutyl, 2,4-dihydroxybutyl, 2-hydroxy-2(p-fluorophenyl)-ethyl, -CH₂ (CO)(substituted or unsubstituted aryl), -CH₂ (CO)(alkyl or substituted alkyl, such as haloalkyl or hydroxyalkyl) and 3,3-difluoro-2-hydroxypent-4-enyl.

Examples of Q₁ include -NH(CO)(CO)-(heterocyclic radical or heteroaryl), -OSO₂ -(aryl or substituted aryl), -O(CO)NH-(aryl or substituted aryl), aminoalkyl, hydroxyalkyl, -NH(CO)(CO)-(aryl or substituted aryl), -NH(CO)(alkyl)(heteroaryl or heterocyclic radical), O(substituted or unsubstituted alkyl)(substituted or unsubstituted aryl), and -NH(CO)(alkyl)(aryl or substituted aryl).

Each of D and D' is independently selected from R₃ and OR₃, wherein R₃ is H, C₁₋₃ alkyl, or C₁₋₃ haloalkyl. Examples of D and D' are methoxy, methyl, ethoxy, and ethyl. In some embodiments, one of D and D' is H.

The value for n is 1 or preferably 0, thereby forming either a six-membered or five-membered ring. This ring can be unsubstituted or substituted, *e.g.*, where E is R₅ or OR₅, and can be a heterocyclic radical or a cycloalkyl, *e.g.* where G is S, CH₂, NR₆, or preferably O.

Each of J and J' is independently H, C₁₋₆ alkoxy, or C₁₋₆ alkyl; or J and J' taken together are =CH₂ or -O-(straight or branched C₁₋₅ alkylene)-O-, such as exocyclic methylenide, isopropylidene, methylene, or ethylene.

Q is C₁₋₃ alkyl, and is preferably methyl.

T is ethylene or ethenylene, optionally substituted with (CO)OR₇, where R₇ is H or C₁₋₆ alkyl.

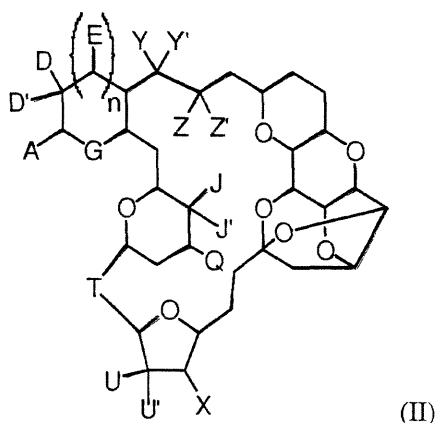
Each of U and U' is independently H, C₁₋₆ alkoxy, or C₁₋₆ alkyl; or U and U' taken together are =CH₂ or -O-(straight or branched C₁₋₅ alkylene)-O-.

5 X is H or C₁₋₆ alkoxy.

Each of Y and Y' is independently H or C₁₋₆ alkoxy; or Y and Y' taken together are =O, =CH₂, or -O-(straight or branched C₁₋₅ alkylene)-O-.

Each of Z and Z' is independently H or C₁₋₆ alkoxy; or Z and Z' taken together are =O, =CH₂, or -O-(straight or branched C₁₋₅ alkylene)-O-.

10 In certain embodiments, the eribulin analogs include compounds having the following formula (II):



In formula (II), the substitutions are defined as follows:

15 A is a C₁₋₆ saturated or C₂₋₆ unsaturated hydrocarbon skeleton, said skeleton being unsubstituted or having between 1 and 10 substituents, inclusive, independently selected from cyano, halo, azido, oxo, and Q₁.

Each Q₁ is independently selected from OR₁, SR₁, SO₂R₁, OSO₂R₁, NR₂R₁, NR₂(CO)R₁, NR₂(CO)(CO)R₁, NR₄(CO)NR₂R₁, NR₂(CO)OR₁, (CO)OR₁, O(CO)R₁,
20 (CO)NR₂R₁, and O(CO)NR₂R₁.

Each of R₁, R₂ and R₄ is independently selected from H, C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ hydroxyalkyl, C₁₋₆ aminoalkyl, C₆₋₁₀ aryl, C₆₋₁₀ haloaryl, C₆₋₁₀ hydroxyaryl, C₁₋₃ alkoxy-C₆ aryl, C₆₋₁₀ aryl-C₁₋₆ alkyl, C₁₋₆ alkyl-C₆₋₁₀ aryl, C₆₋₁₀ haloaryl-C₁₋₆ alkyl, C₁₋₆ alkyl-C₆₋₁₀ haloaryl, (C₁₋₃ alkoxy-C₆ aryl)-C₁₋₃ alkyl, C₂₋₉

heterocyclic radical, C₂₋₉ heterocyclic radical-C₁₋₆ alkyl, C₂₋₉ heteroaryl, and C₂₋₉ heteroaryl-C₁₋₆ alkyl.

Each of D and D' is independently selected from R₃ and OR₃, wherein R₃ is H, C₁₋₃ alkyl, or C₁₋₃ haloalkyl.

5 n is 0 or 1.

E is R₅ or OR₅, wherein R₅ is independently selected from H, C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ hydroxyalkyl and C₁₋₆ aminoalkyl.

G is O.

10 Each of J and J' is independently H, C₁₋₆ alkoxy, or C₁₋₆ alkyl; or J and J' taken together are =CH₂.

Q is C₁₋₃ alkyl.

T is ethylene or ethenylene.

Each of U and U' is independently H, C₁₋₆ alkoxy, or C₁₋₆ alkyl; or U and U' taken together are =CH₂.

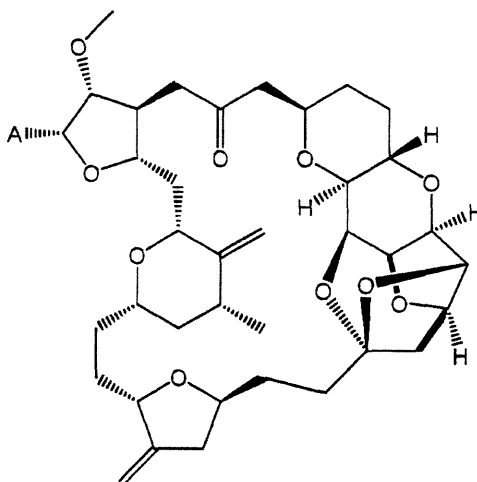
15 X is H or C₁₋₆ alkoxy.

Each of Y and Y' is independently H or C₁₋₆ alkoxy; or Y and Y' taken together are =O.

Each of Z and Z' is independently H or C₁₋₆ alkoxy; or Z and Z' taken together are =O.

20

In some embodiments, the eribulin analogs include compounds having the following formula (III):



(III)

wherein A is a C₁₋₆ saturated or C₂₋₆ unsaturated hydrocarbon skeleton, the skeleton being unsubstituted or having between 1 and 13 substituents, e.g., between 1 and 10 substituents selected from cyano, halo, azido, Q₁, and oxo;

- 5 each Q₁ is independently selected from OR₁, SR₁, SO₂R₁, OSO₂R₁, NR₂R₁, NR₂(CO)R₁, NR₂(CO)(CO)R₁, NR₄(CO)NR₂R₁, NR₂(CO)OR₁, (CO)OR₁, O(CO)R₁, (CO)NR₂R₁, and O(CO)NR₂R₁; and

- each of R₁, R₂, and R₄ is independently selected from H, C₁₋₆ alkyl, C₁₋₆ haloalkyl, C₁₋₆ hydroxyalkyl, C₁₋₆ aminoalkyl, C₆₋₁₀ aryl, C₆₋₁₀ haloaryl, C₆₋₁₀ hydroxyaryl, C₁₋₄ alkoxy-C₆ aryl, C₆₋₁₀ aryl-C₁₋₆ alkyl, C₁₋₆ alkyl-C₆₋₁₀ aryl, C₆₋₁₀ haloaryl-C₁₋₆ alkyl, C₁₋₆ alkyl-C₆₋₁₀ haloaryl, (C₁₋₃ alkoxy-C₆ aryl)-C₁₋₃ alkyl, C₂₋₉ heterocyclic radical, C₂₋₉ heterocyclic radical-C₁₋₆ alkyl, C₂₋₉ heteroaryl, and C₂₋₉ heteroaryl-C₁₋₆ alkyl.

- Hydrocarbon skeletons contain carbon and hydrogen atoms and may be linear, branched, or cyclic. Unsaturated hydrocarbons include one, two, three or more C=C double bonds (sp²) or C≡C triple bonds (sp). Examples of unsaturated hydrocarbon radicals include ethynyl, 2-propynyl, 1-propenyl, 2-butenyl, 1,3-butadienyl, 2-pentenyl, vinyl (ethenyl), allyl, and isopropenyl. Examples of bivalent unsaturated hydrocarbon radicals include alkenylenes and alkylidenes such as methylidyne, ethylidene, ethylidyne, vinylidene, and isopropylidene. In general, compounds of the invention have hydrocarbon skeletons ("A" in formula (I)) that are substituted, e.g., with hydroxy, amino, cyano, azido, heteroaryl, aryl, and other moieties described herein. Hydrocarbon skeletons may have two geminal hydrogen atoms replaced with oxo, a bivalent carbonyl oxygen atom (=O), or a ring-forming substituent, such as --O--(straight or branched alkylene or alkylidene)-O-- to form an acetal or ketal.

C₁₋₆ alkyl includes linear, branched, and cyclic hydrocarbons, such as methyl, ethyl, propyl, isopropyl, butyl, isobutyl, sec-butyl, tert-butyl, pentyl, isopentyl, sec-pentyl, neo-pentyl, tert-pentyl, cyclopentyl, hexyl, isohexyl, sec-hexyl, cyclohexyl, 2-methylpentyl, tert-hexyl, 2,3-dimethylbutyl, 3,3-dimethylbutyl, 1,3-dimethylbutyl, and 2,3-dimethyl but-2-yl. Alkoxy (--OR), alkylthio (--SR), and other alkyl-derived moieties (substituted, unsaturated, or bivalent) are analogous to alkyl groups (R). Alkyl groups, and alkyl-derived groups such as the representative alkoxy, haloalkyl, hydroxyalkyl, alkenyl, alkylidene, and alkylene groups, can be C₂₋₆, C₃₋₆, C₁₋₃, or C₂₋₄.

Alkyls substituted with halo, hydroxy, amino, cyano, azido, and so on can have 1, 2, 3, 4, 5 or more substituents, which are independently selected (may or may not be the same) and may or may not be on the same carbon atom. For example, haloalkyls are alkyl groups with at least one substituent selected from fluoro, chloro, bromo, and iodo. Haloalkyls may have two or more halo substituents which may or may not be the same halogen and may or may not be on the same carbon atom. Examples include chloromethyl, periodomethyl, 3,3-dichloropropyl, 1,3-difluorobutyl, and 1-bromo-2-chloropropyl.

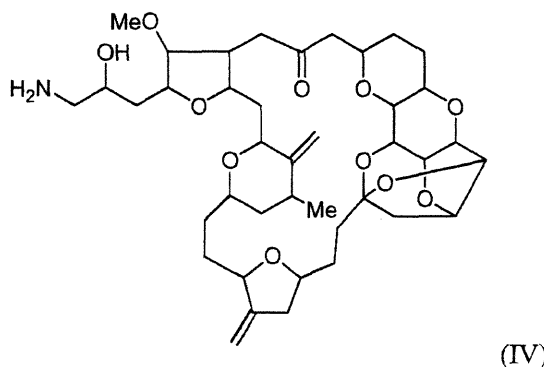
Heterocyclic radicals and heteroaryls include furyl, pyranyl, isobenzofuranyl, chromenyl, xanthenyl, phenoxathieryl, 2H-pyrrolyl, pyrrolyl, imidazolyl (e.g., 1-, 2- or 4-imidazolyl), pyrazolyl, isothiazolyl, isoxazolyl, pyridyl (e.g., 1-, 2-, or 3-pyridyl), pyrazinyl, pyrimidinyl, pyridazinyl, indolizynyl, isoindolyl, 3H-indolyl, indolyl (e.g., 1-, 2-, or 3-indolyl), indazolyl, purinyl, 4H-quinolizynyl, isoquinolyl, quinolyl, phthalazinyl, naphthyridinyl, quinoxalinyl, quinazolinyl, cinnolinyl, pteridinyl, pyrrolinyl, pyrrolidinyl, imidazolidinyl, pyrazolidinyl, pyrazolinyl, piperidyl, piperazinyl, indolinyl, isoindolinyl, and morpholinyl. Heterocyclic radicals and heteroaryls may be linked to the rest of the molecule at any position along the ring. Heterocyclic radicals and heteroaryls can be C₂₋₉, or smaller, such as C₃₋₆, C₂₋₅, or C₃₋₇.

Aryl groups include phenyl, benzyl, naphthyl, tolyl, mesityl, xylyl, and cumenyl.

It is understood that "heterocyclic radical", "aryl", and "heteroaryl" include those having 1, 2, 3, 4, or more substituents independently selected from lower alkyl, lower alkoxy, amino, halo, cyano, nitro, azido, and hydroxyl. Heterocyclic radicals, heteroaryls, and aryls may also be bivalent substituents of hydrocarbon skeleton "A" in formula (I).

The term "eribulin analog" includes eribulin prodrugs. The term "eribulin prodrugs" includes eribulin that has been chemically modified to be inactive or less active until bioactivation (*e.g.*, metabolism *in vivo*) by an enzyme which cleaves the chemically modified portion of the eribulin prodrug, thereby providing the active form of eribulin.

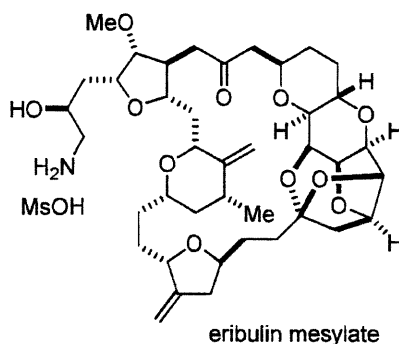
As used herein, the term "eribulin analog" includes all stereoisomers of eribulin and other compounds of formula (I), including diastereoisomers and enantiomers thereof. "Stereoisomers" refers to isomers that differ only in the arrangement of the atoms in space. "Diastereoisomers" refers to stereoisomers that are not mirror images of each other. "Enantiomers" refers to stereoisomers that are non-superimposable mirror images of one another. For example, Formula (IV) encompasses eribulin and such stereoisomers:



The phrase "pharmaceutically acceptable salt," as used herein, is a salt formed from an acid and a basic nitrogen group of Eribulin or an eribulin analog. Examples of such salts include acid addition salts and base addition salts, such as inorganic acid salts or organic acid salts (e.g., hydrochloric acid salt, sulfuric acid salt, citrate, hydrobromic acid salt, hydroiodic acid salt, nitric acid salt, bisulfate, phosphoric acid salt, super phosphoric acid salt, isonicotinic acid salt, acetic acid salt, lactic acid salt, salicylic acid salt, tartaric acid salt, pantothenic acid salt, ascorbic acid salt, succinic acid salt, maleic acid salt, fumaric acid salt, gluconic acid salt, saccharinic acid salt, formic acid salt, benzoic acid salt, glutaminic acid salt, methanesulfonic acid salt, ethanesulfonic acid salt, benzenesulfonic acid salt, p-toluenesulfonic acid salt, pamoic acid salt (pamoate)), as well as salts of aluminum, calcium, lithium, magnesium, calcium, sodium, zinc, and diethanolamine. It will be understood that reference to eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, includes pharmaceutically acceptable salts of eribulin as well as pharmaceutically acceptable salts of an analog thereof. Examples of such pharmaceutically acceptable salts include, but are not limited to, a pharmaceutically acceptable salt of Formula I, a pharmaceutically acceptable salt of Formula II, a pharmaceutically acceptable salt of Formula III or a pharmaceutically acceptable salt of Formula IV.

In a particular embodiment, eribulin mesylate, a pharmaceutically acceptable salt form of eribulin is utilized in the methods of the present invention. Eribulin mesylate is

sold under the trade name HALAVEN[®]. The chemical name for eribulin mesylate is 11,15:18,21:24,28-Trieпоxy-7,9-ethano-12,15-methano-9H,15H-furo[3,2-i]furo[2',3':5,6]pyrano[4,3-b][1,4]dioxacyclopentacosin-5(4H)-one, 2-[(2S)-3-amino-2-hydroxypropyl]hexacosahydro-3-methoxy-26-methyl-20,27-bis(methylene)-, (2R,3R,3aS,7R,8aS,9S,10aR,11S,12R,13aR,13bS,15S,18S,21S,24S,26R,28R,29aS)-methanesulfonate (salt). Eribulin mesylate has the following structure



Eribulin mesylate is label indicated for the treatment of patients with metastatic breast cancer who have previously received at least two chemotherapeutic regimens for the treatment of metastatic disease, including, for example, therapy with an anthracycline and a taxane in either the adjuvant or metastatic setting.

As used herein, the term “biomarker” is intended to encompass a substance that is used as an indicator of a biologic state and includes for example, genes (or portions thereof), mRNAs (or portions thereof), miRNAs (microRNAs), and proteins (or portions thereof). A “biomarker expression pattern” is intended to refer to a quantitative or qualitative summary of the expression of one or more biomarkers in a subject, such as in comparison to a standard or a control.

Various biomarkers which can be used in the methods described herein are summarized in Table 1. Table 1 provides gene abbreviations, Gene ID numbers and accession numbers for transcripts from which encoding nucleotide gene sequences can be identified. For example, gene ABI3 refers to a *Homo sapiens* ABI family, member 3. The nucleotide sequence for human ABI3 transcript variant 1 can be found at Accession Number NM_016428. Reference to a gene (e.g., ABI3) is intended to encompass naturally occurring or endogenous versions of the gene, including wild type, polymorphic or allelic variants or mutants (e.g., germline mutation, somatic mutation) of the gene, which can be found in a subject and/or tumor from a subject. In some embodiments, the sequence of the biomarker gene is at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at

least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to a sequence identified in Table 1 by Accession Number or Gene_ID number. For example, sequence identity can be determined by comparing sequences using NCBI BLAST (e.g., Megablast with default parameters).

As used herein, the phrase “predictive gene signature” refers to expression levels of two or more biomarkers of the present invention in a subject that are indicative of responsiveness to treatment with eribulin, or an eribulin analog. For example, the low level expression of at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 biomarkers from Table 1 in a subject may constitute a gene signature that indicates that the subject will respond positively to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate). Any sub-combination of 2 or more markers from Table 1 may constitute a predictive gene signature of the invention. In another example, the expression of at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 biomarkers from Table 1 under particular threshold levels, or any sub-combination thereof, constitutes a gene signature that indicates that the subject will respond positively to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate).

A “low level of expression” of the biomarker, for example, a biomarker selected from the group of biomarkers listed in Table 1, refers to a level of expression of the biomarker in a test sample (*e.g.*, a sample derived from a subject) that correlates with sensitivity to eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate). This can be determined by comparing the level of expression of the biomarker in the test sample with that of a suitable control. A “low level of expression” also includes a lack of detectable expression of the biomarker.

In some embodiments, the level of expression of the biomarker is determined relative to a control sample, such as the level of expression of the biomarker in normal tissue (*e.g.*, a range determined from the levels of expression of the biomarker observed in normal tissue samples). In these embodiments, a low level of expression will fall below or within the lower levels of this range. In some embodiments, the level of expression of the biomarker is determined relative to a control sample, such as the level of expression of the biomarker in samples (*e.g.*, tumor samples, circulating tumor cells) from other subjects. For example, the level of expression of the biomarker in samples from other subjects can be determined to define levels of expression which correlate with sensitivity to treatment with eribulin, an analog thereof, or a pharmaceutically

acceptable salt thereof (*e.g.*, eribulin mesylate), and the level of expression of the biomarker in the sample from the subject of interest is compared to these levels of expression, wherein a comparable or lower level of expression in the sample from the subject is indicative of a “low level of expression” of the biomarker in the sample. In another example, the level of expression of the biomarker in samples (*e.g.*, tumor samples, circulating tumor cells) from other subjects can be determined to define levels of expression which correlate with resistance or non-responsiveness to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), and the level of expression of the biomarker in the sample from the subject of interest is compared to these levels of expression, wherein a lower level of expression in the sample from the subject is indicative of a “low level of expression” of the biomarker in the sample.

The term “known standard level” or “control level” can refer to an accepted or pre-determined expression level of the biomarker, for example, a biomarker selected from the group of biomarkers listed in Table 1 which is used to compare expression level of the biomarker in a sample derived from a subject. In one embodiment, the control expression level of the biomarker is the average expression level of the biomarker in samples derived from a population of subjects. For example, the control expression level can be the average expression level of the biomarker in breast cancer cells derived from a population of subjects with breast cancer. The population may be subjects who have not responded to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), or the population may be a group of subjects who express the respective biomarker at high or normal levels. In some embodiments, the control level may constitute a range of expression of the biomarker in normal tissue, as described above. For example, the control level may constitute a range of expression of the biomarker in tumor samples from a variety of subjects having breast cancer, as described above.

As further information becomes available as a result of routine performance of the methods described herein, population-average values for “control” level of expression of the biomarkers of the present invention may be used. In other embodiments, the “control” level of expression of the biomarkers may be determined by determining expression level of the respective biomarker in a subject sample obtained from a subject before the suspected onset of breast cancer in the subject, from archived subject samples, and the like.

Control levels of expression of biomarkers of the invention may be available from publicly available databases. In addition, Universal Reference Total RNA

(Clontech Laboratories) and Universal Human Reference RNA (Stratagene) and the like can be used as controls. For example, qPCR can be used to determine the level of expression of a biomarker, and an increase in the number of cycles needed to detect expression of a biomarker in a sample from a subject, relative to the number of cycles
5 needed for detection using such a control, is indicative of a low level of expression of the biomarker.

As used herein, the term "subject" or "patient" refers to human and non-human animals, *e.g.*, veterinary patients. The term "non-human animal" includes vertebrates, *e.g.*, mammals, such as non-human primates, mice, rabbits, sheep, dog, cat, horse, cow,
10 or other rodent, ovine, canine, feline, equine or bovine species. In one embodiment, the subject is a human.

The term "sample" as used herein refers to cells, tissues or fluids isolated from a subject, as well as cells, tissues or fluids present within a subject. The term "sample" includes any body fluid (*e.g.*, blood, lymph, cystic fluid, nipple aspirates, urine and
15 fluids collected from a biopsy (*e.g.*, lump biopsy)), tissue or a cell or collection of cells from a subject, as well as any component thereof, such as a fraction or extract. In one embodiment, the tissue or cell is removed from the subject. In another embodiment, the tissue or cell is present within the subject. Other samples include tears, plasma, serum, cerebrospinal fluid, feces, sputum and cell extracts. In one embodiment, the sample
20 contains protein (*e.g.*, proteins or peptides) from the subject. In another embodiment, the sample contains RNA (*e.g.*, mRNA molecules) from the subject or DNA (*e.g.*, genomic DNA molecules) from the subject.

As used herein, the term "breast cancer" refers generally to the uncontrolled growth of breast tissue and, more specifically, to a condition characterized by anomalous
25 rapid proliferation of abnormal cells in one or both breasts of a subject. The abnormal cells often are referred to as malignant or "neoplastic cells," which are transformed cells that can form a solid tumor. The term "tumor" refers to an abnormal mass or population of cells (*i.e.*, two or more cells) that result from excessive or abnormal cell division, whether malignant or benign, and pre-cancerous and cancerous cells. Malignant tumors
30 are distinguished from benign growths or tumors in that, in addition to uncontrolled cellular proliferation, they can invade surrounding tissues and can metastasize. In breast cancer, neoplastic cells may be identified in one or both breasts only and not in another tissue or organ, in one or both breasts and one or more adjacent tissues or organs (*e.g.* lymph node), or in a breast and one or more non-adjacent tissues or organs to which the
35 breast cancer cells have metastasized.

Eribulin, an analog thereof, or pharmaceutically acceptable salt thereof, can be used to treat breast cancer, and, accordingly, the methods of the present invention can be used in breast cancer and in subjects having breast cancer.

5 In one embodiment, the breast cancer is Estrogen Receptor (ER) negative breast cancer, Progesterone Receptor (PR) negative breast cancer and/or HER-2 negative breast cancer. For example, the breast cancer may be Estrogen Receptor (ER) negative and Progesterone Receptor (PR) negative breast cancer; Estrogen Receptor (ER) negative and HER-2 negative breast cancer; Progesterone Receptor (PR) negative and HER-2 negative breast cancer; or Estrogen Receptor (ER) negative breast cancer, Progesterone
10 Receptor (PR) negative breast cancer and HER-2 negative (triple negative) breast cancer. Assessment of ER, PR and HER-2 status can be done using any suitable method. For example, HER-2 status can be assessed by immunohistochemistry (IHC) and/or gene amplification by fluorescence *in situ* hybridization (FISH), for example, according to National Comprehensive Cancer Network [NCCN] guidelines.

15 The breast cancer can be for example, adenocarcinoma, inflammatory breast cancer, recurrent (*e.g.*, locally recurrent) and/or metastatic breast cancer. In some embodiments, the breast cancer is endocrine refractory or hormone refractory. The terms “endocrine refractory” and “hormone refractory” refer to a cancer that is resistant to treatment with hormone therapy for breast cancer, *e.g.*, aromatase inhibitors or
20 tamoxifen. Breast cancers arise most commonly in the lining of the milk ducts of the breast (ductal carcinoma), or in the lobules where breast milk is produced (lobular carcinoma). Accordingly, in various embodiments of the invention, the breast cancer can be ductal carcinoma or lobular carcinoma. Cancerous cells from the breast(s) may invade or metastasize to any other organ or tissue of the body. For example, cancer cells
25 often invade lymph node cells and/or metastasize to the liver, brain and/or bone.

In various embodiments of the present invention, the subject may be suffering from Stage I, Stage II, Stage III or Stage IV breast cancer. The stage of a breast cancer can be classified as a range of stages from Stage 0 to Stage IV based on its size and the extent to which it has spread. The following table summarizes the stages, which are well
30 known to clinicians:

STAGE	TUMOR SIZE	LYMPH NODE INVOLVEMENT	METASTASIS (SPREAD)
I	Less than 2 cm	No	No
II	Between 2-5 cm	No or in same side of breast	No
III	More than 5 cm	Yes, on same side of breast	No
IV	Not applicable	Not applicable	Yes

Various aspects of the invention are described in further detail in the following subsections.

5

I. Prediction of Responsiveness to Eribulin, an Analog thereof, or a Pharmaceutically Acceptable Salt thereof (e.g., Eribulin Mesylate) in Subjects with Breast Cancer

In one aspect, the invention provides a method for determining whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (e.g., eribulin mesylate),
10 may be used to treat a subject having breast cancer and/or for determining the sensitivity of a breast tumor to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (e.g., eribulin mesylate). The methods involve determining the expression level of at least one biomarker, for example, by assaying a sample derived from a subject having breast cancer. The identification of low levels of expression of at
15 least one biomarker is indicative that eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (e.g., eribulin mesylate) may be used for treatment of the breast cancer and/or that the breast tumor is sensitive to the treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (e.g., eribulin mesylate).

In the methods of the invention, the expression level of at least one biomarker
20 selected from the group of biomarkers set forth in Table 1 is assessed, which, as explained herein, can comprise determining the level of expression of one or more of these genes (e.g., ABI3, ANG) using various approaches, such as determining in a suitable sample the presence of certain DNA polymorphisms or null mutations, determining the level of RNA expressed from a gene, including an mRNA exemplified
25 in Table 1 and/or other transcripts from the gene, or a protein product(s) of any of the foregoing.

TABLE 1: BIOMARKERS OF RESPONSIVENESS TO ERIBULIN, AN ANALOG THEREOF, OR A PHARMACEUTICALLY ACCEPTABLE SALT THEREOF (e.g., ERIBULIN MESYLATE)

GENE NAME	GENE ID	ACCESSION NO.	SEQ ID NO.	NAME
ABI3	51225	NM_016428	1 & 2	Homo sapiens ABI family, member 3 (ABI3), transcript variant 1, mRNA
ANG	283	NM_001097577	3 & 4	Homo sapiens angiogenin, ribonuclease, RNase A family, 5 (ANG), transcript variant 2, mRNA
APBB2	323	NM_173075	5 & 6	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (APBB2), mRNA
CCL26	10344	NM_006072	7 & 8	Homo sapiens chemokine (C-C motif) ligand 26 (CCL26), mRNA
CDC20	991	NM_001255	9 & 10	Homo sapiens cell division cycle 20 homolog (S. cerevisiae) (CDC20), mRNA
CEP152	22995	NM_014985	11 & 12	Homo sapiens centrosomal protein 152kDa (CEP152), mRNA
CFL1	1072	NM_005507	13 & 14	Homo sapiens cofilin 1 (non-muscle) (CFL1), mRNA
CKLF	51192	NM_016326	15 & 16	Homo sapiens chemokine-like factor (CKLF), transcript variant 3, mRNA
COL7A1	1294	NM_000094	17 & 18	Homo sapiens collagen, type VII, alpha 1 (COL7A1), mRNA
CYP4F3	4051	NM_000896	19 & 20	Homo sapiens cytochrome P450, family 4, subfamily F, polypeptide 3 (CYP4F3), mRNA
DYSF	8291	NM_003494	21 & 22	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), transcript variant 8, mRNA
EDIL3	10085	NM_005711	23 & 24	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
ERGIC3	51614	NM_015966	25 & 26	Homo sapiens ERGIC and golgi 3 (ERGIC3), transcript variant 2, mRNA
GNAT1	2779	NM_000172	27 & 28	Homo sapiens guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1 (GNAT1), transcript variant 2, mRNA
GRAMD4	23151	NM_015124	29 & 30	Homo sapiens GRAM domain containing 4 (GRAMD4), mRNA
HYAL2	8692	NM_003773	31 & 32	Homo sapiens hyaluronoglucosaminidase 2 (HYAL2), transcript variant 1, mRNA
IL10	3586	NM_000572	33 & 34	Homo sapiens interleukin 10 (IL10), mRNA
ITFG3	83986	NM_032039	35 & 36	Homo sapiens integrin alpha FG-GAP repeat containing 3 (ITFG3), mRNA
JAM3	83700	NM_032801	37 & 38	Homo sapiens junctional adhesion molecule 3 (JAM3), mRNA
KLHL17	339451	NM_198317	39 & 40	Homo sapiens kelch-like 17 (Drosophila) (KLHL17), mRNA
KRT24	192666	NM_019016	41 & 42	Homo sapiens keratin 24 (KRT24), mRNA
MAD2L1BP	9587	NM_014628	43 & 44	Homo sapiens MAD2L1 binding protein (MAD2L1BP), transcript variant 2, mRNA
MANSC1	54682	NM_018050	45 & 46	Homo sapiens MANSC domain containing 1 (MANSC1), mRNA
MOBKL1B	55233	NM_018221	47 & 48	Homo sapiens MOB1, Mps One Binder kinase activator-like 1B (yeast) (MOBKL1B), mRNA
NCBP1	4686	NM_002486	49 & 50	Homo sapiens nuclear cap binding protein

				subunit 1, 80kDa (NCBP1), mRNA
NMU	10874	NM_006681	51 & 52	Homo sapiens neuromedin U (NMU), mRNA
PAPLN	89932	NM_173462	53 & 54	Homo sapiens papilin, proteoglycan-like sulfated glycoprotein (PAPLN), mRNA
PCDH1	5097	NM_002587	55 & 56	Homo sapiens protocadherin 1 (PCDH1), transcript variant 1, mRNA
PDGFB	5155	NM_002608	57 & 58	Homo sapiens platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog) (PDGFB), transcript variant 1, mRNA
PHOSPHO2	493911	NM_001008489	59 & 60	Homo sapiens phosphatase, orphan 2 (PHOSPHO2), mRNA
PSENEN	55851	NM_172341	61 & 62	Homo sapiens presenilin enhancer 2 homolog (C. elegans) (PSENEN), mRNA
SATB1	6304	NM_002971	63 & 64	Homo sapiens SATB homeobox 1 (SATB1), transcript variant 1, mRNA
SNX11	29916	NM_013323	65 & 66	Homo sapiens sorting nexin 11 (SNX11), transcript variant 2, mRNA
SPTA1	6708	NM_003126	67 & 68	Homo sapiens spectrin, alpha, erythrocytic 1 (elliptocytosis 2) (SPTA1), mRNA
TMEM79	84283	NM_032323	69 & 70	Homo sapiens transmembrane protein 79 (TMEM79), transcript variant 1, mRNA
TMIGD2	126259	NM_144615	71 & 72	Homo sapiens transmembrane and immunoglobulin domain containing 2 (TMIGD2), mRNA
TUBB6	84617	NM_032525	73 & 74	Homo sapiens tubulin, beta 6 (TUBB6), mRNA
TYROBP	7305	NM_198125	75 & 76	Homo sapiens TYRO protein tyrosine kinase binding protein (TYROBP), transcript variant 2, mRNA
YTHDF1	54915	NM_017798	77 & 78	Homo sapiens YTH domain family, member 1 (YTHDF1), mRNA
ZIC5	85416	NM_033132	79 & 80	Homo sapiens Zic family member 5 (odd-paired homolog, Drosophila) (ZIC5), mRNA

Each of the accession numbers identified in Table 1, and their corresponding sequences, are hereby incorporated herein by reference.

In various embodiments, the level of expression of at least 2, 3, 4, 5, 6, 7, 8, 9 or 10 biomarkers selected from the group of biomarkers listed in Table 1 is determined.

In particular embodiments, a predictive gene signature comprising a sub-combination of 2 or more biomarkers selected from the group of biomarkers listed in Table 1 is used. In various embodiments, the level of expression of at least 2, at least 3, at least 4 or at least 5 biomarkers selected from the group of biomarkers listed in Table 1 is determined. For example, the predictive gene signature may include at least 2 biomarkers, *e.g.*, DYSF and EDIL3; GNAT1 and ERGIC3; KRT24 and PAPLN; MANSC1 and PDGFB; PCDH1 and PDGFB; or PHOSPHO2 and PSENEN. In another embodiment, the predictive gene signature may include at least 3 biomarkers, *e.g.*, COL7A1, YTHDF1 and ZIC5; CKLF, IL10 and TUBB6; CDC20, CFL1 and TMEM79; 15 HYAL2, NCBP1 and SNX11; or CEP152, NCBP1 and SATB1. In another embodiment, the predictive gene signature may include at least 4 biomarkers, *e.g.*,

APBB2, CCL26, PSENEN and SATB1; ANG, JAM3, KLHL17 and PAPLN; ITFG3, MAD2L1BP, NMU and PDGFB; SPTA1, TYROBP, SNX11 and PSENEN; GRAMD4, GNAT1, TMIGD2 and YTHDF1; or GRAMD4, HYAL2, PHOSPHO2 and TUBB6. In another embodiment, the predictive gene signature may include at least 5 biomarkers,
5 *e.g.*, CCL26, CDC20, ERGIC3, EDIL3 and PCDH1; DYSF, NMU, PHOSPHO2, PSENEN and SNX11; APBB2, CKLF, CYP4F3, TUBB6 and YTHDF1; or CEP152, MAD2L1BP, SPTA1, TMEM79 and ZIC5.

In particular embodiments, the predictive gene signature may include 2 or more of biomarkers ABI3, ANG, APBB2, CCL26, CDC20, CEP152, CFL1, CKLF, COL7A1,
10 CYP4F3, DYSF, GNAT1, GRAMD4, HYAL2, IL10, ITFG3, JAM3, KLHL17, KRT24, MAD2L1BP, MANSC1, MOBKL1B, NCBP1, NMU, PCDH1, PHOSPHO2, SPTA1, TMIGD2, TYROBP, ZIC5, ERGIC3, PDGFB, PSENEN, SATB1, SNX11, TMEM79 and YTHDF1, *e.g.*, ABI3 and ANG; APBB2 and CCL26; GNAT1 and GRAMD4; IL10 and ITFG3; MACSC1 and MOBKL1B; NMU and PCDH1; or TYROBP and ZIC5. In
15 other embodiments, the predictive gene signature includes at least 3 of the previously recited biomarkers, *e.g.*, ABI3, ANG and APBB2; CCL26, CKLF and COL7A1; DYSF, GNAT1 and HYAL2; JAM3, KLHL17 and KRT24; NCBP1, NMU and PCDH1; SPTA1, TMIGD2 and TYROBP; or ZIC5, MAD2L1BP and CDC20. In other
20 embodiments, the predictive gene signature includes at least 4 of the previously recited biomarkers, *e.g.*, ABI3, ANG, APBB2 and CCL26; CEP152, CFL1, CKLF and COL7A1; KRT24, MANSC1, MOBKL1B and SPTA1; TYROBP, TMIGD2, PHOSPHO2 and NMU; ABI3, GNAT1, KLHL17 and SPTA1; or CEP152, HYAL2, PCDH1 and TMIGD2. In yet further embodiments, the predictive gene signature
25 includes at least 5 of the previously recited biomarkers, *e.g.*, CKLF, COL7A1, GRAMD4, JAM3 and PCDH1; APBB2, CEP152, DYSF, IL10 and TYROBP; CYP4F3, HYAL2, ITFG3, KLHL17 and KRT24; NCBP1, SPTA1, TMIGD2, IL10 and JAM3; or CCL26, PHOSPHO2, SPTA1, TMIGD2 and ZIC5.

In other embodiments, the predictive gene signature may include 2 or more of biomarkers ERGIC3, PDGFB, PSENEN, SATB1, SNX11, TMEM79 or YTHDF1, or
30 any sub-combination thereof, *e.g.*, ERGIC3 and PDGFB; ERGIC3 and PSENEN; ERGIC3 and SATB1; ERGIC3 and SNX11; ERGIC3 and TMEM79; ERGIC3 and YTHDF1; PDGFB and PSENEN; PDGFB and SATB1; PDGFB and SNX11; PDGFB and TMEM79; PDGFB and YTHDF1; PSENEN and SATB1; PSENEN and SNX11; PSENEN and TMEM79; PSENEN and YTHDF1; SATB1 and SNX11; SATB1 and
35 TMEM79; SATB1 and YTHDF1; SNX11 and TMEM79; SNX11 and YTHDF1; or TMEM79 and YTHDF1. In other embodiments, the predictive gene signature includes at least 3 biomarkers, for example, ERGIC3, PDGFB and PSENEN; SATB1, SNX11

and TMEM79; SNX11, TMEM79 and YTHDF1; or ERGIC3, PDGFB and SATB1. In further embodiments, the predictive gene signature includes at least 4 biomarkers, for example, ERGIC3, PDGFB, PSENEN and SATB1; SNX11, TMEM79, YTHDF1 and ERGIC3; or ERGIC3, PDGFB, PSENEN and YTHDF1. In further embodiments, the predictive gene signature includes at least 5 biomarkers, for example, ERGIC3, PDGFB, PSENEN, SATB1 and SNX11; ERGIC3, PDGFB, PSENEN, SATB1 and TMEM79; or PSENEN, SATB1, SNX11, TMEM79 and YTHDF1. In yet further embodiments, the predictive gene signature includes at least 6 biomarkers, for example, ERGIC3, PDGFB, PSENEN, SATB1, SNX11 and TMEM79; PDGFB, PSENEN, SATB1, SNX11, TMEM79 and YTHDF1; or ERGIC3, PSENEN, SATB1, SNX11, TMEM79 and YTHDF1. In yet another embodiment, the predictive gene signature includes 7 biomarkers, for example, ERGIC3, PDGFB, PSENEN, SATB1, SNX11, TMEM79 and YTHDF1.

In various embodiments, the biomarker is not one or more of SPTA1, PAPLN, PCDH1, TMIGD2 and/or KRT24. In a particular embodiment, the biomarker is not SPTA1, PAPLN, PCDH1, TMIGD2 and KRT24. In one embodiment, the biomarker is not SPTA1. In another embodiment, the biomarker is not PAPLN. In another embodiment, the biomarker is not PCDH1. In an alternative embodiment, the biomarker is not TMIGD2. In yet another embodiment, the biomarker is not KRT24.

In particular embodiments, the predictive gene signature may include 2 or more of biomarkers ABI3, ANG, APBB2, CCL26, CDC20, CEP152, CFL1, CKLF, COL7A1, CYP4F3, DYSF, GNAT1, GRAMD4, HYAL2, IL10, ITFG3, JAM3, KLHL17, MAD2L1BP, MANSC1, MOBKL1B, NCBP1, NMU, PHOSPHO2, TYROBP, ZIC5, ERGIC3, PDGFB, PSENEN, SATB1, SNX11, TMEM79, YTHDF1, EDIL3 and TUBB6, *e.g.*, ABI3 and ANG; GRAMD4 and HYAL2; NMU and PHOSPHO2; ZIC5 and PSENEN; or SNX11 and MOBKL1B. In other embodiments, the predictive gene signature includes at least 3 of the previously recited biomarkers, *e.g.*, APBB2, CDC20 and CKLF; COL7A1, DYSF and GNAT1; NCBP1, SATB1 and EDIL3; PSENEN, DYSF and GNAT1; MANSC1, ZIC5 and CFL1; or CKLF, GRAMD4 and NMU. In other embodiments, the predictive gene signature includes at least 4 of the previously recited biomarkers, *e.g.*, ANG, CCL26, CEP152 and JAM3; APBB2, CYP4F3, ITFG3 and TYROBP; CYP4F3, MANSC1, PDGFB and YTHDF1; TUBB6, DYSF, PHOSPHO2 and CDC20; or CKLF, KLHL17, HYAL2 and ZIC5. In yet further embodiments, the predictive gene signature includes at least 5 of the previously recited biomarkers, *e.g.*, IL10, CEP152, COL7A1, TYROBP and ERGIC3; TMEM79, SNX11, PSENEN, GNAT1 and GRAMD4; JAM3, SNX11, KLHL17, MOBKL1B and ERGIC3; or NMU, PHOSPHO2, PDGFB, CFL1 and ANG.

In various methods and or kits of the invention, the biomarker is not ABI3, is not ANG, is not APBB2, is not CCL26, is not CDC20, is not CEP152, is not CFL1, is not CKLF, is not COL7A1, is not CYP4F3, is not DYSF, is not GNAT1, is not GRAMD4, is not HYAL2, is not IL10, is not ITFG3, is not JAM3, is not KLHL17, is not KRT24, is not MAD2L1BP, is not MANSC1, is not MOBKL1B, is not NCBP1, is not NMU, is not PCDH1, is not PHOSPHO2, is not SPTA1, is not TMIGD2, is not TYROBP, is not ZIC5, is not ERGIC3, is not PDGFB, is not PSENEN, is not SATB1, is not SNX11, is not TMEM79, is not EDIL3, is not PAPLN, is not TUBB6 and/or is not YTHDF1.

Any suitable analytical method, can be utilized in the methods of the invention to assess (directly or indirectly) the level of expression of a biomarker in a sample. In some embodiments, a difference is observed between the level of expression of a biomarker, as compared to the control level of expression of the biomarker. In one embodiment, the difference is greater than the limit of detection of the method for determining the expression level of the biomarker. In further embodiments, the difference is greater than or equal to the standard error of the assessment method, and preferably the difference is at least about 2-, about 3-, about 4-, about 5-, about 6-, about 7-, about 8-, about 9-, about 10-, about 15-, about 20-, about 25-, about 100-, about 500- or about 1000-fold greater than the standard error of the assessment method. In some embodiments, the level of expression of the biomarker in a sample as compared to a control level of expression is assessed using parametric or nonparametric descriptive statistics, comparisons, regression analyses, and the like.

In some embodiments, a difference in the level of expression of the biomarker in the sample derived from the subject is detected relative to the control, and the difference is about 5%, about 10%, about 15%, about 20%, about 25%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, or about 90% less than the expression level of the biomarker in the control sample.

The level of expression of a biomarker, for example, as set forth in Table 1, in a sample obtained from a subject may be assayed by any of a wide variety of techniques and methods, which transform the biomarker within the sample into a moiety that can be detected and/or quantified. Non-limiting examples of such methods include analyzing the sample using immunological methods for detection of proteins, protein purification methods, protein function or activity assays, nucleic acid hybridization methods, nucleic acid reverse transcription methods, and nucleic acid amplification methods, immunoblotting, Western blotting, Northern blotting, electron microscopy, mass spectrometry, *e.g.*, MALDI-TOF and SELDI-TOF, immunoprecipitations, immunofluorescence, immunohistochemistry, enzyme linked immunosorbent assays

(ELISAs), *e.g.*, amplified ELISA, quantitative blood based assays, *e.g.*, serum ELISA, quantitative urine based assays, flow cytometry, Southern hybridizations, array analysis, and the like, and combinations or sub-combinations thereof.

5 In one embodiment, the level of expression of the biomarker in a sample is determined by detecting a transcribed polynucleotide, or portion thereof, *e.g.*, mRNA, or cDNA, of the biomarker gene. RNA may be extracted from cells using RNA extraction techniques including, for example, using acid phenol/guanidine isothiocyanate extraction (RNAzol B; Biogenesis), RNeasy RNA preparation kits (Qiagen) or PAXgene (PreAnalytix, Switzerland). Typical assay formats utilizing ribonucleic acid
10 hybridization include nuclear run-on assays, RT-PCR, quantitative PCR analysis, RNase protection assays (Melton *et al.*, *Nuc. Acids Res.* 12:7035), Northern blotting and *in situ* hybridization. Other suitable systems for mRNA sample analysis include microarray analysis (*e.g.*, using Affymetrix's microarray system or Illumina's BeadArray Technology).

15 In one embodiment, the level of expression of the biomarker is determined using a nucleic acid probe. The term "probe", as used herein, refers to any molecule that is capable of selectively binding to a specific biomarker. Probes can be synthesized by one of skill in the art, or derived from appropriate biological preparations. Probes can be specifically designed to be labeled, by addition or incorporation of a label. Examples of
20 molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic molecules.

As indicated above, isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction (PCR) analyses and probe arrays. One method for the determination of
25 mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to the biomarker mRNA. The nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least about 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 250 or about 500 nucleotides in length and sufficient to specifically hybridize under appropriate hybridization conditions to the
30 biomarker genomic DNA. In a particular embodiment the probe will bind the biomarker genomic DNA under stringent conditions. Such stringent conditions, for example, hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45° C., followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65° C., are known to those skilled in the art and can be found in Current Protocols in Molecular Biology, Ausubel *et al.*, eds.,
35 John Wiley & Sons, Inc. (1995), sections 2, 4, and 6, the teachings of which are hereby incorporated by reference herein. Additional stringent conditions can be found in

Molecular Cloning: A Laboratory Manual, Sambrook et al., Cold Spring Harbor Press, Cold Spring Harbor, N.Y. (1989), chapters 7, 9, and 11, the teachings of which are hereby incorporated by reference herein.

5 In one embodiment, the mRNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative embodiment, the probe(s) are immobilized on a solid surface, for example, in an Affymetrix gene chip array, and the probe(s) are contacted with mRNA. A skilled artisan can readily adapt mRNA detection methods for use in determining the level of
10 the biomarker mRNA.

The level of expression of the biomarker in a sample can also be determined using methods that involve the use of nucleic acid amplification and/or reverse transcriptase (to prepare cDNA) of for example mRNA in the sample, *e.g.*, by RT-PCR (the experimental embodiment set forth in Mullis, 1987, U.S. Pat. No. 4,683,202), ligase
15 chain reaction (Barany (1991) *Proc. Natl. Acad. Sci. USA* 88:189-193), self sustained sequence replication (Guatelli *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.* (1988) *Bio/Technology* 6:1197), rolling circle replication (Lizardi *et al.* , U.S. Pat. No. 5,854,033) or any other nucleic acid
20 amplification method, followed by the detection of the amplified molecules. These approaches are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. In particular aspects of the invention, the level of expression of the biomarker is determined by quantitative fluorogenic RT-PCR (*e.g.*, the TaqMan™ System). Such methods typically utilize pairs of oligonucleotide
25 primers that are specific for the biomarker. Methods for designing oligonucleotide primers specific for a known sequence are well known in the art.

The expression levels of biomarker mRNA can be monitored using a membrane blot (such as used in hybridization analysis such as Northern, Southern, dot, and the like), or microwells, sample tubes, gels, beads or fibers (or any solid support comprising
30 bound nucleic acids). See, for example, U.S. Pat. Nos. 5,770,722, 5,874,219, 5,744,305, 5,677,195 and 5,445,934, the contents of which as they relate to these assays are incorporated herein by reference. The determination of biomarker expression level may also comprise using nucleic acid probes in solution.

In one embodiment of the invention, microarrays are used to detect the level of
35 expression of a biomarker. Microarrays are particularly well suited for this purpose because of the reproducibility between different experiments. DNA microarrays provide

one method for the simultaneous measurement of the expression levels of large numbers of genes. Each array consists of a reproducible pattern of capture probes attached to a solid support. Labeled RNA or DNA is hybridized to complementary probes on the array and then detected by laser scanning. Hybridization intensities for each probe on the array are determined and converted to a quantitative value representing relative gene expression levels. See, *e.g.*, U.S. Pat. Nos. 6,040,138, 5,800,992 and 6,020,135, 6,033,860, and 6,344,316, the contents of which as they relate to these assays are incorporated herein by reference. High-density oligonucleotide arrays are particularly useful for determining the gene expression profile for a large number of RNA's in a sample.

Expression of a biomarker can also be assessed at the protein level, using a detection reagent that detects the protein product encoded by the mRNA of the biomarker, directly or indirectly. For example, if an antibody reagent is available that binds specifically to a biomarker protein product to be detected, then such an antibody reagent can be used to detect the expression of the biomarker in a sample from the subject, using techniques, such as immunohistochemistry, ELISA, FACS analysis, and the like.

Other known methods for detecting the biomarker at the protein level include methods such as electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, and the like, or various immunological methods such as fluid or gel precipitation reactions, immunodiffusion (single or double), immunoelectrophoresis, radioimmunoassay (RIA), enzyme-linked immunosorbent assays (ELISAs), immunofluorescent assays, and Western blotting.

Proteins from samples can be isolated using a variety of techniques, including those well known to those of skill in the art. The protein isolation methods employed can, for example, be those described in Harlow and Lane (Harlow and Lane, 1988, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York).

In one embodiment, antibodies, or antibody fragments, are used in methods such as Western blots or immunofluorescence techniques to detect the expressed proteins. Antibodies for determining the expression of the biomarkers of the invention are commercially available. For example, ERGIC-3 specific antibodies are commercially available from Santa Cruz Biotechnology, Inc. (ERGIC-3 (P-16) Antibody and ERGIC-3 (Y-23) Antibody) and Sigma Aldrich (HPA015968, AV47209, HPA015242, SAB4502151). PDGFB specific antibodies are commercially available from Santa Cruz

Biotechnology, Inc. (e.g., PDGF-B (C-5) Antibody and PDGF-B (H-55) Antibody) and Sigma Aldrich (e.g., HPA011972, SAB2101755 and SAB2900226). PSENEN specific antibodies are commercially available from Origene (e.g., Catalog No. TA306367) and Sigma Aldrich (e.g., PRS3981, WH0055851M1, PRS3979 and P5622). Further by way of example, SATB1 antibodies are commercially available from, for example, Abcam (Catalog No. ab49061, ab92307 and ab70004), Abnova Corporation (Catalog No. PAB13379), and Aviva Systems Biology (Catalog No. ARP33362_P050). SNX11 antibodies are commercially available from Abcam (Catalog Nos. ab4128, ab67578, ab76816 and ab76762) and Abnova Corporation (Catalog Nos. PAB6362 and H00029916-B01). TMEM79 Antibodies are commercially available from, for example, Abcam (Catalog No. ab81539) and Sigma Aldrich (Catalog No. SAB2102475). Finally, YTHDF1 antibodies are commercially available from, for example, Abnova Corporation (Catalog No. PAB17446), Aviva Systems Biology (Catalog No. ARP57032_P050) and Santa Cruz Biotechnology (Catalog No. sc-86026).

It is generally preferable to immobilize either the antibody or proteins on a solid support for Western blots and immunofluorescence techniques. Suitable solid phase supports or carriers include any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

One skilled in the art will know many other suitable carriers for binding antibody or antigen, and will be able to adapt such support for use with the present invention. For example, protein isolated from cells can be run on a polyacrylamide gel electrophoresis and immobilized onto a solid phase support such as nitrocellulose. The support can then be washed with suitable buffers followed by treatment with the detectably labeled antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on the solid support can then be detected by conventional means. Means of detecting proteins using electrophoretic techniques are well known to those of skill in the art (see generally, R. Scopes (1982) *Protein Purification*, Springer-Verlag, N.Y.; Deutscher, (1990) *Methods in Enzymology* Vol. 182: *Guide to Protein Purification*, Academic Press, Inc., N.Y.).

Other standard methods include immunoassay techniques which are well known to one of ordinary skill in the art and may be found in Principles And Practice Of Immunoassay, 2nd Edition, Price and Newman, eds., MacMillan (1997) and Antibodies, A Laboratory Manual, Harlow and Lane, eds., Cold Spring Harbor Laboratory, Ch. 9 (1988), each of which is incorporated herein by reference in its entirety.

Antibodies used in immunoassays to determine the level of expression of the biomarker, may be labeled with a detectable label. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by incorporation of a label (e.g., a radioactive atom), coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

In one embodiment, the antibody is labeled, *e.g.* a radio-labeled, chromophore-labeled, fluorophore-labeled, or enzyme-labeled antibody. In another embodiment, an antibody derivative (*e.g.*, an antibody conjugated with a substrate or with the protein or ligand of a protein-ligand pair (*e.g.*, biotin-streptavidin), or an antibody fragment (*e.g.* a single-chain antibody, or an isolated antibody hypervariable domain) which binds specifically with the biomarker is used.

In one embodiment of the invention, proteomic methods, *e.g.*, mass spectrometry, are used. Mass spectrometry is an analytical technique that consists of ionizing chemical compounds to generate charged molecules (or fragments thereof) and measuring their mass-to-charge ratios. In a typical mass spectrometry procedure, a sample is obtained from a subject, loaded onto the mass spectrometry, and its components (*e.g.*, the biomarker) are ionized by different methods (*e.g.*, by impacting them with an electron beam), resulting in the formation of charged particles (ions). The mass-to-charge ratio of the particles is then calculated from the motion of the ions as they transit through electromagnetic fields.

For example, matrix-associated laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) or surface-enhanced laser desorption/ionization time-of-flight mass spectrometry (SELDI-TOF MS) which involves the application of a biological sample, such as serum, to a protein-binding chip (Wright, G.L., Jr., *et al.* (2002) *Expert Rev Mol Diagn* 2:549; Li, J., *et al.* (2002) *Clin Chem* 48:1296; Laronga, C., *et al.* (2003) *Dis biomarkers* 19:229; Petricoin, E.F., *et al.* (2002) 359:572; Adam, B.L., *et al.* (2002) *Cancer Res* 62:3609; Tolson, J., *et al.* (2004) *Lab Invest* 84:845; Xiao, Z., *et al.* (2001) *Cancer Res* 61:6029) can be used to determine the expression level of a biomarker at the protein level.

Furthermore, *in vivo* techniques for determination of the expression level of the biomarker include introducing into a subject a labeled antibody directed against the biomarker, which binds to and transforms the biomarker into a detectable molecule. As

discussed above, the presence, level, or even location of the detectable biomarker in a subject may be detected by standard imaging techniques.

In general, where a difference in the level of expression of a biomarker and the control is to be detected, it is preferable that the difference between the level of
5 expression of the biomarker in a sample from a subject having breast cancer and being treated with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), or being considered for treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), and the amount of the biomarker in a control sample, is as great as possible. Although this
10 difference can be as small as the limit of detection of the method for determining the level of expression, it is preferred that the difference be greater than the limit of detection of the method or greater than the standard error of the assessment method, and preferably a difference of at least about 2-, about 3-, about 4-, about 5-, about 6-, about 7-, about 8-, about 9-, about 10-, about 15-, about 20-, about 25-, about 100-, about 500-,
15 1000-fold greater than the standard error of the assessment method.

In another aspect, the present invention provides methods for determining whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer by determining and/or identifying whether the subject carries at least one gene, selected from the group
20 of biomarkers set forth in Table 1, which contains a polymorphism, for example, a mutation, that results in decreased expression and/or reduced function of the encoded protein, wherein the presence of a polymorphism in at least one gene is indicative that eribulin, an analog thereof, or a pharmaceutically acceptable salt there, will be effective in treating a subject. In another aspect, the present invention provides methods for
25 predicting whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), will be effective in treating a subject having breast cancer by assaying a sample derived from the subject to determine whether the subject carries at least one gene, selected from the group of biomarkers set forth in Table 1, which contains a polymorphism, for example, a mutation, that results in decreased
30 expression and/or reduced function of the encoded protein, wherein the presence of the polymorphism in at least one gene in said sample is indicative that eribulin, an analog thereof, or a pharmaceutically acceptable salt there, may be used to treat said subject. In a further aspect, a method is provided for predicting whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, will be effective in treating a subject
35 having breast cancer, the method comprising determining the presence of a polymorphism that results in reduced expression and/or function in a gene encoding a biomarker selected from the group of biomarkers listed in Table 1 in a sample derived

from said subject, and predicting that eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, may be used to treat said subject based on the presence of the polymorphism.

5 In a further aspect, the present invention provides methods for determining the sensitivity of a breast tumor to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof by determining and/or identifying whether said tumor contains a polymorphism in at least one gene resulting in reduced expression and/or function of the encoded protein, wherein the gene is selected from the group of biomarkers set forth in Table 1. Identification and/or determination that the tumor
10 contains such a polymorphism is indicative of sensitivity of said tumor to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof. In yet another aspect, the present invention is directed to methods for treating a subject having breast cancer with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof by identifying whether a sample derived from said subject has at least one gene, selected
15 from the group of biomarkers set forth in Table 1, which contains a polymorphism resulting in reduced expression and/or function of the encoded protein and administering a therapeutically effective amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate) to the subject when the polymorphism is identified.

20 In another aspect, the present invention provides methods for determining whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer by determining and/or identifying whether the subject carries at least one gene, selected from the group of biomarkers set forth in Table 1, which contains a null mutation, wherein the presence
25 of a null mutation in at least one gene is indicative that eribulin, an analog thereof, or a pharmaceutically acceptable salt there, will be effective in treating the subject. In another aspect, the present invention provides methods for predicting whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer by assaying a sample derived from
30 the subject to determine whether the subject carries at least one gene, selected from the group of biomarkers set forth in Table 1, which contains a null mutation, wherein the presence of a null mutation in at least one gene in said sample is indicative that eribulin, an analog thereof, or a pharmaceutically acceptable salt there, will be effective in treating the subject. In a further aspect, a method is provided for predicting whether
35 eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, may be used to treat a subject having breast cancer, the method comprising determining the presence of a null mutation in a biomarker selected from the group of biomarkers listed in Table 1 in

a sample derived from said subject, and predicting that eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, may be used to treat said subject based on the presence of said null mutation.

5 In a further aspect, the present invention provides methods for determining the sensitivity of a breast tumor to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof by determining and/or identifying whether said tumor contains a null mutation in at least one gene, selected from the group of biomarkers set forth in Table 1. Identification and/or determination that the tumor contains a null mutation is indicative of sensitivity of said tumor to treatment with
10 eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof. In yet another aspect, the present invention is directed to methods for treating a subject having breast cancer with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof by identifying whether a sample derived from said subject has at least one gene, selected from the group of biomarkers set forth in Table 1, which contains a null mutation and
15 administering a therapeutically effective amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate) to the subject when a null mutation is identified.

As used herein, the term “null mutation” refers to a mutation in a genomic DNA sequence that causes the product of the gene to be non-functional or largely absent. Such
20 mutations may occur in the coding and/or regulatory regions of the gene, and may be changes of individual residues, or insertions or deletions of regions of nucleic acids. These mutations may also occur in the coding and/or regulatory regions of other genes which may regulate or control the gene and/or the product of the gene so as to cause the gene product to be non-functional or largely absent. The null mutation may be a
25 deletion of the native gene or a portion thereof. These sequence disruptions or modifications may include insertions, missense, frameshift, deletion, or substitutions, or replacements of DNA sequence, or any combination thereof. For example, the null mutation may result in the insertion of a premature stop codon. The null mutation results in functional inactivation of the gene product by, for example, inhibiting its
30 production partially or completely; disrupting, inhibiting or curtailing the translation of the protein product, or resulting in a nonfunctional protein. The null mutation may be a pre-existing mutation in the subject or a mutation which arose in a tumor. The presence of a null mutation in a biomarker can be indicated by a lack of detectable expression of the biomarker. However, the presence of a null mutation can be determined by other
35 methods. For example, in such embodiments, a sample of the subject’s DNA may be sequenced in order to identify the presence of a null mutation. Any of the well-known methods for sequencing the biomarkers may be used in the methods of the invention,

such as the methods described in, for example, U.S. Patent No. 5,075,216, Engelke *et al.* (1988) *Proc. Natl. Acad. Sci. U.S.A.* 85, 544-548 and Wong *et al.* (1987) *Nature* 330, 384-386; Maxim and Gilbert (1977) *Proc. Natl. Acad. Sci. U.S.A.* 74:560; or Sanger (1977) *Proc. Natl. Acad. Sci. U.S.A.* 74:5463. In addition, any of a variety of automated sequencing procedures can be utilized see, *e.g.*, Naeve, C.W *et al.* (1995) *Biotechniques* 19:448, including sequencing by mass spectrometry (see, *e.g.*, PCT International Publication No. WO 94/16101; Cohen *et al.* (1996) *Adv. Chromatogr.* 36:127-162; and Griffin *et al.* (1993) *Appl. Biochem. Biotechnol.* 38:147-159.

Determining the presence or absence of a null mutation in the sample may also be accomplished using various techniques such as polymerase chain reaction (PCR) amplification reaction, reverse-transcriptase PCR analysis, single-strand conformation polymorphism analysis (SSCP), mismatch cleavage detection, heteroduplex analysis, Southern blot analysis, Western blot analysis, deoxyribonucleic acid sequencing, restriction fragment length polymorphism analysis, haplotype analysis, serotyping, and combinations or sub-combinations thereof.

Any suitable sample obtained from a subject having breast cancer can be used to assess the level of expression, including a lack of expression, of the biomarker, for example, a biomarker provided in Table 1. For example, the sample may be any fluid or component thereof, such as a fraction or extract, *e.g.*, blood, plasma, lymph, cystic fluid, urine, nipple aspirates, or fluids collected from a biopsy (*e.g.*, lump biopsy), obtained from the subject. In a typical situation, the fluid may be blood, or a component thereof, obtained from the subject, including whole blood or components thereof, including, plasma, serum, and blood cells, such as red blood cells, white blood cells and platelets. The sample may also be any tissue or fragment or component thereof, *e.g.*, breast tissue, connective tissue, lymph tissue or muscle tissue obtained from the subject.

Techniques or methods for obtaining samples from a subject are well known in the art and include, for example, obtaining samples by a mouth swab or a mouth wash; drawing blood; or obtaining a biopsy. Isolating components of fluid or tissue samples (*e.g.*, cells or RNA or DNA) may be accomplished using a variety of techniques.

The sample from the cancer may be obtained by biopsy of the patient's cancer. In certain embodiments, more than one sample from the patient's tumor is obtained in order to acquire a representative sample of cells for further study. For example, a patient with breast cancer may have a needle biopsy to obtain a sample of cancer cells. Several biopsies of the tumor may be used to obtain a sample of cancer cells. In other embodiments, the sample may be obtained from surgical excision of the tumor. In this

case, one or more samples may be taken from the excised tumor for analysis using the methods of the invention.

After the sample is obtained, it may be further processed. The cancer cells may be cultured, washed, or otherwise selected to remove normal tissue. The cells may be trypsinized to remove the cells from the tumor sample. The cells may be sorted by fluorescence activated cell sorting (FACS) or other cell sorting technique. The cells may be cultured to obtain a greater number of cells for study. In certain instances the cells may be immortalized. For some applications, the cells may be frozen or the cells may be embedded in paraffin.

II. Treatment with Eribulin, Analogs Thereof, or Pharmaceutically Acceptable Salts Thereof (e.g., Eribulin Mesylate)

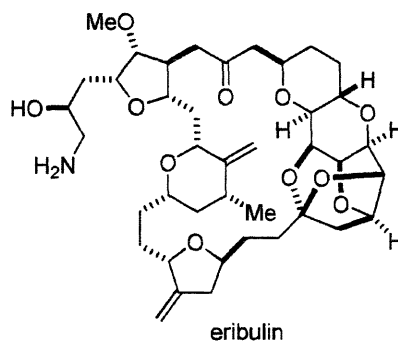
Given the observation that the expression levels of certain biomarkers, for example, those set forth in Table 1, in a subject having breast cancer influences the responsiveness of the subject to eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (e.g., eribulin mesylate), a skilled artisan can select an appropriate treatment regimen for the subject based on the expression levels of the biomarkers in the subject. Accordingly, the present invention provides methods for treating a subject having breast cancer by (i) identifying a subject having breast cancer in which at least one biomarker selected from the group of biomarkers listed in Table 1 has a low level of expression and (ii) administering a therapeutically effective amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (e.g., eribulin mesylate), to the subject. In another aspect, the present invention provides methods for treating a subject having breast cancer by (i) assaying a sample derived from the subject to determine the level of expression of at least one biomarker selected from the group of biomarkers listed in Table 1 and (ii) administering a therapeutically effective amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (e.g., eribulin mesylate) to the subject when a low level of expression of the at least one biomarker is detected in the sample.

In various embodiments, the subject may have been previously treated with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (e.g., eribulin mesylate). In other embodiments, the subject may be under consideration for treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (e.g., eribulin mesylate), for the first time. The level of expression of one or more, e.g., at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10, biomarkers identified in Table 1 is determined. If level of expression of at least one biomarker (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10

biomarkers) is determined to be a low level of expression, treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), is likely to be efficacious. However, it is not necessary that all of the biomarkers assayed have a low level of expression as compared to the respective control. For example,

5 while certain biomarkers may be present at normal or high levels of expression, treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be indicated when, for example, a low level of expression is present for at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 biomarkers.

10 When a low level of expression of one or more of the biomarkers of the invention is found (*e.g.*, due to the presence of a null mutation in the biomarker gene) in a sample derived from a subject having breast cancer, the subject may be treated with eribulin, having the following the structure, with a pharmaceutically acceptable salt of eribulin, or with an eribulin analog or pharmaceutically acceptable thereof.



In some embodiments, a pharmaceutically acceptable salt of eribulin is administered to the subject, such as eribulin mesylate.

20 The treatment regimen for eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), that is selected typically includes at least one of the following parameters and more typically includes many or all of the following parameters: the dosage, the formulation, the route of administration and/or the frequency of administration. Selection of the particular parameters of the treatment

25 regimen can be based on known treatment parameters for eribulin previously established in the art such as those described in the Dosage and Administration protocols set forth in the FDA Approved Label for HALAVEN[®], the entire contents of which are incorporated herein by reference. For example, eribulin mesylate can be administered intravenously

on Days 1 and 8 of a 21 day cycle, for example at a dose of 1.4 mg/m^2 , or if a dose reduction is indicated (*e.g.*, for hepatic or renal impairment), at a dose of 0.7 mg/m^2 or 1.1 mg/m^2 . Various modifications to dosage, formulation, route of administration and/or frequency of administration can be made based on various factors including, for example, the disease, age, sex, and weight of the patient, as well as the severity or stage of cancer (see, for example, U.S. Patent No. 6,653,341 and U.S. Patent No. 6,469,182, the entire contents of each of which are hereby incorporated herein by reference).

As used herein, the term "therapeutically effective amount" means an amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate) as described herein, that is capable of treating breast cancer. The dose of a compound to be administered according to this invention will, of course, be determined in light of the particular circumstances surrounding the case including, for example, the compound administered, the route of administration, condition of the patient, and the pathological condition being treated, for example, the stage of breast cancer.

For administration to a subject, eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), typically is formulated into a pharmaceutical composition comprising eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, and a pharmaceutically acceptable carrier. Therapeutic compositions typically should be sterile and adequately stable under the conditions of manufacture and storage. Pharmaceutical compositions also can be administered in a combination therapy, *i.e.*, combined with other agents, such as those agents set forth below (see, for example, U.S. Patent No. 6,214,865 and U.S. Patent No. 6,653,341, the entire contents of each of which are hereby incorporated herein by reference).

As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Preferably, the carrier is suitable for parenteral (*e.g.*, intravenous, intramuscular, subcutaneous, intrathecal) administration (*e.g.*, by injection or infusion). Depending on the route of administration, the active compound may be coated in a material to protect the compound from the action of acids and other natural conditions that may inactivate the compound.

The pharmaceutical compositions may include one or more pharmaceutically acceptable salts, as defined above.

There are numerous types of anti-cancer approaches that can be used in conjunction with eribulin, an analog thereof, or a pharmaceutically acceptable salt

thereof (*e.g.*, eribulin mesylate) treatment, according to the invention. These include, for example, treatment with chemotherapeutic agents, biological agents (*e.g.*, hormonal agents, cytokines (such as interleukins, interferons, granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), and granulocyte
5 macrophage colony stimulating factor (GM-CSF)), chemokines, vaccine antigens, and antibodies), anti-angiogenic agents (*e.g.*, angiostatin and endostatin), radiation, and surgery, as described in more detail in U.S. Pat. No. 6,653,341 B1 and U.S. Publ. No. 2006/0104984 A1, the teachings of which are incorporated herein by reference in their entirety.

10 The methods of the invention can employ these approaches to treat the same types of cancers as those for which they are known in the art to be used, as well as others, as can be determined by those of skill in this art. Also, these approaches can be carried out according to parameters (*e.g.*, regimens and doses) that are similar to those that are known in the art for their use. However, as is understood in the art, it may be
15 desirable to adjust some of these parameters, due to the additional use of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), with these approaches. For example, if a drug is normally administered as a sole therapeutic agent, when combined with eribulin, according to the invention, it may be desirable to decrease the dosage of the drug, as can be determined by those of skill in
20 this art. Examples of the methods of the invention, as well as compositions that can be used in these methods, are provided below.

Chemotherapeutic drugs of several different types including, for example, antimetabolites, antibiotics, alkylating agents, plant alkaloids, hormonal agents, anticoagulants, antithrombotics, and other natural products, among others, can be used in
25 conjunction with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, according to the invention. Specific, non-limiting examples of these classes of drugs, as well as cancers that can be treated by their use, are as follows.

Numerous approaches for administering anti-cancer drugs are known in the art, and can readily be adapted for use in the present invention. In the case that one or more
30 drugs are to be administered in conjunction with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), for example, the drugs can be administered together, in a single composition, or separately, as part of a comprehensive treatment regimen. For systemic administration, the drugs can be administered by, for example, intravenous infusion (continuous or bolus). Appropriate
35 scheduling and dosing of such administration can readily be determined by those of skill

in this art based on, for example, preclinical studies in animals and clinical studies (*e.g.*, phase I studies) in humans.

Many regimens used to administer chemotherapeutic drugs involve, for example, intravenous administration of a drug (or drugs) followed by repetition of this treatment
5 after a period (*e.g.*, 1-4 weeks) during which the patient recovers from any adverse side effects of the treatment. It may be desirable to use both drugs at each administration or, alternatively, to have some (or all) of the treatments include only one drug (or a subset of drugs).

10 Kits of the Invention

The invention also provides compositions and kits for predicting whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer. These kits include reagents for determining the level of expression of at least one, for example, 1, 2, 3, 4, 5,
15 6, 7, 8, 9 or 10, biomarker(s) selected from the group of biomarkers listed in Table 1 and instructions for use of the kit to predict whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), may be used to treat a subject having breast cancer.

The kits of the invention may optionally comprise additional components useful
20 for performing the methods of the invention. By way of example, the kits may comprise reagents for obtaining a biological sample from a subject, a control sample, and/or eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate).

In one embodiment, the reagents for determining the expression level of at least
25 one biomarker in a biological sample from the subject comprises a nucleic acid preparation sufficient to detect expression of a nucleic acid, *e.g.*, mRNA, encoding the biomarker. This nucleic acid preparation includes at least one, and may include more than one, nucleic acid probe or primer, the sequence(s) of which is designed such that the nucleic acid preparation can detect the expression of nucleic acid, *e.g.*, mRNA,
30 encoding the biomarker in the sample from the subject. A preferred nucleic acid preparation includes two or more PCR primers that allow for PCR amplification of a segment of the mRNA encoding the biomarker of interest. In other embodiments, the kit includes a nucleic acid preparation for each of at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 biomarkers provided in Table 1.

Alternatively, the reagents for detecting expression levels in the subject of one or more biomarkers predictive of responsiveness to eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), can comprise a reagent that detects the gene product of the nucleic acid encoding the biomarker(s) of interest
5 sufficient to distinguish it from other gene products in a sample from the subject. A non-limiting example of such a reagent is a monoclonal antibody preparation (comprising one or more monoclonal antibodies) sufficient to detect protein expression of at least one biomarker in a sample from the subject, such as a peripheral blood mononuclear cell sample.

10 The means for determining the expression level of the biomarkers of Table 1 can also include, for example, buffers or other reagents for use in an assay for evaluating expression (*e.g.*, at either the nucleic acid or protein level).

In another embodiment, the kit can further comprise eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof (*e.g.*, eribulin mesylate), for treating breast
15 cancer or another cancer, as described herein in the subject.

Preferably, the kit is designed for use with a human subject.

The present invention is further illustrated by the following examples which should not be construed as further limiting. The contents of all references, patents and
20 published patent applications cited throughout this application, as well as the Figures and the Appendix of sequences provided herein, are expressly incorporated herein by reference in their entirety.

EXAMPLES

25 **EXAMPLE 1: IDENTIFICATION OF RESISTANCE BIOMARKERS FOR TREATMENT WITH ERIBULIN**

siRNA techniques were employed to “knock down” expression of certain genes and assess the sensitivity of the resulting knock down cells to eribulin. Based on these studies, the expression of those genes set forth in Table 1 were identified as being
30 associated with the sensitivity of breast cancer cells to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof.

siRNA Transfection Optimization and Assay Development

Transfection conditions for human breast cancer cell lines MDA-MB-231 (ATCC Catalog No. HTB26TM) and BT-549 (ATCC Catalog No. HTB122TM) were optimized using transfection reagent DharmaFect 1 from Dharmacon. The MDA-MB-231 and BT-549 cell lines have been reported to be Estrogen Receptor (ER) negative, Progesterone Receptor (PR) negative and HER-2 negative (triple negative). As a non-targeting negative control we used Silencer Negative Control #1 siRNA from Applied Biosystems. The siGENOME TOX (siTOX) Transfection Control (Dharmacon), an RNA duplex designed to induce cell death, was used as a positive control for cell proliferation assays. A reverse transfection procedure in which siRNA was first mixed with transfection reagent and then cells were added to the well, was used in all experiments. Cell viability was compared in cells treated with medium, negative control siRNA and siTOX reagent combined with different amount of DharmaFect 1. Final selected transfection conditions were as follows: MDA-MB-231 cells at 0.035 μ l of DharmaFect 1 per well, while BT-549 cells at 0.05 μ l of DharmaFect 1 per well. Assays and library screening were performed at 50 nM final concentration of siRNAs. Efficacy of transfection was further confirmed by qPCR with control SMARTpool siRNA reagents targeting PPIA and GAPDH genes (Dharmacon).

High-throughput siRNA Screening

The whole human genome siRNA library was purchased from Dharmacon. The library was diluted to 5 μ M. Each well contained 4 SMARTpool siRNA reagents, each directed against a particular gene (four siRNAs targeting the same gene in a single well). More than 18,500 human genes were targeted with this library. 4 μ l of each set of siRNAs from the library plates were transferred to 384-well master plates containing 36 μ l OPTI-MEM medium per well. 40 μ l of diluted DharmaFect 1 reagent were added to each well of the master plate and mixed. 10 μ l of siRNA and transfection reagent mixture per well were distributed into five screening plates. After 10 min incubation, cells in 40 μ l of growth medium were added to each well. Each screening plate included several replicates of negative control siRNA, positive control siTOX as well as medium plus transfection reagent (no siRNA) containing wells. After a 24 hour incubation, 3 screening plates received 10 μ l of DMSO diluted in cell growth medium, while 2 repeats were treated with 10 μ l of eribulin mesylate (E7389) in growth medium, yielding a final concentration corresponding to the IC₂₀ for E7389 for the cell line tested (0.75 nM E7389 for MDA-MB-231; eribulin was provided in a stock solution of DMSO and diluted in growth medium) (see Figure 1). Cell viability was determined at 96 hours after

transfection by CellTiter-Glo luminescent assay from Promega. 10 μ l of CellTiter-Glo solution per well were used. Plates were mixed for 2 minutes on a horizontal shaker, incubated for 10 minutes and read on an EnVision® multilabel plate reader from PerkinElmer.

5

Identification of Primary Hits

Identification of genes with a significant effect on cell sensitivity to E7389 was performed by a method that was similar to the method described for a paclitaxel siRNA screen (Whitehurst *et al.* (2007) *Nature* 446:815-819). Briefly, measurement of each well was normalized by average of medium plus transfection reagent containing reference wells on a plate (32 wells/plate). The biological replicates were averaged for DMSO and E7389-treated plates. For each gene, a two sample t-test was performed to identify significantly different values for wells treated with two different conditions. To narrow down the hit list, the magnitude of response was taken into account by arranging all data according to fold change ratio (average E7389/average DMSO) in ascending order. 364 genes with a fold change among the lowest 5 percentile of the distribution passed the cut-off level. Then, hypothetical open reading frames and genes encoding hypothetical proteins were excluded and the analysis was focused on the 240 remaining genes (see Figure 2).

20

Confirmation Assays

siRNA SMARTpools for the 240 selected genes were ordered in ON-TARGET^{plus} format from Dharmacon. These reagents contain a modified sense strand to prevent interaction with RISC and favor antisense strand uptake. The antisense strand seed region is modified to decrease off-target activity and enhance target specificity. These reagents were used for confirmation secondary screening. To identify common genes influencing sensitivity of cancer cells to E7389, BT-549 breast cancer cells were screened with the 240 selected siRNA pools. The screening was performed using the same protocol as the primary screen with MDA-MB-231 cells, with the final concentration of eribulin mesylate (E7389) in each well corresponding to the IC₂₀ for BT-549 cells (0.25 nM E7389).

30

Data analysis showed that the treatment with 40 out of 240 siRNA pools caused significant differences when comparing E7389-treated wells to carrier-treated wells in both cell lines (Table 2).

To confirm specific down-regulation of 40 genes with siRNA pools, quantitative PCR analysis of targeted mRNAs was performed. MDA-MB-231 and BT-549 cells were transfected with 40 ON-TARGET*plus* siRNAs or non-targeting negative control siRNA according to the above protocol. 48 hours later cells were lysed and cDNAs were synthesized according to the manufacturer's instructions for use of the TaqMan® Gene Expression Cells-to-CT™ Kit (Applied Biosystems). Relative quantities of remaining cDNAs after the treatment with siRNAs were evaluated using QuantiTect SYBR Green PCR Kit with the gene-specific QuantiTect Primer Assays (Qiagen). Results of the analysis are shown in Figure 4. The following 18 genes were down-regulated more than 50 percent in both tested cell lines: CFL1, NMU, MOBKL1B, HYAL2, PSENEN, CYP4F3, ITFG3, EDIL3, YTHDF1, CDC20, CCL26, TMEM79, MANSC1, DYSF, ERGIC3, GRAMD4, NCBP1, SNX11. 14 genes were down-regulated more than 50 percent in at least one cell line (PDGFB, APBB2, SATB1, MAD2L1BP, TUBB6, CEP152, KLH17, COL7A1, CKLF, PHOSPHO2, GNAT1, ABI3, TYROBP, IL10), while other 3 genes were down-regulated more than 35 percent in at least one cell line (ANG, ZIC5, JAM3). Expression of SPTA1, PAPLN, PCDH1, TMIGD2, and KRT24 was either not detectable by this method in MDA-MB-231 cells or didn't change after siRNA treatment in BT-549 cells. The foregoing results indicate that down-regulation of the 40 genes can lead to increased sensitivity to eribulin, an analog thereof, or pharmaceutically acceptable salt thereof.

Table 2. List of 40 overlapping genes from the screening of MDA-MB-231 and BT-549 cells. Fold changes (FC) compared to control and associated p-values are depicted.

gene	Gene ID	MDA-MB-231		BT-549	
		FC	t-test	FC	t-test
PSENEN	55851	0.70	0.03	0.39	0.00
PHOSPHO2	493911	0.56	0.04	0.44	0.02
CCL26	10344	0.71	0.02	0.45	0.03
CDC20	991	0.47	0.03	0.47	0.03
MAD2L1BP	9587	0.47	0.00	0.48	0.01
JAM3	83700	0.63	0.04	0.55	0.00
KLHL17	339451	0.65	0.04	0.57	0.00
PCDH1	5097	0.71	0.02	0.61	0.06
ABI3	51225	0.66	0.04	0.62	0.04
TMIGD2	126259	0.66	0.05	0.62	0.04
NCBP1	4686	0.72	0.04	0.63	0.02
IL10	3586	0.72	0.02	0.64	0.05
ANG	283	0.74	0.02	0.64	0.00
KRT24	192666	0.69	0.01	0.65	0.00
TMEM79	84283	0.66	0.01	0.67	0.02
PDGFB	5155	0.65	0.00	0.68	0.03
SNX11	29916	0.68	0.05	0.68	0.05
CFL1	1072	0.69	0.02	0.68	0.05
CKLF	51192	0.62	0.03	0.70	0.01
TUBB6	84617	0.73	0.01	0.71	0.01
HYAL2	8692	0.67	0.02	0.71	0.05
TYROBP	7305	0.73	0.04	0.71	0.01
APBB2	323	0.70	0.00	0.71	0.02
YTHDF1	54915	0.61	0.02	0.73	0.01
CEP152	22995	0.46	0.03	0.74	0.05
COL7A1	1294	0.73	0.03	0.75	0.05
NMU	10874	0.67	0.00	0.76	0.05
SPTA1	6708	0.38	0.03	0.76	0.02
ERGIC3	51614	0.70	0.05	0.76	0.05
SATB1	6304	0.67	0.02	0.77	0.04
MOBK1B	55233	0.74	0.03	0.77	0.01
GNAT1	2779	0.66	0.04	0.78	0.03
ITFG3	83986	0.73	0.05	0.78	0.05
DYSF	8291	0.26	0.01	0.78	0.05
MANSC1	54682	0.65	0.03	0.78	0.05
EDIL3	10085	0.65	0.01	0.79	0.05
GRAMD4	23151	0.72	0.00	0.79	0.01
ZIC5	85416	0.69	0.03	0.80	0.05
PAPLN	89932	0.71	0.03	0.80	0.01
CYP4F3	4051	0.74	0.02	0.81	0.01

NUCLEIC ACID AND AMINO ACID SEQUENCES OF BIOMARKERS

49

TTTGTGTGTTGGTCTTCGTGCTGGGTCTGGGTCTGACCCACCGACCCTGGCTCAGGATAACTCCAGGTAC ACACACTTCCTGACCCAGCACTATGATGCCAAACACAGGGCCGGGATGACAGATACTGTGAAGCATCA TGAGGAGACGGGGCTGACCTCACCTGCAAGACATCAACACATTTATTCATGGCAACAAGCGCAGCAT CAAGGCCATCTGTGAAAACAAGAAATGGAACCCCTCACAGAGAAAACCTAAGAATAAGCAAGTCTTCTTTC CAGGTACCACTTGAAGCTACATGGAGGTTCCCCCTGGCCTCCATGCCAGTACCGAGCCACAGCGGGGT TCAGAAACGTTGTGTTGCTTGTGAAAATGGCTTACCTGTCCACTTGGATCAGTCAATTTTCCGTCGTCC GTAACCAGCGGGCCCCCTGGTCAAGTGCTGGCTCTGCTGTCTTGCCTTCCATTTCCCTCTGCACCCAGA ACAGTGGTGGCAACATTATTGCCAAGGGCCCAAGAAAGAGCTACCTGGACCTTTTGTTTTCTGTTTGA CAACATGTTTAAATAAATAAAATGTCTTGATATCAGTAAGAA (SEQ ID NO: 3)			
Translated protein sequence			
MVMGLGVLLLLVFLVGLGLTPPTLAQDNSRYTHFLTQHYDAKPQG RDDRYESIMRRRLTSPCKDINTFIHGNKRSIKAICENKNGNPHRENLRISKSSFQV TTCKLHGGSPWPQCQYRATAGFRNVVVACENGLPVHLDQSIFRRP (SEQ ID NO: 4)			
APBB2	323	NM_173075	Homo sapiens amyloid beta (A4) precursor protein-binding, family B, member 2 (APBB2), mRNA
mRNA Sequence			
GCCAAGCCTGGAGAAGTGAATCTCGTCAGCGCCGCTCCCTGCGCGGGACTCGCGGAACGGCACTGAGC ATGCTCAGTTGCCGAGCCCGTTCTGGTCTCAAGTAGGAAGCTAGTGCGCTGTAACCGCATCTGATCTGG GCGCTCCGGGAAGGGCGAGACTGGAGCAGAGCCGCTGGGCGCCGGAGCCGAGGCGAGCCGCGCGCACC ACTGGTTGGAGTTGCTGTGGGTGAGCTGCTGTGGTCTGTAGCCAAGCATCTGTGGTCTGGATCTGCCAG CCGTGGAACAGAAACATTGCTGGATGGAATCCATAAAAGAAAGCTCCTGTGAAAAGCTGAGGCTGAC AATAATTTAAGCAAAATCAGATCGATCTCTTTGGGCTGCCTGACCTCCTTGGGTGCTTGTATTAAATTA CAGACTTTGTGGGGAAGGAGCTTGCCTTCTGAGCTTTGTACCAAGACCTGGGAAACTAACCAT CTCAGTCTTTCTGAGGACTTGGGAACCTGCCAGGCCCTCTGCCAATGTGTGACTGTCTGAGGCTCA CTGTTGTCCAGGCAGCTCATATTTCAAATTATAACCTATTTCTGCACCATGTCTGACGCCTGGTGATCC ATGTCAGAAGTACTTCCAGCTGACTCAGGTGTTGACACCTTGGCAGTGTATATGGCCAGCAGCGGAATA CAGACCTCACAAATCGGAACAGCCAGCCACACCACCAACACCTTAACCTCCGATCCTCCACAATGA ACTGTTGAACGCTGAAATAAAACACACAGAAACCAAGAACAGCACACCTCCCAATGCAGGAAAAATAT GCACTAACTAACATCCAGGCGGCCATGGGCCTCTCGGATCCAGCTGCACAGCCCTGTCTGGGAAATGGCT CTGCCAACATCAAGCTGGTGAAAAATGGGGAGAACCAGCTCCGTAAGGCTGCAGAGCAAGGGCAGCAGGA CCCCAACAAAAACCTGAGCCCCCTGCAGTCATCAACATAAATCTGAGAGTTAGAGGGTAAAGAGCCC CACCCACAGGATTCTCGAGCTGTGAGATTTTACCCTCCAGCCAGGAGAATAAGAGCTTCTTAAATT ACTATGCAGATCTGGAACCTCAGCCAGAGAATAGAGCAGAACCAGGCAATCACCATGGGACTGCGGA AGAGAAATCCAGCCAGTCCAGGGCCAGGCCTCCACCATCATTGGGAATGGCGATTGCTGCTGCAGAAA CCAAACAGACCCAGTCCAGCCCTGAAGACGGCCAAGTAGCCACAGTGTATCCAGCCAGAAACCAAGA AGGATCATCCGAAAACAGGGGCCAAACCGACTGTGCACTGCACCGGATCCAGAACCTGGCACCGAGCGA TGAGGAGTCCAGCTGGACAACGTTGTCCCAAGACAGTGCCTCACCCAGCTCCCGGATGAACAGATATA TGGAGTGATCACTCATTTTCAGACTGATCCAGATTTGCGCCTGGCTGGAAAAGAGTACGATGACATTGCCG GGACCTATTATTGGCACATCCCAACAGGAACGACTCAGTGGGAACGGCCGCTCTCCATCCAGCAGATCT CCAGGGTCTTAGGAAAGGGTCACTTAGTTCTGTAACGCCATCTCCACCCAGAGAACGAGGATTTGCAT GCAGCCACTGTAAACCCGACCCAGTTTAAAGAGTTTGAAGGAGCAACCTACGCTATGCATCTTTGA AACTCAGAAATGCCCCACACCCTGATGATGATGATTCTGTAGTATCAACAGTGACCCAGAACCAAGTG TTTTGCTGTGCGTTCTCTGGGATGGGTAGAGATGGCAGAAGAGGACCTCGCCCCGGTAAAGTAGTGTT GCGGTCAACAACCTGCATCAGGCAACTTTCTACTGCAAAAATGACATCCGAGACACAGTCGGGATTGGG GAGAGGGGAAAGACATGTACCTGATCCTGGAGAATGACATGCTCAGCCTGGTGGACCCCATGGACCGCAG CGTGCTGCACTCGCAGCCCATCGTCAGCATCCGCGTGTGGGGCGTGGGCGCGACAAATGGCCGGGATTTT GCTTATGTAGCAAGAGATAAAGATAACAAGATTTTGAATGTGATGATTTTCGATGTGACACACCAGCAA AAGCCATTGCCACAAGTCTCCACGAGATCTGCTCCAAGATTATGGCTGAACGGAAGAATGCCAAAGCGCT GGCCTGCAGCTCCTTACAGGAAAGGGCCAATGTGAACCTCGATGCCCTTGTCAAGATTTTCCAACACCA AAGACTGAGCTGGTCCAGAAGTTCACGTCAGTACTTGGGCATGTTACCTGTAGACAAACAGTCTGGAA TGGATATTTTGAACAGTGCCATAGAAAATCTTATGACCTCATCCAACAAGGAGGACTGGCTGTCTAGTGAA CATGAACGTGGCTGATGCCACTGTGACTGTGATCAGTGAAAAGAAATGAAGAGGAAGTCTTAGTGGAATGT CGTGTCGATTTCTGCTTTCATGGGTGTTGGGAAGGACGTCCACACATTTGCTTATGATGACGACGG GGAACAGCGCTTTGAGTGCCACGTTTCTGGTGCAGCCTAATGCTGGTAACGTGTCTGAGGCGGTGCA GGCCGCTGCTGTTACGATATCAGAAGTGCTTGGTAGCCAGGCCGCTTCTCAGAAAGTTCGACCACCT CCACCGCCAGCAGATTAGTAACAGAAGAGTCACAACCAATGTAAAACGAGGGGTCTTATCCCTCATTG ACACTTTGAAACAGAAACGCCCTGTACCCGAAATGCCATAGCTGCACATGCAAAAGGACTCGGCTATTTA			

CCTGAAGATTGACTAGCTACACTAAAGAAAATGAACCTCCGCCATCCGACCTTCCATCCAGTTGCTGATGC
TTTGCTTTCAGAGAAATTTACCCCTTAACCAAGCAGTGTTAGACAAGCATGTTCTCTCGTCTTGCCACCATC
ATGTGATATGAAAAGAAGCATGAATAATTTTTTTTGTGTAAGTTACATCATGCGCAGTGGAAGGTCTTT
TTCTTATTGTAAATATTGTGAACATTACTTAACCTCACACACACACAGAGAAGAGTGTGGCCCCACCCCT
CCTAGTGAACTAACGCTGCGTCCCTTGGAAATGAATGATGCGTGAGTTAGTTTCACTGTCTCTTGCGCTGGA
CCTGTCACAAGCAACCTTTAAGTCTACAGCATTGCCCCGTGTTTTCAACATTGGAGTAGGCACATGCATA
GCAGATACCATTGAATTGCTGTAAAAATAGGATGGCGAGTTTGTGTTTTAATTTTTCATAAAAATGAACC
TGTTGGTTGACAAAATGGCTGTGGCATCAGIATAGAAACCACTGGCAGCTTTCCCTGACAAGCTCTT
TGACACATGGACACCATTTCATGTCTACAGCTGTTTGTGGGATGTTGGAAAAAATGAAACTTCAAAAT
GATGAAAAACTAAATTCGAGGAATTAATAATCGAACAAAACATAGCCTTTCTTTTCCGATGGTTTTCAAA
TGATTATTTTTAAAGAGATTAAATAATCATAATGCATTTTGGGTGGGACATATTTCAAACCTCTGCCT
TATATTGTACGGTGCAGCTAGAGAATTATAGTTCACTATGGCCATTCTTACATAAACATTAAGATGAAA
TACTCTCATCAGCCTTTCATCCTTAGTTTGAGAATTAGCTGATATGCAATTTGAAGTTGAGGAAATATC
ATTGATATTTCTATCATGCACGATTATTTAGATTCTACCACCGTGTGATTTTTGCTAGTCCATGTGCT
AGAGGTAACGTTCTGCTGGAATTCTGCATCCAGCTCTATCCCCCTCTGATGCTTTTTGCCAGAAAGCT
GTCTGTCCATCATGTATTGTCCATGGCAACAAATTACATTAGGTGAAACCTTTCCCTGATTTTATGTATT
TAATATTAGAATTTGTTGGACTCAACTAGATATATTTTTTAATTTATATTTTTTCCATTTTACTTTGAAG
ATTTGAAATGTTTACATCTGAGCAAAGTCTACACAGGAGTAATGGACTGTTTAAACAAGTTTCCCAAAACA
GCATTTTCTGCTCCTTCGTATGTAGGTGAGAACTTAGCTGGAAGACATACAAATTTAGACTCTCGTT
GACATTGTCTGTTTTAAAGGAAGTTGCTAAGGCGATCAATCTCAATATTAGTCTTGTTTACTTCTCTTA
ATGTCAAAATTAACATTTACAACATCCAATTATAAAAGTAATGCTTTATGTTTATACACTGCTATGTACT
TGTCAAAATGGTTTTCCACATTTCTATCACATCTGAGCCTTACCAGGTAGAGAAGGTACTAAATACACTTT
AGAAGTAAAAATATGAAGTACCGAGAGGCTAAACCCACTGGCCTAAGATCTCACCAAAGTTCATGAAAA
CAGGACTAGGACCCACGGCTCCCAAAGCCGTTCTGTCTGTGTTGTGCTGCCTCCATATCCGTCAGGAAG
AGCCTTTCCAGAATGATTCTGGGCATATACTAAGAAGAGCAGGTATGGAAGATCTATTGTGAGGGAATC
TTAGAATTTCCCTACACGAGTGGGAGAAAGATGTCCAAATTCCTTACGCAGTGGTATTCTATGATGGTCCC
TATCTAAGTCCAGGACTGTTTTCTTACAGCGTGCCTCAAAAGTGTGTAGAGGGCAGGATTCTACATTCA
CAGCCTGTTCATCTACGAGATTTTCCAGATGCTACTTGTGGTAGACATTCTTAACATGGTACTTAGC
CACCAGAGATCATGATGGAATGAGTGGGTGGCTTTTCTACCTGCCATTCCCTCAGAATTCATGAGGGGTG
GGGACAGGGGGGACCGGAATTGCTTAGCACCCCAATGTTATGACAAAACTATGCTACTTTAGAAACGCA
GTCTGTTTTTACCAAATTGACATACTACTGATCTGAAGTAACAGTGCCATCATAGAATAATCATGCAAT
AAGAAAAATCCTTGCTGTGCCCTTTGAAAAGCTGTTTCAAGAAATCATTACAGTGATCTTTCATCTCGGTG
CTGTAGTGAACATTTTAGTGTGATAAATTTCAAATTTCTAAACAAATTACCCACTTTTATATTGGAAAT
CTCTACCAGAACTCCCTCTTCATTTTTTAAGGCATACATTGCTTGTGTTTCAAGATCAAGAATTCTGAGC
TAGCTTTAAGTAGCAAACTGATTTATATGTGCAATATAGGATGCATTAAGATGAATGATAGCCTTTACA
TATTGAAAACCTTTGCAGACGTTTTGTTTTGAAAATGGCATTGTATAGTAAATGCAAATTAATTTTGAAA
ATTATGTTAAAGAGIATGTTTACAGACATTTCTGCCATGGCCAAAAAGTATGTATGAAAGTATGTGTAT
TTGTTTGTAAAAGGATGCCAATGTTTTTACCTGATATCTTAGTGACACTTCAGTTATCTATGCATTCTTA
GATCTGTGATTCGGTAAACAGGCAGCCATGTTTCCAGATGCCCTTCTATGCTTACCATATTTTAAATTAAC
CTGTTAAATACAGCTTAAATATTTTTATTTTATTCTATTTTTACTGAAATATACTGCATTATTGT
GTTAATGTATTATCTTTCTGGATATTATCTCCAGTGTATCCAGATCTAAGTAATCTCAGTGAATATA
CATTGCCCTAAAAAGTGGTTTTGTAATGATTGTAGTCACATTTCTATTGGGATATGTAGAGAAAAGGCA
AAATGCTTAAAGTTCCTTTTATTTTTTAAAGCAGCTAGATAGACACAGACTTGCCACCTCATACATCTG
CTCCTTGGCAACATCAAGGGGAACGACTAGCCAACATGCCTATGGCTAAAAACTTTCTTTTGCAGACTAA
AGCACTGCTTGGTGCTTCGTTTTTCTACCCCTTCAACATGTGTGATTTCATCTAAGAGATATATACATG
TACACATGGCCTTTGTTTTCCACCTGGATACAAGATCACTCATAGCTAATTAGGACCATGTTTTTTTGTTC
ATCTGTCTTGTGATGAAGGGACATTAGACCCATTTCATTAAAAATAAGTTCTTGGTGATAAACTGTGG
CACTGCTACTTCTTTTTAAATCCACTTTATGATTTCAAGATGGACACTTGTAAAGTACTCGACACAAGG
CCATTGCCCTGGAAGCCCCAGAGCTTTCTCTGTTTGTATGGCCCGTTTCATGTCCAGGCATTGCAACACA
AACTCCTCAAGATTTCAACACACATGACAAGCATTTTCTTAAGTATATTAGCACAATTTAACTAATAA
GCCCCCTCGCTCTCTAGTTGGCCAGGCTTAACCTAATACACATCTAACGTGTGTGCCACACGGCCAGTAG
AAAGTTTAACTTCAGCTTCAGGGCAAAGATACCCACTCACACCGTGTCAACGCAAGCAGTAGTTCTGGC
CTCCAGAGCAGCTTACTTCCCTGAAAGAAGCGTTGTTTTCTTTATGCCCTTTTCTGTTGACCACTT
TTACACATTTAAATGTAATTTGTTGTGAGAATAAATTTAGCTGCATAAAACGTTCCGGCTCATTATCTGA
CATCTTAGTCACATATACAAGGAATAGAAATAGAACTCGGTGTCTCTAGTTATTTTTAAATATTCTTA
CCICAGACTTCTTAGAAATCACTTTAGTAATGGAGCATTTTGTCTTGTATTAGTTACTACATATTTCTGCC
TGGTAAAGAACTAGGAAGTAACCTCAAAATTTGAGTAATCACCCTGTACTTATTGGTGATCAGGAAGGCC
AGCTGGCCTTCCGGACATAGAAGCCTATTTAGTCACCAACTCGAGTCTTTTGTAAAGCGGCTTGTCTAGGA
TTGTGATATTTTAGCACGAAGAAGTTTATCACTTCTTTAAGAACCTGACATCAAAGAATAAAGATAGA
GGGTACACACACTAAATCCAAATGAAAGGTAACTAGAGAAATCAGTTGAATCTGTTTTCAGTTAACTG
TTAGGCGCAGGAAGGCAGATAAACAGAAATTAAGTATGTCCCCGCTTTTTGTTTCATCTTGCACTTCCAC

Translated protein sequence

Homo sapiens chemokine (C-C motif) ligand 26 (CCL26). mRNA

CCL26

10344

NM 006072

mRNA Sequence

Translated protein sequence

MMGLSLASAVLLASLLSLHLGTATRGSDISKTCFQYSHKPLPW
TWVRSYEFTSNCSORAVIFTTKRGKKVCTHPRKKWVOKYISLLKTPKOL (SEQ ID NO: 8)

CDC20

991

NM 001255

Home sapiens cell division cycle 20 homolog

			(S. cerevisiae) (CDC20), mRNA
mRNA Sequence			
GAGGCGTAAGCCAGGCGTGTTAAAGCCGGTCGGAAGTCTCCGGAGGGCAGGGGCTCCGTAGGCACCAAC TGCAAGGACCCCTCCCTCGGGGCGCTCCCATGGCAGATTTCGCTTCGAGAGTGACCTGCACTCGCTG CTTCAGCTGGATGCACCCATCCCAATGCACCCCTGCGCGCTGGCAGCGCAAAGCCAAGGAAGCCGAG GCCCCGCCCCCTACCCATGCGGGCCGCCAACCGATCCCACAGCGCCGGCAGGACTCCGGGCCGAATCC TGGCAAATCCAGTTCCAAGGTTAGACCACTCCTAGCAAACCTGGCGGTGACCGCTATATCCCCATCGC AGTGCTGCCAGATGGAGGTGGCCAGCTTCCTCCTGAGCAAGGAGAACCAGCCTGAAAACAGCCAGACGC CCACCAAGAAGGAACATCAGAAAGCCTGGGCTTTGAACCTGACGGTTTIGATGTAGAGGAAGCCAAGAT CCTTCGGCTCAGTGGAAAACCACAAATGCGCCAGAGGGTTATCAGAACAGACTGAAAGTACTCTACAGC CAAAAGGCCACTCCTGGCTCCAGCCGGAAGACCTGCCGTTACATTCTTCCCTGCCAGACCGTATCTGG ATGCGCTGAAATCCGAAATGACTATTACCTGAACCTTGTGGATTGGAGTTCTGGGAATGTACTGGCCGT GGCACTGGACAACAGTGTGTACCTGTGGAGTGCAAGCTCTGGTGACATCTGCACTTTTGCAAATGGAG CAGCCTGGGGAATATATATCTCTGTGGCTGGATCAAAGAGGGCAACTACTTGGCTGTGGGCACAGCA GTGCTGAGGTGCAGCTATGGGATGTGCAGCAGCAGAAACGGCTTCGAAATATGACCAGTCACTCTGCCCG AGTGGGCTCCCTAAGCTGGAACAGCTATATCTGTCCAGTGGTTACGTTCTGGCCACATCCACCACAT GATGTTTCGGGTAGCAGAACACCATGTGGCCACACTGAGTGGCCACAGCCAGGAAGTGTGTGGGCTGCGCT GGGCCCCAGATGGACGACATTTGGCCAGTGGTGGTAATGATAACTTGGTCAATGTGTGGCCTAGTGTCTC TGGAGAGGGTGGCTGGGTTCTCTGCAGACATTACCCAGCATCAAGGGGCTGTCAAGGCCGTAGCATGG TGTCTCTGGCAGTCCAATGTCTGGCAACAGGAGGGGGCACCAGTGATCGACACATTCGCATCTGGAATG TGTGCTCTGGGCGCTGTCTGAGTGCCGTGGATGCCATTCCCAGGTGTCTCCATCTCTGGTCTCCCCA TTACAAGGAGCTCATCTCAGGCCATGGCTTTGCACAGAACCAGCTAGTTATTGGAAGTACCCAACCATG GCCAAGGTGGCTGAACCAAGGTACACATCCCGGGTCTGAGTCTGACCATGAGCCAGATGGGGCCA CAGTGGCATCCGCAGCAGCAGATGAGACCTGAGGCTATGGCGCTGTTTTGAGTTGGACCCCTGCGCGCGC GCGGGAGCGGGAGAAGGCCAGTGCAGCCAAAAGCAGCCTCATCCACCAAGGCATCCGCTGAAGACCAACC CATCACCTCAGTTGTTTTTTATTTTCTAATAAAGTCATGTCTCCCTTCATGTTTTTTTTTAAAAAAA AAAAAAA (SEQ ID NO: 9)			
Translated protein sequence			
MAQFAFESDLHSLQLDAPIPNAPPARWQRKAKEAAGPAPSPMR AANRSHSAGRTPGRTPGKSSSKVQTPSPKPGGDRYIPHRSAQMEVASFLLSKENQPE NSQTPITKKEHQAWALNLNGFDVEEAKILRLSGKPQNAPEGYQNRKLVLSQKATPGS SRKTCRYIPSLPDRILDAPEIRNDYYLNLVDWSSGNVLAVALDNSVYLWSASSGDILQ LLQMEQPGEYISSVAWIKENYLAAGTSSAEVQLWDVQQKRLRNMTSHSARVGSLSW NSYILSSGSRSGHIIHHHDVRAEHVATLSGHSQEVCGLRWAPDGRHLASGGNDNLVN VWPSAPGEGGWPLQTFTHQGAVKAWAWCPWQSNVLATGGGTSDRHIRIWNVCSGAC LSAVDAHSQVCSILWSPHYKELISGHGFAQNQLVIWKYPTMAKVAELKGHTSRVLSLT MSPDGAIVASAADELRLWRFCFELDPARREREKASAAKSSLIHQIR (SEQ ID NO: 10)			
CEP152	22995	NM_014985	Homo sapiens centrosomal protein 152kDa (CEP152), mRNA
mRNA Sequence			
GCCACCGGGCGAGCTTCTAGTCGGCGATTGAAGGATGCGAGTGCTCCTTAAGGGCTCCGCCCCGTGAG TTCGGTTGTGACTAGGAAGGAGCTAGTGGACTAGAGCCAGGGTAAGGGGATCTGCTAGAAGTTGGTCTTC CGCCAGGACTAGAGTTTCTCGCGGTAACAGCCTCCGTGGCTCCGGAGGACCATGTGATTAGACTTTGG CAGTGTGGCACTACCAGTGCAAAAATGAAGATGAAGAGTATGACGAAGAGGACTATGAAAGAGAGAAAGAG TTGCAGCAGTTACTACAGACCTTCCCATGACATGCTGGATGACGACCTCTCCTCTCCAGAGCTCCAGT ATTCGGACTGCAGCGAGGATGGCACAGACGGACAACCACATCATCTGAGCAATTGGAGATGAGCTGGAA TGAGCAAATGCTGCCCCAAATCTCAAAGTGTAATGGCTATAATGAAATTCAGAGTTTATATGCTGGAGAA AAATGTGGTAATGCTGCGGAAGAAAATAGAAGTAAACTGAAGACCGACATCCTGTGTACCATCTGAAG AAGGTGGAGATGAAGGTGGAAGTGGTTATAGTCTCCTCAAGTAAATGTGAACAGACTGATTTATATCACT TCCTGAAAACCTTAGGCCATATACCAATGGTCAGAAGCAGGAATTTAATAACCAAGCAACCAATGTAATT AAATTTTCAGATCCTCAATGGAACCATTTTCAGGGTCCAGTTGTCAAGGTTTGAACCGTATAATAAAG TGACATATAAACCTTATCAGTCTTCTGCCAGAATAATGGCTACCAGCCAGGAGATAACAGGAAGTGA CACATTGGAAGGCTGCAACAACAATTTTAGGAGCTAATGAGAAGCTGCAAGAAAATATGCAGATTATT CAACTTCAGGTTCTTAACAAAGCAAAAGAGAGACAAGTGGAGAAGCTTAATTGAAAAGTTAAATGAAAGTG AACGTCAAATTCGATATCTGAATCACCAGCTGTAATAATAAAGATGAAAAGGATGGTTTACTCTCAG			

CCTTCGAGAATCACAGAACTCTTTTCAGAAATGGAAAAGAGAGATACAGCTTGAAGCTCAAATAAAA
GCACTGGAGACTCAGATACAAGCATTAAAAGTCAATGAAGAACAGATGATCAAGAAGTCCAGAACAACTG
AAATGGCTCTGGAAAGCTTGAAGCAGCAGCTGGTGACCTTCATCATTCTGAATCATTCAACGAGCTAG
AGAACAGCATGAGAGCATTGTTATGGGCCTCACAAAGAAGTACGAAGAGCAAGTATTGTCTTACAAAAG
AATTTGGATGCCACAGTCACCGCACTTAAAGAACAGGAAGACATTTGCTCTCGTCTGAAAGATCACGTGA
AACAACTGGAAAGGAATCAAGAAGCAATCAAGTTAGAAAAGACTGAGATCATTAAATAGTTGACAAGAAG
TCTAGAGGAGAGTCAAAAGCAGTGTGCCCACTTGTTCAGTCCGGGTCAGTACAAGAGGTGGCTCAGCTA
CAGTTCCAGCTGCAGCAAGCACAGAAGGCACATGCTATGAGTGCACAAATGAACAAGGCTTTGCAAGAAG
AATTAACAGAACTAAAAGATGAAATTTCTCTCTATGAATCTGCTGCAAACTAGGAATACATCCAAGTGA
CTCAGAAGGAGAATTAAATATAGAACTCACTGAATCGTATGTGGATTGGGTATTAATAAGGTCAACTGG
AAAAATCCAAAGTTACCAGCATTGTACAAGAAGAAGACCCAAATGAAGAGCTTTCAAAGATGAGTTCA
TTCTGAAGTTAAAGGCAGAAGTACAGCGTTTGTCTGGGTAGCAACTCAATGAAGCGTCATCTGGTGTCTCA
GTTACAAAATGACCTCAAAGACTGTCTATAAGAAAATTGAAGATCTCCACCAAGTGAAGAAGGATGAAAA
AGCATTGAGGTTGAGACTAAAACAGATACCTCAGAAAAACCAAAGATCAATTATGGCTGAGTCTTCTA
CTTCTGATGTTGTGAGAGATGATATTCTGCTGCTTAAAAATGAAATTCAGTTTTTACAACAACAAAATCA
GGAACCTTAAAGAACTGAAGGAAAACGAGAAAATACAAATCAAGACTTATGTAATCAATGAGACAAATG
GTACAAGATTGACCATGACAAACAGAAGCTGTGGATAGGTGTGAAAGGACTTATCAGCAGCACCATTG
AAGCCATGAAAATATACAAACAGGTGAAAGCCTATTAGCAAGCATGCTTTGGAGAAGCAGCAGCTCTTGA
GGCTTATGAGAGAATCATTGCAACTGAGGTCTGAGTTGGATAAGTTGAATAAGGAGGTGACTGCTGTG
CAGGAATGTACCTAGAAGTGTGCAGAGAGAAGGATAATCTAGAATTGACTCTCAGGAAGACCACTGAAA
AGGAGCAACAGACTCAGGAGAGATCAAGAAAACCTATTCAACAGCTTGAAAAGGAGTGGCAGTCTAA
GCTGGATCAAATATAAAGGCAATGAAAAAGAAGACCTTAGATTGTGGCAGCCAACTGACCAAGTAACC
ACCAGTGATGTTATTTCCAAGAAAGAGATGGCAATATGATAGAAGAGCAGAAGTGCACAAATCCAGCAA
ACTTAGAACAGAGAAGGACATAGCCATCAAGGGGGCTATGAAGAACTCGAAATTGAATTGGAATCAA
ACATTGTGAAAATATTACCAACAGGTAGAAATAGCTGTGCAAAATGCTCATCAGCGATGGCTGGGAGAA
CTACCAGAGCTGGCAGAGTATCAAGCACTTGTGAAGGCAGAACAGAAAAAGTGGGAAGAACAGCATGAGG
TCTCTGTGAACAAAAGGATATCATTGCTGTTTCTGAAGCTAAAGAGAAATGGAAGAGTGAGCTTGAAAA
TATGAGGAAAAATATACCTTCTGGAAGGAATTGGAAGAGAAGATTCTTCTCTCAGAAAGAACTTGAG
TTAAAGAACGAAGAAGTCCCTGTGGTCAATCAGGGCTGAGTTAGCTAAGGCTCGGAGTGAATGGAACAAAG
AAAAGCAAGAAGAAATCCACAGAATCCAAGAACAAAATGAGCAAGATTACCGGCAATTTTTAGATGATCA
CCGAAATAAAATTAATGAGGTGCTTGGCGCAGCTAAAGAAGACTTTATGAAACAAAAAACTGAACTACTT
CTTCAGAAAGGAGACAGAATTACAAACCTTGTCTAGACCAGAGTCGTAGAGAATGGACTATGCGGGAAGCA
AGCGGATCCAACTGGAAATCTATCAGTATGAGGAAGACATCCTGACTGTACTTGGGGTTCTTTTTAAGTGA
TACCCAAAAGGAGCACATCAGTGATTCTGAGGACAAGCAGCTTTTGGAAATCATGTCGACTTGTCTTCA
AAATGGATGCTGTGCAATATTTTGA AAAACTAAAGGGCTGCATACAGAAAGCATTTCAGATACACTTC
CTCTGCTTTGAGAAAACGCTGACCCAGAAATGGA AAAAGAGAAAATATGGCCGAGCTCTCTAAGGATTCTGC
CAGCCAGGGCACTGGCCAAGGAGACCTTGGACCTGCTGCTGGACACCATGCTCAGCCCTTGGCCTTACAA
GCAACAGAAGCAGAAGCTGAAGAGAATAATAAGTTGTTGAAGAATTAATAGAAGAAAACAACGACATGA
AGAATAAATTGGAAGAAATGCAACACTTTGTAAAACACCACCAAGGTCATTGTCAGCAGGGGCCATTGA
AAATGCTTCCTTGCCATGCAAGTGGGGGAGCCTTGGAAAGAACTTCGTGGGCAGTACATTAAAGCTGTAAAA
AAAATTAATGTGACATGCTTCGTTATATTAGGAGAGTAAGGAACGAGCTGCAGAAATGGTAAAAGCAG
AGGTACTGCGAGAACGTCAAGAAACCGCCGAAAGATGCGCAATATATTTGATTGCTTCCAACAGAT
TTTTCAGGATGATGGA AAAAGAGGGGCTGAGAAAAGATTATGAATGCTGCTAGCAAACTTGCTACAATG
GCAAAATTAAGTGAACACCTATTTCTAGTAAGTCCCAAGCAAACTACACAGTCAGCACTGCCCTTAA
CTTCAGAGATGCTGATTGCAGTTAAAAATCAAAAAGAAATGATGTGAATCAGAAAATACCATGTTGTAT
TGAAAGCAAATCAAAATAGTGTAAACACCATCACCAGAACTCTGTGCAACAAAGCTCCCAAGAGGAGGGCA
GCTTGTAACCTTACAAAGGCTGTAGAGAACTCAGAGCATCAGAGCATAAAGCATGTTGGGATCCAAAGAGA
CACATTTGGAATTCAGTTTGGGGATGGTAGTTGCAAGCACCTAAACAGTTTGCCAAGGAATGTTTCTCC
TGAGTTTGTCTTGTGAAGGTGAAGGAGGCTTTGGTTTGCAACAAGAAGAAAGACCTACTCAGTGATAAT
GGTCTGAAATCACTTCCGCATTGAGTGCATACCCCTTTCTTGAACCTTAGGAAATAAACCTTACCTA
GATGTACCCCTGGTCTTCTGAAATCAGGATGCATGCATATAACCTTTCGCGATTCTAATGAAAGACTTGG
TTTAAAAGTATATAAATGCAATCCACTAATGGAAGTGA AAATGCTGCATCTGAGAAAAGTCAAGGTTTG
GATGTTTCAAGAACCTCCAGTAAAAGATGGAGGGGACCTTAGTGACTGCTTGGGCTGGCCTTCCAGCAGTG
CAACCTTTATCCTTTGACAGTCTGGAAGCATCATTGTACATGTTAGGCCACAAGGAACCTTGGAAATACC
AAGTGAATCTGTTAAATCCAACAGTTTTTACCATCCGGTTATCTTTGAGATACAGAGGAAAGTAAATATG
ATTTGTCAAACAAATGAAATGTCAGCGTTATCAAATCCATACCTGTCAGAGAAGAAACCGTATTTGGAGC
CAGGAAGATCAGTGTGAATTTGGACACCCATCTGTCATAAGGCTGATAGATTAAAGTCAGATTTCAA
AAAACAGCAGTACATTACCATCTTCAGTGTGTCAGCAGCCTTCAAGAAAATTAATTGTTCCGCTATCT
AGCCACAAGATAGTGGCTTTGATAGCCCAATTGTTAATCTAGACTAATTATGGTACAGTATTTAAGAAG
AATCATTAAATATTAACAAAATGGAAGGGAAGACCTCATCTGAAAAAATTTGTAGCCCTGGCTCTT
TTGAGATGTTTTAATAACATCTGTTATATAAGTAAAGCATTCTTCTAAAATTGCTTGAGATATTTATGTT

GCCTTAATATTCCAAAGGCCTGATGGTGTATGTATAATCTGCTTTTGTGTGGTGTCTATTTTGGTTTCT AAACCATCTATTTTATACTTATAAATTGACTCACTCTGCAGTGTTAACTTATTTAAATAAACTTGATA TGGTCTGTAAAAAAA (SEQ ID NO: 11)			
Translated protein sequence			
MSLDFGSVALPVQNEDEEYDEEDYEREKELQQLLTDLPHDMLDD DLSSPELQYSDCEDGTGQPHPEQLEMSWNEQMLPKSQSVNGYNEIQSLYAGEKCG NVWEENRSKTEDRHPVYHPEEGDEGGSGYSPPSKCEQTDLYHLPENFRPYTNGQKQE FNNQATNVIKFSDPQWNHFQGPSCQGLEPYNKVITYKPYQSSAQNNGSPAQEI TGSDTF EGLQQQFLGANENSAENMQIIQLQVLNKAKEQLENLIEKLNESERQIRYLNHQLVVI KDEKDLTSLRESQKLFQNGKEREIQLEAQIKALETQIQALKVNEEQMIKKSRTTEM ALESKQQLVLDLHHSSELQRAREQHESIVMGLTKKYEEQVLSLQKNLDATVTALKEQE DICSRLKDHVKQLERNQEAIKLEKTEIINKLTRSLEESQKQCAHLLQSGSVQEVQALQ FQLQQAQKAHAMSANMNKALQEELTELKDEISLYESAACKLGIHPSDSEGELNIELTES YVDLGIKKVNWKSKSVTSIVQEEDPNEELSKDEFILKLKAEVQRLLGNSNMKRHLVSQ LQNDLKDCHKKIEDLHQVKKDEKSIEVETKTD TSEKPNQLWPESSTDVVRDDILL KNEIQVLQQNQELKETEGKLRNTNQDLNQMROMVQDFDHDQKQEAVDRCERTYQQHH EAMKTQIRESLLAKHALEKQQLFEAYERTHLQLRSELDKLNKEVTAVQECYLEVCREK DNLELTLRKTTKEQQTQEKIKEKLIQOLEKEWQSKLDQTIKAMKKKTLDCGSQTDQV TTSVDISKEMAIMIEEQKCTIQONLEQEKDIAIKGAMKKLEIELELKHENITKQVE IAVQNAHQRWLGELPELAEYQALVKAQKWEQHEVSVNKRISFAVSEAKEKWKSEL ENMRKNILPGKELEEKIHSLOKELELKNEEVPVIRAEAKARSEWNKEQEEIHRIQ EQNEQDYRQFLDDHRNKINEVLAAAKEDFMKQKTELLQKETELOTCLDQSRREWMTQ EAKRIQLEIYQYEDILTVLGVLLSDTQKEHISDSEDKQLLEIMSTCSSKWMVSQYFE KLKGCIQKAFQDTLPLLVENADPEWKKRNMAELSKDSASQGTGQGDGPAAGHHAQPL ALQATEAAEENNKVVEELIEENNDMNKLEELQTLCKTPPRSLSAGAIENACLPSCG GALEELRGQYIKAVKKIKCDMLRYIQESKERAAMVKAEVLRERQETARKMRKYLYIC LQQILQDDGKEGAEEKIMNAASKLATMAKLEETPISSKSQSKTQTSALPLTSEMLIAV KKSQRNDVNQKIPCCIESKNSVNTITRTLCEQAPKRAACNLQRLLENSEHQS IKHV GSKETHLEFQFGDGSCHLNLSLRNVSPFVPCGEGGGFGLHKKDLSDNGSESLPH SAAYPFLGTLGNKPSRPTPGPSESGCMHITFRDSNERLGLKVYKCNPLMESENAASE KSQGLDVQAFPPKDGGLSDCLGWPSSTLSDSREASVHGRPQGTLEIPSESVKS KQFSPSGYLSDTESNMICQTMKCQRYQTPYLSEETTYLEPGKISVNCGHPSRHKADR LKSDFKLSSTLPSSVCQQPSRKLIVPLSSQDSDGSDSPFVNLD (SEQ ID NO: 12)			
CFL1	1072	NM_005507	Homo sapiens cofilin 1 (non-muscle) (CFL1), mRNA
mRNA Sequence			
GGCCGGCGGGAAGACTCCGTTACCCAGCGAGCGAGCGGCGGCGCAGGGCCAGCGGACTCCATTTCGGT CGGCTCGCGGTGGGAGCGCCGGAAGCCCCCGCCACCCTCATTGTGCGGCTCCTACTAAACGGAAGGGGC CGGGAGAGGCCGCGTTCAGTCGGGTCCCGGCAGCGGCTGCAGCGCTCTCGTCTTCTGCGGCTCTCGGTGC CCTCTCCTTTTCGTTTCCGGAACATGGCCTCCGGTGTGGCTGTCTCTGATGGTGTATCAAGGTGTTCA ACGACATGAAGGTGCGTAAGTCTTCAACGCCAGAGGAGGTGAAGAAGCGCAAGAAGCGGTGCTCTTCTG CCTGAGTGAGGACAAGAAGAACATCATCTGGAGGAGGGCAAGGAGATCTCTGGTGGGCGATGTGGGCCAG ACTGTCGACGACCCCTACGCCACCTTTGTCAAGATGCTGCCAGATAAGGACTGCCGCTATGCCCTCTATG ATGCAACCTATGAGACCAAGGAGAGCAAGAAGGAGGATCTGGTGTATTATCTTCTGGGCCCCGAGTCTGC GCCCCCTAAGAGCAAAATGATTTATGCCAGCTCCAAGGACGCCATCAAGAAGAAGCTGACAGGGATCAAG CATGAATTGCAAGCAAAGTCTACGAGGAGGTCAAGGACCGCTGCACCTGGCAGAGAAGCTGGGGGGCA GTGCCGTATCTCCCTGGAGGGCAAGCCTTTGTGAGCCCTTCTGGCCCCCTGCCGAGCATCTGGCAG CCCCACACCTGCCCTTGGGGTTGCAGGCTGCCCCCTTCTGCCAGACCGAGGGGCTGGGGGGATCCCA GCAGGGGGAGGGCAATCCCTTACCCCAAGTTCGCAACAGACCCCCACCCCTGGATTTTCTTCTCCC TCCATCCCTTGACGGTTCTGGCCTTCCCAAAGTGTCTTTGATCTTTTGATTCCTCTTGGGCTGAAGCAGA CCAAGTTCCTCCAGGACCCCAAGTGTGGGGGAGCCTGTATTTTTTAAACAACATCCCATTTCCCCAC CTGGTCTCTCCCTTCCATGCTGCCAAGTCTAACCGCAATAGTGACTCTGTGCTGTGCTTTAGTTC TGTGTATAAAATGAATGTTGTGGAGATGACCCCTCCCTGTGCCGGCTGTTCTCTCCCTTTCCCTGG TCACGGCTACTCATGGAAGCAGGACCAAGTGAAGGACCTTCGATTAAAAAAAAGACAATAAAAAA (SEQ ID NO: 13)			
Translated protein sequence			

MASGVAVSDGVIKVFNDMKVRKSSSTPEEVKKRKKAVLFLCSEDK KNIILEEGKEILVGDVGQTVDDPYATFVKMLPDKDCRYALYDATYETKESKEDLVFI FWAPESAPLKSMIYASSKDAIKKLTGIKHELQANCYEEVKDRCTLAEKLGGSAVIS LE GKPL (SEQ ID NO: 14)			
CKLF	51192	NM_016326	Homo sapiens chemokine-like factor (CKLF), transcript variant 3, mRNA
mRNA Sequence			
ATGCGCGCAAGAGAGCGGGAAGCCGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCG GTGCTATCGCTTCGAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGG GCTGCAGACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCGCTTCAGTGTAAGGC CACGTGAAGATGCTGCGGCTGGTGTTCGACTTGTGACAGCAGTATGCTGCTTGCCGACGGGGCCCTTA TTACCGGAAGCTTCTGTTCAATCCAGCGGTCTTACCAGAAAAAGCCTGTGCATGAAAAAAGAAGT TTTGTAATTTATATTACTTTTAGTTTGATACTAAGTATTAAACATATTTCTGTATTCTCCACATATT TTCTGCAGTTATTTAACTCAGTATAGGAGCTAGAGGAAGAGATTTCGAAGTCTGCACCCCGCGCAGAG CACTACTGTAACCTTCAAGGGAGCGCTGGGAGCAGCGGGATCGGGTTTCCGGCACCCGGGCTGGGTGG CAGGGAAGAATGTGCCGGGATCCGCCCTCAGGGATCTTTGAATCTCTTTACTGCTGGCTGGCCGGCAGCT CCG (SEQ ID NO: 15)			
Translated protein sequence			
MDNVQPKIKHRPFCFSVKGHVKMLRLVLFALVTAVCCCLADGALIY RKLLFNPSGPYQKKPVHEKKEVL (SEQ ID NO: 16)			
COL7A1	1294	NM_000094	Homo sapiens collagen, type VII, alpha 1 (COL7A1), mRNA
mRNA Sequence			
GATGACGCTGCGGCTTCTGGTGGCCGCGCTCTGCGCCGGGATCCTGGCAGAGCGCCCCGAGTGCGAGCC CAGCACAGGGAGAGAGTGACCTGCACGCGCCTTTACGCGCTGACATTGIGTTCTTACTGGATGGCTCCT CATCCATTGGCCGAGCAATTTCCGCGAGGTCCGCGAGCTTTCTCGAAGGGCTGGTGCTGCCTTTCTCTGG AGCAGCCAGTGACAGGGTGTGCGCTTTGCCACAGTGACAGCAGTACACCCACGGACAGAGTTCCGGC CTGGATGCACTTGGCTCTGGGGGTGATGTGATCCGCGCCATCCGTGAGCTTAGCTACAAGGGGGGCAACA CTCGCACAGGGGCTGCAATTCATGTGGCTGACCATGTCTTCTGCCCCAGCTGGCCCGACCTGGTGT CCCCAAGGCTGCACTCTGATCACAGACGGGAAGTCCCAGGACCTGGTGACACAGCTGCCCAAAGGCTG AAGGGGCAGGGGGTCAAGCTATTTGCTGTGGGGATCAAGAAATGCTGACCCCTGAGGAGCTGAAGCGAGTTG CCTCACAGCCCACAGTGACTTCTTCTTCTTCTCAATGACTTCAGCATCTTGAGGACACTACTGCCCT CGTTTCCCGGAGAGTGTGCACGACTGTGCTGGTGGCGTGCTGTGACCCGACCTCCGGATGACTCGACCTCT GCTCCACGAGACCTGGTGCTGTCTGAGCCAAGCAGCCAATCCTTGAGAGTACAGTGACAGCGGCCAGTG GCCCTGTGACTGGCTACAAGGTCCAGTACACTCCTCTGACGGGGCTGGGACAGCCACTGCCGAGTGAGCG GCAGGAGGTGAACGTCCAGCTGGTGAGACCAAGTGTGCGGCTGCGGGGTCTCCGGCCACTGACCGAGTAC CAAGTGACTGTGATTGCCCTCTACGCCAACAGCATCGGGGAGGCTGTGAGCGGGACAGCTCGGACCACTG CCCTAGAAGGGCCGGAAGTACCATCCAGAATACCACAGCCACAGCCTCCTGGTGGCCTGGCGGAGTGT GCCAGGTGCCACTGGCTACCGTGTGACATGGCGGGTCTCAGTGGTGGGCCCCACAGCAGCAGGAGCTG GGCCCTGGGCAGGGTTCAAGTGTGCTGCGTGACTTGGAGCCTGGCACGGACTATGAGGTGACCGTGAGCA CCCTATTTGGCCGAGTGTGGGGCCCGCACTTCCCTGATGGCTCGCACTGACGCTTCTGTTGAGCAGAC CCTGCGCCCCGTCATCCTGGGCCCCACATCCATCCTCCTTTCTGGAACCTGGTGCTGAGGCCCGTGGC TACCGGTTGGAATGGCGGCGTGAGACTGGCTTGGAGCCACCGCAGAAAGTGGTACTGCCCTCTGATGTGA CCCGTACCAGTTGGATGGGCTGCAGCCGGGCACTGAGTACCGCCTCACACTCTGACTCTGTGGAGGG CCACGAGGTGGCCACCCCTGCAACCGTGGTTCCCACTGGACCAAGAGCTGCCTGTGAGCCCTGTAACAGAC CTGCAAGCCACCGAGCTGCCCGGGCAGCGGGTGGCAGTGTCTGGAGCCCACTGCCCTGGTGCCACCGAGT ACCGCATCATTGTGCGCAGCACCAGGGGGTTGAGCGGACCTGGTGTCTCCTGGGAGTCAGACAGCATT CGACTTGGATGACGTTACGGCTGGGCTTAGCTACACTGTGCGGGTGTCTGCTCGAGTGGGTCCCCGTGAG GGCAGTGCCAGTGTCTCACTGTCCGCGGGAGCCGAAATCCACTTGCTGTTCAGGGCTGCGGGTTG TGGTGTGAGATGCAACGCGAGTGAGGGTGGCTGGGGACCCGTCCCTGGAGCCAGTGGATTTCGGATTAG CTGGAGCACAGGCAGTGGTCCGAGTCCAGCCAGACACTGCCCCAGACTCTACTGCCACAGACATCACA GGGCTGCAGCCTGGAACCACTACAGGTGGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG CAGTATCGTGGCTCGAACGGACCCACTGGGCCAGTGAGGACGGTCCATGTGACTCAGGCCAGCCAGCTC ATCTGTACCAATTACCTGGACCAAGGTTCTTGGCGCCACAGGATACAGGTTTCTTGGCACTCAGCCAC GGCCAGAGAAATCCAGTTGGTTCTTGGGGAGGCCACGGTGGCTGAGCTGGATGGACTGGAGCCAGATA			

CTGAGTATACGGTGTCATGTGAGGGCCCATGTGGCTGGCGTGGATGGGCCCCGTCCTCTGTGGTTGTGAG
 GACTGCCCTGAGCCTGTGGGTCGTGTGTCGAGGCTGCAGATCCTCAATGCTTCCAGCGACGTTCTACGG
 ATCACCTGGGTAGGGGTCCTGAGGCCACAGCTTACAGACTGGCTGGGGCCGGAGTGAAGGCGGCCCCA
 TGAGGCACCAGATATCTCCAGGAAACACAGACTCTGCAGAGATCCGGGGTCTCGAAGGTGGAGTCAGCTA
 CTCAGTGCAGTGTGACTGCACTTGTGCGGGACCGCGAGGGCACACCTGTCTCCATTGTGTACTACGCCG
 CCTGAGGCTCCGCCAGCCCTGGGGACGCTTACGTTGGTGCAGCGCGGGGAGCACTCGCTGAGGCTGCGCT
 GGGAGCCGGTGGCCAGAGCGCAGGGCTTCCCTTCTGCACTGGCAACCTGAGGGTGGCCAGGAACAGTCCCG
 GGTCTTGGGGCCGAGCTCAGCAGCTATCACCTGGACGGCTGGAGCCAGCGACACAGTACCGCGTGAGG
 CTGAGTGTCTAGGGCCAGCTGGAGAAGGGCCCTCTGCAGAGGTGACTGCGCGCACTGAGTCACTCGTG
 TTCCAAGCATTGAACACGTGTGGTGGACACCTCGATCGACTCGGTGACTTTGGCCTGGACTCCAGTGT
 CAGGGCATCCAGCTACATCCTATCTTGGCGGCCACTCAGAGGCCCTGGCCAGGAAGTGCCTGGGTCCCCG
 CAGACACTTCCAGGGATCTCAAGCTCCAGCGGGTGACAGGGCTAGAGCCTGGCGTCTCTTACATCTTCT
 CCCTGACGCTGTCTTGGATGGTGTGCGGGGTCTGAGGCACTGTGCACACAGACGCCAGTGTGCCCCCG
 TGGCCTGGCGGATGTGGTGTCTCTACCACATGCCACTCAAGACAATGCTACCGTGGGAGGCTACGAGG
 AGGGTCTGTGAGCGTCTGGTGTGGCACTTGGGCTCTTGGGCCACAGGCAGTTACGTTGGCTGTCTGT
 CTTACAGTCTCGGCCCTCCCCACTGTTCCTCCACTGAATGGCTCCCATGACCTTGGCATTATCTTGCAAAG
 GATCCGTGACATGCCCTACATGGACCCAAGTGGGAACAACCTGGGCACAGCCGTGGTACAGCTCACAGA
 TACATGTTGGCACCAGATGCTCTTGGGCGCGCCAGCAGTACAGGGGTGATGGTCTGTAGTGGATG
 AACCTTGTGAGAGGTGACATATTCAGCCCCATCCGTGAGGCCACAGGCTTCTGGGCTTAATGTGGTGAATG
 GGAATGGCTGGAGCGGACCCAGAGCAGCTGCGTGCCTTGGCGCGGGGTATGGACTCTGTCCAGACCTTC
 TTCGCGTGGATGATGGGCCAAGCCTGGACCAAGCAGTCACTGGTCTGGCCACAGCCCTGTGTACAGGCAT
 CCTTCACTACTCAGCCCCGGCCAGAGCCCTGCCAGTGTATTGTCCAAAGGGCCAGAAGGGGAACCTGG
 AGAGTCCGCTGAGAGGACAGTGGGCTTCTGGCGACCTGGCCTCCCGGGCAGGACCGGTGCTCCCG
 GGCCCCCAGGGGCCCTTGGAAAGTGCCTGCAAGGGCGAGAGGGGCTTCCCTGGAGCAGATGGGCGTC
 CAGGCAGCCCTGGCGCGCGCGGAATCTGGGACCCCTGGAGCCCTGGCCTAAAGGGCTCTCCAGGGTT
 GCCTGGCCCTCGTGGGACCCGGGAGAGCGAGGACCTCGAGGCCCAAGGGGAGCCGGGGGCTCCCGGA
 CAAGTCACTCGGAGGTGAAGGACCTGGGCTTCTTGGGCGGAAAGGGGACCTGGACCATCGGGCCCCCTG
 GACCTCGTGGACCACTGGGGGACCCAGGACCCCGTGGCCCCCAGGGCTTCTTGGAAACAGCCATGAAGGG
 TGACAAAGGCGATCGTGGGGAGCGGGGTCCCCCTGGACCAAGGTGAAGGTGGCATTGCTCTGGGGAGCCT
 GGGCTGGCGGCTTCCCGGAAGCCTTGGACCCCAAGGCCCTTGGCCCCCTTGGAAAGAAAGGAGAAA
 AAGGTGACTCTGAGGATGAGCTCCAGGCCCTCCAGGACAACCTGGGTCTCCGGGTGAGCAGGGCCACG
 GGGACCTCTTGGAGCTATTGGCCCCAAAGGTGACCGGGGCTTCCAGGGCCCCCTGGGTGAGGCTGGAGAG
 AAGGGCAACCTGAGACCCCAAGGCCAGCGGGATCCCGGGGCTGCCAGGGGTGTCTGGACGTCTTGGAG
 CCAAGGTCTCTGAAGGGCCACAGGACCCACTGGCCGCAAGGAGAGAAGGGGAGCCTGGTCCGCCCTGG
 GGACCTGCACTGGTGGGACCTGTCTGTGTGGACCCAAAGGAGAAAAGGGAGATGTGGGGCCCGCTGGG
 CCCAGAGGAGCTACCGGAGTCCAAGGGGAACGGGGCCACCCGGCTTGGTCTTCTTGGAGACCCTGGCC
 CCAAGGTGAGCCTTGGAGACCGGGGTCCCATTTGGCCTTACTGGCAGAGCAGGACCCCAAGGTGACTCAGG
 GCCTCTTGGAGAGAAGGGAGACCTGGGCGGCTGGCCCCCAGGACCTGTGGCCCCGAGGACGAGAT
 GGTGAAGTTGGAGAGAAGGTGACGAGGGTCTCCGGGTGACCCGGGTTTGCCTGGAAAAGCAGGCGAGC
 GTGGCTTCCGGGGGACCTGGAGTTCGGGGGCTGTGGGTGAAAAGGAGACAGGGAGATCTTGGAGA
 GGATGGACGAAATGGCAGCCCTGGATCATCTGGACCCAAAGGTGACCGTGGGGAGCCGGGTCCCCCAGGA
 CCCCCGGGACGGCTGGTAGACACAGGACCTGGAGCCAGAGAGAAGGGAGAGCCTGGGGACCGCGGACAAG
 AGGGTCTCTGAGGGCCCAAGGGTGATCTTGGCTTCCCTGGAGCCCCCTGGGGAAGGGGCATTGAAGGGTT
 TCGGGGACCCCAAGGCCACAGGGGACCCAGGTGTCCGAGGCCACAGCAGAGAAAAGGGTGACCGGGGT
 CCCCCTGGGCTGGATGGCCGGAGCGGACTGGATGGGAAACCAGGAGCCGCTGGGCCCTCTGGGCCGAATG
 GTGCTGCAGGCAAGCTGGGGACCCAGGGAGAGACGGGCTTCCAGGCCTCCGTGGAGAACAGGGCTCCC
 TGGCCCCCTTGGTCCCCCTGGATTACCGGGAAGCCAGGCGAGGATGGCAAACCTGGCCTGAATGGAAAA
 AACGGAGAACCTGGGGACCTTGGAGAAGACGGGAGGAAGGGAGAGAAAGGAGATTACGGCGCCTCTGGGA
 GAGAAGGTCTGTATGGCCCCAAGGGTGAGCGTGGAGCTCCTGGTATCCTTGGACCCAGGGGCTCCAGG
 CCTCCAGGGCCAGTGGGCCCTCTTGGCCAGGGTTTCTTGGTGTCCAGGAGGCACGGGCCCAAGGGT
 GACCGTGGGGAGACTGGATCCAAAGGGGAGCAGGGCTTCCCTGGAGAGCGTGGCTTGCAGGAGAGCCTG
 GAAGTGTGCCGAATGTGGATCGGTTGTGGAACTGCTGGCATCAAGGCATCTGCCCTGCGGGAGATCGT
 GGAGACCTGGGATGAGAGCTCTGGTAGCTTCTGCTGTGCCCCGAACGGCGTCCAGGCCCCAAGGGGGAC
 TCAGGCGAACAGGGCCCCCAGGCAAGGAGGGCCCCATCGGCTTCTTGGAGAACCGGGGTGAAGGGCG
 ACCGTGGAGACCTTGGCCCTCAGGGGCCACCTGGTCTGGCCCTTGGGAGAGGGGGCCCCCGGGCCTTC
 CGGCCTTGGCGGGGAGCCTGGAAAGCCTGGTATTCCTGGGCTTCCAGGCAGGGCTGGGGGTGTGGGAGAG
 GCAGGAAGGCCAGGAGAGAGGGGAGAACGGGAGAGAAAGGAGAACGTGGAGAACAGGGCAGAGATGGCC
 CTCCTGGACTCCTTGAACCCCTGGGCCCCCGGACCCCTGGCCCCAAGGTGTCTGTGGATGAGCCAGG
 TCCTGGACTCTCTGGAGAACAGGGACCCCTGGACTCAAGGGTCTAAGGGGAGCCGGGACGCAATGGT
 GACCAAGGTCCCCAAGGAGACAGGGGTGTGCCAGGCATCAAGGAGACCGGGGAGAGCCTGGACCGAGGG
 GTCAGGACGGCAACCCGGGTCTACCAGGAGAGCGTGGTATGGCTGGGCTGAAGGGAAGCCGGGTCTGCA

GGGTCCAAGAGGCCCCCTGGCCAGTGGGTGGTCATGGAGACCTGGACCACCTGGTGCCCCGGGTCTT GCTGGCCCTGCAGGACCCCAAGGACCTTCTGGCCTGAAGGGGAGCCTGGAGAGACAGGACCTCCAGGAC GGGGCCTGACTGGACCTACTGGAGCTGTGGGACTTCTGGACCCCCCGGCCCTTCAGGCCTGTGGGTCC ACAGGGGTCTCCAGGTTTGCCTGGACAAGTGGGGGAGACAGGGAAGCCGGGAGCCCCAGGTGAGATGGT GCCAGTGGAAAAGATGGAGACAGAGGGAGCCCTGGTGTGCCAGGGTCACAGGTCTGCCTGGCCCTGTCTG GACCTAAAGGAGAACCTGGCCCCACGGGGGCCCTGGACAGGCTGTGGTGGGGTCCCTGGAGCAAAGGG AGAGAAGGGAGCCCCCTGGAGGCCTTGCTGGAGACCTGGTGGGTGAGCCGGGAGCCAAAGGTGACCGAGGA CTGCCAGGGCCGCGAGGCGAGAAGGGTGAAGCTGGCCGTGCAGGGGAGCCCGGAGACCCTGGGGAAGATG GTCAGAAAGGGGCTCCAGGACCCAAAGGTTTCAAGGGTGACCCAGGAGTGGGGTCCCGGGCTCCCTGG GCCTCTGGCCCTCCAGGTGTGAAGGGAGATCTGGGCCTCCCTGGCCTGCCCGGTGCTCCTGGTGTGTTT GGGTTCCTGGGTGAGACAGGCCCTCGAGGAGAGATGGGTGAGCCAGGCCCTAGTGAGAGCGGGGTCTGG CAGGCCCCCAGGGAGAGAAGGAATCCCAGGACCCCTGGGGCCACCTGGACCACCGGGGTGAGTGGGACC ACCTGGGGCTCTTGGACTCAAAGGAGACAAGGGAGACCCTGGAGTAGGGTGCCTGGGCCCCGAGGCGAG CGTGGGAGCCAGGCATCCGGGGTGAAGATGGCCGCCCGGCCAGGAGGGACCCGAGGACTCACGGGGC CCCCCTGGCAGCAGGGGAGAGCGTGGGGAGAAGGGTGATGTTGGGAGTGCAGGACTAAAGGGTGACAAGGG AGACTCAGCTGTGATCTTGGGGCTCCAGGCCACCGGGTGCCAAGGGGGACATGGGTGAACGAGGGCCT CGGGCTTGGATGGTGACAAAGGACCTCGGGGAGACAATGGGGACCTGGTGACAAGGGGAGAGAGGAG AGCCTGGTGACAAGGGCTCAGCCGGGTTGCCAGGACTGCGTGGACTCCTGGGACCCAGGGTCAACCTGG TGCAGCAGGGATCCCTGGTGACCCGGGATCCCAGGAAAGGATGGAGTGCCTGGTATCCGAGGAGAAAA GGAGATGTTGGCTTCATGGGTCCCGGGCTCAAGGGTGAACGGGGAGTGAAGGGAGCCTGTGGCCTTG ATGGAGAGAAGGGAGACAAGGGAGAAGCTGGTCCCCAGGCCGCCCGGGCTGGCAGGACACAAAGGAGA GATGGGGGAGCCTGGTGTGCCGGGCCAGTCGGGGGCCCTGGCAAGGAGGGCCTGATCGGTCCCAAGGGT GACCAGGGCTTTGACGGGCAGCCAGGCCCAAGGGTGACAGGGCGAGAAAGGGGAGCGGGGAACCCAG GAATTGGGGCTTCCAGGCCCCAGTGGAAATGATGGCTCTGCTGGTCCCCAGGGCCACCTGGCAGTGT TGGTCCCAGAGGCCCCGAAGGACTTCAGGGCCAGAAGGGTGAGCGAGGTCCCCCGGAGAGAGAGTGGTG GGGGCTCCTGGGGTCCCTGGAGCTCCTGGCGAGAGAGGGGAGCAGGGGCGGCCAGGGCCTGCCGTCTC GAGGCGAGAAGGGAGAAGCTGCACTGACGGAGGATGACATCCGGGGCTTGTGCGCCAAGAGATGAGTCA GCACTGTGCCTGCCAGGGCCAGTTCATCGCATCTGGATCAGGACCCCTCCCTAGTTATGCTGCAGACACT GCCGGCTCCAGCTCCATGCTGTGCTGTGCTCCGCGTCTCTCATGCAAGAGGAGGAAGAGCGGGTACCCC CTGAGGATGATGAGTACTCTGAATACTCCGAGTATTCTGTGGAGGAGTACCAGGACCCCTGAAGCTCCTTG GGATAGTGTATGACCCCTGTTCCCTGCCACTGGATGAGGGCTCCTGCACTGCCTACACCTGCGCTGGTAC CATCGGGCTGTGACAGGCAGCACAGAGGCCGTGCACCCCTTTGTCTATGTTGGCTGTGGAGGGAATGCCA ACCGTTTGGGACCCGTGAGGCCTGCGAGCGCGCTGCCACCCCGGGTGGTCCAGAGCCAGGGGACAGG TACTGCCAGGACTGAGGCCAGATAATGAGCTGAGATTGAGCATCCCTGGAGGAGTGGGGTCTCAGC AGAACCCCACTGTCCCTCCCTTGGTGCTAGAGGCTGTGTGCACGTGAGCGTGCCTGTGCACGTCCGT ATTTGAGTACTTGGTCCCGTGGGTCTAGCCTTCCCCCTGTGGACAAACCCCAATTGTGGCTCCTGCCA CCCTGGCAGATGACTCACTGTGGGGGGTGGCTGTGGGCAGTGAGCGGATGTGACTGGCGTCTGACCCGC CCCTTGACCCAAGCCTGTGATGACATGGTGTGATTCTGGGGGGCATTAAAGCTGCTGTTTTAAAGGC (SEQ
ID NO: 17)
Translated protein sequence
MTLRLLVAALCAGILAEAPRVRAQHRERVCTRLYAADIVFLLD GSSSIGRSNFRVRSFLEGLVLPFSGAASAQGVRFATVQYSDDPRTIEFLDALGSGGD VIRAIRELSYKGNTRTGAAILHVADHVFLPQLARPGVPKVCILITDGKSQDLVDTAA QRLKGQGVKLFVAVGIKNADPEELKRVASQPTSDFFFFVNDFSILRTLPLVSRVCTT AGGVPTTRPPDDSTSAPRDLVLSEPSQSLRVQWIAASGPVTGYKVQYTPLTGLGQPL PSEQEVNVPAGETSVRLRGLRPLTEYQVTIVIALYANSIGEAVSGTARTTALEGPFLT IQNTTAHSLLVAVRSVPGATGYRVITWRVLSGGPTQQQELGPGQGSVLLRDLEPGTDYE VTVSTLFRSGVPATSLMARTDASVEQTLRPVILGPTSILLSWNLVPEARGYRLEWRR ETGLEPPQKVVLPSDVTRYQLDGLQPGTEYRLTLYTLLEGHEVATPATVVP TGPELPV SPVTDLQATELPGQVRVRSWSPVPGATQYRIIVRSTQGVERTLVLPQSQTAFDLDVQ AGLSYTVRVRSARVGPREGSASVLTVRREPETPLAVPGLRVVVS DATRVVAVGVPVPGA SGFRISWSTGSGPESSQTLPPDSTATDITGLQPGTTYQVAVSVLRGREGGPAAVIVAR TDPLGPVRTVHVTQASSSSVTITWTRVPGATGYRVSWHSAHGPEKSQLVSGEATVAEL DGLEPDTEYTVHRAHVAGVDGPPASVVVRIAPEPVGRVSRLQILNASSDVLRIITWVG VTGATAYRLAWGRSEGGPMRHQILPGNTDSAEIRGLEGGVSYSVRV TALVGDREGTPV SIVVTPPEAPPALGTLHVVRGEHSLRLRWEVPVRAQGFLHWHQPEGGQEQSRVLGP ELSSYHLDGLEPATQYRVRLSVLGPAGEGPSAEVTARTESPRVPSIELRVVDTSIDSV TLAWTPVSRASSYILSWRPLRGPGQEVPGSPQTLPGISSQVRVTGLEPGVSYIFSLTP VLDGVRGPEASVTQTPVCPRLADVFLPHATQDNAHRAEATRVLRLV LALGPLGP QAVQVGLLSYSHRPSPLFPLNGSHDLGIILQIRIDMPYMDPSGNNLGTAVVTAHRYML

APDAPGRRQHVPGVMLLVDEPLRGDIFSPIREAQASGLNVMLGMAGADPEQLRRLA
 PGMDSVQITFFAVDDGPSLDQAVSGLATALCQASFTTQPRPEPCPVYCPKGQKGEPPGEM
 GLRGQVGPDPGLPGRGTGAPGPQGGPSATAKGERGFPGADGRPGSPGRAGNPGTPG
 APGLKGSPLPGPRGDPGERGPRGPKGEPGAPGQVIGGEGPLPGRKGDGPGSPGPPGP
 RGPLGDPGPRGPPGLPGTAMKGDGDRGERGPPGPGEGLIAPGEPGLPGLPGSPGPQG
 PVGPPGKKGEKGDSEAGPLPGQPGSPGEGQPRGPPGAIGPKGDRGFPGLGEAGEK
 GERGPPGPAGSRGLPGVAGRPGAKGPEGPPGPTGRQGEKGEPRGPDPAVVGPAVAGP
 KGEKGDVGPAGPRGATGVQGERGPPGLVLPDGPDKGDPGDRGPIGLTGRAGPPGDSG
 PPGEKGDGPRGPPGPGVGPGRDGEVGEKGEDEGPPDGLPGKAGERGLRGAPGVRGP
 VGEKGDQGDGPDGDRNGSPGSSGPKGDRGEPGPPGPPGRLVDTGPGAREKGEPRGQ
 EGPRGPKGDGPLPGAPGERGIEGFRGPPGPGQDGPVGRPAGEKDRGPPGLDGRSGLD
 GKPGAAGPSGNGAAGKAGDPGRDGLPGLRGEQGLPGPSGPPGLPGKPGEDGKPLNG
 KNGEPGDPGEDGRKGEKGDSDGASGREGRDGPKEGAPGILPGQGGPGLPGVGPFGQ
 GFPGVPGGTGPKGDRGETGSKGEQGLPGERGLRGEPSVNPVDRLLLETAGIKASALRE
 IVETWDESSGFLPVERRRGPKGDSGEQPPGKEGPIGFPERGLKGDGDPGPPQGP
 PGLALGERGPPGPGSLAGEPGKPGIPGLPGRAGGVGEAGRPERGERGEKGERGEGGR
 DGPPGLPGTGPFPGPPGPKVSVDEPGPLSGEQGPPGLKGAKEPGSNGDQGPKGDRG
 VPGIKGDRGEPGPRGQDGNPGLPGERGMAGPEGKPLGQGRGPPGPPVGGHGDGPPGA
 PGLAGPAGPQGPSGLKGEPPGETGPPGRGLTGPTGAVGLPGPPGPSGLVGFQGSPLPG
 QVGETGKPGAPGRDASGKDGDRGSPGVPGSPGLPGVGPKEGPGPTGAPGQAVVGLP
 GAKGEKGAAGGLAGDLVGEPAKGDRLPGPRGEKGEAGRAGEPGDPGEDGQKGAAPGP
 KGFGKDPGVGVPGSPGPPGPPGVKDLGLPLPGAPGVVGFPGQTGPRGEMGQPPGSG
 ERGLAGPPREGIPGLPGLPPGPPGSGVSGPPGASGLKGDGDPVGLPGPRGERGEPGR
 GEDGRPGQEGPRGLTGPPGSRGERGEKGDVGSAGLKGDKGDSAVILGPPGPRGAAGDM
 GERGPRGLDGDGKPRGNDGPDGDKSGKEPGDKGSAGLPLGLRGLGPPQGPAGAIPG
 DPGSPGKDGVPGRGEKGDVGFMPGRGLKGERGVKGACGLDGEKGDKEAGPPGRPGL
 AGHKGEMGEPGVPQGSGAPGKEGLIGPKGDRGFDGQPGPKGDQGEKGERGTPGIGGFP
 GPSGNDGSAGPPGPPGSGVGRGPEGLQGGQKGERGPPGERVVGAPGVGAPGERGEQGR
 GGPAGPRGEKGEAALTEDDIRGFVRQEMSHCACQGFIIASGSRPLPSYAADTAGSQL
 HAVPVLRVSHAEERVPPEDEYSEYSEYSVEEYQDEAPWDSDDPCSLPLDEGSCT
 AYTLRWYHRAVTGSTEAHPFVYGGCGGNANRFGTREAERRCPPRVVQSGTGTAQD (SEQ ID NO: 18)

CYP4F3	4051	NM_000896	Homo sapiens cytochrome P450, family 4, subfamily F, polypeptide 3 (CYP4F3), mRNA
--------	------	-----------	---

mRNA Sequence

AGAAGAAGGGGAGAGGAGGTTGTGTGGGACAAGGTGCTCCTGACAGAAGGATGCCACAGCTGAGCCTGTC
 CTCGCTGGGCCCTTTGGCCAATGGCAGCATCCCCGTGGCTGCTCCTGCTGCTGGTTGGGGCCTCCTGGCTC
 CTGGCCCCCATCCTGGCCTGGACCTATACCTTCTATGACAAGTCTGCCGCTCCGGTGTITCCCGCAAC
 CCCCAGAACCGAATTGGTTCTTGGGTACCTGGGCTGATTACAGCTCGGAGGAGGCTCTCTATACAC
 ACAAAGCCTGGCATGCACCTTCGGTGATATGTGCTGCTGGTGGGTGGGGCCTGGCACGCAATCGTCCGC
 ATCTTCCACCCACCTACATCAAGCCTGTGCTCTTTGCTCCAGCTGCCATTGTACCAAAGGACAAGGTCT
 TCTACAGCTTCTGAAGCCTGGCTGGGGATGGGCTCCTGCTGAGTGTGGTGAAGAGTGGAGCCGCCA
 CCGTCGGATGCTGACGCTGCTTCCATTTCAACATCCTGAAGCCTATATGAAGATTTTCAATGAGAGT
 GTGAACATCATGCATGCCAAGTGGCAGCTCCTGGCCTCAGAGGGTAGTGCCCGTCTGGACATGTTTGAGC
 ACATCAGCCTCATGACCTTGGACAGTCTGCAGAAATGTGTCTTCAGCTTTGACAGCCATTGCCAGGAGAA
 GCCCATGTAATATATATGGCGCCATCTGGAGCTCAGTGCCCTTGTGACAAAAAGACACAGCAGATCCTC
 CTGTACATAGACTTCTGTATTATCTACCCCTGATGGGCAGCGTTTCCGAGGGCCTGCCGCTGGTGC
 ACGACTTCACAGATGCCGTATCCAGGAGCGGCGCCGACCCCTCCCTAGCCAGGGTGTGTGACTTCTC
 CCAAGCCAAGGCCAAATCCAAGACTTTGACTTTCATTGATGTACTCCTGCTGAGCAAGGATGAAGATGGG
 AAGAAGTTGTCCGATGAGGACATAAGAGCAGAAGCTGACACCTTTATGTTGAGGGCCATGACACCACAG
 CCAGTGGTCTCTCCTGGGTCTGTACCACCTTGCAAAGCACCCGGAATACCAGGAGCGCTGTCGGCAGGA
 GGTGCAAGAGCTTCTGAAGGACCGTGAGCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCCCTTC
 CTGACCATGTGCATTAAAGGAGAGCCTGAGGCTGCATCCCCAGTCCCTGCCGTCTCTCGCTGCTGCACCC
 AAGACATTGTGCTCCAGACGGCCGGGTCTATCCCAAGGCATTATCTGCCTCATCAGTGTITTTGGAAC
 CCATACAACCCAGCCGTGTGGCCGACCTGAGGTCTATGACCCCTTTGCTTTGACCCAAAGAACATC
 AAGGAGAGGTACCTCTGGCTTTTATCCCTTCTCAGCAGGGCCAGGAAGTGCATCGGGCAGGCGTTTCG
 CGATGGCGGAGATGAAGGTGGTCTTGGGGCTCACGCTGCTGCGCTTCCGCGTCTCCTGACACACCGA
 GCCCCGAGGAAGCCGAGCTGGTCTGCGCGCAGAGGGCGGACTTTGGCTGCGGGTGGAGCCCTGAGC
 TGAGTTCTGCAGAGACCCACTCTGACCCCACTAAATGACCCCTGATTATCAAAAGTGAAGGCTAGAAAT

TACCCTAAGACCCTGTTCCACAGTCCTGTATTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTG TTCAAACAGAAAGACGCTTGTGCGTGAAATGTTTCATGGCAGCCCTATTACAGTAGCCAAACGATGAAAAC AACCCCAAGCTATATATTACCAGATGAAAGGATAAAACAAAATATGGTCCATCCATACAATGGAGTATTAC ACAGCCATAAAAAGGAATGAAGCAGTGATCCCCACTACACTGTGGATGAACCTGAATGCATGATACTGA ATGAAAGACATCAGATGCAAAAGGTCACATAGTGTACTGTCTTTTATATGAAATTTCCAGAACAGGCCA ATCTGAAGAGATGTATAGTGGATTGGTGGCTTTACGACAGCTGTGGGGAGGTGGGACTGAGGAGCGACTGC TAATCAGGATGGGGTTTCTCTCGGGATGGTGAAAATGTTCCGGACCTAGATAGTGATGAAGGTAGCACG ACACTGTGAGTGCCTAAATGCTATTGAATTGGACACTTTAGAATGGTTGAAATAGTGATTTTTATGTGA ATTCTACCTAAACATGCTATTACAGCTCATATATACTTTTTCCATCTGGATTCTTCACAAAGAATATGT TGTGAGCATCTTTCCATGATATTAATCATCTTAGGAAACATTATTTTGTGTTCTTCAAAATGTGCATGT TAAGTATTCAAATCAGTCTTAAATTTTTAAAAATAATGTAATTTAGAAAATAATTTAAAGGTTTTGTTT CAGTTTGTAAGATTTCTTTTCTGGCACTTTAATGGCTTGAGGTATCATTATCAGTTACAAATTGAGTTAT TCCTCATCAATGACTTTTGGAGTAGAGATTTTATTTTATAGCAATAGATGCACAGATATTCCTGTAAAG ATACAGGTGTGGTTAGACACTTTTCTAGAACAGGCATGCCCTGCAAACCTCCACAGACACTGACTGTTTTT GTCCTATTAAGAAGTAGACCACTGAGAAGGGAGAAGGTGACATTTTAGCTTTCCAGGTAAAGTGGTTT TCATCCTCACACCAATTTTATGGACTGGACGTTAACTCTCTTGTCTCAAGGTCACCTGAGTGGAAGAGTG GGGATAAATCTGGTTCTGTTTGGCATCAGAGGCCATGACTTTTCTACCACAGAAGTAATTTTCAAAGTAA GTCTCTGCCCTAGGCACATCAGATCACCTGGGGACCACTCCAGAGTGAGTAGACAAGACTTTGACAGGGG TGCTAATTTTTTTTTTTTGGAGATGGAGTCTCGCTCTGTGCCCA (SEQ ID NO: 19)			
Translated protein sequence			
MPQLSLSSGLWPMMAASPWLLLLLVGASWLLARILAWTYTFYDN CCRLRCFPQPKNRWFGLHGLIHSSEGLLYTQSLACTFGDMCCWVGPWHAIVRIF HPTYIKPVLFAPAIIVPKDKVFSFLKPWLGDGLLLSAGEKWSRHRRLTPAFHFNIL KPYMKIFNESVNIMHAKWQLLASEGSARLDMFEHISLMTLDSLQKCVSFDSSHQKEKP SEYIAAILELSALVTKRHQQIILYIDFLYYLTPDGQRFRACRLVHDFDVAIQERRR TLPSQGVDDFLQAKAKSKTLDIDVLLLSKDEDDGKKLSDEDIRAEADTFMEGHDTTA SGLSWVLYHLAKHPEYQERCRQEVQELLKDRPKIEWDDLAQLPFLTMCIKESRLH PPVPAVSRCCQTQDIVLPDGRVIPKGIICLISVFGTHHNPVWPDPEVYDFFRFPKNI KERSPLAFIPFSAGPRNCIGQAFAMAEMKVVLGLTLLRFRVLPDHTEPRRKPELVLRA EGGLWLRVEPLS (SEQ ID NO: 20)			
DYSF	8291	NM_003494	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF), transcript variant 8, mRNA
mRNA Sequence			
GCGGCCGCCGCCAGCCAGGTGCAAAATGCCGTGTCAATTGGGAGACTCCGCAGCCGGAGCATTAGATTAC AGCTCGACGGAGCTCGGGAAGGGCGGGGGGTGGAAGATGAGCAGAAGCCCTGTTCTCGGAACGCCGG CTGACAAGCGGGGTGAGCGCAGCCGGGGCGGGGACCCAGCCTAGCCCACTGGAGCAGCCGGGGGTGGCCC GTTCCCTTTTAAAGAGCAACTGCTCTAAGCCAGGAGCCAGAGATTCGAGCCGGCCTCGCCCAAGCCAGCCT CTCCAGCGAGGGGACCCACAAGCGGCGCCTCGGCCCTCCCGACCTTTCCGAGCCCTCTTTGCGCCCTGGG CGCAGCGGGGCCCTACACGCGCCAAGCATGCTGAGGGTCTTCATCCTCTATGCCGAGAACGTCCACACACC CGACACCGACATCAGCGATGCTTACTGCTCCGCGGTGTTTGAGGGGTGAAGAAGAGAACCAAGTCATC AAGAACAGCGTGAACCTGTATGGAATGAGGGATTGTAATGGGACCTCAAGGGCATCCCCCTGGACCAGG GCTCTGAGCTTCATGTGGTGGTCAAAGACCATGAGACGATGGGGAGGAACAGGTTCTTGGGGGAAGCCAA GGTCCCACTCCGAGAGGTCTCGCCACCCCTAGTCTGTCCGCCAGCTTCAATGCCCCCTGCTGGACACC AAGAAGCAGCCACAGGGCCTCGCTGGTCTGCAAGGTGTCTACACACCGCTGCTGGAGCTGTGCCCC TGTTCCCGCCCCCTACTCCTCTGGAGCCCTCCCGACTCTGCTGACCTGGATGTAGTGGCAGACACAGG AGGAGAGGAAGACACAGAGGACCAGGGACTCACTGAGATGAGGCGGAGCCATTCTGGATCAAAGCGGA GGCCCGGGGCTCCCACCACCCCAAGGAACTACCTTCACGTCTCCGCCCACTACCCGGGATCAAAA GAAAGCGAAGTGCGCCTACATCTAGAAAGCTGTGTCAGACAAACCGAGGATTCCAGATCAGGGTCCA GGTGATCAGGGGCGCCAGCTGCCGGGGGTGAACATCAAGCCTGTGGTCAAGGTTACCGCTGCAGGGCAG ACCAAGCGGACGCGGATCCACAAGGGAACAGCCCACTCTTCAATGAGACTCTTTCTTCAACTTGTTTG ACTCTCTTGGGGAGCTGTTTGATGAGCCATCTTTATCACGGTGGTAGACTCTCGTTCTCTCAGGACAGA TGCTCTCTCGGGGAGTTCCGGATGGACGTGGGCACCATTTACAGAGAGCCCCGGCACGCCTATCTCAGG AAGTGGCTGTCTCTCAGACCTGATGACTTCTCTGCTGGGGCCAGAGGCTACCTGAAAACAAGCCTTT GTGTGCTGGGGCTGGGGACGAAGCGCCTCTGGAGAGAAAAGACCCCTCTGAAGACAAGGAGGACATTGA AAGCAACCTGCTCCGGCCACAGGCGTAGCCCTGCGAGGAGCCCACTTCTGCCTGAAGGTCTTCGGGGCC GAGGACTTGCCGCAGATGGACGATGCCGTGATGGACAACGTGAAACAGATCTTTGGCTTCGAGAGTAACA			

AGAAGAACTTGGTGGACCCCTTTGTGGAGGTCAGCTTTTGGGGGAAAAATGCTGTGCAGCAAGATCTTGGA
 GAAGACGGCCAAACCTCAGTGAACAGACAATCACACTGCCTGCCATGTTTCCCTCCATGTGCGAAAAA
 ATGAGGATTTCGTATCATAGACTGGGACCGCTGACTCACAATGACATCGTGGCTACCACCTACCTGAGTA
 TGTGAAAAATCTCTGCCCCCTGGAGGAGAAATAGAAGAGGAGCCTGCAGGTGCTGTCAAGCCTTCGAAAGC
 CTCAGACTTGGATGACTACCTGGGCTTCCCTCCCCACTTTTGGGCCCTGCTACATCAACCTCTATGGCAGT
 CCCAGAGAGTTTACAGGCTTCCCAGACCCCTACACAGAGCTCAACACAGGCAAGGGGGAAGGTGTGGCTT
 ATCGTGGCCGGCTTCTGCTCTCCCTGGAGACCAAGCTGGTGGAGCACAGTGAACAGAAGGTGGAGGACCT
 TCTTGGGATGACATCCTCCGGGTGGAGAAGTACCTTAGGAGGCGCAAGTACTCCCTGTTTGGCGCCTTC
 TACTCAGCCACCATGCTGCAGGATGTGGATGATGCCATCCAGTTTGGGTGAGCATCGGGAACCTACGGGA
 ACAAGTTCGACATGACCTGCCTGCCGTGGCTCCACCCTCAGTACAGCCGTGCAGTCTTTGACGGGTG
 CCACTACTACTACCTACCTTGGGGTAACGTGAAACCTGTGGTGGTGTGTCATCCTACTGGGAGGACATC
 AGCCATAGAATCGAGACTCAGAACCAGCTGCTTGGGATTGTGACCGGCTGGAAGCTGGCCTGGAGCAGG
 TCCACCTGGCCCTGAAGGCGCAGTGCTCCACGGAGGACGTGGACTCGCTGGTGGCTCAGCTGACGGATGA
 GCTCATCGCAGGCTGCAGCCAGCCTCTGGGTGACATCCATGAGACACCTCTGCCACCACCTGGACCAG
 TACCTGTACCAGCTGCGCACCCATCACTGAGCCAAATCACTGAGGCTGCCCTGGCCCTGAAGCTCGGCC
 ACAGTGAGCTCCCTGCAGCTCTGGAGCAGGCGGAGGACTGGCTCCTGCGTCTGCGTGGCCCTGGCAGAGGA
 GCCCCAGAACAGCCTGCCGACATCGTCATCTGGATGCTGCAGGGAGACAAGCGTGTGGCATAACAGCGG
 GTGCCCCGCCACCAAGTCTCTTCTCCCGCGGGGTGCCAACTACTGTGGCAAGAATTGTGGGAAGCTAC
 AGACAATCTTTCTGAAATATCCGATGGAGAAGGTGCTGGCGCCCGGATGCCAGTGCAGATACGGGTCAA
 GCTGTGGTTTGGGCTCTCAGTGGATGAGAAGGAGTTCAACCAGTTTGTGAGGGGAAGCTGTCTGTCTTT
 GCTGAACCTATGAGAACGAGACTAAGTTGGCCCTTGTGGGAACCTGGGGCACAACGGGCCCTCACCTACC
 CCAAGTTTCTGACGTACCGGGCAAGCTCAAGCTACCCAGGACAGCTTCCGCCCTCGGCCGGCTGGAC
 CTGGGCTGGAGATTGGTTCTGTGTCCGGAGAAGACTCTGCTCCATGACATGGACGCCGGTCACTGAGC
 TTCGTGGAAGAGGTGTTTGAAGACAGACCCGGCTTCCCGAGGGCCAGTGGATCTACATGAGTGACAACT
 ACACCGATGTGAACGGGGAGAAGGTGCTTCCCAAGGATGACATTGAGTGCCCACTGGGCTGGAAGTGGGA
 AGATGAGGAATGTCCACAGACCTCAACCGGGCTGTTCGATGAGCAAGGCTGGGAGTATAGCATACCATC
 CCCCCGAGCGGAAGCCGAAGCACTGGGTCCCTGCTGAGAAGATGTACTACACACACCGACGGCGGGCGCT
 GGGTGGCCCTGCGCAGGAGGGATCTCAGCCAAATGGAAGCACTGAAAAGGCACAGGCAAGGCGGAGGGCGGA
 GGGCAGGGCTGGGAGTACGCCCTCTCTTTTGGCTGGAAGTTCCACCTCGAGTACCGCAAGACAGATGCC
 TTCCGCCCGCCGCTGGCGCCGTGCGATGGAGCCACTGGAGAAGACGGGGCTGCGCTGTGTGGCC
 TTGAGGGGGCCCTGGCGGGCTGTGATGACAAGAGTGAAGATTCCATGTCCGTCTCCACCTTGAGCTT
 CGGTGTGAACAGACCCACGATTTCTGCTATTCGACTATGGGAACCGCTACCATCTACGCTGTCTACATG
 TACCAGGCGCGGGACCTGGCTGCGATGGACAAGGACTCTTTTCTGATCCCTATGCCATCGTCTCCTTCC
 TGCACCAGAGCCAGAAGACGGTGGTGGTGAAGAACACCCCTTAACCCACCTGGGACCAGACGCTCATCTT
 CTACGAGATCGAGATCTTTGGCGAGCCGGCCACAGTTGCTGAGCAACCGCCAGCATTGTGGTGGAGCTG
 TACGACCATGACACTTATGGTGCAGACGAGTTTATGGGTGCTGCTGCTGTCAACCGAGTCTGGAACGGA
 TGCCACGGCTGGCCCTGGTTCCCACTGACGAGGGGCGAGCCAGCCGTCGGGGGAGCTGCGCTCTTTTGA
 GCTCATCCAGAGAGAGAAGCCGGCCATCCACCATATTCTGGTTTTGAGGTGCAGGAGACATCAAGGATC
 CTGGATGAGTCTGAGGACACAGACCTGCCCTACCCACCACCCAGAGGGAGGCCAACATCTACATGGTTT
 CTCAGAACATCAAGCCAGCGCTCCAGCGTACCGCCATCGAGATCCTGGCATGGGGCTCGCGAACATGAA
 GAGTTACCAGCTGGCCAACATCTCCTCCCCAGCCTCGTGGTAGAGTGTGGGGCCAGACGGTGCAGTCC
 TGTGTCTACAGGAACCTCCGGAAGAACCCCACTTTGACATCTGCACCCCTCTTCATGGAAGTGATGTCTG
 CCAGGGAGGAGCTTACTGCCCCCATCACCGTCAAGGTATCGATAACCGCCAGTTTGGCCCGCGGCC
 TGTGGTGGGCCAGTGTACCATCCGCTCCCTGGAGAGCTTCTGTGTGACCCCTACTCGCGGAGAGTCCA
 TCCCCACAGGGTGGCCAGACGATGTGAGCCTACTCAGTCTGGGGAAGACGTGCTCATCGACATTGATG
 ACAAGGAGCCCTCATCCCCATCCAGGAGGAAGAGTTTCATCGATTGGTGGAGCAAATCTTTGGCTCCAT
 AGGGGAGAGGGAAAAGTGGCGCTCCTACCTGGAGAAGGATTTTGACACCTGAAGGTCTATGACACACAG
 CTGGAGAAATGTGGAGGCCTTTGAGGGCTGTCTGACTTTTGTAAACCTTCAAGCTGTACCGGGGCAAGA
 CGCAGGAGGAGACAGAAGATCCATCTGTGATTGGTGAATTAAGGGCCTCTTCAAAATTTATCCCTCCC
 AGAAGACCCAGCCATCCCCATGCCCCAAGACAGTTCCACCAGCTGGCCGCCAGGGACCCAGGAGTGTG
 TTGGTCCGTATCTACATTGTCCGAGCATTTGGCCTGCAGCCCAAGGACCCCAATGGAAGGTGTGATCCTT
 ACATCAAGATCTCCATAGGGAAGAAATCAGTGAGTGACCAGGATAACTACATCCCCTGCACGCTGGAGCC
 CGTATTTGGAAGATGTTTCGAGCTGACCTGCACCTCTGCCCTGGAGAAGGACCTAAAGATCACTCTCTAT
 GACTATGACCTCCTCTCAAGGACGAAAAGATCGGTGAGACGGTCTGTCGACCTGGAGAACAGGCTGTCTGT
 CCAAGTTTGGGGCTCGCTGTGGACTCCACAGACCTACTGTGTCTCTGGACCGAACCAAGTGGCGGGACCA
 GCTCCGCCCTCCAGCTCCTCCACCTCTTCTGCCAGCAGCATAGAGTCAAGGCACCTGTGTACCGGACA
 GACCGTGTAAATGTTTCAGGATAAAGAAATATTCATTGAAGAGATAGAGGCTGGCAGGATCCCAAAACCCAC
 ACCTGGGGCCAGTGGAGGAGCGTCTGGCTCTGCTGTGCTTCAGCAGCAGGGCCTGGTCCCGGAGCAGT
 GGAGTCCGGCCCTCTACAGCCCCCTGCAGCCAGACATCGAGCAGGGGAAGCTGCAGATGTGGGTGCGAC
 CTATTTCCGAAGGCCCTGGGGCGGCTGGACCTCCCTTCAACATCACCCACCGGAGAGCCAGAAGGTTTT
 TCCTGCGTTGTATTATCTGGAATACCAGAGATGTGATCTGGATGACCTGAGCCTCACGGGGGAGAAGAT

GAGCGACATTATGTGAAAGGTTGGATGATTGGCTTTGAAGAACACAAGCAAAAGACAGACGTGCATTAT
CGTTCCTCGGGAGGTGAAGGCAACTTCAACTGGAGGTTCATTTTCCCTTCGACTACCTGCCAGCTGAGC
AAGTCTGTACCATTGCCAAGAAGGATGCCTTC TGGAGGCTGGACAAGACTGAGAGCAAAATCCAGCACG
AGTGGTGTTCCAGATCTGGGACAATGACAAGTTCTCCTTTGATGATTTTCTGGGCTCCCTGCAGCTCGAT
CTCAACCGCATGCCCAAGCCAGCAAGACAGCCAAAGAAGTGCTCCTTGGACCAGCTGGATGATGCTTTTCC
ACCCAGAATGGTTTTGTGTCCCTTTTTGAGCAGAAAACAGTGAAGGGCTGGTGGCCCTGTGTAGCAGAAGA
GGGTGAGAAGAAAATACTGCGCGGCAGCTGGAAATGACCTTGGAGATTTGTAGCAGAGAGTGAAGCATGAG
GAGCGCCTGCTGCCAGGGCCGGGATGAGCCCAACATGAACCTTAAGCTTGAGGACCCAAGCGCCCCG
ACACCTCCTTCTGTGGTTTACCTCCCCATACAAGACCATGAAGTTCATCCTGTGGCGGCGTTTCCGGTG
GGCCATCATCCTCTTCATCATCCTCTTCATCCTGCTGCTGTTTCTGGCCATCTTCATCTACGCCCTCCCCG
AACTATGCTGCCATGAAGCTGGTGAAGCCCTTCAGCTGAGGACTCTCCTGCCCTGTAGAAGGGGCCGTGG
GGTCCCTCCAGCATGGGACTGGCCTGCCTCCTCCGCCAGCTCGGCGAGCTCCTCCAGACCTCCTAGGC
CTGATTGTCCTGCCAGGGTGGGCAGACAGACAGATGGACCGGCCACACTCCCAGAGTTGCTAACATGGA
GCTCTGAGATCACCCACTTCCATCATTTCTTCTCCCCCAACCAACGCTTTTTTGGATCAGCTCAGAC
ATATTTTCAGTATAAAACAGTTGGAACCACAAAAAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO: 21)

Translated protein sequence	
1	MAKQK
2	MAKQK
3	MAKQK
4	MAKQK
5	MAKQK
6	MAKQK
7	MAKQK
8	MAKQK
9	MAKQK
10	MAKQK
11	MAKQK
12	MAKQK
13	MAKQK
14	MAKQK
15	MAKQK
16	MAKQK
17	MAKQK
18	MAKQK
19	MAKQK
20	MAKQK
21	MAKQK
22	MAKQK
23	MAKQK
24	MAKQK
25	MAKQK
26	MAKQK
27	MAKQK
28	MAKQK
29	MAKQK
30	MAKQK
31	MAKQK
32	MAKQK
33	MAKQK
34	MAKQK
35	MAKQK
36	MAKQK
37	MAKQK
38	MAKQK
39	MAKQK
40	MAKQK
41	MAKQK
42	MAKQK
43	MAKQK
44	MAKQK
45	MAKQK
46	MAKQK
47	MAKQK
48	MAKQK
49	MAKQK
50	MAKQK
51	MAKQK
52	MAKQK
53	MAKQK
54	MAKQK
55	MAKQK
56	MAKQK
57	MAKQK
58	MAKQK
59	MAKQK
60	MAKQK
61	MAKQK
62	MAKQK
63	MAKQK
64	MAKQK
65	MAKQK
66	MAKQK
67	MAKQK
68	MAKQK
69	MAKQK
70	MAKQK
71	MAKQK
72	MAKQK
73	MAKQK
74	MAKQK
75	MAKQK
76	MAKQK
77	MAKQK
78	MAKQK
79	MAKQK
80	MAKQK
81	MAKQK
82	MAKQK
83	MAKQK
84	MAKQK
85	MAKQK
86	MAKQK
87	MAKQK
88	MAKQK
89	MAKQK
90	MAKQK
91	MAKQK
92	MAKQK
93	MAKQK
94	MAKQK
95	MAKQK
96	MAKQK
97	MAKQK
98	MAKQK
99	MAKQK
100	MAKQK

MLRVFILYAENVHTPTDITDISDAYCSAVFAGVKKRTKVIKNSVNP
VWNEGFEDWLKGIPLDQGSLEHVVKDHETMGRNRLGLEAKVPLREVLATPPLSASFN
APLLDTKKQPTGASLVLQVSYTPLPGAVPLFPPTPLEPSPTLPDLVDVADTGGEEDT
EDQGLTGDEAEPLDQSGGPGAPTTPRKLPSRPPPHYPGIKRKRSAPTSRLKLLSDKPQ
DFQIRVQVIEGRQLPGVNIKPVVKVTAGQTKRTRIHKNSPLFNELTLFNLFDSPGE
LFDEPIFITVVDLSRLRTDALLGEFRMDVGTIYREPRHAYLRKWLLLSDDPDDFSAGAR
GYLKTSLCVLPGPDEAPLERKDPSEDKEDIESNLLRPTGVALRGAHFCLKVFRADLP
QMDDAVMDNVKQIFGFESNKKNLVDPPFEVSFAGKMLCSKILEKTANPQWNQNTLPA
MFPSPCEKMRIRIIDWDRLTHNDIVATTYLSMSKISAPGGEIEEEPAGAVKPSKASDL
DDYLGFLPTFGPCYNLYGSPREFTGFPDPYTELNTGKGEGVAYRGRLLLLSLETKLVE
HSEQKVEDLPADDILRVEKYLRRRKYSLFAAFYSATMLQDQVDDAIQFEVSIIGNYGNKF
DMTCPLPLASTTQYSRAVFDGCHYYLPWGNVKKPVVVLSSYWEDISHRIETQONLLGIA
DRLEAGLEQVHLALKAQCSTEDVDSLVAQLTDELIAGCSQPLGDIHETPSATHLDQYL
YQLRTHHLSQITAAALAKLGHSELPAALEQAEDWLLRLRLALAEPPQNSLPDIIVWML
QGDKRVAYQRPVAHQVLFSSRGANYCGKNCGLQITFLKYPMEKVPGARMPVQIRVKL
WFGLSVDEKEFNQFAEGKLSVFAETIYENETKLALVGNWGTGLTYPKFSDVTGKIKLP
KDSFRPSAGWTWAGDWFVCPKLTLLHDM DAGHLSFVEEVFENQTRLPGGQWLYMSDNY
TDVNGEKVLPKDDIECPLGWKWEDEEWSLDLNRVADDEQGWESITIPPERKPKHWVPA
EKMYTHRRRRWRVRLRRRDLQSOMEALKRHRQAEAEGEWEYASLFGWKFHLEYKRTDA
FRRRWRRRMEPLEKTGPAAVFALEGALGGVMDKSEDSMSVSTLSFGVNRPTISCIF
DYGNYHLRCMYQARDLAAMDKDSFSDPYAIVSFLHQSQKTVVVKNLTNPWDQTLI
FYEIEIFGEPATVAEQPPSIVVELYDHDITYGADEFMGRICQPSLERMPRLAWFPLTR
GSQPSGELLASFELIQREKPAIHHPGFVEQETSRILDESEDITLPIPPPQREANIYM
VPQNIKPALQRTAIEILAWGLRNMKSYQLANISSPSLVVECGGQTVQSCVIRNLRKNP
NFDICTLFMEVMLPREELYCPPITVKVIDNRQFGRRPVVGQCTIRSLESFLCDPYSAE
SPSPQGGPDDVSLSPGEDVLIDIDDKLEPLIQEEEFIDWWSKFFASIGEREKCGSY
LEKDEDTLKVYDTQLENVAEFGLSDFCNTFKLYRGKTQEETDPSVIGEGKGLFIY
PLPEDPAIMPPRQFHQLAAQGECLVRIYVRAFGLPKDPNGKCDPYIKSIGKK
SVSDQDNYPCTLEPVFGKMFELTCTLPLEKDLKITLYDYDLLSDEKIGETVVDLEN
RLLSKFGARCGLPQTYCVSGPNQWRDQLRPSQLLHLFCQQHRVKAPVYRTDRVMFQDK
EYSIEIEAGRIPNPHLGPVEERLALHVLQQQGLVPEHVESRPLYSPLQPDIEQGKLQ
MWVDLFPKALGRPGPFNITPRRARRFLRCIWNTRDVLDDLSLTGKMSDIYVKG
WMIGFEEHKQKTDVHYRSLGGEGNFNWRFIFFPDYLPAEQVCTIAKKDAFWRLDKTES
KIPARVVFIWDDNDFSFDDFLGSLQLDLNRMPPKPAKTAKKCSLDQLDDAFHPEWFS
LFEQKTVKGWVPCVAEEGKKILAGKLEMTLEIVAESHEERPAGQGRDEPNMNPKE
DPRRPDTSFLWFTSPYKTMKFIWRRFRWAIILFIILFILLFLAIFYAFPNYAAMK
LVKPF (SEQ ID NO: 22)

EDIL3	10085	NM_005711	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
-------	-------	-----------	--

mRNA Sequence	
1	5'-GAG-3'
2	5'-GAG-3'
3	5'-GAG-3'
4	5'-GAG-3'
5	5'-GAG-3'
6	5'-GAG-3'
7	5'-GAG-3'
8	5'-GAG-3'
9	5'-GAG-3'
10	5'-GAG-3'
11	5'-GAG-3'
12	5'-GAG-3'
13	5'-GAG-3'
14	5'-GAG-3'
15	5'-GAG-3'
16	5'-GAG-3'
17	5'-GAG-3'
18	5'-GAG-3'
19	5'-GAG-3'
20	5'-GAG-3'
21	5'-GAG-3'
22	5'-GAG-3'
23	5'-GAG-3'
24	5'-GAG-3'
25	5'-GAG-3'
26	5'-GAG-3'
27	5'-GAG-3'
28	5'-GAG-3'
29	5'-GAG-3'
30	5'-GAG-3'
31	5'-GAG-3'
32	5'-GAG-3'
33	5'-GAG-3'
34	5'-GAG-3'
35	5'-GAG-3'
36	5'-GAG-3'
37	5'-GAG-3'
38	5'-GAG-3'
39	5'-GAG-3'
40	5'-GAG-3'
41	5'-GAG-3'
42	5'-GAG-3'
43	5'-GAG-3'
44	5'-GAG-3'
45	5'-GAG-3'
46	5'-GAG-3'
47	5'-GAG-3'
48	5'-GAG-3'
49	5'-GAG-3'
50	5'-GAG-3'
51	5'-GAG-3'
52	5'-GAG-3'
53	5'-GAG-3'
54	5'-GAG-3'
55	5'-GAG-3'
56	5'-GAG-3'
57	5'-GAG-3'
58	5'-GAG-3'
59	5'-GAG-3'
60	5'-GAG-3'
61	5'-GAG-3'
62	5'-GAG-3'
63	5'-GAG-3'
64	5'-GAG-3'
65	5'-GAG-3'
66	5'-GAG-3'
67	5'-GAG-3'
68	5'-GAG-3'
69	5'-GAG-3'
70	5'-GAG-3'
71	5'-GAG-3'
72	5'-GAG-3'
73	5'-GAG-3'
74	5'-GAG-3'
75	5'-GAG-3'
76	5'-GAG-3'
77	5'-GAG-3'
78	5'-GAG-3'
79	5'-GAG-3'
80	5'-GAG-3'
81	5'-GAG-3'
82	5'-GAG-3'
83	5'-GAG-3'
84	5'-GAG-3'
85	5'-GAG-3'
86	5'-GAG-3'
87	5'-GAG-3'
88	5'-GAG-3'
89	5'-GAG-3'
90	5'-GAG-3'
91	5'-GAG-3'
92	5'-GAG-3'
93	5'-GAG-3'
94	5'-GAG-3'
95	5'-GAG-3'
96	5'-GAG-3'
97	5'-GAG-3'
98	5'-GAG-3'
99	5'-GAG-3'
100	5'-GAG-3'

AGAAAGCCCCGAGCCGCGCGGAGAACAGCGACAGCCGAGCGCCCGGTCCGCCTGTCTGCCGGTGGGT CTGCCTGCCCGCGCAGCAGACCCGGGGCGGCCGCGGGAGCCCGCGCCCGCCCGCGCCTCTGCCGGG ACCCACCCGAGCGGAGGGCTGAGCCCGCGCGGGCTCCCCGAGCTCACCCACCTCCGCGCGCCGGAGC GCAGGCAAAAGGGGAGGAAAGGCTCCTCTCTTTAGTCACCACTCTCGCCCTCTCCAAGAATTTGTTAAC AAAGCGCTGAGGAAAGAGACGTCTTCTTTGAAATCTTTAGTAGGGGCGGAGTCTGCTGCTGCCCTGCGCT GCCACCTCGGCTACACTGCCCTCCGCGACGACCCCTGACCAGCCGGGTCACGTCCGGGAGACGGGATCA TGAAGCGCTCGGTAGCCGTCTGGCTCTTGGTCGGGCTCAGCCTCGGTGTCCCCAGTTCGGCAAAGGTGA TATTTGTGATCCCAATCCATGTGAAAATGGAGGTATCTGTTTGCCAGGATTGGCTGATGGTTCCCTTTTC TGTGAGTGTCCAGATGGCTTCACAGACCCCAACTGTTCTAGTGTGTGGAGGTTGCATCAGATGAAGAAG AACCAACTTCAGCAGGTCCCTGCACTCCTAATCCATGCCATAATGGAGGAACCTGTGAAATAAGTGAAGC ATACCGAGGGGATACATTATAGGCTATGTTTGTAAATGTCCCGAGGATTAAATGGGATTCTGTCAG CACAACTAAATGAATGCGAAGTTGAGCCTTGCAAAAATGGTGGAATATGTACAGATCTTGTGCTAACT ATTCCTGTGAGTGGCCAGGCGAATTTATGGGAAGAAATGTCAATACAAATGCTCAGGCCCACTGGGAAT TGAAGGTGGAATTATATCAAACCAGCAAATCAGAGCTTCCTCTACTCACCAGGCTCTTTTGGACTCCAA AAATGGTATCCCTACTATGCACGTCTTAATAAGAAGGGGCTTATAAATGCGTGAGACGCTGCAGAAAATG ACAGATGGCCGTGATTAGATAAATTTGCAAAGGAAAAAGAGATTACTGGTGTGATTACCCAAGGAGC CAAGAGGATTGGAAGCCAGAGTATATAAATCCTACAAAATTGCTACAGTAATGATGGAAGACTTGG GCAATGTACAAAGTGAAGGCACCAATGAAGACATGGTGTTCGTGGAAACATTGATAACAACACTCCAT ATGCTAACTCTTTCACACCCCCATAAAAGCTCAGTATGTAAGACTCTATCCCCAAGTTTGTGGAAGACA TTGCATTTTGCGAATGGAATCTTGTGCTGTGAACGTGCGGGTTGTTCTGAGCCTCTGGGTATGAATCA GGACATATACAAGACTATCAGATCACTGCCTCCAGCATCTTCAGAAGCTCAACATCAATGTTCACTT GGGAACCAAGGAAAGCTCGGCTGGACAAGCAAGGCAAAGTGAATGCCTGGACCTCTGGCCACAATGACCA GTCACAATGGTTACAGGTGGATCTTCTTGTTCACCAAAAGTACTGGCATCATTACACAAGGAGCTAAA GATTTTGGTGCATGTACAGTTTGTGGCTCCTACAACTGGCTTACAGCAATGATGGAGAAGACTGGACTG TATACCAGGATGAAAAGCAAAGAAAAGATAAGGTTTCCAGGGAAATTTTGACAATGCACTCAGAAA AAATGTCATCGACCTCCCATCTATGCACGACACATAAGAAATCCTTCCTTGGTCTGGTACGGGAGGATC ACATTGCGGTGAGCTGCTGGGCTGCACAGAGGAGGAATGAGGGGAGGCTACATTTACAACCTCTTC CCTATTTCCCTAAAAGTATCTCCATGGAATGAACGTGTGCAAAATCTGTAGGAACTGAATGGTTTCTTT TTTTTTTCATGAAAAGTGTCTCAATATAGGTAGGCAACTAACGGTGTTTTTAAGGGGTCTAAGCCTGC CTTTCAATGATTTAATTTGATTTTATTTATCCGTCAAATCTCTTAAGTAACAACACATTAAGTGTGAA TTACTTTTCTCATGTGTTTCTGAATTATTCGCATTGGTAGAAATATATTAGGGAAGAAAGTAGCCTT CTTTTATAGCAAGAGTAAAAAGTCTCAAAGTCATCAAATAAGAGCAAGAGTTGATAGAGCTTTACAA TCAATACTCACCTAATCTGATAAAAGGAATACTGCAATGTTAGCAATAAGTTTTTCTTCTGTAATGA CTCTACGTTATCTGTTTCCCTGTGCCTACCAACACGTGCAATGTTTATTACAAAATTTTAAAGAAGAA TATGTAACATGCAGTACTGATATTATAATTCTCATTTTACTTTCATTATTTCTAATAAGAGATTATGTA CTTCTTTTTCTTTAGTTCTATTCTACATTCTTAATATTGTATATTACCTGAATAATTCAATTTTTTCT AATTGAATTTCTTATTAGTTGACTAAAAGAAGTGCATGTTTACTCATATATGTAGAACATGACTGCCTA TCAGTAGATTGATCTGTATTTAATATTCGTTAATTAATCTGCAGTTTATTTTTGAAGGAAGCCATAAC TATTTAATTTCCAAATAATTGCTTCATAAAGAAATCCCATACTCTCAGTTTGACAAAAGAACAAAAATA TATATGCTCTTTAAATTTAAATCTTCATTTAGATGGTAATTACATATCCTTATATTACTTTAAAAAAT CGGCTTATTTGTTTATTTTATAAAAAATTTAGCAAAGAAATATTAATATAGTGTGCATAGTTTGGCCAA GCATACATCATTTCTTTGTTTCAGCTCCACATTTCCGTGAAACTAACATCTTATTGAGATTTGAAACT GGTGGTAGTTTCCCAGGAAGGCACAGGTGGAGTT (SEQ ID NO: 23)			
Translated protein sequence			
MKRSVAVWLLVGLSLGVPQFGKGDICDPNCPENGIGICLPGLADG SFSCECPDGFIDPNCSSVVEVASDEEPTSAAGPCTPNPCHNGGTCEISEAYRGDTFIG YVCKCPRGFNGIHQHNINECEVEPCKNGGICTDLVANYSECPGEFMRNCQYKCSG PLGIEGGIISNQITASSTHRALFGLQKWYPYARLNKKGLINAWTAAENDRWFPWQI NLQRKMRVTGVITQAKRIGSPYIKSYKIAYSNDGKTWAMYKVKGTMEDMVFRGNID NNTPYANSFTPIKAQYVRLYPQVCRHCTLRMELLGCELSGCSEPLGKMSGHIQDYQ ITASSIFRTLNMDFWEPRKARLDKQKVNAWTSGHNDQSQWLQVDLLVPTKVTGII TQAKDFGHVQFVGSYKLAYSNDGEHWTVYQDEKQRKDKVFQGNFDNDTHRKNVIDPP IYARHIRILPWSWYGRITLRSELLGCTEEE (SEQ ID NO: 24)			
ERGIC3	51614	NM_015966	Homo sapiens ERGIC and golgi 3 (ERGIC3), transcript variant 2, mRNA
mRNA Sequence			
GTGGCTCCAGGCCGGAAGAGGGAGTCTGTAGGGGCGGGCGGCTGGCGTCCCCTTTCCGGCCGGTCCCCA			

TGGAGGCGCTGGGGAAGCTGAAGCAGTTCGATGCCTACCCCAAGACTTTGGAGGACTTCCGGGTCAAGAC CTGCGGGGGCGCCACCGTGACCATTGTCAGTGCCCTTCTCATGCTGCTACTGTTCTGTCCGAGCTGCAG TATTACCTCACCACGGAGGTGCATCCTGAGCTCTACGTGGACAAGTCGCGGGGAGATAAACTGAAGATCA ACATCGATGTACTTTTTCCGCACATGCCTTGTGCCTATCTGAGTATTGATGCCATGGATGTGGCCGGAGA ACAGCAGCTGGATGTGGAACACAACCTGTTCAAGCAACGACTAGATAAAGATGGCATCCCCGTGAGCTCA GAGGCTGAGCGGCATGAGCTTGGGAAAGTCGAGGTGACGGTGTTTGACCTGACTCCCTGGACCTGATC GCTGTGAGAGCTGCTATGGTGTGCTGAGGCAGAAGATATCAAGTGTCTGTAACACCTGTGAAGATGTGCGGGA GGCATATCGCCGTAGAGGCTGGGCCTTCAAGAACCCAGATACTATTGAGCAGTGCCGGCGAGAGGGCTTC AGCCAGAAGATGCAGGAGCAGAAGATGAAGGCTGCCAGGTGTATGGCTTCTTGGAACTCAATAAGGTGG CCGAAACTTCCACTTTGCCCTGGGAAGAGCTTCCAGCAGTCCCATGTGCACGTCCATGACTTGCAGAG CTTTGGCCTTGACAACATCAACATGACCCACTACATCCAGCACCTGTCAATTTGGGGAGGACTATCCAGGC ATTGTGAACCCCTGGACCACACCAATGTCACCTGCGCCCAAGCCTCCATGATGTTCCAGTACTTTGTGA AGGTGGTGCCCATGTGTACATGAAGGTGGACGGAGAGGTACTGAGGACAAATCAGTTCTGTGTGACCG ACATGAGAAGGTTGCCAATGGGCTGTGGGCGACCAAGGCCCTTCCCGAGTCTTCGCTCTCTATGAGCTC TCGCCCATGATGGTGAAGCTGACGGAGAAGCACAGGTCTTCCACCCACTTCTGCAGAGGTGTGTGCGCCA TCATTGGGGCATGTTACAGTGGCTGGACTCATCGATTGCTCATCTACCACTCAGCACGAGCCATCCA GAAGAAAATTGATCTAGGGAAGACAACGTAGTCACCCTCGGTGTCTTCTCTGTCTCTTTCTCCCTGG CCTGTGGTTGTCCCCAGCCTCTGCCACCTCCACCTCCTCGGTCAGCCCCAGCCCCAGGTTGATAATC TATTGATTGATTGTGATAGTAAAAA (SEQ ID NO: 25)			
Translated protein sequence			
MEALGKLGKQFDAYPKTLEDFRVKTCGGATVTIVSGLLMLLFLS ELQYYLTTEVHPELYVDKSRGDKLKINIDVLFPHMPCAYLSIDAMDVAGEQQLDVEHN LFGKRLDKDGIPVSSEAEERHELKKEVTVDFDPSLDPRCESCYGAEEDIKCNTCE DVREAYRRRGWAFKNPDTIEQCRREGFSQKMQEQKNEGCQVYGFLEVNVAGNFHFAP GKSFQQSHVHVHDLQSFGLDNINMTHYIQHLSFGEDYPGIVNPLDHTNVTAPQASMMF QYFVKVVPVVMKVDGEVLRNQFSVTRHEKVANGLLDGQGLPGVFVLYELSPMMVKL TEKHSRSTHFLIGVCAIIGGMFTVAGLIDSLIYHSARAIQKKIDLGKTT (SEQ ID NO: 26)			
GNAT1	2779	NM_000172	Homo sapiens guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1 (GNAT1), transcript variant 2, mRNA
mRNA Sequence			
AGTTGATTGCAGGTCTCTCTGGGGCCAGAAGGGTGCCCTGGGAGGCCAGGTTCTGGGGATCCCTCCATCC AGAAGAACCACCTGCTCACTCTGTCCCTTCGCTGCTGCTGGACCATGGGGCTGGGGCCAGTCTGAG GAGAAGCATCCAGGGAGCTGGAAGAAGCTGAAAGAGGACGCTGAGAAGGATGCTCGAACCGTGAAGC TGCTGCTTCTGGGTGCCGTGAGTCCGGGAAGAGCACCATCGTCAAGCAGATGAAGATTATCCACCAGGA CGGGTACTCGCTGGAAGAGTGCCTCGAGTTTATCGCCATCATCTACGGCAACACGTTGCAGTCCATCCTG GCCATCGTACGCGCCATGACCACACTCAACATCCAGTACGGAGACTCTGCACGCCAGGACGACGCCCGGA AGCTGATGCACATGGCAGACACTATCGAGGAGGGCACGATGCCCAAGGAGATGTCCGACATCATCCAGCG GCTGTGGAAGGACTCCGGTATCCAGGCCTGTTTGTAGCGCGCTCGGAGTACCAGCTCAACGACTCGGCG GGCTACTACCTCTCCGACCTGGAGCGCTGGTAACCCCGGGCTACGTGCCACCGAGCAGGACGTGCTGC GCTCGCGAGTCAAGACCACTGGCATCATCGAGACGAGTTCTCTCTCAAGGATCTCACTTCCGGATGTT CGATGTGGGCGGCGAGCGCTCGGAGCGCAAGAAGTGGATCCACTGCTTCGAGGGCGTGACCTGCATCATC TTCATCGCGGCGCTGAGCGCTACGACATGGTGCTAGTGGAGGACGACGAAGTGAACCGCATGCACGAGA GCCTGCACCTGTTCAACAGCATCTGCAACCACCGCTACTTCGCCACGACGTCCATCGTGTCTTCTCTTAA CAAGAAGGACGCTTCTTCGAGAAGATCAAGAAGGCGACCTCAGCATCTGTTTCCCGGACTACGATGGA CCCAACACCTACGAGGACGCCGGAACACTACATCAAGGTGCAGTTCCCTCGAGCTCAACATGCGGCGCGACG TGAAGGAGATCTATTCCACATGACGTGCGCCACCGACACGACGAGAAGCTCAAATTGTCTTCGACGCTGT CACCAGATCATCATCAAGGAGAACCTCAAAGACTGTGGCTTCTCTGAGGCCAGGGCCTGTGCTGCAGT CGGGGACAAGGAGCTTCCGTCGGCAAGGCCGGGGCACAATTTGCACTCCCTCAGCTAGACGCACAGAC TCAGCAATAAACCTTGCATCAGGCTCCAGCTGTCTTCTTGGTGGAGGACTTAATTATCACAAGTCAT GGGCATTTATTAAGTCCCAGTGTGGGTTGGGCATGAAGTGGGAAGATGGCCCCCAGGAGGAAGTA CCTGGCTGACAAGGTGGGGCACTCTGGGGGTATGGGACCAACTCATGGCTTTTACGGGAGTTGAGGA GAGAGGAGCTGTGGAATAATTCACTGGGACAGTCTTGGATCAAGAGGGAGTTTTGAGGTGGAGGCTCAT TCTGGCAGGGACCGTAGTGTCTACAGCCCCAGAAACATGGGCTTATGGCCACAGGAGTTCAGTGGAGCA AGAGCAGGGGAGGAGAGAGCTGGACAGGTGCCCAAAGCCAGTCCGAGGGCCTGGGCTTCTCAGAAGGTG ATGGAGAGTCTTGAAGCCCTCGAGGCAGGAACATAATGACAGGCTGGGATTAGGTTGAGGGAAGTGAG			

GCACACTCACCTTGGGTGCAACATTTAAGGCGATGCCAAAAATTTAGTAACCAAGGTAAATAATATTAG GATAATATTTTTAAAAATCAAATGAATGCAAAACCCCAATGAATGAAATATCAAAATCCAACAGAGGA TCAAACAGAGGCATGCTAAGATATATTGGGGCTTGAAGCAAAGGGAAACTATTTGTTGCTATATGTTTG TAGGGATTTTTTGGCAGTTTTAAAAATACATGTATCATAAAGTTTACTATCTCAGCCACTTGCCGGTGTA TAGTTTGGTGGTGTAAAGTACATTCTAATGTTGTACAACACCGCAACTGTTTCTATCTCCAGAACTCCTT TCCTCTTGTAACCTGTAACCTCTGTACCCATGAAAAATAACCCCCATTCTGCCTTCCCCGGCTCCT GGCATCCACCAATTCTACTTTCCATCTCTATGAATGTGACTGCTCTAAGTGCCTCAGATGTGTGGGTCCAT GAAGTCTTTGTCTTTTGGCACTGGCTTATTTCACTTAGCATCATGTCTTCAAGGTTTATTTCATGTGTAG CATATGGCAGAATCTCCTTCTCTTTTAAAGTTGAATAATATTCATTGTATATATTCACACTTTGTTTA TTTATTCTATCTATTGATGAATGGTTACATCTGCCTTTTGGCTATTGTGAATAATGCTGCTATGAACATGG GTGTACAAATCTCTCAAAAAAAAAAAAAAAAAA (SEQ ID NO: 27)			
Translated protein sequence			
MGAGASAEKHSRELEKKLKEDAEDARTVKLLLLGAGESGKST IVKQMKIIHQDGYSLKECLEFIAIIYGNLQSLAIVRAMTTLNIQYGDSARQDDARK LMHMDTIEEGTMPKEMSDIIQRLWKDSGIQACFERASEYQLNDSAGYYLSDLERLVT PGYVPTQDVLRSRVKTTGIIETQFSFKDLNFRMFDVGGQSRERKKWIHCFEGVTCII FIAALSAYDMVLVEDDEVNRMHESLHLFNSICNHRYFATTSIVLFLNKKDVFFFEKIKK AHLISICFPDYDGPNTYEDAGNYIKVQFLELNMRRDVKEIYSHMTCATDTQNVKVFVDA VTDIIKENLKDCLF (SEQ ID NO: 28)			
GRAMD4	23151	NM_015124	Homo sapiens GRAM domain containing 4 (GRAMD4), mRNA
mRNA Sequence			
CGTCATGTTAGGGTGAAGCAGAGGACCTCAGTGCTGAACATGCTAAGGAGGTTGGACAAAATCAGGTTCA GAGGTACAAGAGAGATGACTTCCTCGATCTAGCGGAGTCTCAAATGCCTCGGACACCGAATGCAGCGA CGAAATCCCCCTGAAGGTACCGCGGACCTCGCCCCGGGACAGCGAGGAGCTGAGGGACCTGCTGGTCCA GGGACCTCATCATGGCCACAGGAGTCCAGGACTTTAACCAGCAGAGTTTGATCGACTGAATGAGATCA AAGTTCACCTGGAAATTGCCTTATTGGAAAAACATTTCTTACAGGAGGAGCTCCGGAAGCTGCGAGAAGA AACCAACGCGGAGATGCTGCGGCAGGAGCTGGACCGCGAGCGGAGCGGCGGATGGAGCTGGAGCAGAAG GTGCAGGAGGTGCTGAAGGCCAGAACCGAGGAGCAGATGGCTCAGCAGCCCCAAAAGGCGAGGCCCAGG CCAGCAATGGAGCAGAGCGCCGGAGCCAGGGGCTGTCTCGCGCTGCAGAGTGGTTCTACGAGCGGTT CGGGGAGTACGTGGAGGACTTCCGGTTCCAGCCGAGGAGAACACTGTGGAGACAGAGGAACCCCTGAGC GCCCCGAGGTTAACTGAAATATGAGACGGCTCAAGCGCGGTGCCAAGCCGGTCACTAATTTGTGAAGA ACCTCTCTGCCTTATCCGACTGGTACTCCGCTACACGCTGCCATTGCCTTACCGGTGACATGAATGC CGTGTGGCATGGCTGGGCCATCCCATTGTTCTTATTTCTAGCAATCTGAGGTTATCCCTCAATTACCTC ATCGCCAGGGGGTGGCGGATACGTGGAGCATCGTGCCGGAAGTGTCTGAGCCCGTGAACCTGCAAGAAG AAGACCTGACTGTGTCTGAGAAGTTCAGCTGGTGTGGACGTCGCCAGAAAGCCAGAACCTTTTCGG GAAGATGGCTGACATCCTGGAGAAGATCAAGAATGTTCATGTGGGTCCAGCCGAGATCACACAGAAG CTGTATGTGGCGCTCTGGGCTGCCTTCTGGCTCCTGCTTCTTCCCTACCGCTGGTGGGGCTTGGCG TGGGACTCTATGCTGGTATCAAGTCTTCTCTATTGATTCATCTTTAAACGCTGCCGAGGCTGCGCGC CAAGTACGACACGCCCTATATCATCTGGAGGAGTCTCCCCACCGACCCGAGCTCAAGGAGCGCTCCAGC GCCGAGTCTCACGCAGGCTGCAGACGACCTCGTCACGGAGCTACGTACCAGCGCACCGGCCGGCCTGG GTAAAGAGGAGGAGCGCCGGTGCCTTCCACAGCACCAAGAAGGGCAATTTCCACGAGATCTTCAATCTGAC AGAAAACGAGCGTCCGCTGGCGGTGTGCGAGAATGGCTGGCGCTGCTGCCTCATCAACAGGGACCGGAAG ATGCCCACGGACTACATCAGGAACGGGGTGTCTACGTACGGAGAATTACTTGTGCTTCGAAAGCTCCA AATCTGGGTCTCTCAAAGAGGAACAAAGTCATCAAGCTAGTGGACATCACGGACATCCAGAAGTACAAGGT CCTGTCTGTCTCCAGGCTCAGGCTAGGGATGCGCTGTGACGCCATCCACCCAGAAACCGCTCGTG TTTGGTGCCATGGTGACAGGGATGAGGCTTTCAGACCATTTCTCAGCCAGTACATCAAGATCACCTCAG CGGCAGCGTCTGGCGGGGACAGCTAGTATTGACTTGCCAGGACGTTGCTGGAAATTTCTTTTTCTTTTT CTTTTTCTTTTTTTTTTTTACGATTTGGTAGTGGAAACAATTGGACATCCTCATGAGCTTTTGAATAA TTCTCTTGACCTGTGGTTCTATTGTGTTGACCTCTGCGTTTTATCGACCAAGAAGGGGCCAGGGCTCAC AGGGACGGGGTGGCCCTCTCCACAGGGCACGTCAGGTGCCTCTGAGGGCCACCCGACAGCTGGGGGAG GGGGCAGAGGCCCTCGGGGGCCGTGGAGAAGACACAGGACCCCTGGCCCTGCCCTTCTCCGTTCCAG CCTGGACAGAGAACTCTCCAGCCACCCCAAGAGGTTCTCGCAACCTTGTGTCCCGCTCTCCAGAGGCC AGAAGCTCGTCCACCACCAAGCCATAGCTGAAGAGTGCGGGGCCCTTCTCTGGGGACAGAAAGATGT CGTCAAGGAGGGACATGGGGGCCCTTTCACCAACCAAGAGAAAGGGGCTGGCGGCCCTCTCTCTCTTA CATGAGACCTCTCTGTGCATTTGCCCTTGGTGCCGGGCTGGGGCCGGGCGAGTGACCCTGCCTGCGCT CCACACTCGCTCCACGGGAACAGAGAGGGTGAGAAGGGCCCCACCCCTCGCCTGCCCTCAGTGTCTTTGGT			

GGCACCTTCCTTGCTGGCTCCAGGGCGCTCAGCACCGCTCTGTAAGGGCTGCCTGCTGCTCTCGGCC TGACACGCCGGCCAGGAGGTCTGTAGCTGGGGACCAGTAAGGGCACAGGATGGTGCAAGTAAAAGCACAT CTTTCTCACACTTTGCTCTTTGGAAGGCCAGGAGAACATCCGCGAAGGTGTTGGAGGTGCTCCGAGCA CTGTGGCATGCTGGCAGATGGCCCCAGGCTGCGGTGCTGGTGGTGGGGAGGAAGTGGGGAGG AGTGTTCGGGACCATGGTGGCCAGGCTGCAGCCGCTTTGGGCCATCCGAGAGGCTCTGGCAGCCCCT GTGCTTAGGGAGCAACCGTGAGCCGAGCCAGAGGCTGGGCTGCACGCTGCAGCCGACATGCGAC AGCGTTCCTCCCCCGCTGCTAGCCGGTGCCGGTCCGGGCACAGACCCCCAGCCCCGCTGCCC CAGGGAAGCCTGGGCTTCCCGGGAACAAGGTGGCAITGTGGAGGGAGCGCCCGCAGGACCTGGTCTGCTG GGGCCGCTGCGCTGGGCTGAAGGGAGGAAAGGCGCTTGGGCTCCTGGAAGGAGGTGGCCACCCCGC GGGCTGCGTGTCTGCTGGGGCGGATCCCGCAGCTCCCTCAGCTTGTCTGAGTCCCTTGGGTGCTGTTG AGATTGTGTTTTTTGAAGAAACAGAAGATCTATTTTTTACAGCGAGCAAGCTGTTTTCTTATTTTTG TATCCTTTTTTTCAGATGTAATTTTTATCTTTGCTCCGATCCTCATTTGCTGGTGTGGGTGAGGGATCCGGC GGCATGGGCTGGTTTACCCCCCTTACAGAGGGCGCCGAGAGTCACACGCTGGTGCCGGGGGTGCTTTGGG GGGAGCTGCGCCGATCACCAGATTAAGCACATGTCTATCCAGGCGGTGGAGCGGAGCCCCGTGGCTC TGGAGTGCAGCGGAGCTTGGCGTCAGGATGACACACGCGGCTTTCCCGAATGGGGAGACAGAACCCCTC TGAGCCGTGGGTCTGGCTCCTGTAGGGGACTGGCTCTTTGGTGCACAGGGGAGGGGACATATCCAG TGAACCCACCTTGGCGCTGAGGCAACACAGGCTGGGCACTGACCCACCCAGGGGCGGTGCAGAGG CAGTGCCCGCAGACAATGGCCACACCTCTCTCCCAGGGCCCGCAGTGCCCAAGGATGGGTCCGGGGCC TCGGGGCCAATGAGCGCTCTTCCTAGGTGCTGGGATTCAGTCCCCAAACACAGCGGGAGGGGTCCCTGG GGCAGATGGGGCTTTACAGCGTCGGGTGGTTAGTTCGAGTCCCTTTTGTGGAGAAAGGAGATGAAAA CTGACCACGTGCCAGGTGTGGCCGAAGCCCCAGGGAGGGCCACATTCGGGGAGCGGGGGGTGCGGGGAG GGCCACCGACTGGCTCTGCTGCCAGCAGGCCCTCCCTGGAAGTCTCGGGAGCGGAGCGCGGATCGG CACGGGCTCTGGGCTCCCCGTGGAGAGAAGCTGTAGTTTTTACCAAATTGTGTACATCTGGGCAGATGTT TAATTTCTGTGACTAATCACTGAAGTAGACGAATGTTAAATTTTTATGTCTGAAGCCTGAGTCTATTTT GGATCTGTAAATAATCATTGCCAGTGTGACTTTTGTTCACAAAAGGATTGTACTGTATTAAGAACCGAT GAAAAAAATTCCTGTAAACATTTTTTAAGAAAACCTTGTGTTTAAAGAAAAAGTATTGTATAAATT ATAATTTTTATTAAATAAACCTAAATGCTTTGTGCTAAGGCTCAAAAAAAAAAAAAAAAAAAAAA (SEQ ID			
NO: 29)			
Translated protein sequence			
MLRRLDKIRFRGHKRDDFLDLAESPNASDTECSDEIPLKVPRTS PRDSEELRDPAGPGTLIMATGVQDFNRTEFDRLEIKGHLEIALLEKHFLOEELRKLK EETNAEMLRQELDRERQRRMELEQKVQEVVKARTEEQMAQQPPKQQAQASNGAERRSQ GLSSRLQKWFYERFGEYVEDFRFQPEENTVETEEPLSARRLTENMRRLKRGAKPVTNF VKNLSALSDWYSVYTSIAIAFTVYMNVAWHGWAIPFLFLAILRLSLNYLIARGWRIQW SIVPEVSEPVPEPKEDLTVSEKFQVLVDVAQKAQNLFKGMADILEKIKNLFMWVQPEI TQKLYVALWAAFLASCFFPYRLVGLAVGLYAGIKFFLIDFIFKRCPRLRKYDTPYII WRSLPDPLKERSAAVSRRLQTTSSRSYVPSAPAGLGKEEDAGRFSHTKGNFHEI FNLTENERPLAVCENGWRCLINRDRKMPTDYIRNGVLVVTENYLCFESSKSGSSKRN KVIKLVDTIDIQYKVLVLPGSGMGIADVSTPSTQKPLVFGAMVHRDEAFETILSQYI KITSAAASGGDS (SEQ ID NO: 30)			
HYAL2	8692	NM_003773	Hom sapiens hyaluronoglucosaminidase 2 (HYAL2), transcript variant 1, mRNA
mRNA Sequence			
TTTCTCTCAGGGGCGAGCAGGAAGTGAAGGAGAAAGGCTGGGATGGGAGGCGGGAGCGGATGGGAGGGA ATGGGGTTTATCAAGTCTCGGCGAGCTGCCAACGGGCGAGCAGCTGGCGCAAGTAGCCTAGCTGGAGAG GCTACCCAGGAAGGAGGAGGAGGCCACCGACCTACTGGGCGGACGGACTCCACACAGTTCTTCTGAGCTGG TGCCAGGCGAGGTGACACCTCTGCAGCCCCAGCATGCGGGCAGGCCCAGGCCCCACCGTTACATTGGCC CTGGTCTGGCGGTGTCATGGGCCATGGAGCTCAAGCCACAGCACCACCCATCTTCACTGGCGGGCCCT TTGTGGTAGCGTGGGACGTGCCACACAGGACTGTGGCCACGCTCAAGGTGCCACTGGACCTGAATGC CTTTGATGTGCAGGCCTCACCTAATGAGGGTTTTGTGAACAGAATATTACCATCTTCTACCGCGACCGT CTAGGCCTGTATCCACGCTTCGATTCTGCCGAAGGTCTGTGCATGGTGGTGTGCCACAGAATGTCAAGCC TTTGGGCACACCGGAAGATGCTGCAGAAACGTGTGGAGCACTACATTCCGACACAGGAGTCTCGGGGGCT GGCGGTATCGACTGGGAGGACTGGCGACCTGTGTGGGTGCGCAACTGGCAGGACAAAGATGTGTATCGC CGGTTATCACGCCAGCTAGTGCCAGTCTGTCACCTGACTGGCTCCAGACCGCATAGTCAAACAGGCAC AATATGAGTTTGTGTTTCGAGCACAGCAGTTCATGCTGGAGACACTGCGTTATGTCAAGGCAGTGGCGCC CCGGCACCTCTGGGGCTTCTACCTCTTCTGACTGCTACAATCATGATTATGTGCAGAACTGGGAGAGC TACACAGGCCGCTGCCCTGATGTTGAGGTGGCCCGCAATGACCAGCTGGCTGGCTGTGGGCTGAGAGCA			

CGGCCCTCTTCCCGTCTGTCTACCTGGACGAGACACTTGCTTCCCTCCCGCCATGGCCGCAACTTTGTGAG CTTCCGTGTTTACGAGGCCCTTCGTGTGGCTCGCACCACCATGCCAACCATGCACCTCCAGCTACGTC TTCACAGACCCACCTACAGCCGAGGCTCAGGGGCTTAGTGAGATGGACCTCATCTCTACATTGGCG AGAGTGGCGCCCTGGGCGCAGCTGGTGTATCCTCTGGGGTGACGCGGGGTACACCACAAGCAGGAGAC CTGCCAGTACCTCAAAGATTACCTGACACGGCTGCTGGTCCCCTACGTGGTCAATGTGTCTGGGCCACC CAATATTGCAGCCGGGCCCAGTGCCATGGCCATGGGCGCTGTGTGCGCCGAACCCAGTGCCAGTACCT TCCTGCATCTCAGCACCAACAGTTTTCCGCTTAGTGCCATGGCCATGCACCTGGTGAACCCAGCTGCGACC TGTGGGGGAGCTCAGTTGGGCGACATTGACCACCTGCAGACACACTTCCGCTGCCAGTGCTACTTGGGC TGGAGTGGTGAGCAATGCCAGTGGGACCATAGGCAGGCAGCTGGAGGTGCCAGCGAGGCCTGGGCTGGGT CCCACCTCACCAGTCTGCTGGCTCTGGCAGCCCTGGCCTTTACCTGGACCTGTAGGGGTCTCCTGCCTA GCTGCCTAGCAAGCTGGCCTCTACCACAAGGCTCTCTTAGGCATGTAGGACCCTGCAGGGGTGGACAA ACTGGAGTCTGGAGTGGGCGAGAGCCCCAGGAAGCCAGGAGGGCATCCATACCAGCTCGCACCCCCCTG TTCTAAGGGGGAGGGGAAGTCCCTGGGAGGCCCTTCTCTCCCTGCCAGAGGGGAAGGAGGGTACAGCTG GGCTGGGGAGGACCTGACCTACTCCTTGCCCTAGATAGTTTATTATTATTATTTGGGGTCTCTT TTGTAAATTAAACATAAAACAATTGCTTCTCTGCTTGGATTTTGT (SEQ ID NO: 31)			
Translated protein sequence			
MRAGPGPTVTLLVLAVSWAMELKPTAPPIFTGRPFVVAWDVPT QDCGPRLLKVLPLDLNADFVQASPNEGFVNQNIITIFYRDLRLGLYPRFDSAGRSVHGGVPQ NVSLWAHRKMLQKRVEHYIQTQESAGLAVIDWEDWRPVVWRNQDKDVYRRLSRQLVA SRHPDWPDRIVKQAYEFEEFAAQFMLETLRVYKAVRPRHLWGFYLFPCYNHDYVQ NWESYTGRCPDVEVARNDQLAWLWAEESTALFSPVYLDELASSRHGRNRFVSFRVQEAL RVARTHHANHALPVYVFTRPTYSRRLTGLSEMDLISTIGESAALGAAGVILWGDAGYT TSTETCYLKDYLTRLVVPVNVSWATQYCSRAQCHGHGRCVRRNPSASTFLHLSTN SFRLVPGHAPGEPQLRPVGELSWADIDHLQTHFRQCQYLGSWGEQCQWDHRQAAGGAS EAWAGSHLTSLALLAALFTWTL (SEQ ID NO: 32)			
IL10	3586	NM_000572	Homo sapiens interleukin 10 (IL10), mRNA
mRNA Sequence			
ACACATCAGGGGCTTGCTCTTGCAAAACCAACCAAGACAGACTTGCAAAAGAAGGCATGCACAGCTC AGCACTGCTCTGTTGCCTGGTCTCTTGACTGGGGTGAGGGCCAGCCAGGCCAGGGCAGCCAGTCTGAG AACAGCTGCACCCACTTCCCAGGCAACCTGCCTAACATGCTTCGAGATCTCCGAGATGCCTTCAGCAGAG TGAAGACTTTCTTTCAATGAAGGATCAGCTGGACAACCTGTTGTTAAAGGAGTCTTGCTGGAGGACTT TAAGGGTTACCTGGGTTGCCAAGCCTGTCTGAGATGATCCAGTTTACCTGGAGGAGGTGATCCCCAA GCTGAGAACCAAGACCCAGACATCAAGGCGCATGTGAACCTCCCTGGGGGAGAACCTGAAGACCCTCAGGC TGAGGCTACGGCGCTGTATCGATTTCTTCCCTGTGAAACAAGAGCAAGGCCGTGGAGCAGGTGAAGAA TGCCTTTAATAAGCTCCAAGAGAAAGGCATCTACAAAGCCATGAGTGAGTTTGACATCTTCATCAACTAC ATAGAGCCTACATGACAATGAAGATACGAACTGAGACATCAGGGTGGCGACTCTATAGACTCTAGGAC ATAAATTAGAGGTCTCCAAAATCGGATCTGGGGCTCTGGGATAGCTGACCCAGCCCCCTTGAGAAACCTTA TTGTACCTCTCTTATAGAATATTTATTACCTCTGATACCTCAACCCCATTTCTATTTATTTACTGAGCT TCTCTGTAACGATTAGAAAGAAGCCCAATATATAATTTTTTCAATATTTATTATTTTACCTGTTT TTAAGCTGTTTCCATAGGGTGACACACTATGGTATTTGAGTGTTTTAAGATAAATTATAAGTTACATAAG GGAGGAAAAAAATGTTCTTTGGGGAGCCAACAGAAGCTTCCATTCCAAGCCTGACCACGCTTTCTAGCT GTTGAGCTGTTTTCCCTGACCTCCCTCTAATTTATCTTGCTCTGCGGCTTGGGGCTTCCCTAAGTCTACA ATACTCTTAGGAAGAGAAAACAGGGAGCCCCCTTGTATGATTAATTCACCTTCCAGTGTCTCGGAGGGAT TCCCCIAACCTCATCCCCAACCACTTCATTCTTGAAAGCTGTGGCCAGCTTGTTATTTATAACAACCTA AATTTGGTTCTAGGCCGGGCGCGGTGGCTCACGCCGTGAATCCCAGCACTTTGGGAGGCTGAGGCGGGTG GATCACTTGAGGTCAGGAGTTCCTAACCCAGCTGGTCAACATGGTGAAACCCCGTCTCTACTAAAAATAC AAAAATTAGCCGGGCATGGTGGCGCGCAGCTGTAATCCAGCTACTTGGGAGGCTGAGGCAAGAGAATTG CTTGAACCCAGGAGATGGAAGTTGCAGTGAGCTGATATCATGCCCTGTACTCCAGCCTGGGTGACAGAG CAAGACTCTGTCTCAAAAAATAAAAAATAAATTGGTTCTAATAGAACTCAGTTTAACTAGAAT TTATTCAATTCCTGGGAATGTTACATTGTTTGTCTCTTCATAGCAGATTTAATTTTGAATAAATA AATGTATCTTATTCACATC (SEQ ID NO: 33)			
Translated protein sequence			
MHSSALLCLVLLTGVRASPGQGTQSENSCTHFPNLPNMLRDL RDAFSRVKIFFQMKDQLDNLKESLLEDFKGYLGCQALSEMIQFYLEEVMPOAENQD PDIKAHVNSLGENLKLRLRLRRCHRFLPCENKSKAVEQVKNFKNLQEKGIYKAMSE FDIFINYIEAYMTMKIRN (SEQ ID NO: 34)			

ITFG3	83986	NM_032039	Homo sapiens integrin alpha FG-GAP repeat containing 3 (ITFG3), mRNA
mRNA Sequence			
AGTGACGCCAGGGGGCGGGGCCAGCGGCGCGGTGCGGGTGAGAGGCCGCGGGCGGCAGGTCCACCTGGGCTT GCGAAGGCACAGATTCCCGTCCACAGCTCACGACCAGATGCACCAGCAGGAGTCCACATCGAGGACGTC CTCCGGGCACTCCACGACCAGTGACCAGGAGTTAACTTTGGGATGTGCCCGTGATGTTGGACCACAAG GACTTAGAGGCCGAAATCCACCCCTTGAATAAAGAAAGAAATCGCAGGAAATCTGGGAAATCCAT CAAAAAATGAGGATAACGTGAAAAGCGCGCTCCACAGTCCCGGCTCTCCCGGTGCCGAGCGGCGGCTT TTTTCTTTTCATTGTTCTCTGCCTTTTGTGGTGTTCGTCTCTCATTCTGTCATCCCGTGTCCAGACCGG CCGGCGTCCACGGAATGTGGAGGATAGACTACAGTGGCGCTGTTATCTATGACTTTCTGGCTGTGGATG ATATAACCGGGACAGGATCCAAGATGTTCTTTTCTTTATAAAAAACACCAACAGCAGCAACAATTTTCTAG CCGATCTGTGTGGACGAAGGCTTTTCTCTCCCTGCACCTTTGCAGCTGCTGTGTGCGGGGCCAACGGC AGCAGCTCTGGGAGAGACCTGTGGCCCAAGACGTGGCCCTCGTGGAGTGTGCTGTGTCGCCAGCCAAGAG GCAGTGAGGCACCTTCTGCCTGCATCCTGGTGGGCAGACCCAGTTCTTTTCATTGCAGTCAACTTGTTCAC AGGGGAAACCTGTGGAACACAGCAGCAGCTTCAGCGGGAATGCGTCCATCCTGAGCCCTCTGCTGCAG GTGCTGTGTGGACGGCGATGGGGCCCCAGACCTGCTGGTCTCACCAGGAGCGGGAGGAGGTTAGTG GCCACCTCTACTCCGGCAGCACCGGGCACCAGATTGGCCTCAGAGGCAGCCTTGGTGTGGACCGGGGAAAG TGGCTTCTCTTACGTCACCGAGCAGGTGCCCCACTACATCTCTTTCCCTGCGCAAGCTCCCTCTGC GGCTGCTGTGTAAGGCTCTTACGAGAAGGTGACCGGGAGCGGCGGCGGCTTCAAGAGTGACCCGCACT GGGAGAGCATGCTCAATGCCACCAACCGCAGGATGCTTTCCACAGCTCTGGAGCAGTGGCTAGCTGAT GCATGTCCAGGGAACCGCGGTGCAGATGTGCTTCTTGTGGGCTCAGAGGCCTTCGTGCTGCTGGACGGG CAGGAGCTGACGCTCGTGGACACCAAGGCAGCCATGTCTTGAGAAAACCCATCTTCGGCCGCTACA AACCAGACACCTTGGCTGTAGCCGTTGAAAACGGAACCTGGCACCAGACAGACAGATCTGTTTCTGGACCT TGGCACTGGAGCCGCTCTGTGTAGCTTAGCCCTCCCGAGCCTCCCTGGGGGTCCACTGTCCGCCAGCCTG CCGACCGCAGACCAACCGCTCAGCCTTCTTCTCTGGGGCTCCACGAGCTGGGGAGCACCAGCGAGACGG AGACCGGGGAGGCCCGGCACAGCCTGTACATGTTCCACCCACCTGCGCGCGTGTGCTGGAGCTGGC CAATGTCTCTACCCACATTGTGCGCTTTGACGCGCTCTGTTTGGCCAAAGCCGCCACGCCCTACATC CTTCTGACAGGCCCGGCAGACTCAGAGGCACCGGCCCTGCTCTGTGATCAAGCACAGGTGCGGGACC TTGTCCCAAGCAGCAGGCTGGTCCGCTGGGTGAGGTGGGCCAGACAGTGACCAAGCCATCAGGGACCG GTTCTCCCGGCTGCGGTACCAGAGTGAGGCGTAGAGGCACGCCAGCCAGAGCCTGTGGAGAGACTCCGCC TGCTGACACTAAACGCTCTGGGAAGTGGGCCCTTCCCTGGGTCTCTGCACTGACTCCCCACTCTGACC CTGGTGATGGTCCGCACTGGGCAGCAGCAGCCTTACCAGTCTCTCATGATCACCCAGGGACCTGCATG GGTGAGGGGACACCTTGGGCTCTCTCCCGCCAGCATCTCTCTGAGTCCCCACACAGGGCCTCACTCT GCACCCACACAGGTCCCGCTCACACAGGCAGCCTTCATAGTGGTCTCCCTGGCCACCTTGGGCAGAGC TGGGTCTACAGCACCCCATCCTTACCCGCTGCCCTCTCTCTGCAAGCTTCTCCCAAGCCAGGTGCGGGCC ATCGCGTAGAAAGAACAGGGTGTCCCGGGACAGGCCGTCCCCACCCATCTGTAGAAGTCCATTCC CCTTTTCCCTCTGTGCTCTGTCCCCAAGGAGTCATGGAACCTCAGGGTACTGGGCTCAACGGGAACCT GAGACAGCTCCAGCTTCGAGCCCTTCCCGAGCTACAGGGGATCTCTAGCATGGGGGTGTGACTTG GTTCTTTGACCAGGTCTCTGTGAGGAAGCCTGAGCAAGGGTCTCCCCAGCAGGATGGGTGGGGCCTGC TCTGGAGCTGAGCCGTGGCCGCTCACAGGTGTCTTAGTGGTGTGTCAGCTGTCTACTGGCTGCATGTG CTGTGAATATCCCAAGGAACCTGGCTGTGGAATGCGTGTGTTGGTCACTGTGCCCCTCTCAGTAGACACT GGAGCTGCTCTGTCCCTGAAGAGGCCCGGTGCCCGCAGGATGGCAAGCGCTGCTCTCCCTTCCCGTG CTCACACGCCACGCCGTGCCACCCGATGCAGGACTACCTCTGTGCTTGTGCTCTCTGAGGCCCAAGG GCAGCCATGGTGTCTGTACTGCTCGGGCGGCCAGGTACAGAGCCTGAGCTTCGTAGCCAAAGCAGCC TGATGACCCACCCACGAAGAAGCAGAATAAACATTTTGCAGTGCCTGAAAAACCCCGGTGGTCA GGCGTGAGCCTAAAAA (SEQ ID NO: 35)			
Translated protein sequence			
MLDHKDLEAEIHLKNEERKSQENLGNPSKNEEDNVKSAPPQSRL SRCRAAAFFLSLFLCLFVVVVSFVIPCPRPASQRMWRIDYSAAVIYDFLAVDDING DRIQDVLFLYKNTNSSNFSRSCVDEGFSSPCTFAAAVSGANGSTLWERPVAQDVALV ECAVPQPRGSEAPSACILVGRPSSFIAVNLFTGETLWNHSSFSGNASILSPLLQVPD VDGDGAPDLLVLTQEREESVGHLYSGSTGHQIGLRGSLVDGESGFLHVRTGAIHYI LFPCASSSLCGCSVKGLYEKVTGSGGPFKSDPHWESMLNATRRMLSHS3GAVRYLMHV PGNAGADVLLVGSEAFVLLDGOELTPRWTPKAAHVLRKPIFGRYKPDTLAVAVENGTE TDRQILFLDLGTGAVLCSLALPSLPGGPLSASLPTADHRSAFFFWGLHELGSTSETET GEARHSLYMFHTLPRVLELANVSTHIVAFDAVLFEPSRHAAYILLTGPADSEAPGL VSVIKHKVRDLVPSSRVVRLGEGGPDSDQAIRDIFSRLRYQSEA (SEQ ID NO: 36)			

JAM3	83700	NM_032801	Homo sapiens junctional adhesion molecule 3 (JAM3), mRNA
mRNA Sequence			
<p> TAGACCTCAGCTTCCTCTGTCAACCATGGTGCCGGCTCGGCTGGGCCCGGCGGTCGCCATGGTAACTGGGG CGGGTCGCAGGGTCCTGGCAGGCTGGGCGCATGCGCGCGGGGACTACAAGCCGCGCCGCGCTGCCGCTGG CCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGGCCACCGCGACTCCGGCTCTGCGCTCGGCTGCCTGAC TTCCTCCCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATCTCAAATCCAGCAATCGAACCC CAGTGGTACAGGAATTGAAAGTGTGGAACGTCTTTCATCATTACGGATTTCGACAGACAAGTGACCCAG GATCAGTGGGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTGACAACAAAATTCAGGGAGAC TTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAGACTCAG CCCTTTATCGCTGTGAGGTGCTTGCCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAAC TGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACA CTGCACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCACTGC CCACGGATTCCAGAGCCAATCCAGATTTTCGCAATCTCTTTCCACTTAAACTCTGAAACAGGCACCTTT GGTGTGTACGCTGTTTCAAGGACGACTCTGGGCGAGTACTACTGCATTGCTTCCCAATGACCGAGGCTCA GCCAGGTGTGAGGAGCAGGAGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTTCTGG TTGTCTTGTGTACTGGCCCTGATCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAA CAATAAACAGGATGGAGAAAGTTACAAGAACCAGGGAACAGATGGAGTTAACTACATCCGCACTGAC GAGGAGGGCGACTTCAGACACAAGTCATCGTTTGTGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAG AGCGCACGTGCACATACCTCTGTAGAACTCCTGTCAAGGCGAGGAGCTGATGCACTCGGACAGAGC TAGACACTCATTGAGAAGCTTTTCGTTTTGGCCAAAGTTGACCACTACTCTTCTTACTCTAACAAGCCAC ATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAAGGAAGCGAACTGGGTGCCGT CACTGAGTTGGGTTCCATACTGTTTCTGGCCTGATTCCCGCATGAGTATTAGGGTGATCTTAAAGAGTT TGCTCACGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTCACTACTGGTTCAGCAGCCACG ACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGAAACCCAGAAAAAG GCTTCTTACAGCAGCCTTACTTCATCGGCCACAGACACCACCGAGTTTCTTCTTAAAGGCTCTGCT GATCGGTGTTGCAGTGCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAG GAAGGTAAATTTGGTGTGGAAGAGGGATCTTGCCCTGAGGAACCCGTGTTGTCCAACAGGGTGTGAGGAT TTAAGGAAAACCTTCGCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGT ATTTTAAATAATTTTACATCTAAATTTTGTCTAAGGATGTATTTGATTATTGAAAAGAAAATTTCTATT TAACTGTAAATATATTGTACATAATGTTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGA AGTTCCAAGCTACTAGTGTTAAATTTGAAAATATCAATAATTAAGAGTATTTTACCAAGGAATCCTCTC ATGGAAGTTTACTGTATGTTCCTTTTCTCACACAAGTTTTAGCCTTTTTCACAAGGGAACCTATACGT CTACACATCAGACCATAGTTGCTTAGGAAACCTTTAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTG CATCTCTTCAAAGAAACCTCTCAGGTTAGCTTTGAACTGCCCTCTTCTGAGATGACTAGGACAGTCTGT ACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAGATGCCAGTCAGCTCCTGGGGTTGCGCCAG GCGCCCCCGCTTACGTCACTGTTGCCCTCGCTGCTGCCAGGAGGCCCTGCCATCCTTGGGGCTTGGCAG TGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGCTCTCAGGTGGGCACTG CAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAAACAGACCTCTTTTGGTTATG GATGGCTCACAAAATAGGGCCCCAATGCTATTTTTTTTTTAAGTTTGTTTAATTATTGTTAAGATT GTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGATC CCACTGTTCCTCTTTGCCACAGAGAAAGCAGCCAGAGCCACAGGCTCTGTGCGATTTCAAACAAACCA TGATGGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCCTGGCGG GGAGGAAAGTGAAACGCCTGAATCAAAGCAGTTTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGGAG ACACTGCTCCCATTTTGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGT TCTCAGCCTCACATGCCCTGCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGTGAGAA GGAGCACTCCACTGTGTGCTGGAGAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTTG GGTTTTTATACTTTGACAGCTTTTTTTTAAATGTCATACATGAGACTGTGTGACTTTTTTTAGTTATGT GAAACACTTTGCCCGAGGCCCTGGCAGAGGCAGGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTG TCTGTGCTATGGCATCCTGGATGCTTAGCATGCAAGTTCCCTCCATCATTGCCACCTTGGTAGAGAGGGA TGGCTCCCCACCCCTCAGCCTTGGGGATTACGCTCCAGCCTCCTTCTTGGTTGTATAGTATAGGGTAG CCTTATTGCCCTCTTCTTATACCCATAAACCTTCTACACTAGTGCCATGGGAACCCAGGTCTGAAAAAG TAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATACTGAGACTAGACGGAAGGAATACTC GTGTATTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCTGCCTTTGGATG GATGTTGCTGTACAGATGCTACAGACTTGTAATAACACCGTAATTGGCATTGTTTAACTCATTT TATAAAGCTTCAAAAAAACCAAAAAACCCAAA (SEQ ID NO: 37) </p>			
Translated protein sequence			

MVPARLGPAVAMVTGAGRRVLGWAHARGDYKPRRAAAGPSATL DMALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVOEFESVELSCIITD SQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLGRAEILGKTSLKIWNVTRDSALYRC EVVARNDRKEIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSW YRNDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCE EQEMEVDNLNIGGIIGVVLVLAVALILTGICCAAYRRGYFINNKQDGESYKNPGKPD GVNYIRTDEEGDFRHKSSFVI (SEQ ID NO: 38)			
KLHL17	339451	NM_198317	Homo sapiens kelch-like 17 (Drosophila) (KLHL17), mRNA
mRNA Sequence			
AGTGAGCGACACAGAGCGGGCCGCCACCGCCGAGCAGCCCTCCGGCAGTCTCCGCGTCCGTTAAGCCCGC GGGTCTCCGCGAATCGGCGGTGGGTCCGGCAGCCGAATGCAGCCCCGAGCGAGCGCCCGGCCGCGAGG ACGCGAGAGCCCGGAGCAGCGCAGCCCGGGGCCCCGGGCCCGAGGCGCCGCGCCTCCACCGCCGAGCCGC CGGCCCCCGAGGCAGAGCGCACGCGGCCCGGGCAGGCTCGGCCCGCAGCCCCCATGGAGGGAGCCGTGCA GCTGCTGAGCCGCGAGGGCCACAGCGTGGCCCACTCCAAAGCGGCACTACCACGATGCCTTCGTGGCC ATGAGCCGCGATGCGCCAGCGCGGCTCTGTGCGACATCGTCTGACGCTGGCTGCCAAGAGAGATCCGTG CGCACAAAGTGGTGTGGCTCTGCGACCCCTACTTCCACGCCATGTTACAAATGAGATGAGCGAGAG CCGCCAGACCCACGTGACGCTGCACGACATCGACCCTCAGGCCCTGGACCAGCTGGTGCAGTTTGCTTAC ACGGCTGAGATTGTGGTGGGCGAGGGCAATGTGCAGACTCTGCTCCAGCCGCGAGTCTCTGCGAGCTGA ATGGCGTCCGAGACGCTGTGCAAGTTTCTACTGAGTCAGCTCGACCCCTCCAACTGCCTGGGTATCCG GGGCTTTGCCGATGCGCACTCTGCGAGCAGCTGCTCAAGGCCGCCACAGGTACGTGCTGCAGCACTTC GTGGACGTGGCCAAGACCGAGGAGTTTATGCTGCTGCCCTGAAACAGGTTCTGGAACGTGCTCTAGCG ACAGCCTGAACTGTGCTTACAGAGGAGGAGTCTACCGAGCCGCTCTGAGCTGGGTGAAACACGACGCTGGA CGCCCGCAGGCAGCATGTCCACGGCTCATGAAGTGTGTGCGGCTGCCCTTGTGAGCCGCGACTTCTGT CTGGGCCACGTGGATGCCGAGAGCTGGTGAGGCACACCTGACTGCAAGGACCTCTCATCGAGGCC TGAAATTCCACCTGTGCTGCTGAGCAGAGGGCGTCTTAGGCACCGCCGACACGTCCTCCGGCGCTGCGA GGGGGCCGGGCTGTGCTTTTGTGTGGGCGGCGGAGCCTGTTTGCCATCCACGGAGACTGTGAGGCC TACGACACGCGCACCGACCGCTGGCAGCTGGTGGCTCCATGTCCACGCGCCGGGCCCGGGTGGGAGTGG CTGCGGTGGGGAACCGGCTCTATGCTGTGGGCGGCTATGATGGGACCTCAGACCTGGCTACCGTGGAGTC CTAGCACCCCGTGACTAACACGTGGCAGCCGAGGTGTCCATGGGCAAGGCCAAGCTGCTGGGTGTG GCCGCTTGATGACTCCTGTACTCGCCCGCGGCTATGACGGGCGCTCTGCTGAAACAGTGTGTAAC GCTACGACCCCTGACCGGAACGTGGACGTCCGTGCTGCCATGAGCACCGGAGGCGCTATGTGCGAGT GGCCACGCTTGATGGGAACCTGTATGCTGTGGGCGGCTACGACAGCTCTCACACCTGGCCACTGTGGAG AAGTATGAGCCCCAGGTGAACGTGTGGTCCGCGTGGCGTCCATGCTGAGCCGACGACGTCAGCGGGCG TGGCGGTGCTGGAGGGTGCCCTGTACGTGGCAGGGGGCAACGACGGCACCAGCTGCCTCAACTCGGTAGA GAGATACAGTCCAAAGGCTGGAGCCTGGGAAAGCGTGGCGCCCATGAATATCCGAGGAGCAGCGATGAC CTGGTGGCTAGGACGGATGGTTGTACGCGGTGGGGGTAACGACGGTAGCTCCAGCTCAACTCCATCG AGAAGTACAAACCGAGGACCAACAAGTGGGTGGCCGCATCCTGCATGTTACCCGCGCAGCAGTGTGGG TGTGGCGGTGCTGGAGCTGCTCAATTTCCCGCCGCCATCTCCCGACGCTGTCCGTGTCTTCCACGAGC CTCTGACCCACCTACCACGAGGCTGCAGCCTCCACATGCCTTAAGGGGACCGTGGCCCCCACCAGG GACGTCCTGCGCCATCCGTTACGCTCTGCAATCCATTCCTCATGCTTTATTAGTTGTTTATTATT TAGTTATTTATCTTATTATTGAGGGGTGAGGAGTGCCACGGCTGCCCGTTTACACCTTTAGCGTCTGGT CCTCCTGCGTGTCTCCCTCCACTGCCTGCATGGGGGCGCGGGGAGTGACCAGGCGGGGGCCTCACC CCCCAGGGCCGTGGCTGCTCAGACCTTGACGGCTGTGGAGCAAGAGGCCCTGGGTCTCTCAAGCAGCT GCAGACCCGAGCTCGAATTTTGCACATGGCGGGGTCCCGGGAAGGGTGGGGAGCAGTTGTCTTCTGTC GTCGTCTGCGGTGTGCCATCTTCTGGATCTGTAGTGGGTGCACACGCTGCACTGGGACCCACACA GCAATACGAGTCCAACTTAATAAACACATTCTGGGGTTCCTCAAAAAAAAAAAAAAAAAA (SEQ ID NO:			
39)			
Translated protein sequence			
MQPRSERPAGRTQSPHEGSPGPGPEAPPPPPQPPAPEAERTRP RQARPAAPMEGAVQLLSREHGSVAHNSKRHYHDAFVAMSRMRQRLLCDIVLHVAAKE IRAHKVVLASCSPIYHAMFTNEMSESQTHVTLHDIDPQALDQLVQFAYTAIEIVGEG NVQTLPLPAASLLQLNGVRDACKFLLSLDPSNCLGIRGFADAHSCSDLKAAHRYVL QHFVDVAKTEEFMLPLKQVLELVSSDSLNVPSSEEVYRAVLSWVKHVDVARRQHVPR LMKCVRLPLLSRDFLLGHVDAESLVRHHPDCKDLLIEALKFHLLPEQRGVLGTSRTRP RRCEGAGPVLFAVGGGSLFAIHGDCEAYDTRTDRWHVASMSTRRARVGVAAVGNRLY AVGGYDGTSLATVESYDPVTNTWQPEVSMGTRRSCLGVAALHGLLYSAGGYDGASCL			

NSAERYDPLTGTWTSVAAMSTRRRYVRVATLDGNLYAVGGYDSSSHLATVEKYEPQVN VWSPVASMLSRSSAGVAVLEGALYVAGGNDGTSLNSVERYSPKAGAWESVAPMNIR RSTHDLVAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRSSVGVAVLEL LNFPSPSPTLSVSSTSL (SEQ ID NO: 40)			
KRT24	192666	NM_019016	Homo sapiens keratin 24 (KRT24), mRNA
mRNA Sequence			
ACTCTTCGTCATCACCTCTCCTATTGCGCTGGACAAGCTCATGTTTGAGGAGCACCATGTCTTGCTCGT CTCGCGCCTCCTCCTCAGGGCTGGAGGCAGCAGCTCAGCCAGGGTGTCTGCTGGTGAAGCAGCTTCAG CAGTGAAGCAGATGTGGTCTGGGGGCGAGCTCGGCCAGGGCTTCCGAGGAGGAGCCAGCAGCTGCAGC CTGAGTGGGGGGTCTAGCGGTGCTTTTGGGGGCGAGCTTTGGAGGGGGCTTTGGTAGCTGCTCAGTAGGGG GTGGTTTGGGGGAGCTTCAGGCTCTGGGACAGGATTGGTGGGGGTTCTAGCTTTGGCGGGGTCTCTGG ATTTGGCAGGGGTTCTGGATTCTGTGGGAGTTCTAGATTACAGCAGTGGTGCTACTGGAGGCTTCTACAGC TATGGTGGTGGTATGGGAGGTGGTGTGGCGATGGGGGGCTTTTCTCTGGAGGGGAAAAGCAAACCATGC AGAACCTCAATGACCGCTTGGCCAATTACCTAGACAAGGTCAGAGCCCTGGAGGAGGCTAACACTGATCT GGAGAACAAAATCAAGGAGTGGTATGACAAATATGGGCTGGGTCTGGAGACGGTGGATCGGGAAGAGAT TATAGCAAATACTATTCAATAATTGAAGATCTCAGAAACCAGATCATTGCTGCCACTGTTGAAAATGCTG GGATCATTTTGCACATTGACAATGCCAGATTGGCTGCTGATGACTTCAGACTGAAGTATGAGAACGAGCT GTGTCTCCGGCAGAGCGTGGAGGCTGACATCAATGGCCTGCGGAAAGTCTGGATGACCTGACTATGACC CGCTCTGACCTGGAGATGCAGATTGAGAGTTTACCAGGAGCTAGCCTACCTGAGGAAGAACACGAGG AGGAAATGAAGAATATGCAAGGAAGCTCTGGAGGGGAGGTGACCGTAGAAATGAATGCTGCGCCAGGGAC CGACTGACCAAAATTACTGAATGACATGAGGGCGCAGTACGAGGAGCTGGCTGAGCAAAACCGCCGAGAG GCTGAGGAGCGGTTCAACAAGCAGAGCGCATCACTACAAGCACAATCTCCACTGATGCTGGGGCAGCCA CTTCTGCCAAGAATGAGATAACAGAACTAAAACGTACCCTGCAAGCCCTGGAATTGAGCTTCAGTCCCA ACTGGCCATGAAAAGCTCCCTGGAGGGAACCTTGGCTGACACAGAAGCTGGCTACGTGGCTCAGCTGTCA GAAATTCAAACGCAGATCAGTGCCCTGGAGGAGGAGATCTGCCAGATCTGGGGTGAGACTAAATGCCAGA ACGCAGAGTACAAGCAATTGCTGGACATCAAGACACGCCTGGAGGTGGAGATCGAGACCTACCGCCGCCCT GCTCGATGGAGAGGGAGGTGGTTCTAGTTTTGCAGAAATTTGGTGGTAGAACTCAGGATCTGTAAACATG GGATCCAGGGATCTGGTATCTGGTGACTCAAGATCTGGAAGCTGTTCTGGTCAAGGACGAGATTCAAGCA AGACTAGAGTGACTAAGACTATCGTAGAGGAGTTGGTGGATGGCAAGGTGTCTCGTCTCAAGTCAGCAG TATTTCTGAGGTGAAAGTTAAATAAGGAACCTCCAGATCAACAAAAGTGTCTTTCAAAGAAAAAATC AAGAAGGACACAAGCGAAGAAATGGCATCAATCTAGGCATCTTTCTGGATAATTTAGGAAAAGCTTCAG TCCAGAAATGGATGACTAGCCAACTTTTCTGCATCTTCTTATTTCTCATTAGAAATGCTCTTGAAATAGC TGAATTAACAACCTTTGCTTTAATTGTTTCTATGCTTCAATAAAATTTACTTTGCAAGTTAAAAA AAAAAA (SEQ ID NO: 41)			
Translated protein sequence			
MSCSSRASSSRAGSSSARVSAGSSSFSSGSRCLGGSSAQGFR GGASSCSLSGGSSGAFGGFSGGGFGSCSVGGGFGGASGSGTGFGGGSSFGGVSGFGRG SGFCGSSRFSSGATGGFYSGGGMGGVGDGGLFSGGEKQTMQNLNDRLANYLDKVRA LEEANTDLENKIKEWYDKYGPSSGDSGRDYSKYYSIIEDLRNQIIAATVENAGIIL HIDNARLAADDFRLKYENELCLRQSV EADINGLRKVLDDLTMRSDLEMQIESFTEEL AYLRKNHEEEMKNMQSSGGEVTVMNAPGTDLTLLNDMRAQYEELAEQNRREAE RFNKQSASLQAQISTDAGAATS AKNEITELKRTLQALEIELQSQLAMKSSLEGLADT EAGYVAQLSEIQTQISALEEEICQIWGETKQNAEYKQLLDIKTRLEVEIETYRRLD GEGGSSFAEFGRN SGSVNMGSRDLVSGDSRSGSCSGQGRDSSKTRVTKTIVEELVD GKVVSSQVSSISEVKVK (SEQ ID NO: 42)			
MAD2L1BP	9587	NM_014628	Homo sapiens MAD2L1 binding protein (MAD2L1BP), transcript variant 2, mRNA
mRNA Sequence			
ATTCTAACCGCAAGGAGTAGCGGAGGGGAGGTGCTGATGGCGGCGCCGGAGGCGGAGGTTCTGTCCTCAG CCGCAGTCCCCTGATTGGAGTGGTATGAGAAGTCCGAAGAACTCACGCCTCCAGATAGAACTACTTGA GACAAAGCTCTACGCAGGAACCTCTCAACGCTTCGGAGGCCTTTTGCCCAAGAGACTGCATGGTACCAGTG GTGTTTCTGGGCTGTGAGCCAGGAAGGCTGCTGTCAGTTTACTTGTGAACCTCTAAAGCATATCATGT ATCAACGCCAGCAGCTCCCTCTGCCCTATGAACAGCTTAAGCACTTTTACCGAAAACCTTCTCCCCAGGC AGAGGAGATGCTGAAGAAGAAACCTCGGGCCACCCTGAGGTGAGCAGCAGGAAATGCCAACAGCCCTG GCAGAACTGGAGAGTGTCTCAGCCACCTGGAGGACTTCTTTGCACGGACACTAGTACCGCAGTGCTGA			

TTCTCCTTGGGGGCAATGCCCTAAGCCCCAAGGAGTTCTATGAACTCGACTTGTCTCTGCTGGCCCCCTA CAGCGTGGACCAGAGCCTGAGCACAGCAGCTTGTTTGGCGCCGTCTCTCCGAGCCATATTATGGCTGAT GCCTTTAGCGAGCTTTCAGGCTCCTCCACTCATGGGCACCGTCGTCATGGCACAGGGACACCGCAACTGTG GAGAAGATTGGTTTCGACCCAAGCTCAACTATCGAGTGGCCAGCCGGGGCCATAAACTGACTGTGACCCCT GTCAATGTGGCAGACCTTCCATCCGAACACGGCTTGGGAAGACTACATTGGTTCCAGGCACCACTGACA TTTAAAGGCTTCCGCGAGTGAATGAGTGTCTTTAATCCTAAAAACACAATGGCTGAATTATCTTTCTCC ATGTGGCGCTGAATCACCCTCTGGTTTGGAGCTAGAGTTGCTTCTGGTGAGAGAGGAAGCAACTCTCC TTCTGGTTGTCTGCCCTCCCTCAGATTTCTGATAGGCTGATGGCATGTGGCTGTGACTGTGACTGTAAAT CATTGTGAACAACATCTCTTTGAATCAAAGGTTGATTTTCCAGAGGGTGCTGGGTGAGGCATTTCTAT TAGGAGTTGGAAAGCAAAAATGGGTCCATAGACACTCTATGGAGGTGTCCCTTTCTGCTCTTTGCTGTGT CCTTTCAGAATTTTACCAGGAACATAATGTGGATGTGACTTATGAACCTAAATATAAAATAAATAGATT CTTATTATATTTTCTGAAAAA (SEQ ID NO: 43)			
Translated protein sequence			
MAAPEAEVLSSAAVPDLEWYEKSEETHASQIELLETSSSTQEPLN ASEAFCPRDCMVPVFPVPGPVSQEGCCQFTCELLKHIMYQRQQLPLPYEQLKHFYRKPS PQAEEMLKKPRATTEVSSRKCCQALAELESVLSHLEDDFFARILVPRVLILLGGNALS PKFELYDLSSLAPYSVDQSLSTAACLRLRFRAIFMADAFSELQAPPLMGTVMMAQGH RNCGEDWFRPKLNYRVP SRGHKLTVLSCGRPSIRTAWEDYIWQAPVTFKGFRE (SEQ ID NO: 44)			
MANSC1	54682	NM_018050	Homo sapiens MANSC domain containing 1 (MANSC1), mRNA
mRNA Sequence			
AACCACAAAACCCGCCAGGCCGGTGCGGGAGCTGCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCCCGC GCGGATTCGCGGTCCTTCCCGCGGGCGGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCG GGGTCTCTCGACGCCAGAGAGAAATCTCATCTGTGCGAGCCTTCTTAAAGCAAACCTAGACAGAGG GAGGATTATCCTTGACCTTTGAAGACAAAACCTAACTGAAATTTAAAAATGTTCTTCGGGGGAGAAGGGA GCTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATTGCCTCAA AAAGAGTCTAGAAGATGTGTCTGATGACATCCAGTCATCTCTTCTAAGGGAATCAGAGGCAATGAGCCC GTATATACTTCAACTCAAGAAGACTGCATTAATTTCTGCTGTTCACAAAAACATATCAGGGGACAAAG CATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGTCC CAACGAGGAAGCCTGTCCATTGAAACAGCAAAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCA TCTTTGACCAAGAAATTTGCCAAGCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAAATTTGAC AAGCAGTCACTCCCTAGCCCATCATCACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACAC ACTTTCTCAGAAGTTTGGATCTCAGATCACTTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCAG CTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAAATTTTCTCTGATCAAGAAATAGCTCATC TGCTGCCTGAAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCTAC TCCAAAGCCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCCAGCCACAGCTG GCCACCACAGCTCCACCTGTAACCACTGTCACCTTCTCAGCTTCCACGACCTCATTCTACAGTTTTTA CACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTAC GGACTCGAAAGGCAGCTTAGAAACCATACCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAAT GTGTATAACCTACTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGCGG AAGGTAGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTCCAGAAAATCAGTACGGCCTTCCATT TGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTGGTGCTCTTCTGCTGATAGGCCTCGTCTCTCGTG GGTAGAATCTCTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGATTATTTGATCAATGGGATCT ATGTGGACATCTAAGGATGGAACCTGGTGTCTCTTAATTCATTTAGTAACCAGAAAGCCCAATGCAATGA GTTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTGTATTTTGAAGACAGGAAATGCCCTTCTGCTTT CCTTTTTTTTTTTTGGAGACAGAGTCTTGCTTTGTTGCCAGGCTGGAGTGCACTAGCACGATCTCGGCT CTCACCGCAACCTCCGCTCTCTGGGTTCAAGCGATTCTCTGCTCAGCTCCTAAGTATCTGGGATTAC AGGCATGTGCCACCACACCTGGGTGATTTTTGTATTTTGTAGTAGAGACGGGTTTACCAATGTTGGTACG GCTGTGCTCAAACCTGACCTAGTGATCCACCTCTCGGCTTCCAAAGTGCTGGGATTACAGGCATG AGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGGAATGAAGTGGGAACCAATTA GGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCTATGTAAGTAATAAAGTATA ATTGCCATATAAATTTCAAATCAACTGGCTTTTATGCAAGAAACAGGTTAGGACATCTAGGTTCCAA TTCAATTCATCTTGGTTCCAGATAAAATCAACTGTTTATATCAATTTCTAATGGATTGCTTTCTTTT TTATATGGATTCTTTTAAACTTATTCAGATGTAGTTCTTCCAATTAATATTG (SEQ ID NO: 45)			
Translated protein sequence			
MFFGGESLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSS			

<p>LSKGIRGNEPVYTSTQEDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPN EEACPLKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDY SKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIHL LPENVSAIPATVAVASPHHTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTS QPPTTLISTVFTRAAATLQAMATTAVLTTFQAPTDSKGSLETIPFTEISNLTNTGN VYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSVPENQYGLPFKWLIGSLLF GVLFLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI (SEQ ID NO: 46)</p>			
MOBK1B	55233	NM_018221	Homo sapiens MOB1, Mps One Binder kinase activator-like 1B (yeast) (MOBK1B), mRNA
mRNA Sequence			
<p>GCGAGGTGGGGTAGCGGGCAAGCGGGCGCCGAGGTTTGCAAAGGCTCGCAGCGGCCAGAAACCCGGCT CCGAGCGGGCGGGCCCGGCTTCCGCTGCCCCGTGAGCTAAGGACGGTCCGCTCCCTCTAGCCAGCTCCGA ATCCTGATCCAGCGGGGGCCAGGGGCCCCCTCGCTCCCTCTGAGGACCGAAGATGAGCTTCTCTTCA GCAGCCGCTCTTCTAAACATTCAAACCAAAGAAGATATCCCTGAAGGATCTCATCATGTAACCTTT AAAACATGCAGAAGCAACTCTAGGAAGTGGGAATCTGAGACAAGCTGTTATGTTGCCTGAGGGAGAGGAT CTCAATGAATGGATTGCTGTGAACACTGTGGATTCTTTAACCAGATCAACATGTTATATGGAATATTA CAGAATTCTGCACGAAGCAAGCTGTCCAGTCATGTCTGCAGGTCGAGATATGAATATCACTGGGCAGA TGGTACTAATATTAAGCAATCAATGTTCTGCACCAAAATACATTGACTATTTGATGACTTGGGTT CAAGATCAGCTTGATGATGAAACTCTTTTCTTCTAAGATTGGTGTCCATTTCCTCAAAACCTTTATGT CTGTGGCAAAGACTATTCTAAAGCGTCTGTTCAAGGTTTATGCCCATATTTATCACCAGCACCTTGATT TGTGATGCAGCTGCAAGAGGAGGCCCCACCTCAACACCTCTTTAAGCACTTTATTTCTTTGTTTCAAGG TTTAATCTGATTGATAGCGGTGAGCTGGCACCTCTTCAAGAATTAATAGAGAACTTGGATCAAAAGACA GATAAATGTTTCTTCTAGAACACAGTTACCCCCCTTGCTTCATCTATTGCTAGAACTATCTCATTGCTATC TGTATAGACTAGTGATACAACTTTAAGAAAACAGGATAAAAAGATACCCATTGCCTGTGTCTACTGAT AAAATTATCCCAAAGGTAGGTTGGTGTGATAGTTTCCGAGTAAGACCTTAAGGACACAGCCAAATCTTAA GTACTGTGTGACCACTCTTGTGTTATCACATAGTCATCTTGGTTGTAATGTGATGGTTAAGCTGTA GCTTATAAATTTACTTATTATCTTTTACTCATTACTCAGTCATTTCTTTACAAGAAAATGATTGAATC TGTTTTAGGTGACAGCACAATGGACATTAAGAATTTCCATCAATAATTTATGAATAAGTTTCCAGAACAA ATTTCTTAATAACACAATCAGATTGTTTATCTTTTATTTTACGAATAAAAAATGTATTTTTCAGTAA AAAAA (SEQ ID NO: 47)</p>			
Translated protein sequence			
<p>MSFLFSSRSKTFKPKKNIPESHQYELLKHAEATLGSGNLRQA VMLPEGEDLNWIAVNTVDFNQINMLYGTITEFCTEASCPVMSAGPRYEHWADGTN IKKPIKKSAPKYIDYLMTWQDQLDDELTFPSKIGVPFPKNFMSVAKTILKRLFRVYA HIYHQHFD SVMQLQEEAHLNLSFKHF IFFVQEFNLIDRRELAPLQELIEKLGSKDR (SEQ ID NO: 48)</p>			
NCBP1	4686	NM_002486	Homo sapiens nuclear cap binding protein subunit 1, 80kDa (NCBP1), mRNA
mRNA Sequence			
<p>ATTGAGAGGCCACCGGGAACCATTTGAGAAGCCCCGAGGACCGGCTGAGCGGAGGCGGAGACTAGAGC GGCCGCCGCGACGACCCGCCCTTACGGCGTACGACGACCGCGGCCCGGGGGCTCTGAGTGGCCAAAGCGGC GGCACTTTCTGCGTGGCCCCGGAAGGACATAGAGCGGAAGGCGGGAGAAAGAAGTAGCCGGCAGGCGGAG GCAGCCCGAGGGGGCGGTTGCATGTGTGCCAGACGTTCTGAGCCCACTGAGCTTCTCAGCCGGCTGTC GCAGCGCTAGCCCCACCGCGGCCCTCTCCTGCGCTTCCGGGGCCGTGGCGAGCTAGTGCCTGCGTG CCGGCCCATCCGCGCGCTTGCAGCTGTCTTGCCTGCGGCCAGCGCCAGACAGTTCTGCGAGCGCTTAC CGCTGGCTCTCGGTTCCGCGGCGCACCGGAGGGCAGCATGTGCGGGCGGGGCACAGCGACGAGAACG ACGGTGGGCAGCCTCACAAAAGGAGAAAGACCTCTGATGCAAATGAACTGAAGATCATTGGAATCTTT AATATGTAAAGTAGGAGAAAAGAGTGCTCTTTGGAGAGCAACCTAGAAGGCTTGCTGTTGTTTGG GAAGCTGATCTTCTAATACTACAAGAGCAAGATCTTAAGGCTTCTTTGTACAGTTGCACGCTATTACCTG AGAAGCTGACAATTTATACAACATTAGTTGGACTACTGAATGCCAGGAATTACAATTTTGGTGGAGAATT GTAGAAGCCATGATTCGTCAACTTAAAGAATCATTGAAAGCAACAATTATAATGAAGCCGTGATTG GTCCGTTTTTATCTGATCTTGTGAATTGTCAATGTGATTGCCGCCCATCAATGGTTGCTATGTTGAAA ATTTGTAAAGCGTAACCTCAGGAAGAAGATGTACCTCAGGTGCGACGAGATTGGTATGTGTATGCATTTCT GTCTATTTGCCCTGGGTTGGAAAGGAGTTGTACGAAAAGAAAGATGCAGAGATGGACCGCATCTTTGCC AACACTGAAAGCTATCTTAAAGACGCCAAAGACTCATGTACCCATGTTACAGGTATGGACTGCTGATA AACCACATCCACAAGAAGAGTATTTAGATTGCCGTGGGGCCAGATTGAGAAATTGAAAAGGATCGCTG</p>			

GCAGGAACGGCACATCCTAAGACCTTATCTTGCCTTTGACAGCATCCTGTGTGAAGCACTGCAGCACAAAT
CTGCCTCCTTTTACACCACCTCCTCACACTGAAGATTGAGTGTACCCAAATGCCAAGGGTCATCTTCAGAA
TGTTTGATTACACAGATGATCCCGAGGGTCTGTGTCATGCCAGGGAGTCATTGAGTGGAAAGATTGTAAT
AGAAGAGAATCTTCACTGCATCATTAAAGTCCCACTGGAAGGAAAGGAAGACTTGTGCTGCACAGTTAGTG
AGCTATCCAGGGAAGAACAAGATCCCTTGAAGTACACATAGTTGAGGTGATCTTTGCAGAGCTGTTTC
AACTTCCAGCACCCCTCACATTGATGTGATGTACACAACACTCCTCATTGAACTGTGCAAACCTTCAACC
TGGCTCTCTACCCCAAGTTCTTGCACAGGCAACTGAAATGCTATACATGCGTTTGGACACAATGAACACT
ACCTGTGTAGACAGGTTTATTAATTGGTTTTCTCATCATCTAAGTAACCTCCAGTTCCGTTGGAGCTGGG
AAGATTGGTCAGATTGTCTTAGTCAAGATCCTGAAAGTCCCAAACCGAAGTTTGTAAAGAGAAGTTCTAGA
AAAATGTATGAGGTTGTCTTACCATCAGCGTATATTAGATATTGTTCTCTACCTTCTCAGCTCTGTGT
CCTGCAAACCCAACTGCATTTACAAGTATGGAGATGAAAGTAGCAATTCTCTTCTGGACATTCTGTTG
CCCTCTGTGTTAGCTGTTGCTTTTAAAGTAAGGCAACCAATGATGAAATCTTCAGCATCTGAAAGATGT
ACCAAATCCTAACCCAGGATGATGACGACGATGAAGGATTGAGTTTAAACCCATTGAAATAGAGTCTTT
GTACAGACTCTGCTACACTTGGCAGCCAAATCATTGAGCCACTCCTTCACTGCTCTTGCAGAGTTTCATG
AAGTCTTCAAAACCCTAGCTGAAAGTGAAGGAAAGTTACATGTGCTAAGAGTTATGTTTGGAGTCTG
GAGGAACCATCCACAGATGATTGCTGTACTAGTGGATAAGATGATTGCTACACAAATGATTGATTGTGCT
GCCGTAGCAAATGGATCTTCTCTTCCAGAACTATCTCGTGACTTTACCAGATTGTTTGTGTTGGGAAATTT
TGCACCTCTACAATTGTAAGATGAACAAACATGTCCTGAAGATCCAGAAAGAGCTGGAAGAAGCTAAAGA
GAAACTTGCTAGGCAACACAAACGGCGAAGTGATGATGACGACAGAAGCAGTGACAGGAAAGACGGGGTT
CTTGAGGAACAAATAGAACGACTTCAGGAAAAAGTGGAAATCTGCTCAGAGTGAACAAAAGAAATCTTTTCC
TCGTTATATTTTACGCGTTTATCATGATCTTGACCGAGCACCTAGTACGATGCGAAACTGATGGGACCAG
TGTATTAAACCATGGTATAAGAAGTGTATAGAGAGGCTGCAGCAGATCTTCTTACAGCATCACCAAATA
ATCCAGCATACATGGTGACCTTGGAGAACCTTCTCTTCACTGCTGAATTAGACCCCTCATATCTTGGCCG
TGTTCCAGCAGTTCTGTGCCCTGCAGGCCTAAGGGTCAATTTTTCTCATGTCAAGGTTTTTTTTGATAT
CTTAAATAAATTTGTCTTATTTTTTGTGTTTGAATGCTTGTCTTCTGTAGTATCCTTTCACCTCTTA
AAGGAAACAAAGGGGAAGAGGACAGTGAATGAACATGGCATTACTTTAATTGCCCTGAAAAGCAAATAC
TTCTTACCGGCAGTAATGTGACTATGACCATGATAATTATATATGTGACAGATACAAATCTCTGTGAT
CAGTTTGTATTTTTTTCTCTTAAAGGCACAAAATAATTGGTTTGGAGTATGTGAAACACTAGAGGTCA
ACCTTACATAGTATATAGAAGTGTATGGGTTTACCCAGCTACCCAGTAGCATAACTTTTACAGCTCGGGG
ATGAATTAACTAGCTGAATAAACTAAAGTATGGTTTTTAACTTTGGCATTTCATGATTTATCATC
TCACTCTACTCTAAAACCTGGTGGTTTTCTTACTGAAGGTGTTCTCCATTTGAAATTTTCTCAGAGTAT
TTTTAAGTAGTATCTTAAAGACATGACTTGTAGTAATAAAAGTGTACTAGTTGGAAGAGTAGCTCTCA
AATTTGTCTTAATGTAAATCACCTGGGAATCTTCAAGTTATTTTGAATTTAAACCACCGTCTGGGGGT
GGAACGAGACATCCTCAGTAATCCTTAAAGTTTCCCGAGGTGATCCAGGTTTGGTCACCATATCTTA
GAGCATCTACTCACTTCTCTAGCCTTGGGGTTATTTGTCCAAGGTCTTGTAGTGAGTTACAGAATACTA
AAGTGGATGTAGAAGTGGTCAGATTGACTGAACTATACCTGAATTAGATGTGAGTTAGATTTTGT
ATATGGAACCTGATCCAAAACTACGAAGTCTGAGCTGTTTCTGTATAGTACTGATGCTGAAATAA
GATGACAGCAGTTTGTAAAATAATACACAAATATGAGGAATTGCTGACATTCCAAATTTCTCAGAGTAT
TAGACTTTTTTCAATTAACCTTAGAAAAAATTACCAGTAATCCTACAACACTACTGGTAGTGTGTTGTG
ATTTGCACAAAATAGGTATAATTTTTCTTATACATCCCAAGTTTATGATGCATTAAGCGTTTTGCATA
TTTTGATATATTTTGTCTTGGTTTACCATACATTTTAGTGGCTACAGAATGTAGTCTGCTTAATAAATG
GGAATTCCTAGAATGTTTAAATACCACTATTTAAGCAAAAATACAAAATATCCAGAAAAATCCAGGTT
GCGTGGCTGGTTAGTAAAGGACTAAAACCCAGGTTCTTGGCTAAATGTTTTCGTTTATCTGTTATCTT
TCCCATTGCTTAAAGCACAGCAAACTATGTAATTATATATAATTACAGTTGACCCTGAAACAACATGGG
TTTGAACGTGTGAGTCTCCTTACACACAGGTTTTCTTCCACCCCTGAGATGGCAAGACCCAGCCCTTGT
CTTCTCAGCCTGCTCAACGTGAAGATGATGAGGATGAAGACCTTTATGATGATCCACTTCTACTTATTA
AATAGTAAATATATTTTTTCTTATGATTTTATTTCTTTCTAGCTTCATAAGAATATAGCATATGG
GCTGGGCGCAGTGGCTCACGCTGTAAATCCAGCACTTTGGGAGGCTGAGGCGGGCGGATCACAAGGTCA
GGAGATTGAGACCATCCTGGCTAACACAGTGAACCCCTGTCTCTACTAAAAACACAAAACTTAGCCAGG
CGTGGTGGTACATGGCTGTAGTCCCAGCTACTTGGGAGGCTGAGACAGGAGAATCGCTTGAACCTGGGAG
GTGGAGGTTTCACTGAGCCAAAGATTGTGCCACTGCACCTCCAGCCTGGGTGATGGAGCGAGGCTCTGTCTC
AAAAAGAAAAAAATATATAGCATATAACATACAAAATGAGTTTATCAACTGTTTGTATTGGTAAAGTC
AGCAGTGGGCTATTGGTGGTTAAGTTTTGGGGGAGTCAAAAGTTACATGCAAATTTTTACTGTGCGGGG
TGTCAGCATCCCTAACCCCATGTTGTTCAAGGGTCAACTGTAGTTTAAATGACTCCTGTCTCAAAAAAC
CAAAGGATAACCTTAAAGGATTGGTAACCTTGACTCAAACTGCTTTGTAATCTTTTCAATGTACTG
AAAAGTGTGGCTAGTTATGTTTGTATCCACATCTAGAGAAAATTTGTAGGTTTAAATTTCTTTCTTGG
TCTCTCTTCAATGATAATGGTTGCTTTTAAACAGCTGTTGCTGATGTGGTCTGCTGTCTCCAGTCTA
GCAGCTTTAGTGTATGGAAAAATTGAAGTAGGAATTGAGTTTTGAAGAAATAAAGGTGTAAGAGCAAACA
TTCAACAGTTGCTGTCCCGAGTAATGAAGTTTACACAGACAAAAGATGGCATGTCACTGTACATCATACC
TTGCAATAAATAATTCGTTAAATTGTGCTGGTGAATTTAAACATGCTTTTGTCAAAGTAAA (SEQ ID NO:

AGGCAGGGCCATGGGCACCCCTGCTCAGCCTCCTGTGGAGGAGGCTCCAGTCCCGCTCCGTGTACTGCAT
 CTCGCTGACGGGGCCGGCATCCAGGAGGCGGTGGAGGAGGCTGAGTGTGCCGGGCTGCTGGGAAGCCC
 CCTGCCATTAGGCCCTGTAACCTGCAGCGCTGTGCAGCCTGGAGCCCGGAGCCCTGGGGAGAGTGTCTG
 TCAGTTGTGGCGTTGGCGTCCGGAAGCGGAGCGTTACTTGCCGGGGTGAAAGGGGTCTTTGTCCATAC
 CGCAGCGTGCTCCTTGGAGACCGGCCACCTCTGACTGAGCCCTGTGTGCATGAGGACTGCCCCCTCCTC
 AGTGACCAGGCCCTGGCATGTGGGCACCTGGGGTCTATGCTCCAAGAGCTGCAGCTCGGGCACTCGGAGGC
 GACAGGTCACTGTGCCATTGGGCCGCCAGCCACTGCGGGAGCCTGCAGCACTCCAAGCCTGTGGATGT
 GGAGCCTTGTAACACGCAGCCCTGTCACTCCCCAGGAGGTCCCAGCATGCAGGATGTGCACACCCCT
 GCCAGCAACCCCTGGATGCCGTTGGGCCCTCAGGAGTCCCCTGCTCAGACTCCAGAGGCCAGTGGTGGG
 CAGCCCAGGAACACCCCTCAGCCAGGGGTGACCACAGGGGAGAACGAGGTGACCCAGGGGCGACCAAGG
 CACCCACCTGTAGCCCTGGGCCCGCTCCCTCTCTGCAGCAGCCCCATAACCAGCAACCCCTGCGGTGCG
 GGCTCAGGGCCCCACGACTGCAGACACAGTCTCACGGGTGCTGCCCGATGGCCACACGGCATCTCTCG
 GGCTCAGTGGCAAGGCTGCCCTGGGGCCCCCTGTGCAGCAGCAGGTACGGGTGCTGCCCTGACAGGGT
 ATCTGTGCTGAGGGGCCCCATCACGCTGGCTGCACAAAGTCGTATGGTGGTGACAGCACCAGGGGCGCATG
 CCCAGTCAAGGGCAGTGGCTTCTACAGTCCACAACCCACAGCCCGAGCCAGGCCAGAGAATGAGCCATG
 GTGAGTGCCGGGCTCCAGTCTTGGCTGTTGCTATGACAACGTGGCCACTGCAGCCGCTCCTCTTGGGGA
 AGGCTGTGTGGGCCAGCCAGCCATGCCTACCCCGTGGGTGCTGCTGCCAGTGCCCATGGCTCTTGC
 GCAGACTGGGCTGCCCGTGGTACTTCTGTGCTCTGTGGGCCAATGTAACCGCTTCTGGTATGGCGGCT
 GCCATGGCAATGCCAATAACTTTGCTCGGAGCAAGAGTGATGAGCAGCTGCCAGGGATCTCTCCATGG
 GCCCCGCTGCTCCCGAGCCTGGGGCTTCTGGAAGGAGCACCCACAGGATGGTGGCGGCAGCAGTCTTGCA
 GGCGAGCAGGAACCCAGCCAGCACAGGACAGGGGCGCGGTGCAGAGAAAGCCCTGGCCTTCTGGTGGTC
 TCTGGCGGCAAGACCAACAGCCTGGGCCAGGGGAGGCCCCCCACACCCAGGCCCTTTGGAGAATGGCCATG
 GGGCAGGAGCTTGGGTCCAGGGCCCTGGACTGGGTGGAGATGCCGGATCACAGGCCACCTTCCAC
 AGCTCCTCTACAGGATTAGCTTGGCAGGTGTGGAGCCCTCGTTGGTGCAGGCAGCCCTGGGGCAGTTGG
 TGCGGCTCTCTGCTCAGACGACACTGCCCGGAATCCAGGCTGCCCTGGCAGAAAGATGGCCAGCCAT
 CTCTCTGACAGGCACAGGCTGCAGTTCGACGGATCCCTGATCATCCACCCCTGCAGGCAGAGGACGCG
 GGCACCTACAGCTGTGGCAGCACCCGGCCAGGCCGCGACTCCCAGAAGATCCAACCTTCGCATCATAGGGG
 GTGACATGGCCGTGCTGTCTGAGGCTGAGCTGAGCCGCTTCCCTCAGCCAGGGACCCAGCTCAGGACTT
 TGGCCAAAGCGGGGCTGTCTGGGCCCTGGGGGCCATCCCTCTTACACCCACAGCCTGCAACACAGGCTG
 GCTTTGACAGCAACACAGCCCGGGTGGTGGATGCCAGTCCAGGCCAGCGGATCCGCTGCGGTG
 CCGAAGGCTTCCCGCCCCAGCCATCGAGTGGCAGAGAGATGGGCAGCCTGTCTCTTCCAGACACCA
 GCTGCAGCCTGATGGCTCCCTGGTCATTAGCCGAGTGGCTGTAGAAGATGGCGGCTTCTACACCTGTGTC
 GCTTTCAATGGGCAGGACCGAGACCAGCGATGGGTCCAGCTCAGAGTTCGGGGGAGCTGACAATCTCAG
 GACTGCCCCCTACTGTGACAGTGGCAGAGGGTGATACGGCCAGGCTATTGTGTGTGGTAGCAGGAGAAAG
 TGTGAACATCAGGTGGTCCAGGAACGGGCTACCTGTGCAGGCTGATGGCCACCGTGTCCACAGTCCCCA
 GATGGCACGCTGCTCATTTACAACCTGGCGGCCAGGGATGAGGGCTCCTACAGTGCAGTGCTTACCAGG
 GGAGCCAGGCAGTGCAGCCGAGCACCGAGGTGAAGGTGGTCTCACCAGCACCCAGCCCGCCAGCCAGGGA
 CCCTGGCAGGGACTGCGTCGACAGCCAGAGCTGGCCAACTGTGATTGTATCTGCAAGGCCAGCTTTGT
 GGCAATGAGTATTACTCCAGCTTCTGCTGTGCCAGCTGTTACGTTTCCAGCCTCAGCTCAGCCATCT
 GGCAGTAGGGATGAAGGCTAGTTCCAGCCCCAGTCCAAAATAGTTATAGGGCTAGGGAGAAAGGAAGAT
 GGACTCTTGGCTTCCCTCTCTGCTGGCTGGCAAAGGGAGTTATCTTCTGGAATACATTAGCTCTTTCAAAA
 CCCACCCAGTGTTTAGCCTCAACGGCAGCCAGTTACCAGCTTCTCTCTGTAGCCTTCCAGCAGTGTGTGCA
 TCTCTGACATAACCACAGGCTGCTGTTTCAAGAAGAGCAATCTGTTTGGATAAGAAAAACCTTTACTTT
 ACAGCTTCCCTTTATAATTTGTTACACAGGAATAGTTAAATGCATTTGTTTGTGTTTGTGAGACAGA
 GTTTCACCTTTGTTGCCAGGCTGGAGGGCAATGGCGCGATCTCAGCTCACTGCAAGCTCCCGTCTCCTGG
 GTTCTTGATTCTCTGTGTGTCAGCCTTCTGAGTAGCTAGGATTACAGATGCCTATCACCATGCCTGGGTAA
 TTTTGTATTTTTAGTTGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTTCTGACCTCAGA
 TGATCTGCCCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCAGCCAGCCATCAATG
 CATTTTTTTTATTTTTTTTTTGGAGACAGATTTGCACTTCTTGGCCAGGCTGGAGTACAATGGTGCAT
 CTGGCTCACTGCAACCTCCACCTCCTGGGTTCAAGCGCTTCTCCAGCCTCAGCCTCCTGAGTAGCTGGG
 ATTACAGGTATGTGCCACCATGCCCTGGCTAATTTTGTATTTTAGTAGAGACGGGGTTTCTCCATGTTGG
 TCAGACTGGTCTTGAACCTCCGACCTCAGGTAATCCGCGCGCTCGGCTCCCAAAATGCTGGGATTAGA
 GGTGTGAGCCACTGTGCCAGCCCATCAATGTGTTTTAAAGCTAGCTGTGAGGGTTCCACTTAATTTAAA
 GCTGGGCAGGGAGATGTGAATGATTTCAAAGTTAACACCTGTTTGTGTTTCTAAAGGGCATGCCAAGTCC
 TGCTGATCAGGGAAGTATTCTGTGCTAAAATCAGCGATGGTTTCAATGCTCTAGTCTCTCTCACCCCTCT
 AGGCAGTGCATCAGTCACTCTAAATCTGGTGCAGAGGGTTAACAGCATAACCCCTGTTGGCAAAAATGGA
 ATAGATGTTAAGACCTCAATAGGGATTGGGATGAAACAGCTGCAGTTAGCACTGTTATCTGAGCATGA
 AAGAACGGAACGCTCCTTACGTCGAGATGTGGACCTTGAAGCCCTCCTGAGGCCAACATGCAATCT
 GGCTGTGACGGTTCACTGACACCTGTGTAAAGCTGACCAGCTGCTCTGTACAGTGACAATGAGGAGCC
 CCTCTCTCCTTAAAGTAGGAATCTGTGAAGCAAAATGTTGCTGCAAGACAAATCAGACTGTCACTCA
 TAAAAACAGCATTAGCAGGATGAGGATAGCAATGGGGAAGGGTTGTGGGCAATGCAGTAACAGGGAAAT

GGCTTCAGAAATGGTTTGAGTTGGAAGACAACATTCTTCATCTCTCAGGACTTCTAATTCCTTGATGCTA AAAGAAGAGGCATGGATTCTATGAGCTTCCAAGTCCCTTTTCCACTTTAACCTTCTACAAATCTTTTCAGAG GACTGCCTAGTAGCAAAGGTTATTCTGGACACAGGAAAGACGGGCATTACAGGGACCAAAGCTCTGAAA GGTGACTTTTATTACCAACACACTGGCTGGAAAAGGGACAAACCACATCACGGGTGAGTGATACTTCTCA GTCTTCTCTACTCATTCAACAAAGGAAATGTGGGCTGGGGCAGAGGTCTTTTTTCATTTAATACTGGAAA AATATTGAAGAGCATCCATGTTCACTTATGGCTGGTTTTGCTATAGAAATTGGAATAAAGGCCACTTT TTTGAATCCCCAGTTTAATTAATAAAAAAAAAAAAAAAAAA (SEQ ID NO: 53)			
Translated protein sequence			
MRLLLVPLLLAPAGSSAPKVRQSDTWGPWSQWSPCSRCTCGG GVSFRRPCYSQRRDGGSSCVGPARRSHRSCRTECPDGARDFRAEQCAEFDGAEFQGR RYRWLPYYSAPNKCELNCIPKGENFYKHEAVVDGTPCEPKRDVCVDGSCRVVGCD HELDSSKQEDKCLRCGGDGTTCYPVAGTFDANDLSRAVKNVRGYYLNGHWITIEARA LPAASTILHYERGAEDLAPERLHARGPTSEPLVIELISQEPNPGVHYEYHLPRLRPS PGFSWSHGSWSDCSAECGGGHQSRLVFCTIDHEAYPDHMCQRQPRPADRRSCNLHPCP ETKRWKAGPWAPCSASC GGGSQSRSVYCISSDGAGIQEAVEEAECAGLP GKPPAIQAC NLQRCAAWSPEPWGECVSCGVGVRKRSVTCRGERGSL LHTAACSLDRPPLTEPCVH EDCPLLSDQAWHVGTWGLCSKSCSSGTRRRQVICAIGPPSHCGSLQHSKPV DVEPCNT QPCHLPQEVPSMQDVHTPASNPWMPLGPQESPASDSRGQWAAQEHPSARGDHRGERG DPRGDQGTHTLSALGPAPSLQPPYQQPLRSGSGPHDCRHS PHGCCPDGHTASLGPQWQ GCPGAPCQQSRYGCCPDRVSVAEGPHHAGCTKSYGGDSTGGMPRSRAVASTVHNTHQP QAQQNEPSECRGSQFGCCYDNVATAAGPLGEGCVGQPSHAYPVRCLLPSAHGSCADWA ARWYFVASVGQCNRFYWGCHGNANNFASEQECMSSCQGLHGPRRPQPGASGRSTHT DGGGSSPAGEQEPSQHRTGA AVQRKPWPSGGLWRQDQPGPGEAPHQTQAFGEWPWGQE LGSRAPGLGGDAGSPAPPFHSSSYRISLAGVEPSLVQAALGQLVRLSCSDDTAPESQA AWQKDQGPISDRHRLQFDGSLIIHPLQAEDAGTYSCGSTRPGRDSQIKLRIIGGDM AVLSEAELSRFQPRDPAQDFGQAGAAGPLGAIPSSHQPANRLRLDQNPVRVDASP GQIRIMTCRAEGFPFPAIEWQRDQGPVSSPRHQLQPDGSLVISRVAVEDGGFYTCVAF NGQDRDQRWVQLRVLGELTISGLPPTVTVPEDTARLLCVVAGESVNIWRNRNGLPVQ ADGHRVHQSPDGTLLIYNLRARDEGSYTC SAYQGSQAVSRSTE VKVVSFAPTAQPRDP GRDCVDQPELANCDLILQAQLCGNEYYSFCCASC SRFQPHAQPIWQ (SEQ ID NO: 54)			
PCDH1	5097	NM_002587	Homo sapiens protocadherin 1 (PCDH1), transcript variant 1, mRNA
mRNA Sequence			
CGCAAAGCCGCCGGGCTGCTGCGCCAGAGCCAGCCGGAGCCGGAGCCGGAGCCCGAACTGCAGCTCCAG CCCCAGCCGTGCGGAGCCGCAGCCAGCCGGGCGGCGCGGCTCATGGACAGCGGGCGGGCGGGCCG GCGTGCCTGGGAGGCGCCCTCCTGATTCTGGGCGCTCCAGGATGGAGCACCTGAGGCAGCCCGAGC CCTGGGGGGCAACGGCTACTGCTGCCCTCCATGCTGCTAGCACTGCTGCTCCTGCTGGCTCCATCCCCAG GCCACGCCACTCGGGTAGTGTAAGGTGCCGAGGAACAGCCACCCAACACCCTCATTGGGAGCCTCGC AGCCGACTATGGTTTTCCAGATGTGGGCACCTGTACAAGCTAGAGGTGGGTGCCCCGTACCTTCGCGTG GATGGCAAGACAGGTGACATTTTCACCACCGAGACCTCCATCGACCGTGAGGGGCTCCGTGAATGCCAGA ACCAGCTCCCTGGTGATCCCTGCATCCTGGAGTTTGAGGTATCTATCACAGACCTCGTGCGAATGGCAG CCCCCGGCTGCTAGAGGGCCAGATAGAAGTACAAGACATCAATGACAACACACCCAACCTTCGCCTACCA GTCATCACTCTGGCCATCCCTGAGAACACCAACATCGGCTCACTCTTCCCCATCCCGTGCGTTCAGACC GTGATGCTGGTCCCAACGGTGTTGGCATCCTATGAGCTGCAGGCTGGGCTGAGGCCAGGAGCTATTTGG GCTGCAGGTGGCAGAGGACCAGGAGGAGAAGCAACCACAGCTCATTGTGATGGGCAACCTGGACCGTGAG CGCTGGGACTCCTATGACCTCACCATCAAGGTGCAGGATGGCGGCAGCCCCCAGCGCCAGCAGTGCCC TGCTGCGTGTACCGTGCTTGACACCAATGACAACGCCCCAAGTTTGAGCGGCCCTCCTATGAGGCCGA ACTATCTGAGAAATAGCCCCATAGGCCACTCGGTATCCAGGTGAAGGCCAATGACTCAGACCAAGGTGCC AATGCAGAAATCGAATACACATTCACCAGGCGCCCGAAGTTGTGAGGCGTCTTCTTCGACTGGACAGGA ACACTGGACTTATCACTGTTCAAGGCGCGGTGGACCGTGAGGACCTAAGCACCTGCGCTTCTCAGTGCT TGCTAAGGACCGAGGCACCAACCCCAAGAGTGCCCGTGCCAGGTGGTTGTGACCGTGAAGGACATGAAT GACAATGCCCCCACCATTGAGATCCGGGGCATAGGGCTAGTGACTCATCAAGATGGGATGGCTAACATCT CAGAGGATGTGGCAGAGGAGACAGCTGTGGCCCTGGTGAGGTGTCTGACCGAGATGAGGGAGAGAATGC AGCTGTCACCTGTGTGGTGGCAGGTGATGTGCCCTTCCAGCTGCGCCAGGCCAGTGAGACAGGCAGTGAC AGCAAGAAGAAGTATTTCTGCACTACACCCCCCTAGACTACGAGAAGGTCAAAGACTACACCATTG AGATTGTGGCTGTGGACTCTGGCAACCCCCCACTCTCCAGCACTAACTCCCTCAAGGTGCAGGTGGTGGA			

CGTCAATGACAACGCACCTGTCTTCACTCAGAGTGTCAGGTGCGCTTCCCGGAAACAACAAGCCT GGTGAAGTGATTGCTGAGATCACTGCCAGTGATGCTGACTCTGGCTCTAATGCTGAGCTGGTTTACTCTC TGGAGCCTGAGCCGGCTGCTAAGGGCCTCTTACCATCTCACCCGAGACTGGAGAGATCCAGGTGAAGAC ATCTCTGGATCGGGAACAGCGGGAGAGCTATGAGTTGAAGGTGGTGGCAGCTGACCGGGGCAGTCTTAGC CTCCAGGGCACAGCCACTGTCTTGTCAATGTGCTGGACTGCAATGACAATGACCCCAATTTATGCTGA GTGGCTACAACCTTCTCAGTGATGGAGAATGCCAGCACTGAGTCCAGTGGGCATGGTGAATGCTATTGA TGGAGACAAGGGGGAGAATGCCAGGTGCAGCTCTCAGTGGAGCAGGACAACGGTGACTTTGTTATCCAG AATGGCACAGGCACCATCTATCCAGCCTGAGCTTTGATCGAGAGCAACAAAGCACCTACACCTTCCAGC TGAAGGCAGTGGAATGGTGGCGTCCCACCTCGCTCAGCTTACGTTGGTGTCAACATCAATGTGCTGGACGA GAATGACAACGCACCCCTATATCACTGCCCCCTCTAACACCTCTCACAAGCTGCTGACCCCCAGACACGT CTTGGTGAGACGGTCAGCCAGGTGGCAGCCGAGGACTTTGACTCTGGTGTCAATGCTGAGCTGATCTACA GCATTGCAGGTGGCAACCCCTATGGACTCTTCCAGATTGGGTACATTAGGTGCCATCACCTTGGAGAA GGAGATTGAGCGGCGCCACCATGGGCTACACCGCTTGGTGGTGAAGGTGAGTACCGCGGCAAGCCCCCA CGCTATGGCACAGCCTTGGTCCATCTTTATGTCAATGAGACTCTGGCCAACCGCACGCTGCTGGAGACCC TCCTGGGCCACAGCCTGGACACGCCGCTGGATATTGACATTGCTGGGGATCCAGAATATGAGCGCTCCAA GCAGCGTGGCAACATTCTCTTTGGTGTGGTGGCTGGTGGTGGCGTGGCCTTGCTCATCGCCCTGGCG GTTCTTGTGCGCTACTGCAGACAGCGGGAGGCCAAAGTGGTTACCAGGCTGGTAAGAGGAGACCAAGG ACCTGTATGCCCCCAAGCCAGTGGCAAGGCCCTCCAAGGGAAACAAAAGCAAAGGCAAGAAGAGCAAGTC CCCAAAGCCCGTGAAGCCAGTGGAGGACGAGGATGAGGCGGGCTGCAGAAGTCCCTCAAGTTCAACCTG ATGAGCGATGCCCCTGGGGACAGTCCCCGCATCCACCTGCCCTCAACTACCCACAGGCAGCCTGACC TGGGCGGCCACTATCGCTCTAACTCCCCACTGCCTTCCATCCAGCTGCAGCCCCAGTCACCTCAGCCTC CAAGAAGCACAGGTGGTACAGGACCTGCCACCTGCAACACATTCGTGGGCACCGGGGACACCACGTCC ACGGGCTCTGAGCAGTACTCCGACTACAGCTACCGCACCAACCCCCCAATACCCAGCAAGCAGGTAG GCCAGCCCTTTACGCTCAGCACACCCAGCCCTACCCACCCCTACCCAGGAGCCATCTGGACCGAGGT GTGGGAGTGATGGAGCAGGTTTACTGTGCTGCCCCTGTTGGGGGCCAGCTGAGCCAGCAGTGGGAGGT GGGGCCTTAGTGCCTACCGGGCACACGGATTAGGCTGAGTGAAGATTAAGGGAGGGTGTGCTCTGTGGT CTCTCCCTGCCCCCTCCCCACTGGGGAGAGACTGTGATTGCCAAGTCCCTGGACCTGGACCAGCTA CTGGGCCTTATGGGTGGGGGTGGTAGGCAGGTGAGCGTAAGTGGGGAGGGAAATGGGTAAGAAGTCTAC TCCAAACCTAGGTCTCTATGTCAGACCAGACCTAGGTGCTTCTTAGGAGGGAAACAGGGAGACCTGGGG TCCTGTGGATAACTGAGTGGGGAGTCTGCCAGGGGAGGGCACCTTCCATTGTGCTTCTGTGTGATTG TGCATTAACTCTTCTCACCACCTAGGCTTCTGGGGCTGGGTCCACATGCCCTTGACCTTGACCAATAAA GTTCTCTATTTTTGGAAAAA A (SEQ ID NO: 55)			
Translated protein sequence			
MDSGAGGRRCEAALLILGPPRMEHLRHSPGPGGQRLLLPSMLL ALLLLLAPSPGHATRVVYKVPPEEQPNTLIGSLAADYGFDPVGHLYKLEVGAAPYLVRVD GKTGDIFFTETSIDREGLRECQNQLPGDPCILEFEVSIIDLQVNGSPRLLEGQIEVQD INDNTNFASPVITLAIPTENTNIGSLFPIPLASDRDAGPNGVASVELQAGPEAQELFG LQVAEDQEEKQPQLIVMGNLDRERWDSYDLTIKVDGGSPPRASSALLRVTVLDTNDN APKFERPSYEAELSENSPIGHSVIQVKANDSDQGANAEIEYTFHQAPEVVRLLRLDR NTGLITVQGPVDREDLSLRFVSLAKDRGTNPKSARAQVVVTVKDMNDNAPTIEIRGI GLVTHQDGMANISEDVAEETAVALVQVSDRDEGENAAVTCVVGDPVFFQLRQASSETGS DSKKKYFLQTTPLDYEKVDYTIETIIVAVDSGNPPLSSTNSLKVQVVDVNDNAPVFTQ SVTEVAFPENNKPEVIAEITASDADSGSNAELVYSLEPEPAAKGLFTISPETGEIQV KISLDREQRESYELKVVAADRGSPLQGTATVLVNVLDNDNDPKFMLS GYNFVSMEN MPALSPVGMVTVIDGDKGENAQVQLSVEQDNGDFVIQNGTGILSSLSFDREQQSTYT FQLKAVDGGVPPRSAYVGVITINVLDENDNAPYITAPSNTHKLLTPQTRLGETVSQVA AEDFDSGVNAELIYSIAGGNPYGLFQIGSHSGAITLEKEIERRHHGLHRLVVKVSDRG KPPRYGTALVHLYVNETLANRTLLETLLGHSLDTPLDIDIAGDPEYERSKQKRNILFG VVAGVVAVALIALAVLVRYCRQREAKSGYQAGKKETKDLYAPKPSGKASKGNKSKGK KSKSPKPKVPVEDEDEAGLQKSLKFNLMSDAPGDSPRIHLPLNYPGSPDLGRHYRSN SPLPSIQLQFQSPSASKKHQVVDLPPANTFVGTGDTTSTGSEQSDYSYRTPPKYP SKQVGQPFQLSTPQLPHPYHGAIWTEVWE (SEQ ID NO: 56)			
PDGFB	5155	NM_002608	Homo sapiens platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog) (PDGFB), transcript variant 1, mRNA

mRNA Sequence			
CCTGCCTGCCTCCCTGCGCACCCGACGCTCCCCGCTGCCTCCCTAGGGCTCCCTCCGGCCGCCAGCG CCCATTTTTTCATTCCCTAGATAGAGATACTTTGCGCGCACACATACATACGCGCGCAAAAGGAAAAA AAAAAAAAAAGCCACCTCCAGCCTCGCTGCAAAGAGAAAACCGGAGCAGCCGAGCTCGCAGCTCGC AGCTCGCAGCCCGCAGCCCGCAGAGGACGCCAGAGCGGCGAGCGGGCGGGCAGACGGACCGACGGACTC GCGCCGCGTCCACCTGTGCGCCGGGCCCAGCCGAGCGCGCAGCGGGCACGCCGCGCGCGGGAGCAGCCG TGCCCGCCGCGCGGGCCCCGCGCCAGGGCGCACACGCTCCCGCCCCCTACCCGGCCCGGGCGGGAGTTT GCACCTCTCCCTGCCCAGGTGCTCGAGCTGCCGTTGCAAAGCCAACTTTGAAAAAGTTTTTTGGGGGAG ACTTGGGCCTTGAGGTGCCAGCTCCGCGCTTTCCGATTTTGGGGGCTTTCCAGAAAATGTTGCAAAAA AGCTAAGCCGGCGGGCAGAGGAAAACGCTGTAGCCGCGAGTGAAGACGAACCATCGACTGCCGTGTTTC CTTTTCTCTTGGAGTTGGAGTCCCCTGGGCGCCCCACACGGCTAGACGCTCGGCTGGTTCGCGACG CAGCCCCCGCGCGTGGATGCTCACTCGGGCTCGGGATCCGCCCAGGTAGCGGCCTCGGACCCAGGTCTT GGCCCAGGTCTCTCCCTGCCCCCAGCGACGGAGCCGGGGCCGGGGCGGGCGGCCCGGGGGCATGCG GCTGAGCGCGGCTGCAAGAGGCTGAGCGCTGATCGCCGCGGACCCGAGCCGAGCCCTCCCGGCTCC CAGCCCCCACCTGGCCGCGGGGGCGGCGCGCTCGATCTACGCTCCGGGGCCCCGCGGGGGCGGGGCC GGAGTCGGCATGAATCGCTGCTGGGCGCTCTTCTGTCTCTGTCTGTCTACCTGCGTCTGGTCAGCGCCG AGGGGGACCCATTCCCGAGGAGCTTTATGAGATGCTGAGTGACCACTCGATCCGCTCCTTTGATGATCT CCAAGCCTGCTGCACGAGACCCCGGAGAGGAAGATGGGGCCGAGTTGGACCTGAACATGACCCGCTCC CACTCTGGAGGCGAGCTGGAGAGCTTGGCTCGTGGAGAAGGAGCCTGGGTTCCCTGACCATTTGCTGAGC CGGCCATGATCGCGAGTGCAAGACGCGCACCGAGGTGTTGAGATCTCCCGCGCCTCATAGACCGCAC CAAGCCCAACTTCTGTTGTGGCGCCCTGTGTGGAGGTGCAGCGCTGCTCCGGTGTGCAACAACCCGC AACGTGCAGTGCCGCCCCACCCAGGTGACGTGCGACCTGTCTCAGGTGAGAAAGATCGAGATTGTGCGGA AGAAGCCAATCTTTAAGAAGGCCACGGTGACGTGGAAGACCACCTGGCATGCAAGTGTGAGACAGTGGC AGCTGCACGGCCTGTGACCCGAAGCCCGGGGGTTCCCAGGAGCAGCGAGCCAAAACGCCCAAACCTCGG GTGACCATTCGGACGGTGCAGTCCGCGGCCCCCCAAGGGCAAGCACCAGAAATTCAAGCACACGCATG ACAAGACGGCACTGAAGGAGACCTTGGAGCCTAGGGGCATCGCGAGGAGAGTGTGTGGGCGAGGGTTATT TAATATGGTATTTGCTGTATTGCCCCATGGGGTCTTGGAGTGATAATATTGTTTCCCTCGTCCGCTCTG TCTCGATGCTGATTTCGACGGCCAATGGTGCTTCCCCACCCCTCCACGTGTCCGTTCCACCTTCCATC AGCGGGTCTCTCCAGCGGCTCCGCGCTTGGCCAGCAGCTCAAGAAGAAAAAGAGGACTGAACCTC CATCGCATCTTCTTCCCTTAACCCAAGAACTTGGGATAAGAGTGTGAGAGAGACTGATGGGGTCGCTC TTTGGGGGAAACGGGCTCTTCCCTGCACCTGGCCTGGGCCACACCTGAGCGCTGTGGACTGTCTTGAG GAGCCCTGAGGACCTCTCAGCATAGCCTGCCTGATCCCTGAACCCCTGGCCAGCTCTGAGGGGAGGCACC TCCAGGCAGGCCAGGCTGCCTCGGACTCCATGGCTAAGACCACAGACGGGCACACAGACTGGAGAAAACC CCTCCACGGTGCCCAACACACAGTCACTCGTCTCCCTGGTGCCTCTGTGCACAGTGGCTTCTTTTCGT TTTCGTTTTGAAGACGTGGACTCTCTTGGTGGGTGTGGCCAGCACACCAAGTGGCTGGGTGCCCTCTCA GGTGGGTAGAGATGGAGTTTGTGTTGAGTGCTGTAGATGTTGACCTGGGTATCCCTGCTCTCTGTC CACCCCTTCTCCCCACACTCCACTCTGATTACCTCTTCTCTGGTTCCCTTTCATCTCTCTACCTCCAC CCTGCATTTTCTCTTGTCTGGCCCTTCAGTCTGCTCCACCAAGGGGCTCTTGAACCCCTTATTAAGGC CCCAGATGATCCAGTCACTCTCTCTAGGGCAGAAGACTAGAGGCCAGGGCAGCAAGGGACCTGCTCAT CATATTTCAACCCAGCCACGACTGCCATGTAAGGTTGTGAGGGTGTGTACTGCACAAGGACATTGTATG CAGGGAGCACTGTTACATCATAGATAAAGCTGATTTGTATATTTATTATGACAATTTCTGGCAGATGTA GGTAAAGAGGAAAAGGATCCCTTTTCTAATTCACACAAAGACTCCTTGTGGACTGGCTGTGCCCTGATG CAGCCTGTGGCTTGGAGTGGCCAAATAGGAGGGAGACTGTGGTAGGGGCAGGGAGGCAACTGCTGTCC ACATGACCTCCATTTCCCAAAGTCTCTGCTCCAGCAACTGCCCTTCCAGGTGGGTGTGGGACACCTGGG AGAAGGTCTCCAAGGGAGGGTGACGCCCTCTTGCCCGCACCCCTCCCTGCTTGCACACTTCCCCATCTTT GATCCTTCTGAGCTCCACCTCTGGTGGCTCCTCCTAGGAAACCAGCTCGTGGGCTGGGAATGGGGGAGAG AAGGGAAAAGATCCCAAGACCCCTGGGGTGGGATCTGAGCTCCACCTCCCTTCCACCTACTGCACT TTCCCCCTTCCCGCTTCCAAAACCTGCTTCTTTCAGTTTGTAAAGTCGGTGATTATATTTTGGGGGCT TTCTTTTATTTTAAATGTAAATTTATTTATATCCGTATTTAAAGTTGTAAAAAAAATAACCACA AAACAAACCAAATGAAAAAAAAAAAAAAAAA (SEQ ID NO: 57)			
Translated protein sequence			
MNRWALFLSLCCYLRLVSAEGDPIPEELYEMLSDHSIRSFDDL QRLHGDPEEDGAELDNMTRSHSGGELESLARGRRSLGSLTIAEPAMIAECKTRTE VFEISRRLIDRTNANFLVWPPCQVEVQRCSGCCNNRNQCRPTQVQLRPVQVRKIEIVR KKPIFKKATVTLEDHLACKCETVAAARPVTRSPGGSQEQRAKTPQTRVTIRTVRVRP PKGKHKRFKHTHDKTALKETLGA (SEQ ID NO: 58)			
PHOSPHO2	493911	NM_001008489	Homo sapiens phosphatase, orphan 2 (PHOSPHO2),

			mRNA
mRNA Sequence			
<p>AACAAGGGAGGTGCTGCAGTTGGCGGTCGGGCTAGAGAAGAGAGGCGCCTGCGCTTGCGAGCTGGGCTTG TGAGTGGGGCTGCCGAGAGGGCAGGCGTGGGGCGAGGCCAAGGACTGAACCCGAGGAGCGTCACGGGC GCCGGGGCGGCTGCCGACGGCGGGACTGGGTTTTCTATCAGATGTTCCACGTAATAATGCTGGAGTTAAG AAGTTTCCATTATTTTGTCTCCAAACCAGAAGACTCTGTTCCCTGTATATAGAATAGGAGTAATATTTGAA AACAACTGGCTGATGTTTAAAACTGAAGATTGTCATGATTGTTTATCTAATCCCAATGCTGAAGTAAGA TTGCTTGGAAATACTAAGTTGGGTAATCCAAATCTATTTCTGGAACCATGAAAATTTTGTAGTTTTT GACTTTGACAATACAATCATAGATGACAATAGTACACTTGGATTGTACAATGTGCTCCCAACAAAAAGC TTCCTATTGAACTACGTGATTCTTATCGAAAAGGATTTTGGACAGAATTTATGGGCAGAGTCTTTAAGTA TTTGGGAGATAAGGGTGTAAGAGAACATGAAATGAAAAGAGCAGTGACATCATTGCCTTTCACTCCAGGG ATGGTGGAACCTTCAACTTTTATAAGAAAGAATAAGGATAAAATTTGACTGCATTATTATTTTCAGATTCAA ATTCCGTCTTTCATAGATTGGGTTTTAGAAGCTGCCAGTTTTTCATGACATATTTGTAAAGTGTTTACAAA TCCAGCAGCTTTTAAATAGCAATGGTCATCTCAGTGTGAAAATTATCATACTCATTCTTGCAATAGATGC CCAAAGAATCTTTGCAAAAAGGTAGTTTGTATAGAATTTGTAGATAAACAGTTACAACAGGGAGTGAATT ATACACAAATTTGTTTATTTGTTGATGGTGGAAATGATGCTCCAGTCACTTTTAAAGAAATGATGA TGTTGCCATGCCACGAAAGGATATACCTTACAGAAAACCTTTCCAGAATGTCTCAAAATCTTGAGCCT ATGGAATATTCTGTTGTAGTTTGGTCTCAGGTGTTGATATAATTTCTCATTTACAATTTCTAATAAAGG ATTAATATGTCAGCAAAAAAAAAAAAAA (SEQ ID NO: 59)</p>			
Translated protein sequence			
<p>MKILLVDFDNTIIDNSDTWIVQCAPNKKLP IELRDSYRKGFW TEFMGRVFKYLGDKGVREHEMKRAVTSLPF TPGMVELFNFIRKNKDKFDCIIISDNS VFIDWVLEAASFHDIFDKVFTNPAAFNSNGHLTVENYHTHSCNRCPKNLCKKVVLIEF VDKQLQQGVNYTQIVYIGDGGNDVCPVTF LKNDVAMPKGYTLQKTLSRMSQNLEPM EYSVVWSSGVDIISHLQFLIKD (SEQ ID NO: 60)</p>			
			Homo sapiens presenilin enhancer 2 homolog (C. elegans) (PSENEN), mRNA
PSENEN	55851	NM_172341	
mRNA Sequence			
<p>CTCGCCCAAAGAAGACTACAATCTCCAGGGAAACCTGGGGCGTCTCGCGCAAACGTCATAACTGAAAGT AGCTAAGGCACCCAGCCGGAGGAAGTGAGCTCTCCTGGGGCGTGTTGTTTCGTATCCTTGCACTCGTT ACTTAGGGTCAAGGCTTGGGTCTTGCCCCGAGACCCTTGGGACGACCCGGCCCCAGCGCAGCTATGAAC CTGGAGCGAGTGCCAATGAGGAGAAATTGAACCTGTGCCGGAAGTACTACCTGGGGGGGTTTGCTTTCC TGCCTTTCTCGGTTGGTCAACATCTTCTGGTTCTTCGAGAGGCCTTCCTTGTCCAGCCTACACAGA ACAGAGCCAAATCAAAGCTATGTCTGGCGCTCAGCTGTGGGTTCCTCTTCTGGGTGATAGTGCTCACC TCCTGGATCACCATCTTCCAGATCTACCGGCCCCGCTGGGGTGCCCTTGGGGACTACCTCTCCTTCACCA TACCCTGGGCACCCCTGACAACCTCTGCACATACTGGGGCCCTGCTTATTCTCCAGGACAGGCTCCT TAAAGCAGAGGAGCCTGCTCTGGGAGCCCTTCTCAAACCTCTAAGACTGTTTTTCATGTCCCAAGCTTCT CTGCTGACATCCCCCAATAAAGGACCCTAACTTTCAAAAAAAAAAAAAA (SEQ ID NO: 61)</p>			
Translated protein sequence			
<p>MNLERVSNEEKLNLCKRYLGGFAFLPFLWLNVNIFWFFREAFLV PAYTEQSQIKGYVWRSVAGFLFWIVLTSWITIFQIYRPRWGALGDYLSFTIPLGTP (SEQ ID NO: 62)</p>			
			Homo sapiens SATB homeobox 1 (SATB1), transcript variant 1, mRNA
SATB1	6304	NM_002971	
mRNA Sequence			
<p>TTTCTCGCTCGCTCCCGTTCCCGGACGCGGCGGATGAGCCGCGCCCGCTGGGGAAGGCTCCGGGCGGCG GCGGGCGGCGGGAGGAGGCTGCGTGCTCGGGGCTGGGGCTGCGAGCGGGGTGATTTGTATTAAATGA GGAGGAGGAAGAAGAGGCACCCACAGCGGCAGCGGCGGCGGCGGCGGAGCAGCAGCAGGAGCAGCGGCG GAGAGGGCTGCAGCCCGGGCGGACGCGCGGAGCCGAGCGGGGCACGGCGCGGCGGACAGCAGCGGCGGG ATGAGTCAACTAATAATTTAATGGGGGACAGAGCGGACGAGGGGTAGAGCTAGCGAGGGAGAGAGCGA GAGAAGCAGCCCGTCCGGGACTCGCGTCACTCAGCACACACACAACACACACACCTCTCCC TGTGCCACCCAGCAACACCCGGCCTGTCACACAACAACACGCGCGGCGCCCTCTATCCTGCCCGGGG GCCCAGCCGAAAGCCAGGCGACTCTAGAGACGCTGCCCGCCCCCTCTTTCATTTCGGGAAACTCGTG</p>			

<p>GTCTTAAAAGTTTTAAATAGAGAAAATGTGCTTTACACAGTTGCCTATAAAAAGTGCTCTATGTTATCCA AGCAATTCATACTATAAGCTTCACCTCTATTGTTGTATGCAATTTTTACTATCATGCAAATAAGCTTAGG TAAATAAACTAATAGATCACCTTAGAAAATTATGCAATTAATGTGAAAATAATTGATGTTTGCAATGTG TCTTCCTTTGGTTTACAATCAATTTTTAAGCTACATCTGTATAAAATTTCTGTATAAAGGTGTATTCTTT TTTTATGAGTTTATGGCTATGAAAACAGCTATTTTGTACAGCTGGCTGTTTTTATAAGTGTATCACAAT TTCTTTTATGCAGAAATGTTCTGACTAGGAGTGGTTATTGACTGTAACACACAATTAATAATTGTTTGTA TCGTATGACATGGTAGGGTTTGTCTGCTTATGTGAAGTAACTAAAGGAGTCAAAGGATGGCCCTCTCATT TAGGTGCATGTTAATAACTTGTATTATTTCACTGATTTTAAAAAGAGCAATTGACAAGTTACTTGAAACACT GTAAATTTAAATCACAAACACATGCTCATTTTTAAATAGGTATGAAATTTACACAATGAAAATAACCTGTT TGGTTAACATTTTGTCTAATAAGTAGAGATAGGATGGTCAAAAGACTCTCCGACAAAACAAATCCAGTC TCTAGCAGTTATGTTGTTAGAAATGGA (SEQ ID NO: 63)</p>			
Translated protein sequence			
<p>MDHLNEATQGKEHSEMSNNVSDPKGPPAKIARLEQNGSPLGRGR LGSTGAKMQGVPLKHSGLMKTNLRKGTMLPVFCVVEHYENAIEYDCKEEHAEFVLVR KDMLFNQLIEMALLSLGYSHSSAAQAKGLIQVGKWNVPVLSYVTDAPDATVADMLQDV YHVVTLKIQHLHSCPKLEDLPPEQWSHTTVRNALKDLLKDMNQSSLAKECPLSQSMISS IVNSTYYANVSAAKQEFGRWYKHFKKTKDMMVEMDSLSELSQGANHVNFQQPVPVG NTAEQPPSPAQLSHGSPSVRTPLPNLHPGLVSTPISPQLVNLQQLVMAQLLNQQYAVN RLLAQSSLNQYLNHPPVSRSMNKPLeQQVSTNTEVSSEIYQWVRDELKRAGISQAV FARVAFNRITQGLLSEILRKEEDPKTASQSLLVNLRAMQNFLQPEAERDRIYQDERER SLNAASAMGPAPLISPPSRPPQVKTAIATERNGKPENNTMNNINASIYDEIQEMKR AKVSQALFAKVAATKSQGWLCCELLRWKEDPSPENRTLWENLSMIRFLSLPQPERDAI YEQESNAVHHHGDPRPHIIHVPAEQIQQQQQQQQQQQQQQAPPPPPQPPQPPQTGPRL PPRQPTVASPAESDEENRQKTRPRTKISVEALGILQSFIDVGLYPDEEAIQTLQAQL DLPKYTIKFFQNRYYLKHGKCLKDNSGLEVDVAEYKEEELLKDLEESVQDKNTNLT FSVKLEELSVEGNTDINTDLKD (SEQ ID NO: 64)</p>			
SNX11	29916	NM_013323	Homo sapiens sorting nexin 11 (SNX11), transcript variant 2, mRNA
mRNA Sequence			
<p>CCGCGCTCCCAAGTGAGTGGAGGGGGGATCCCGACTCCAGTCCGGGGCCTTGGCCAGCGGAGCCGCGCTA TTCGGAAGCGGGAATCCCACTCAGAGCCCGGGCCTGTAGGGGCGGGGCGTCCCGGGCACCCGGGATTGGG GCGTCTCCCGTCGTGCACCGGGGCACCGCGACTCACC CGGAAGGAGAGCCGTGATCTGGCTATATGGT GGGGCGCGGGCGGTGTGCTGTGGGGAGCTGGTGTCTTCTCAGATGTTTCTTCCAATGGGCTTTTGGT GTAGGATGTGCGGAGAACCAAGAACAGGAGGAGGTGATTACAGTGCCTGTTTACAGACCCCGAGTGCAGAA TGAGGGCTCCTGGAACCTTTATGTGGATTATAAGATATTCCTCCATACCAACAGCAAAGCCTTTACTGCC AAGACTTCCCTGTGTGCGGCGCGGCTACCGTGAGTTCTGTGTGGCTGAGAAAGCAGCTACAGAGAAATGCTG GTTTGGTGCCTGTTCCTGAACCTTCTGGGAAGTCAACCTTCTTCGGCACCTCAGATGAGTTCATTGAGAA GCGACGACAAGGTCTGCAGCACTTCTTGAAGGTCTGTCAGAGTGTGGTTCTCTGTCAGACAGCCAG TTGCACCTATTCCTGCAAAGCCAGCTCTCGGTGCTGAGATAGAAGCCTGTGTCCAGGGCCGAAGTACCA TGACTGTGTCTGATGCCATTCTTCGATATGCTATGTCAAACGTGGCTGGGCCCAGGAAGAGAGGCAGAG CTCTTCTACCTGGCTAAAGGAGACCAGCCTAAGAGTTGCTGCTTTCTTCCAAGATCGGGTAGGAGGAGC TCTCCCTCACCGCCTCCCACTGAAGAAAAGGACCAATTAGAAGTGTGGGCTCCAGTTGTTGACTCTGAGG TTCTTCTCTTGGAAAGTCCCACTCTCCACCCCTCTCCTCACCATTATGCTGTGATTTTGGAAAGACCCAA AGAGGGAACCTCCACTCTTCAGTCTGTGAGGAGGGCTGTGGGAGGAGATCATGCTGTGCCCTTTGGACCTT GGTCAGTTAGAAACAGTTTGGAAAAGTGAAGTCTGGGTTCTGCTCTGAGATGGTCAGAGAAGATGCGGG CCAGGAGACTTACTCAGGTGGGACTGGGCACAGGGCAGGATGTGGGAGGCTGGGCTGCTTAGTGTCTTC TAGTCACCTCTGCTTGGGCTGATTGACAGAGGTCAAGTATTACAGCCCTTATGCCTCTTCCATGGGAAC AAATACTGTGAGATGTTTGAAGTTAAACATAAGACACAGGGGCTGTTGCTTTTGAACAGAACCTATA TTACTCTCTGGGATCTGAGTTTCTGCAGGTCAATTTGTATGTAGGACCAGGAGTATCTCCTCAGGTGACC AGTTTGGGGACCCGATGTGGCAAATTTAAGCTGCCATATTGAACATCATCCCACTGGGAGTGGTTAT GTTGTATCCCCATCTTGGCTGGCTTCAGTTTTTGTCTGTAGCCCTAGAGCACTTTGTTTGTGGGAGGCTGG CCTCTTGCCTACCTCCTTGCATGGACAGGGGGATGAATATTTACTTTCCACCTCCTTGCTTTTCTTTTC ACTGATACCACTGAATGGAACGGTGTGTGACTCCTGCTGCTGGGGATTTATGTCCCAGACCTTAGCC TGGTGTAGTGGAGCCTGAGACCTGCACAACAGCTCATGGTATGCATGAGAGAGAAGTGGCTGGCCACAG CCAGAGGGAACAGTAACAGCCAGGGGCTTTATTTGGGAAAGGCTGTCCCGGCTGTTACTGTCTCTT CTGGTTATAAAGCAGACATGTGGCCATCTTTCCGAGGGTTAGAGTGGGCTCCTTTCTTTTGGAAATCC</p>			

<p>TTTTCTTCTCCTTTGGTAGCAGCTCCCTGCCTCCAGGGCTTCCGCCACCAGCGTCTCTGCTGTGTGCGC AGTGCACTGGGGTGAAGGGCTTTGTTTCTGCTGCCTGAAAGAGAGGGCTCTGGGGATGGAGATGAGAA ACAACACGCTCTCCTTCAGACAATGAGGCATTCTGCTCCTGCTGCCATTCTTCATCTCCACTGAGAGC CAGAGCTGGTAGGAGCCGAGTGCCACAGGCATTCTGCATTGCTCTACTCTTAGGTTTGTGTGTGATCC TTCCCTCCCTGTGCGCCACTCCTCCTCCTCTGGCTATCCTACCTGTCTGTGGGCTCTTTTACTACCA GCCTATGCTGTGGGACTGTGATGGCATTAGTTCAGAGTGGAGGGCTTTGGCCTGAAATAAAATGCAAG TATT (SEQ ID NO: 65)</p>			
Translated protein sequence			
<p>MGFWCRMSENQEEVITVRVQDPRVQNEGSWNSYVDYKIFLHT NSKAFTAKTSCVRRRYREFVWLRLQRLNAGLVPVPELPGKSTFFGTSDEFIEKRROG LQHFLEKVLQSVLLSDSQLHLFLQSLVPEIEACVQGRSTMTVSDAILRYAMSNCG WQEQERQSSSHLAGDQPKSCFLPRSGRRSSPSPPPSEKDHLEWVAPVVDSEVPSL ESPTLPPLSSPLCCDFGRPKEGTSTLQSVRRVAVGGDHAVPLDPGQLETVLEK (SEQ ID NO: 66)</p>			
SPTA1	6708	NM_003126	Homo sapiens spectrin, alpha, erythrocytic 1 (elliptocytosis 2) (SPTA1), mRNA
mRNA Sequence			
<p>TATGTCTTCTAAAGATAATGTGCGATTGTGTATGGCTGATGGGATTCTAGGACCAAGCAAGAGGTTTTTTT TTTTCCCCACATACTTAACGTTTCTATATTTCTATTTGAATTCGACTGGACAGTTCCATTGAAATTATT TCTCTCTCTCTCTCTCTGACACATTTATCTTGCCAGGTTCTAAACCTTTAGGAAAAATGGAGCAATT TCCAAGGAAACCGTTGTGGAGAGCAGTGGGCCAAAGGTTTTGGAACAGCAGAAGAGATCCAGGAGAGG CGTCAGGAAGTGTGACTCGGTATCAAAGTTTCAAGGAGCGGGTCGCTGAGAGGGGTGAGAAGCTTGAGG ATTCTATCACTTACAAGTTTCAAGCGAGATGCAGATGATCTGGGGAAGTGGATCATGGAGAAAGTCAA TATCTTAACCGATAAGAGCTATGAAGACCCAACCTAATATACAGGGGAAATATCAGAAGCATCAATCCCTT GAAGCAGAGGTGCAAAACAAAATCAAGACTCATGTCTGAACTGGAAAAAACAAGGAAGAAGCATTTACCA TGGGTCATTCTGCCACGAAGAAACGAAGGCCCATATAGAGGAGCTACGCCACCTGTGGGACCTGCTGTT AGAGCTGACCTGGAGAAGGGTGACCAGTTGCTGCGGGCCCTGAAGTTCCAGCAGTATGTACAGGAGTGT GCTGACATCTTAGAGTGGATTGGAGACAAGGAGGCTATAGCGACATCAGTGGAGCTAGGTGAAGACTGGG AGCGCACCGAAGTTCTGCATAAGAAATTTGAAGACTTCCAAGTGGAGCTGGTAGCTAAAGAAGGGAGAGT TGTTGAAGTGAACCAATATGCCAATGAGTGTGCGGAGGAAACCACTGACCTACCTTAATTCAGTCT AAGCAAAATGGTGAAGTGTGCTGGGAGCGCTTCGTGTTTGGCTCTCCAGAGACAGAAAGCTCTGT CCAATGCTGCAAACTTACAACGATTCAAAGGGATGTGACTGAAGCCATCCAGTGGATCAAGGAGAAGGA ACCTGTACTCACCTCTGAGGACTATGGCAAAGACCTTGTGCTCTGAAGGACTGTTTCACAGTCACAAG GGACTTGAGAGAAATCTTGCTGTCATGAGTGACAAGGTGAAGGAGTATGTGCTAAAGCAGAGAAGCTGA CACTTTCCCATCTTCAGATGCACCTCAGATCCAGGAGATGAAAGAAGATCTGGTCTCCAGCTGGGAGCA TATTCGTGCCCTGGCCACCAGCAGATATGAAAACTGCAGGCTACTTATTGGTACCATCGATTTTCATCT GACTTTGATGAACCTCAGGCTGGATGAACGAGAAGACTGCTGCGATCAATGCTGATGAGCTGCCAACAG ATGTGGCTGTGGTGAAGTGTGCTGAGCAGGCATCAGCAGCATAAGCATGAGATTGACTCTTACGATGA CCGATTTCAATCTGCTGATGAGACTGGTCAAGACCTCGTGAATGCCAATCATGAAGCCTCTGATGAAGT CGGGAAAGATGGAATACTTGACAACAACCTGGACTGCCCTGCTGGAACCTGTGGGACGAGCGTCATCGTC AGTATGAGCAGTGTGACTTTTCTCTCTTACAGAGACAGTGAAGTGGACAGTGGATGAGTAG ACAAGAGGCTTCTGGAAAACGAGGATCTGGGAACTCACTGGGAGTGCAGAAGCCTTCTTTCAGAAG CATGAAGACTTTGAGGAAGCCTTTACTGCCCAGGAAGAGAAGATCATAACTGTAGACAAGACTGCAACCA AATTGATTGGTGATGACCATTTATGATTCAGAGAACATCAAGGCTATCCGTGACGGGCTGTAGCCCCGGC GGATGCCCTACGTGAAAAGGCTGCCACTAGACGTAGATTGCTGAAGGAGTCATTGCTTCTGCAAAAAGCTG TATGAGGACTCAGATGACCTAAAGAACTGGATCAACAAGAAGAAAAAGTTGGCAGATGATGAAGATTACA AGGACATACAGAACTTGAAGAGCAGGTTCAAAGCAGCAAGTCTTTGAAAAGGAGTTGGCAGTTAATAA GACCCAGCTGGAACATACAGAAAAGTGGCCAAAGAGATGATTGAGGGTGGTCACTATGCTCTGACAAAT GTGACCACTCGTCTGAGTGAAGTTGCCAGCCTCTGGGAGGAGTTGCTGGAGGCTACAAAACAGAAAGGGA CCGAGTTGCATGAGGCCAACAGCAGCTGCAATTTGAAAATAATGCAGAAGATTTGCAGCGCTGGCTGGA GGATGTTGAGTGGCAAGTCACCTCTGAGGATTATGGGAAAGGCTGGCCGAGGTACAGAATCGACTCAGG AAACACGGCCTCTTGAGTGGCTGTGGCTGCTCGTCAGGATCAGGTGGATATCCTTACAGACCTGGCTG CATATTTTGAAGAAATAGGCCATCCTGATTCTAAGGATATAAGGGCAAGGCAAGAGTCTTGGTATGCCG ATTTGAAGCTCTGAAGAGCCACTGGCCACCCGAAAGAAGAGCTCTTAGACCTTCTCCATCTGCAGCTG ATTTGTAGAGACACAGAGGATGAGGAGGCTGGATCCAAGAGACTGAACCCTCAGCTACTTCCACCTACC TTGGAAGGACCTGATTGCTTCCAAAAGCTTCTGAATAGGCATAGAGTCATCCTGGAGAACATTGCCAG CCATGAACCACGCATTCAAGAGATAACAGAAAGGGGAAACAAAATGGTAGAGGAAGGACACTTTGCTGCA GAAGATGTGGCCTCTAGGTCAGAGTTTGAACCAGAATATGGAGTCTCTCCGTGCTCGAGCTGCTAGGC</p>			

GACAAAATGATCTTGAAGCCAATGTCCAGTTCCAGCAGTACCTGGCTGACCTGCATGAAGCAGAAACATG
GATCAGAGAGAAGGAACCTATTGTAGATAATACTAATATGGTGTGATGAAGAAGCAGCTGGGGCTCTT
CTAAAGAAGCATGAGGCCCTTTCTATTAGATCTCAATTCATTTGGAGACAGTATGAAAGCTCTGCGGAATC
AGGCAAACGCTGCCAGCAACAACAGGCTGCACCAGTGGAGGGAGTTGCTGGAGAACAAGGGTTCATGGC
TTTATATGACTTCCAGGCCCGCAGCCCCGAGAAGTCACCATGAAGAAAGGTGATGTCTTAACGCTGCTC
AGTTCCATCAATAAGGACTGGTGGAAAGGTGGAAGCTGCTGATCATCAGGGCATTGTCCCAGCTGTCTATG
TCAGAAGACTGGCCACGATGAGTTCCCGATGCTCCACAGCGGCGACGAGAAGAGCCAGGAAACATCAC
CCAGCGCCAGGAGCAGATTGAGAACCAATACCGCTCCCTCTTGGATCGGGCAGAAGAACGAGACGTCGT
CTATTGGCAACGTTATAATGAATTTTATTGGCCTATGAGGCAGGAGACATGCTGGAATGGATTCAAGAGA
AAAAGGCAGAAAACACTGGAGTGGAACTAGATGATGTTTGGGAGCTGCAGAAAAAGTTTGATGAGTTCCA
AAAGGATTTGAATACCAATGAGCCTCGGCTAAGGGATATCAACAAGGTAGCTGATGATCTACTATTTGAA
GGACTTCTAACACCAGAAGGAGCTCAAAATCCGGCAGGAATTGAATTCGGCTGGGGTTCTTTGCAGAGGC
TTGCAGATGAACAGCGGCAGCTGCTGGGCAGTGGCCATGCTGTTGAAGTGTTCACAGAGAAGCAGATGA
CACGAAGGAGCAGATTGAGAAGAAATGCCAGGCCCTCAGTGTGTCAGACCTGGCTCAGATCTGTTTCACT
GTTTCAAGCTTCTCAGCGACGGCATGAGGGCTTTGAAAGGGACCTCGTACCCCTGGGAGATAAGGTGACCA
TACTGGGGGAGACAGCAGAGCGGCTCAGTGGCTTCCATCCAGATGCCACTGAGGACCTGAGGAGAGAA
AATGGAGCTGAATGAGGCCTGGGAAGACCTGCAGGGGCGTACAAAGGATCGTAAGGAGAGCCTAAATGAG
GCCCAGAAATTTACCTGTTTCTCAGCAAGGCCAGGGATCTGCAGAACTGGATCAGTAGCATTGGTGGCA
TGGTATCATCACAGGAGCTGGCCGAAGACTTAACTGGCATAGAGATCTTGTGGAGAGACATCAGGAGCA
CCGTGCTGACATGAGGCGAGAGGCTCCCACTTCCAGGCCTTAGAGGACTTCAGTGCAGAACTTATCGAC
AGTGGGCACCATGCTAGCCCTGAAATGAAAAAAGCTTCAAGCTGTCAAGCTAGAGAGAGATGATTTGG
AGAAGGCTTGGGAAAAACGCAAGAAGATCCTAGACCAGTGCCTGGAGTTGCAGATGTTCCAGGGGAACTG
TGATCAAGTTGAGAGCTGGATGGTGGCAGTGAGAAATCCCTGAGGTGAGATGACAAAAGTTCCCTTAGAC
AGTCTGGAGGCTTTGATGAAGAAACGGGACGATTTGGACAAAGCAATCACTGCCAGGAAGGGAAGATCA
CTGACCTAGAACATTTTGTGAGAGCCTCATTGCTGATGAACACTATGCCAAAGAAGAGATTGCTACGCG
GCTCCAACGTGTACTAGACAGGTGGAAGGCTCTCAAAGCACAACCTGATTGATGAGCGGACAAAGCTTGG
GACTATGCCAACCTTAAACAATTTCTACCGAGACCTTGAGGAGCTGGAAGAATGGATCAGTGAAGTGTGTC
CCACAGCCTGTGATGAATCCTACAAAGACGCCACTAACATTAGAGGAAATACCTGAAACACCAGACCTT
TGCACATGAAGTCGATGGCCGATCTGAGCAGGTGCATGGCGTCATCAACCTGGGGAACTCCCTGATTGAG
TGTAGCGCTTGTGATGGCAATGAAGAGGCCATGAAGGAGCAACTGGAACAGCTGAAGGAACATTGGGATC
ATCTCCTTGAGAGAAACAAATGACAAAGGGAAGAAGCTCAATGAGGCCAGTCTGTCACAGAGGTTCAACAC
AAGCATCCGGGACTTTGAGTTCTGGCTCTCAGAGGCAGAGACATTGCTGGCCATGAAAGATCAGGCCAGG
GACTTGGCTTTCAGCAGGAACCTACTCAAGAAGCATCAGCTATTGGAGAGAGAGATGTTGGCTCGAGAGG
ATGCACTCAAGGACCTGAATACATTGGCTGAAGATTGCTCTCCAGCGGGACTTTCAACGTTGATCAGAT
TGTGAAGAAAAAGATAATGTCAACAAGCGTTTCTGAATGTCCAAGAATTGGCAGCTGCACACCACGAA
AAATTGAAAGAGGCCATGCTTGTTCAGTTCTTCCAGGATCTAGATGATGAGGAATCCCTGGATAGAGG
AGAAGTTGATACGAGTGAGCTCCAGGACTATGGGAGAGATCTTCAGGGGTTTCAAGCTTGTCTGAAGAA
GCACAAACGCTAGAGGGGAGCTGGTGGCCCATGAGCCTGCCATCCAGAATGTGCTGGAATAGGCGAG
AAGCTGAAAGACAAGGCTGCTGTGGGGCAAGAGGAGATCCAGTTGCGGCTGGCTCAGTTTGTGAACACT
GGGAGAAGCTCAAAGAGTTGGCCAAGGCCGAGGACTTAAGTTGGAAGAATCCCTAGAATACTTGCAATT
CATGCAGAAATGCTGAGGAAGAGGAAGCTTGGATCAATGAAAAGAATGCTTTGGCTGTCCGAGGAGATTGT
GGAGATACATTAGCTGCTACTCAGAGCTTGCTAATGAAGCATGAAGCTTTGGAAGATGACTTTGCTGTCC
ATGAGACCCGAGTACAAAATGTGTGTGCACAAGGAGAAGACATCTAAATAAGGTGTTGCAGGAGGAAAG
TCAGAACAAAGAGATTTCTTCCAAGATAGAGGCTCTGAATGAAAAGACCCCTTCTCTGGCTAAGGCAATA
GCTGCTTGGAAAGTTGCAATTGGAAGACGATTATGCTTTTCAAGGAATCACTGGAAGGCTGATGTGGTAG
AGGCTTGGATAGCTGATAAGGAAACAAGCTTAAAGACCAATGGCAATGGTGCAGACCTTGGTGACTTCTT
CACTCTTCTGGCAAAACAGGACACTCTGGATGCCAGTCTGCAGAGTTTCCAGCAAGAGAGACTTCCCGAG
ATCACTGACCTGAAGGACAAACTGATTTCTGCTCAACACAACCAGTCTAAAGCCATTGAAGAGCGTTATG
CCGCTCTGCTGAAGCGCTGGGAACAGTTGCTGGAAGCCTCGGCAGTCCACAGACAGAAATGCTGGAGAA
ACAGCTGCCTCTACAGAAGGCTGAGGACCTGTTCTGGAATTTGCACATAAGGCTTCAGCTTTGAACAAC
TGGTGTGAAAAGATGGAAGAAAACCTTGTGAGAGCCTGTGCACTGTGTCTCCCTGAATGAAATTCGGCAGC
TGCAGAAAGACCATGAGGACTTCTTGGCTCCCTGGCTAGGGCTCAAGCAGACTTTAAATGTTTGTGGA
GCTAGACCAGCAGATTAAAGGCTTAGGTGTGCTTCCAGCCCTTATACCTGTTAACAGTGGAGGTGCTG
GAAAGGACCTGGAAGCACCTATCTGACATCATAGGAACGGGAGCAGGAGCTGCAAAAGGAAGAGGCAA
GACAGGTCAAGAACTTTGAGATGTGTGAGGAGTTTGAACAGAATGCCAGTACCTTCTTCAATGGAATCT
GGAAACCAGGGCTTACTTTCTGGATGGATCATTGTCAAAGAAACAGGAACCTTGAATCTCAGCTGGAA
GCAATAAAAAGAAAACAGAAGGAGATCCAGGCGATGAAGCGTCAACTAACCAAGATTGTGGACCTGGGGG
ACAACTTGGAAAGACGCTCTGATCCTTGATATCAAAATACAGCACCATTGGATTGGCTCAGCAGTGGGACCA
GCTCTACAGCTTGGGTTGCGGATGCAACACAACCTGGAGCAACAGATCCAGGCCAAGGACATCAAGGT
GTGAGTGAAGGAGACTTAAAGGAATTTAGCACAATCTATAAACACTTTGATGAGAATTTGACAGGGCGCC
TGACTCACAAGAGTTCCGGTCTGCTGAGAGGACTCAATTACTACTTGCCCATGGTGGAGGAGGATGA

ACATGAGCCCAAGTTTGAGAAGTTCCTGGATGCTGTGGATCCAGGGAGGAAGGGCTATGTCTCACTGGAG
GACTATACTGCTTTCTGATTGACAAGGAGTCAGAAAACATCAAGTCCAGTGATGAAATAGAGAATGCCT
TCCAAGCCCTGGCAGAGGGCAAGTCATATATTACCAAAGAAACATGAAGCAGGCCCTTACCCCGAGGCA
AGTGTCAATTCTGTGCCACACATATGCAGCAATATATGGACCCACGGGGTCGAAGCCATCTCTCTGGCTAT
GACTACTTGTGGCTTCACCAATTCTCTACTTTGGCAACTAATAAGCAGCTCCTCGTGGATCGTAGAAAACTCT
TAGTGTGCTGGGAAATTTACTCTGGGGGCAAAAGAGTACAGGCAAAATGTGGAAGATAAAAGATGGCCCTCGTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCTTGTGTTTGTGTGCATATTACATTTATTGTAGGATCTT
AAAAAATCTCAAGGGTGGGAGATAGAAAGGTTAATAGAGTTGGAGGAGTGGAAAGCTATTTTGTATGCAAC
TAGTCACTGCTGAGGGGTGTCAAAGTTTCTATTTTATTGTTCTGTTTGGCACGCTTTATCATTTTGC
TTTATTCCGATTATAGAATAAAGTAATTCTTTTAAAAAATATTTTTTGGGGCAAAGTTAAGTAAAAATGTT
GAGCTTCTATATTTCTGGGAAGCTGTACTCATATAAGAGTGGGCAGCTAATTTTACTGTAAAGAAGGGCCA
TGGTATAGTAGATAAATAAAATCCAAGGCAATTTTCAAACAATTTTTTAAACTTTGGAAATGTGTTTAA
TTTAAATTGAAAAATAAAGATATTGTGATTTTCTGGGG (SEQ ID NO: 67)

Translated protein sequence	
1	MAKQK
2	MAKQK
3	MAKQK
4	MAKQK
5	MAKQK
6	MAKQK
7	MAKQK
8	MAKQK
9	MAKQK
10	MAKQK
11	MAKQK
12	MAKQK
13	MAKQK
14	MAKQK
15	MAKQK
16	MAKQK
17	MAKQK
18	MAKQK
19	MAKQK
20	MAKQK
21	MAKQK
22	MAKQK
23	MAKQK
24	MAKQK
25	MAKQK
26	MAKQK
27	MAKQK
28	MAKQK
29	MAKQK
30	MAKQK
31	MAKQK
32	MAKQK
33	MAKQK
34	MAKQK
35	MAKQK
36	MAKQK
37	MAKQK
38	MAKQK
39	MAKQK
40	MAKQK
41	MAKQK
42	MAKQK
43	MAKQK
44	MAKQK
45	MAKQK
46	MAKQK
47	MAKQK
48	MAKQK
49	MAKQK
50	MAKQK
51	MAKQK
52	MAKQK
53	MAKQK
54	MAKQK
55	MAKQK
56	MAKQK
57	MAKQK
58	MAKQK
59	MAKQK
60	MAKQK
61	MAKQK
62	MAKQK
63	MAKQK
64	MAKQK
65	MAKQK
66	MAKQK
67	MAKQK
68	MAKQK
69	MAKQK
70	MAKQK
71	MAKQK
72	MAKQK
73	MAKQK
74	MAKQK
75	MAKQK
76	MAKQK
77	MAKQK
78	MAKQK
79	MAKQK
80	MAKQK
81	MAKQK
82	MAKQK
83	MAKQK
84	MAKQK
85	MAKQK
86	MAKQK
87	MAKQK
88	MAKQK
89	MAKQK
90	MAKQK
91	MAKQK
92	MAKQK
93	MAKQK
94	MAKQK
95	MAKQK
96	MAKQK
97	MAKQK
98	MAKQK
99	MAKQK
100	MAKQK

MEQFPKETVVESSGPKVLETAEEIQERRQEVLTTRYQSFKVERVAE
RGQKLED SYHLQVFKRDADDLGKWI MEKVNI LTKSYEDPTNIQGYQKHQSLEAEVQ
TKSRLMSELEKTRERERTMGHSAHEETKAHIEELRHLWDLLELTLEKGDQLLRALKE
QQYVQECADILEWIGDKEAIATSVELGEDWERTEVLHKKFEDFQVELVAKEGRVVEVN
QYANECAEENHPDLPLIQSKQNEVNAAWERLRGLALQRQKALSNAANLQRFKRDVTEA
IQWIKAKEFVLTSEDYKGDLVASEGLFHSKGLERNLAVMSDKVKELCAKAELTLSH
PSDAPQIQEMKEDLVSSWEHILRALATSRYEKLQATYWYHRFSSDFDELSGWMNEKTAA
INADELPTDVAGGEVLLDRHQHKHEIDSYDDRFQSADETGQDLVNANHEASDEVREK
MEILDNNWTALLELWDERHRQYEQCLDFHLFYRDSEQVDSWMSRQEAFLNEDLGNSL
GSAEALLQKHEDFEEAFTAQEEKIITVDKTATKLIGDDHYDSENIKAIRDGLLARRDA
LREKAATRRRLKESLLQLKLYEDSDDLKNWINKKKKLADDEDYKD IQNLKSRVQKQQ
VFEKELAVNKTQLENIQKTGQEMIEGGHYASDNVTTRLSEVASLWEELEATKQKGTQ
LHEANQQLQFENNAEDLQRWLEDVWQVTSYEDYKGGLAEVQNRLRKHGLLESAVAARQ
DQVDILTDLAAAYFEEIGHPSDKDIRAQESLVCRFEALKEPLATRKKKLLDLLHLQLI
CRDTEDEBAWIQTESPATSTYETLGKDLIASKKLLNRHRVILENIASHEPRIQEITERG
NKMVEEGHFAEDVASRVKSLNQNMESLRARAARRQNDLEANVQFQQYLADLHEAETW
IREKEPIVDNTNYGADEEAAGALLKKHEAFLLDLNSFGDSMKALRNQANACQQQQAAP
VEGVAGEQRVMALYDFQARS PREVTMKG DVLTLLSSINKDWWKVEAADHQGIVPAVY
VRLLAHDEF PMLPQRRREEP GNI TQRQE QIENQYRSLLDRAEERRRRLQRYNEFLLA
YEAGDMLEWIQEKAENTGVELDDVWELQKKFDEFQKDLNTNEPRLRDINKVADDLLF
EGLLTPEGAQIRQELNSRWGSLQRLADEQRQLGSAHAVEVFHREADDTKEQIEKKCQ
ALSAADPGS DLF SVQALQRRHEGFERDLVPLGDKVTILGETAERLSESHPDATEDLQR
QKMEINAEWEDLQGRTKDRKESLNEAQKFYFLFSKARDLQNWISSIGGMVSSQELAE
LTGIEILLERHQEHRADMEAEAPTFAQLED FSAELIDSGHASPETIEKKLQAVKLERD
DLEKAWERKKILDQCLELQMFQGNCDQVESWMVARENSLRSDDKSSLSLEALMKKR
DDLDKAITAQEGKITDLEHFAESLIADEHYAKEE IATRLQRVLD RWKALKAQ LIDERT
KLGDYANLQKFYRDL EELEW ISEMLPTACDESYKDATNIQRKYLKHQTF AHEVDGRS
EQVHGVINLGNSLIECSACDGNEEAMKEQLEQLKEHWDHLLERTNDKGKLINEASRQ
RFNTSIRDFEFWLSEAE TLLAMKDQARDLASAGNLLKKHQLLEREMLAREDALKDLNT
LAEDLLSSGTFNVQDQIVKKKDNVNKRFLNVQELAAAHHEKLKEAYALFQFFQDLDEE
SWIEEKLIRVSSQDYGRDLQGVQNLLKKHKRLEGE LVAHEPAIQNVLDMAEKLKD KAA
VGQEEIQRLAQFVEHWEKLELAKARGLKLEESLEYLQFMQNAEEEEAWNEKNALA
VRGDCGDTLAATQSLMKHEALENDFAVHETRVQNVCAQGEDILNKVLQEESQNKES
SKIEALNEKTPSLAKAIAAWKLQLEDDYAFQEFNWKADVVEAWIADKETS LKTNGGA
DLGDFLTLLAKQDTLDASLQSFQQERLPEITDLKDKLISAQHNQSKAIEERYAALLKR
WEQLLEASAVHRQKLEKQLPLQKAEDLFVEFAHKASALNNWCEKMEENLSEPVHCVS
LNEIRQLQKDHEDFLASLARAQADFKCLLELDQQIKALGVPSSPYTWLTVEVLERTWK
HLSDIIEEREQELQKEEARQVKNFEMCQEF EQNAS TFLQWILETRAYFLDGSLLKETG
TLESQLEANKRKQKEIQAMKRQKLTIVIDLGDNLLEDALILDIKYSTIGLAQQWDQLYQL
GLRMQHNLQEQIQAKDIKGVSEETLKEFSTIYKHF DENLTGR LTHKEFRSCLRG LNY
LPMVEEDEHEPKFEKFLDAVD PGRKGYSLEDYTAFLIDKESENIKSSDEIENAFQAL
AEGKSYITKEDMKQALTPEQVSFCATHMQQYMDPRGRSHLSGYDYVGFTNSYFGN (SEQ ID NO: 68)

TMEM79	84283	NM_032323	Homo sapiens transmembrane protein 79
--------	-------	-----------	---------------------------------------

			(TMEM79), transcript variant 1, mRNA
mRNA Sequence			
AGGTTTTGAGACACAGGTAAAGGGAGGGAGACAGAGAGAAATACTTGCAGAGCCAGCAGGTAGCTGGGCA GCTCCTTCCCGGACGGACGGATGGACAGACGCTGGGGACCCCTCCACTCCATATGGAAAGATGACATGACC TTGTGGTAGATCCAGAACTGAGGCCCCAGGATGACAGAACAGGAGACCCTGGCCCTACTGGAAGTGAAG AGGTCTGATTCCCCAGAGAAGAGCTACCCACAGGCCTTGGTTCCCAATGGCCGGCAGCCAGAAGGGGAAG GTGGGGCCGAATCCCCGGGAGCTGAGTCCCTCAGAGTGGGGTCTTCAGCTGGATCTCCACAGCCATAGA GGGGGCTGAGGATGGTCTAGACAGCACAGTAAGTGAGGCTGCCACCTTGCCCTGGGGGACTGGCCCTCAG CCCAGTGTCTCCGTTCCCGGATCCCCCTGGCTGGCGGGACATTGAACCAGAGCCCCCTGAGTCAGAACCCAC TTACCAAGCTAGAGGAGCTGCCCCAAGACGATGCCAACCTGCTGCCTGAGAAAGCGGCCCTGCCTTCGT GCCTATTGACCTACAGTGCATTGAGCGGCAGCCCCAAGAAGACCTTATCGTGCCTGTGAGGACGGCGAG GGCGAGTGCCGAACCTTCATGCCCCCGGGTACCCACCCCGACCCACTGAGCGCAAGTGGGCTGAGG CAGTGGTGAGGCCCTGGCTGTTCCGTGGGGGCTGCGGGAGCTGTGGAGACCGTGAGTGGCTAAGGGC TGTGGCTCCGTGGGAGCCGCACTCATTCTCTCCCTTGCCCTACTATACGGGGCATATGCCTTCCTGCCG TTTGTATGTCACGGCTGCCACCATGAGTTCCCGCTGATCTACACACTGCGCTGCGGGGTCTTTGCCA CCTTCCCATTTGTCTGGGATCCTGGTGTACGGGCTGAGCCTGTTATGCTTTTTCGCCCTTCGGCCCTT TGGGGAGCCACGGCGGAGGTGGAGATCCACCGCGATATGTGGCCAGTCGGTCCAGCTCTTTATTCTC TACTTCTTCAACCTGGCCGTGCTTTCCACTTACCTGCCCCAGGATACCCTCAAACCTGCTCCCTCTGCTCA CTGGTCTCTTTGCCGTCTCCCGGCTGATCTACTGGCTGACCTTTGCCGTGGGCGCTCTCTCCGAGGCTT CGGCTACGGCCTGACGTTTCTGCCACTGCTGTGATGCTGATGTGGAACCTTACTACATGTTCTGTTGGTG GAGCCGGAGCGCATGCTCACTGCCACCGAGAGCCGCTGGACTACCCGGACCACGCCGCTCGGCCTCCG ACTACAGGCCCCCGCCCTGGGGCTGAGCCTCTCCGCCCTCGCCCTCGGAGTAGGGGGTAGCGGCTTGGGT CTGACACATCTTTGAACCTTGTGGCCAGGCCTGGAATTGCCCCCAGGCCTAGGACCGCGGTGGGTGGAA CCCTGTCTACTGCCCCAACAGGGACTCCAATCAATCGGAGTTCTCCCTTGCCGGAGCTGCCCTTACCTT TGGGGCCCCGAGACAGTCATAAGGGATGGACTTAGTTTTCTTGCAGGGAAAAAGGTGGACAGCCGTGTTTC TTAAGGATGCTGAGGGCATGGGGCCAGGACCAGGGGAGAGGCACAGCTCCTTCTGAGCAGCCTCTCACC ACTGCCACAAGGCTCCCTAATGCTGTTCTGCTCCACTCCCCGGCTTCCGTGAGGCAGGAGGCAGAGC CACAGCCAAGGCCCTGACCACTTCTGTGCCAGTTGCTAAGCAGAGCGCCTCAGGGACGCTGGAATGCC TTAAGGATAGAGGCTGGGCATCACATCAATGGGACTGTGGTGTGTTGGTGAAAACTTCTGAGGATCTG GATTGAGACCCCTCATGACTGGCCTATTTACTGTTTACAGCTGGCCAGTGCCAGAGCTGCTGCTCTTTTA CCCTTTTATGGCCCCGTGTAACCTCCCACTTTAACTGCCCAGAGGCATGCCTCTCCCACAGGAAGAGGG GAGCAGACAGGGAAATCTGCCTACCAAGAGGGGTGTGTGTCTTTGTGCCACACGTGGTGGCTGGGGA GTGCTGGATGGTGGGTGGTTGATGTTAACCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT GTGTGTGTGTAACAATAAATTACTACAGTCAAAAAAAAAAAAAA (SEQ ID NO: 69)			
Translated protein sequence			
MTEQETLALLEVKRSDSPEKSSPQALVPNGRQPEGEGGAESPGA ESLRVSSAGSPTAIEGAEDGLDSTVSEAATLPWGTGPQPSAPFPDPPGWRDIEPEPP ESEPLTKLEELPEDDANLLPEKAARAFVPIDLQCIERQPQEDLIVRCEAGEGECRTFM PPRVTHPDPTEKWAEEAVVRPPGCSGCGSGCDREWLRAVASVGAALILFPCLLYGA YAFLPFDVPRLPMTSSRLIYTLRCGVFATFPIVLGILVYGLSLLCFPSALRPFGEPRRE VEIHRRYVAQSVQLF ILYFFNLAVLSTYLPQDILKLLPLLGLFAVSRLIYWLTFVG RSFRGFGYGLTFLPLLSMLMWNLYMFVVEPERMLTATESRLDYPDHARSASDYRPRP WG (SEQ ID NO: 70)			
TMIGD2	126259	NM_144615	Homo sapiens transmembrane and immunoglobulin domain containing 2 (TMIGD2), mRNA
mRNA Sequence			
GGAAGTCTGTCAACTGGGAGGGGGAGAGGGGGGTGATGGGCCAGGAATGGGGTCCCCGGGCATGGTGCTG GGCCTCCTGGTGCAGATCTGGGCCCTGCAAGAAGCCTCAAGCCTGAGCGTGACGAGGGGCCCAACTTGC TGCAGGTGAGGCAGGCGAGTCAGGCGACCCTGGTCTGCCAGGTGGACAGGCCACAGCCTGGGAACGGCT CCGTGTTAAGTGGACAAAGGATGGGGCCATCCTGTGTCAACCGTACATCACCAACGGCAGCCTCAGCCTG GGGGTCTGCGGGCCCCAGGGACGGCTCTCTGGCAGGCACCCAGCCATCTCACCTGCACTGAGCCCTG TGAGCCTCAACCACAGCGGGCGTACGTGTGCTGGGCGGCGGTAGAGATTCTGAGTTGGAGGAGGCTGA GGGCAACATAACAAGGCTCTTTGTGGACCCAGATGACCCACACAGAACAGAAACCGGATCGCAAGCTTC CCAGGATTCTCTCTGCTGCTGCTGGGGGTGGGAAGCATGGGTGTGGCTGCGATCGTGTGGGGTGCTTGGT TCTGGGGCCCGCAGCTGCCAGCAAAGGGACTCAGGTAACAGCCCAGGAAATGCATTCTACAGCAACGT			

CCTATACCGCCCCGGGGGGCCCCAAAGAAGAGTGAGGACTGCTCTGGAGAGGGGAAGGACCAGAGGGGC CAGAGCATTTATTCAACCTCCTTCCCGCAACCGGGCCCCCGCCAGCCGCACCTGGCGTCAAGACCTGCC CCAGCCCGAGACCCTGCCCGAGCCCGAGCCCGGCCACCCCGTCTCTATGGTCAGGGTCTCTCTTAGACC AAGCCCCACCCAGCAGCCGAGGCCAAAAGGGTTCCCCAAAGTGGGAGAGGAGTGAGAGATCCCAGGAGAC CTCAACAGGACCCACCCATAGGTACACACAAAAGGGGGGATCGAGGCCAGACACGGTGGCTCACGCC TGTAATCCCAGCAGTTTGGGAAGCCGAGGCGGGTGGAACTTGAGGTCAGGGGTTTGGAGCAGCCCTGG CTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCGACAGAG TGAGACTCCGTCTCAAAAAAACAAGCAGGAGGATTGGGAGCCTGTCAGCCCCATCCTGAGACCCCG TCCTCATTTCTGTAATGATGGATCTCGCTCCCACTTTCCCCAAGAACCTAATAAAGGCTTGTGAAGAAA AAGCAAAAAAAAAAAAAAAAAA (SEQ ID NO: 71)			
Translated protein sequence			
MGSPGMVLGLLVQIWLQEASSLSVQQGPNLLQVRQGSQATLVC QVDQATAWERLRVKWKDGAAILCQPYITNGSLSLGVCGPQGRLSWQAPSHLTLQLDPV SLNHSGAYVCWAAVEIPELEEAEGNITRLFVDPDDPTQNRNRIASFPGFLFVLLGVGS MGVAAIVWGAWFWRRCQQRDSGNSPGNAFYSNVLYRPRGAPKKSEDCSGEGKDQRG QSIYSTSFPQAPRQPHLASRPCSPRCPSPRPGHPVSMVRVSPRPSPTQQPRPKGF PKVGEE (SEQ ID NO: 72)			
TUBB6	84617	NM_032525	Homo sapiens tubulin, beta 6 (TUBB6), mRNA
mRNA Sequence			
GGGCACGAGGGCAGAGCCAGTTCTAGCGCAGAGCCGCGCCCGCCATGAGGGAGATCGTGACATCCAGG CGGGCCAGTGCGGGAACAGATCGGCACCAAGTTTGGGAAGTGATCAGCGATGAGCACGGCATCGACCC GGCCGGAGGCTACGTGGGAGACTCGGCGCTGCAGCTGGAGAGAATCAACGTCTACTACAATGAGTCATCG TCTCAGAAATATGTGCCAGGGCGCCCTGGTGGACTTAGAGCCAGGCACCATGGACAGCGTGCGGTCTG GGCCTTTTGGGCAGCTTTTCCGGCCTGACAACCTCATCTTTGGCCAGACGGGTGCAGGGAACAACCTGGGC GAAAGGGCACTACACGGAGGGCGCGGAGCTGGTGGACGCAGTGCTGGACGTGGTGCAGGAGGAGTGCGAG CACTGCGACTGCCTGCAGGGCTTCCAGCTCAGCAGCTCGCTGGCGGCGGCACGGGCTCAGGCATGGGCA CGCTGCTCATCAGCAAGATCCGTGAGGAGTTCCCGGACCGCATCATGAACACCTTCAGCGTCATGCCCTC GCCCCAAGGTGTCGGACACGGTGGTGGAGCCCTACAATGCCACACTGTCGGTGCACCACTGGTGGAGAAT ACAGACGAGACCTACTGCATCGACAACGAGGCGCTCTATGACATCTGCTTCCGCACTCTGAAGCTGACAA CGCCCACTACGGGGACCTCAACCACCTGGTGTCCGCCACCATGAGTGGGGTACCCACCTCGCTGCGCTT CCCGGGCCAGCTCAATGCTGACCTGCGCAAGCTGGCGGTGAACATGGTGCCTTCCCGCGCTGCACTTC TTATGCTTGGCTTCGCGCCGCTACACAGCCGCGGACCCAGCAGTACCGGGCCCTGACCGTGCCCGAGC TCACCCAGCAGATGTTTCGACGCGAGGAACATGATGCCCGCTGCGATCCGCGCCATGGCCGCTACCTGAC CGTGCCACCGTGTTCCGCGGGCCCATGTCCATGAAGGAGGTGGACGAGCAGATGCTGGCCATCCAGAGT AAGAACAGCAGCTACTTCGTGGAGTGGATTCCCAACAACGTGAAGGTGGCCGTGTGCGACATCCCGCCCC CGCGCCTGAAGATGGCCTCCACCTTCATCGGCAACAGCAGGCCATCCAGGAGCTGTTCAAGCGCATCTC CGAGCAGTTTCTCAGCCATGTTCCGCGCGCAAGGCCCTTCTGCACTGGTTACGGGTGAGGGCATGGATGAA ATGGAGTTCACCGAGGCGGAGAGCAACATGAACGACCTGGTATCCGAGTACCAGCAGTACCAGGATGCCA CCGCCAATGACGGGGAGGAAGCTTTTGGAGATGAGGAAGAGGAGATCGATGGATAGTCGGAATAGAGCCG CCCCAATCAGATCCTACAACACGCAAGTTCCTTCTGAACCTGGTGCCTCCTACCTATGGCCCTGAA TGGTGCAGTGGTTAATTGTGTTGGTGTGCGCCCTCACAAATGCAGCCAAGTCATGTAATTAGTCATCT GGAACAAAGACTAAAAACAGCAGAGAATTGCGGGTTTACCCAGTCAGAAGATCACACCATGGAGACTTT CTACTAGAGGACTTGAAAGAGAACTGAGGGGCCACAAAATAAACTTCACCTTCCATTAAAGTGTTCAGCA TGTCTGCAAAATTAGGAGGGAGTTAGAAACAGTCTTTTTCATCTTTGTGATGAAGCCTGAATTTGTGCGG TGTTGCCTTATATGAATATGCAGTATGGGACTTTGAAATAATGATTATAATAAAATACTAAACGTGTGT CTTCAAAAAAAAAAAAAAAAAA (SEQ ID NO: 73)			
Translated protein sequence			
MREIVHIQAGQCGNQIGTKFWEVISDEHGIDPAGGYVGDSALQL ERINVYNESSSQKYVPRAALVDLEPGTMDSVRSQPFQGLFRPDNFIQGTGAGNNWA KRHYTEGAELVDAVLVDVRKECEHCDLQGFQLTHSLGGGTGSGMGTLLISKIREFP DRIMNTFSVMPSPKVSQDTPVEPNATLSVHQLVENTDETYCIDNEALYDIFRTLKLT TPTYGDLNLHVSATMSGVTTSLRFPQQLNADLRKLAVNMVFPRLHFFMPGFAPLTSR GSQQYRALTVPELTQQMFDAARNMAACDPRHGRYLTVAIVFRGPMMSKVEDEQMLAIQ SKNSSYFVEWIPNNVAVVCDIPRGLKMASTFIGNSTAIQELFKRISEQFSAMFRRK AFLHWFTEGMDMEFTEAESNMNDLVSEYQQYQDATANDGEEAFEDDEEEIDG (SEQ ID NO: 74)			
TYROBP	7305	NM_198125	Homo sapiens TYRO protein tyrosine kinase

			binding protein (TYROBP), transcript variant 2, mRNA
mRNA Sequence			
AGACTTCCTCCTTCACTTGCTGGACGCTGCGCCACATCCCACGGCCCTTACACTGTGGTGTCCAGCAG CATCCGGCTTCATGGGGGACTTGAACCCTGCAGCAGGCTCCTGCTCCTGCTCCTGCTGGCTGTAAG TGGTCTCCGTCTGTCCAGGCCAGGCCAGAGCGATTGCAGTTGCTCTACGGTGAGCCCGGCGTGCTG GCAGGGATCGTGATGGGAGACCTGGTGCTGACAGTGCTCATTGCCCTGGCCGTGTACTTCTGGGCCGGC TGGTCCCTCGGGGCGAGGGGCTGCGGAGGCGACCCGGAACAGCGTATCACTGAGACCGAGTGCCTTA TCAGGAGCTCCAGGGTCAGAGGTGCGATGTCTACAGCGACCTCAACACACAGAGGCCGTATTACAAATGA GCCCCAATCATGACAGTCAGCAACATGATACCTGGATCCAGCCATTCTGAAGCCCAACCTGCACCTCAT TCCAACCTCTACCGGATACAGACCCACAGAGTGCCTATCCCTGAGAGACCAGACCGCTCCCCAATACTCT CCTAAATAAACATGAAGCACAAAAACAAAAA (SEQ ID NO: 75)			
Translated protein sequence			
MGGLEPCSRLLLLPLLLAVSGLRPVQAQASDCSCSTVSPGVLA GIVMGDLVLTVLIALAVYFLGRLVPRGRGAAEATRKQRITETESPYQELQGRSDVYS DLNTQRPYYK (SEQ ID NO: 76)			
YTHDF1	54915	NM_017798	Homo sapiens YTH domain family, member 1 (YTHDF1), mRNA
mRNA Sequence			
GCGTGACGCTGACGCCGCGCAGTCTCGTCCCTGCCGCCGCTCGCCGCTGCTGTGCGCCGCCGCCGCC GCCATTGGAGTCGACGCCCTCTCAGTGCGTCCGCGTCCCGGGCTACCGCCGCTGCCGCTCGCCAGGGG CCCGCGCGCCAGCAGCCGCCGCCGCCGCCGCCGCCGCGGCGCCCGGGGAATTGGCGCGGGGCCCGGGGCG CCGAGCTAGGGTGACAGGCCCGGCCCTCTAGGGGAGGCCCGAGCCGGCGGGCGCCCCGCCCGCTCTA GTTGTTTATGAAGCATGTGCGCCACCAGCGTGACACCCAGAGAACAAAAGGACAAGATAATAAAGTACA AAATGGTTTCTTACATCAGAAGGATACAGTTTATGACAATGACTTTGAGCCCTACCTTACTGGACAGTCA AATCAGAGTAACAGTTACCCCTCAATGAGCGACCCCTACCTGTCCAGCTATTACCGCCGCTCCATTGGAT TTCTTTACTCCCTCAATGAGGCTCCGTGCTTACTGCAGGGGACCTCCGATTCCATACCTCACCACCTA CGGACAGCTCAGTAACGGAGACCATCATTTTATGCACGATGCTGTTTTTGGGCAGCCTGGGGGCTGGGG AACAACTATCAGCAGAGGTTCAATTTTTTCCCTGAAAACCTGCGTTCTCAGCATGGGGGACAAGTG GGTCTCAAGGTGACGAGACCCAGAGCTCCGCGTATGGGAGCAGCTACACCTACCCCCGAGCTCCCTGGG TGGCAGGTTGGTTGATGGGCAGCCAGGCTTTTACAGCGACACCCCTCAGCAAGGCCCGCGGATGAACAGC CTGGAGCAGGGCATGGTTGGCTTGAAGATTGGGGACGTGAGTCTCTCCGCCGCTAAGACGGTGGGCTCTG TCGTGACGAGCGTGGCACTGACTGGTGTCTTTCTGGCAACGGTGGGACAAATGTGAACATGCCAGTTTCT AAAGCCGACCTCGTGGGCTGCCATTGCGCAGCAAGCCTGCAAAACACAGCCATAAATGAAAACAAAGAGC GGGCTGTATGGGGGTGGGCTGCCCCCTCCACCCATAAAGCATAACATGGACATTGGCACCTGGGATA ACAAGGGGCTGTGCCGAAGGCCCTCAGTCCCCAGCAGGACCCCTCTCCACAGGCTGCCCCACAGCCCCA GCAGGTGGCTCAGCCTCTCCAGCACAGCCCCAGCTTTGGCTCAACCGCAGTATCAGAGCCCTCAGCAG CCACCCAGACCCGCTGGGTTGCCCCAGCAACAGAAACGCGGCGTTTGGGCAGAGCGGAGGGGCTGGCA GCGATAGCAACTCTCTGGAAACGTCCAGCCTAATTCTGCCCCAGCGTCGAATCCCAACCCGCTCTTGA AAAAGTGAAGGCTGCTACAGCTACAACCCGAAAGAGTTTGAAGTGAATCTGAAAAGCGGGCGTGTGTTT ATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCAGAGC ACGGCAACAAGCGCTTGGACAGCGCTTCCGCTGCTGAGCAGCAAGGGGCGCGTCTACCTGCTCTTACG CGTCAATGGGAGTGGGCATTTTGTGGGGTGGCCGAGATGAAGTCCCCGTGGACTACGGCACCAGTGCC GGGGTCTGGTCTCAGGACAAGTGAAGGGGAAGTTTGAAGTCCAGTGGATTTTGTAAAGGATGACCCA ATAACCAAGCTCCGCGACATCAGGCTGGAGAATAACGACACAAACCGGTCACAACTCCCGGGACACCCA GGAGGTGCCCTTAGAAAAAGCCAAGCAAGTGTGAAAATTATCAGTTCTTACAAGCACACACCTCCATC TTCGACGACTTTGCTCACTACGAGAAGCGCCAGGAGGAGGAGGTGGTGGCAAGGAACGGCAGAGTC GAAACAAACAATGAGGGCGAACCAAGTTTCTTACATGTTCTAACGTTTGACTTTGAAAACAGTTTAAACA CGTGTGCTTGGTCACTCCAGTGTGCTGCTCCCGTGCAGGGGTTGAGTGTGTCATCTTTGCTTTCTGTG GTTGATTTTGGCCAGATGGATCTGCATTTATTTGACTTTTCTATGTATTATAATCCTGTAGAAGTCA CTAATAAAGGAGTATTTTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAATGTAAGTATCCTTA AAAACAAAGCATCTATTTTGGCAGAAATTGTGTTCTTAAATTCAGTCATTTGATTTCTGTGAGACTTCA TATTTCTCATCCCTTATTTGCTTTTATAGCAACATAAGAAACCATGAGTCATTTTGTCTTTAGAGTATT CTGATAAAATCTCTTGAATAACTGAAATCAAAAGGTTAATGATTTTTTGTTCATTCGATTTGTCTATT TATTATCTGTTATCGGTCTAAAGTGCTAATTTACCAATTGATTTTTCTGCTAGACAGATAACTTTAAT			

TTTTCAAATTGGCAGACACTTTTTTTTTTTTTTTGAAAATCTTTCCTTCCAGATCTGTTGCCCACTGAA
CAGCCACCCGTCCTCAGTGTCTGGTGTCCGATTGGGCTGGATGGTGTIGGGGCATGATGTGTGGAGGA
ACTGGAAGGTGCTTTAGGCTGTGTTCAAGGTCGGGCATTCTTTGTGTGTTCACATCTTTTTAAATTTTA
CACCTTTTCTTAAGAATTCTAATGCCGTCTTAAGTTTTATACCAATAATGCTGAGCTTTAAGTGTAGGA
TCTGGTAGTACAGACAGTGTGATGGATGATGCTGCTGGTTGTAAATTCATCGTGTGTGTCTAATTTTTT
TTCTGTGTGAATGGGTAAAAACAAAACAAACTTTTTTAGAAGATGAATTTGCTGTCATGTTTTGTGGA
ATGAGGGACCGTTGAGCTCACTACCACCTGGAGTTTGAGTTGAAGCATGAAAAATGGTGCCCATGCCTGAC
GCTCCAGCGCTGGATCTGCAGTGCCTTTAGAGGATCCTTACCGTCTAGAGCAGCAGCGCTTCTG
AAAACACTTCTGTCTCAAAAGACCCCTCTGAGTTAACGTTTCAGTGTATCATTAGACTGTATTTAGAGCG
TGTCACCTTCTGAACTGTTACTGCCTGAATGGAGTCTGGAGCATTAGGGTTTTTCTCTAGGAGAA
TACAAGCCTTAATAAAACAATACTATTTAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO: 77)

Translated protein sequence	
1	MAKQK
2	MAKQK
3	MAKQK
4	MAKQK
5	MAKQK
6	MAKQK
7	MAKQK
8	MAKQK
9	MAKQK
10	MAKQK
11	MAKQK
12	MAKQK
13	MAKQK
14	MAKQK
15	MAKQK
16	MAKQK
17	MAKQK
18	MAKQK
19	MAKQK
20	MAKQK
21	MAKQK
22	MAKQK
23	MAKQK
24	MAKQK
25	MAKQK
26	MAKQK
27	MAKQK
28	MAKQK
29	MAKQK
30	MAKQK
31	MAKQK
32	MAKQK
33	MAKQK
34	MAKQK
35	MAKQK
36	MAKQK
37	MAKQK
38	MAKQK
39	MAKQK
40	MAKQK
41	MAKQK
42	MAKQK
43	MAKQK
44	MAKQK
45	MAKQK
46	MAKQK
47	MAKQK
48	MAKQK
49	MAKQK
50	MAKQK
51	MAKQK
52	MAKQK
53	MAKQK
54	MAKQK
55	MAKQK
56	MAKQK
57	MAKQK
58	MAKQK
59	MAKQK
60	MAKQK
61	MAKQK
62	MAKQK
63	MAKQK
64	MAKQK
65	MAKQK
66	MAKQK
67	MAKQK
68	MAKQK
69	MAKQK
70	MAKQK
71	MAKQK
72	MAKQK
73	MAKQK
74	MAKQK
75	MAKQK
76	MAKQK
77	MAKQK
78	MAKQK
79	MAKQK
80	MAKQK
81	MAKQK
82	MAKQK
83	MAKQK
84	MAKQK
85	MAKQK
86	MAKQK
87	MAKQK
88	MAKQK
89	MAKQK
90	MAKQK
91	MAKQK
92	MAKQK
93	MAKQK
94	MAKQK
95	MAKQK
96	MAKQK
97	MAKQK
98	MAKQK
99	MAKQK
100	MAKQK

MSATSVDTRTKGQDNKVVQNSLHQKDTVHDNDFEPYLTGQSNQ
SNSYPSMSDPYLSSYPPSIGFPYSLNEAPWSTAGDPPIPYLTITYGQLSNGDHHFMHD
AVFGQPGGLGNNIYQHRFNFFPENPAFSAWGTSGSQGQQTQSSAYGSSYTYPPSSLG
TVVDGQPFGHSDTLKAPGMNSLEQGMVGLKIGDVSSSAVKTVGSVVSSVALTGVLSG
NGGTNVNMPVSKPTSWAAIASKPAKPQPKMKTSGPVMGGGLPPPIKHNDIGTWDN
KGFVPKAPVPQQAPSPQAAPQPQVAQPLPAQPPALAQPYQSPQPPQTRWVAPRNR
NAAFGQSGGAGSDSNSPQGNVQNSAPSVESHVPLEKLEKAAHNSYNPKEFEWNLSGRVF
I I KSYSEDDIHSRIKYSIWCS TEHGKRLDSAFRCMSSKGPVYLLF SVNGSGHFCGVA
EMKSPVDYGTSAQVWSQDKWKGF DVQWIFVKDVPNNQLRHIRLENNNDNKVPTNSRDT
QEVPLEKAKQVLKIISSYKHTTSIFDDFAHYEKRQEEEEVVVRKERQSRNKQ (SEQ ID NO: 78)

ZIC5	85416	NM_033132	Homo sapiens Zic family member 5 (odd-paired homolog, Drosophila) (ZIC5), mRNA
------	-------	-----------	--

mRNA Sequence	
1	5'-ATG-3'
2	5'-TAC-3'
3	5'-GAC-3'
4	5'-TAA-3'
5	5'-GAA-3'
6	5'-TGA-3'
7	5'-GTT-3'
8	5'-GTT-3'
9	5'-GTT-3'
10	5'-GTT-3'
11	5'-GTT-3'
12	5'-GTT-3'
13	5'-GTT-3'
14	5'-GTT-3'
15	5'-GTT-3'
16	5'-GTT-3'
17	5'-GTT-3'
18	5'-GTT-3'
19	5'-GTT-3'
20	5'-GTT-3'
21	5'-GTT-3'
22	5'-GTT-3'
23	5'-GTT-3'
24	5'-GTT-3'
25	5'-GTT-3'
26	5'-GTT-3'
27	5'-GTT-3'
28	5'-GTT-3'
29	5'-GTT-3'
30	5'-GTT-3'
31	5'-GTT-3'
32	5'-GTT-3'
33	5'-GTT-3'
34	5'-GTT-3'
35	5'-GTT-3'
36	5'-GTT-3'
37	5'-GTT-3'
38	5'-GTT-3'
39	5'-GTT-3'
40	5'-GTT-3'
41	5'-GTT-3'
42	5'-GTT-3'
43	5'-GTT-3'
44	5'-GTT-3'
45	5'-GTT-3'
46	5'-GTT-3'
47	5'-GTT-3'
48	5'-GTT-3'
49	5'-GTT-3'
50	5'-GTT-3'
51	5'-GTT-3'
52	5'-GTT-3'
53	5'-GTT-3'
54	5'-GTT-3'
55	5'-GTT-3'
56	5'-GTT-3'
57	5'-GTT-3'
58	5'-GTT-3'
59	5'-GTT-3'
60	5'-GTT-3'
61	5'-GTT-3'
62	5'-GTT-3'
63	5'-GTT-3'
64	5'-GTT-3'
65	5'-GTT-3'
66	5'-GTT-3'
67	5'-GTT-3'
68	5'-GTT-3'
69	5'-GTT-3'
70	5'-GTT-3'
71	5'-GTT-3'
72	5'-GTT-3'
73	5'-GTT-3'
74	5'-GTT-3'
75	5'-GTT-3'
76	5'-GTT-3'
77	5'-GTT-3'
78	5'-GTT-3'
79	5'-GTT-3'
80	5'-GTT-3'
81	5'-GTT-3'
82	5'-GTT-3'
83	5'-GTT-3'
84	5'-GTT-3'
85	5'-GTT-3'
86	5'-GTT-3'
87	5'-GTT-3'
88	5'-GTT-3'
89	5'-GTT-3'
90	5'-GTT-3'
91	5'-GTT-3'
92	5'-GTT-3'
93	5'-GTT-3'
94	5'-GTT-3'
95	5'-GTT-3'
96	5'-GTT-3'
97	5'-GTT-3'
98	5'-GTT-3'
99	5'-GTT-3'
100	5'-GTT-3'

GCGGCCGCAAGCAGCGGGGGCGAATCCCCGCTGGGTTCGAGGGCTGAACGGGAGCCAATCGAGCAGCCGAG
GCTACTGCCAATACCGGGCTCCCTCCAATCCCACCCGTGCCATTTCAAAAATCTCGGTCCCCTGTGCA
GCTCAAAATGTGGTGTTCACCTCTGCCAATCGCTGGAGGATAGAGTGGGAACAGGAATAAGCAGAGTTAAGA
GGCCAGGACAAAAAGAGTTAAAGAGCGCCCAATACATACATGTTTTGAAGGCGGGCAGAGGGAATAAG
TCCCCCAGTCAGGGGTCTATGGGCGTGATTGTGTAGTTCTGTATGGAGCCCCCTTTGAGCAAGAGGAACCC
GCCAGCGTGTAGATTAGCGATTGTGGCAACGGCTCAGGTCCAGCGCTTCAAGATATGACAGGTTCCCG
GCGCTGGCCGGCCCGCGCCCACTCCCAACTCCGGGCGCGCTCGCGCACTCCCGCTTCGGGAGCACTTG
GCGCTGACCCCGCGTGGCCACCACTCCGCTCGGACCCGAGCACATGGCCCAGGCGAGCACGCTGGGCCCT
CAGCCCTCCCTCCCAGGCGTTCCCGGCACACCCGGAGGCTCCGGCAGCCGCGCCCGTGTGTCAGCCTTG
GTCGCGCACCCCGCGCGGGCAGCTACCCCTGCGGGCGGGGCGAGCAGTGGCGCGCAGCCCTCCGCGCCCC
CGCCCCCAGCCCCCTCTCTCTCTCCACCCCTTCACCCCTCCCCCTCCCGCGCTCTCTCTCTCTCTG
CTCTCGGGCTACACCACCACCAACAGTGGCGGCGGGCGGCGAGCAGCGGCAAGGCCACAGCAGGGACTTC
GTCTCCGGAGGGACCTTTCGCCACGGGCCCCCGCGCGGCCATGCACGGGGCCCCGCTCGGAGGGGAGC
AGCGGTTCGGCAGCGGCTCCCCCAGCACCCGCGCCGCTCCCACTCGCGCGCATGTTTCATCTCCGC
CAGCGGCACCTACGCGGGCCCGGACGGCAGCGCGCGGCCGCGCTTTCGCCGCGCTGCACGACAGCCG
GGGGCCCCAGGCGGCCACCCGCAACCCGCTCAACGGCCAGATGCGCTTGGGGCTGGCGGCGGCAGCGGCAG
CCGCGCGGGCTGAGCTGTACGGCCGCGCGGAACCGCCCTTCGCGCCGCGCTCTGGGGACGCGCACTACGG
GGCGGTTCGCGCCGAGCGCGCGGCCGCTGACGGCTACGGAGCCGTGAACCTTAAACCTGAACCTGGCG
GCTGCGGCGGCGGAGCAGCGGCGGGCCCGGGCCCCACCTGCAGCACCACGCGCGCCCCCGGCGCGCG
CGCCGCCCGCGGCGCCGCGCAGCACCCCGCACCAGCACCAACCCCCACCTCCAGGGGCGGCTGGGGCCTT
CCTGCGCTACATCGCGCAGCCAATCAAGCAGGAGCTCATCTGCAAGTGGATCGACCCCGACGAGCTGGCC
GGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCCACGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT
GCTCCAAAAATTTCCGGCACCATGCACGAGCTGGTGAATCAGCTCAGCGTGAGCAGCTGGGAGGCCCCGA
GCAGAGCAGCCACGCTCTGCTTCTGGGAGGACTGTCCGCGCGAGGGCAAGCCCTTCAAGGCCAAATACAAG
CTCATCAACCACATCCGCGTGCACACGGCGGAGAAGCCCTTTCCCTGCCCTTTCCCGGCTGCGGCAAGG
TCTTCGCGCGCTCCGAGAACCCTCAAGATCCACAAGCGTACTCATACAGGGGAAAAGCCTTTCAATGTGA
ATTTGATGGCTGTGACAGGAAGTTTGCCAATAGCAGTGATCGGAAGAAACATTTCCCATGTCCACACCAGT
GACAAGCCCTACTACTGCAAGATTCTGAGGCTGTGACAAATCCTACACTCACCCAAGCTCCCTGAGGAAGC
ACATGAAGATTACTGCAAGTCCCCGCCACTTCTCCAGGACCCCTTGGTTACTCATCAGTGGGGACTCC
AGTGGGCGCCCCCTGTCTCCCTGTGCTGTGGACCCAGCCAGGAGTCACTCGCAGACTCTGTCCCCTCAGGTG
ACCAACCTCAATGAGTGGTACGTTTGGCAGGCCAGTGGGGCCCCCAGCCACTCCACACCCCTTCCAGCA
ACGGAACCACTCTGAGACTGAAGATGAGGAAATTTACGGGAACCTGAAGTTGTGCGGACGATACATTA

GAATTTATTATTAATAATAATAAGTGAAATAATAAGTGGGAGTCCTTGGACCACATCCTAACCTGAGACA
 ATGCCGAGCCTGAGACAAACCCGTGACTCAGACTTGCCACCGGGTCTAATTAGCCCTATTTATTAGTAT
 GAAACCTATGGTGTGTTGTACATTTAATTAATTTAATTAAGATATTTGGGCTTTTTTTTTTTTTCTT
 AAAAAACAAACAAAAACAAACAGCTGGACTTGTACATTGCAGGAGGATGGGGCTGGGGGCAAAATTGTA
 CCAAGGAAAATGAATGGAGAGATTAGTTAATGGCGATACACACTGCCGATGCAATATATATATATATA
 TATATACATATATATATATATATTTTTTTTTTAAAGGGGGAGAAAAAGAGCATTAAAGTCAGAACTTAACA
 CAGCACCAAGGCCCTCTGCATTTCCAGAGTGCCTCTCAAATGCCTTTGACACCATAACCATGGGCTGCTT
 TTGAGCCTCCTTGTGGACCCTAATTCTGCCAAGGCCCTTTGATTGTAAACCACACACCTGCTGCATTGC
 CAACAGATCCTGTTCCGTACCTGTGTCCAAAAACATTTGTAAAAACCTTTGAGTTTAATATTTGTAATT
 TTTAATTTCCACTCTTTTATTACTGATCTTAGCTTAATACAATATTTTATACAGGATTATTCTTCAGT
 ATCCTACTGTGTGATTTTTAAAAAAGATGCAGCAACCTTAATATATCTCCATATCTTGTGCTACTGTGAT
 TGTTCAGCAAAAGTGGAGAGAAGAAAAGCTGCTGCAAAAGACAACCTGTGAAACTGTGATATTTATAAAA
 ATAGAAGAAATTCAGTGCTTTCTTTTCTATATGTTTTTTTTTTTTTATCTGAATCTCAGATACTGC
 CTCCTAAGTGTCCAACTTCTTGTGTAATAAGAGATTCTGTTTTCGATCCTAAGTCTTTTGGGAGTGC
 CAACATTCAGTCAAGTCTTGAGGAGGTGTGATGATGGCATCATGCCTATTTTTTTGGAAAGCTGTTGT
 TTTTAAACAGGCCAACACCTCTTTTATACGTGTGTATCAGCCTTTTAAAAAGTCTATTTTTCAATGCCT
 GAACTGCATTTTAATGCATTTTCTTCCACCTGAGCACTGAGCACACCAAACCTGGAATCCATTTGAAAAI
 GACAGTGTGTGAAGTGTATGATTTACATTAAGAGAGGGGAGGAGTTGCCATACATATTAATAATTTTTTA
 AAAGTTTATAGTTACCACCAAACACTGATGAATGTGTGACCTTTGCCAGAGCTGTCAAGCTAGGATAAA
 AAAGTCAAGGACCTAGGACAATAACTCTTAGTCGATTTATTTTCGGTTGGTACAACACATCTCCTGTGC
 AAAATGTAGTCCATCAGAAACATCCTACAGATACACTAAGAGCACTAATTTATCCTTAGAGACCCCGAA
 GACACCCCTCCCGAGGGTTGTAGAAATTTGTTTTGTGTGCTGTGAGTGGTTGATGTAGCTTGTCTATT
 GTTAATAACTTGTATGTGAACACTATTATTTGTACAGTTGAATTAATTTATTTTCAGACATCATCTTTT
 TTTTTTCTTTCTGGAAGAGTTCAAAGCACACCAAAGAATTATATTATACATTTTGGTGAAAGATTGTC
 ATTTATGATCCATGGTTTATTTAAAAAAGGAAAGAAAATGGAATAATATTTTAAAGCTTACTTG
 AATGAACAACGTAATGTGAAAACCAAGACTCTTCTGTCATGCTTTTTTGCATTGTGTTGATAAGATTAT
 ATATAGTTTATAGATATATTATATTACTAGTACAGTGCATGGTGCTGTCACCTTGAAAGCCTTTCAATGT
 TGTCTTCAGATTGTTGTGATGAATATGAAACATGCAGACCCCTCCTTTATAAAGAAAAAGACCTTAAACT
 TGAATATGAGATAAATTTACATTTTAAAGTTTATTTGATTTTCATATTATTCACCTTCAAAGCCCTTTC
 AAATAGAAAAGGTATGAACTTTTGGGGGATAATTTATGTATCGTAAACTTATTAGAACAAATATTCTT
 GATGTATAATGAGTTGTTTTATTTATACAACCTTTTCAATGGTAGTTGCACTATTCTTTATTATGCTAC
 AGGTTTATTTATTATGAACAAAGGAATATGTATTTTATGTATTTTACCATGCATAGGTTAACTCTTTC
 CACAGATTTATTGGTTCTTGATACACCTAAAAATAAAAAAATGTGTACCTCCAATAGAGAGCAAGCAAG
 AATGATTATGAAGTAACAAATTTAATAAAGTATTCTTGTATTATTAATAAAAAA (SEQ ID NO: 79)

Translated protein sequence

MFLKAGRGNKVPPVRVYGPDCVVLMEPPLSKRNPPALRLADLAT
 AQVQPLQNMTGFPALAGPPAHSQLRAVAHLRLDLGADPGVATTPLGPEHMAQASTL
 GLSPPSQAFPAHPEAPAAARAAALVAHPGAGSYPCGGSSGAQPSAPPPPAPPLPPT
 PSPPPPPPPPPPPALSGYTTTNSGGGSSGKGHSRDFVLRDLSATAPAAAMHGAPLG
 GEQSRGTGSPQHPAPPPHSAGMFIASGTYAGPDGSGGPALFPALHDTPGAPGGHPHP
 LNGQMRGLGAAAAAAAAAELYGRAEPPFAPRSGDAHYGAVAAAAAALHGYAVNLLN
 NLAAAAAAGPGPHLQHHAPPPAPPPPPAPQHPHQHHPHLPGAAGAFRLYMRQPI
 KQELICKWIDPELAGLPPPPPPPPPPPPAGGAKPCSKTFGTMHELVNHVTVEHV
 GGPEQSSSHVCFWEDCPREGKPFKAKYKLINHIRVHTGEKPFPCPFPGCGKVFARSEN
 LKHKRHTHGEKPFKCEFDGCDRKFANSSDRKKHSHVHTSDKPYCKIRGCDKSYTHPS
 SLRKHKMKHCKSPPPSPGLGYSSVGTPVGAPLSPVLDPARSHSSTLSPQVTNLNEWY
 VCQASGAPSHLHTPSSNGTTSETEDEEIIYGNPEVVRTIH (SEQ ID NO: 80)

CLAIMS

What is claimed is:

- 5 1. A method for determining whether eribulin, an analog thereof, or a
pharmaceutically acceptable salt thereof, may be used to treat a subject having breast
cancer, the method comprising
- determining the level of expression of a biomarker selected from the group of
biomarkers listed in Table 1 in a sample derived from said subject, wherein a low level
10 of expression of the biomarker is indicative that eribulin, an analog thereof, or a
pharmaceutically acceptable salt thereof, will be effective in treating said subject.
2. A method for determining whether eribulin, an analog thereof, or a
pharmaceutically acceptable salt thereof, may be used to treat a subject having breast
15 cancer, the method comprising
- assaying a sample derived from said subject to determine the level of expression
in said sample of a biomarker selected from the group of biomarkers listed in Table 1,
wherein a low level of expression of the biomarker is indicative that eribulin, an analog
thereof, or a pharmaceutically acceptable salt thereof, will be effective in treating said
20 subject.
3. A method for predicting whether eribulin, an analog thereof, or a
pharmaceutically acceptable salt thereof, may be used to treat a subject having breast
cancer, the method comprising
- 25 determining the level of expression of a biomarker selected from the group of
biomarkers listed in Table 1 in a sample derived from said subject, and
- predicting that eribulin, an analog thereof, or a pharmaceutically acceptable salt
thereof, will be effective in treating a subject having breast cancer when said sample is
determined to have a low level of expression of said biomarker.
- 30 4. A method for determining the sensitivity of a breast tumor to treatment
with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, the
method comprising

determining the level of expression of a biomarker selected from the group of biomarkers listed in Table 1 in said tumor, wherein a low level of expression of the biomarker in said tumor indicates that said tumor is sensitive to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof.

5

5. A method for determining the sensitivity of a breast tumor to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, the method comprising

10 determining the level of expression of a biomarker selected from the group of biomarkers listed in Table 1 in said tumor, and

identifying said tumor as being sensitive to treatment with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, when there is determined to be a low level of expression of said biomarker in said tumor.

15 6. The method of claim 4 or 5, wherein a sample of the breast tumor is obtained from a subject having breast cancer.

7. A method of treating a subject having breast cancer, the method comprising

20 identifying a subject having breast cancer in which a biomarker selected from the group of biomarkers listed in Table 1 has a low level of expression, and

administering a therapeutically effective amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, to said subject.

25 8. A method of treating a subject having breast cancer, the method comprising

assaying a sample derived from said subject to determine the level of expression in said sample of a biomarker selected from the group of biomarkers listed in Table 1, and

30 administering a therapeutically effective amount of eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, to said subject when a low level of expression of the biomarker is detected in said sample.

9. The method of any one of claims 1-8, wherein the pharmaceutically acceptable salt of eribulin is eribulin mesylate.

5 10. The method of any one of claims 1-3 or 6-8, wherein said subject has not been previously treated with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof.

10 11. The method of any one of claims 1-3 or 6-8, wherein said subject has been previously treated with eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof.

12. The method of any one of claims 1-3 or 6-8, wherein said breast cancer is an Estrogen Receptor (ER) negative breast cancer.

15

13. The method of any one of claims 1-3 or 6-8, wherein said breast cancer is a Progesterone Receptor (PR) negative breast cancer.

14. The method of any one of claims 1-3 or 6-8, wherein said breast cancer is a HER-2 negative breast cancer.

20

15. The method of any one of claims 1-3 or 6-8, wherein said breast cancer is an Estrogen Receptor (ER) negative and Progesterone Receptor (PR) negative breast cancer.

25

16. The method of any one of claims 1-3 or 6-8, wherein said breast cancer is an Estrogen Receptor (ER) negative and HER-2 negative breast cancer.

17. The method of any one of claims 1-3 or 6-8, wherein said breast cancer is a Progesterone Receptor (PR) negative and HER-2 negative breast cancer.

30

18. The method of any one of claims 1-3 or 6-8, wherein said breast cancer is an Estrogen Receptor (ER) negative, Progesterone Receptor (PR) negative and HER-2 negative breast cancer.

5 19. The method of any one of claims 1-8, wherein at least 2 biomarkers selected from the group of biomarkers listed in Table 1 have a low level of expression

20. The method of any one of claims 1-8, wherein the level of expression of at least 3 biomarkers selected from the group of biomarkers listed in Table 1 have a low
10 level of expression.

21. The method of any one of claims 1-8, wherein the level of expression of at least 4 biomarkers selected from the group of biomarkers listed in Table 1 have a low level of expression.

15

22. The method of any one of claims 1-8, wherein the level of expression of at least 5 biomarkers selected from the group of biomarkers listed in Table 1 have a low level of expression.

20 23. The method of any one of claims 1-8, wherein there is a low level of expression of said biomarker as compared to a control.

24. The method of claim 23, where said biomarker is not expressed at a detectable level.

25

25. The method of any one of claims 1-8, wherein the level of expression of said biomarker is determined at the nucleic acid level.

26. The method of claim 25, the level of expression of said biomarker is
30 determined by detecting cDNA.

27. The method of claim 25, the level of expression of said biomarker is determined by detecting mRNA or miRNA.

28. The method of claim 25, the level of expression of said biomarker is
5 determined by detecting DNA.

29. The method claim 25, wherein the level of expression of said biomarker is determined by using a technique selected from the group consisting of polymerase chain reaction (PCR) amplification reaction, reverse-transcriptase PCR analysis, quantitative reverse-transcriptase PCR analysis, Northern blot analysis, RNAase protection assay, digital RNA detection/ quantitation, and combinations or sub-combinations thereof.
10

30. The method of any one of claims 1-8, wherein the level of expression of
15 said biomarker is determined at the protein level.

31. The method of claim 30, wherein the presence of the protein is detected using an antibody or antigen binding fragment thereof, which specifically binds to the protein.
20

32. The method of claim 31, wherein the antibody or antigen binding fragment thereof is selected from the group consisting of a murine antibody, a human antibody, a humanized antibody, a bispecific antibody, a chimeric antibody, a Fab, Fab', F(ab')₂, ScFv, SMIP, affibody, avimer, versabody, nanobody, a domain antibody, and an antigen binding fragment of any of the foregoing.
25

33. The method of claim 31, wherein the antibody or antigen binding fragment thereof is labeled.

34. The method of claim 33, wherein the antibody or antigen binding fragment thereof is labeled with a label selected from the group consisting of a radio-label, a biotin-label, a chromophore-label, a fluorophore-label, and an enzyme-label.
30

35. The method of claim 28, wherein the level of expression of said biomarker is determined by using a technique selected from the group consisting of an immunoassay, a western blot analysis, a radioimmunoassay, immunofluorimetry,
5 immunoprecipitation, equilibrium dialysis, immunodiffusion, electrochemiluminescence immunoassay (ECLIA), ELISA assay, immunopolymerase chain reaction and combinations or sub-combinations thereof.

36. The method of claim 35, wherein the immunoassay is a solution-based
10 immunoassay selected from the group consisting of electrochemiluminescence, chemiluminescence, fluorogenic chemiluminescence, fluorescence polarization, and time-resolved fluorescence.

37. The method of claim 35, wherein the immunoassay is a sandwich
15 immunoassay selected from the group consisting of electrochemiluminescence, chemiluminescence, and fluorogenic chemiluminescence.

38. The method of any one of claims 1-3, 6 or 8, wherein said sample comprises a fluid, or component thereof, obtained from said subject.
20

39. The method of claim 38, wherein the fluid is selected from the group consisting of blood, lymph, serum, plasma, cystic fluid, nipple aspirates, urine, sputum, and fluid collected from a biopsy.

25 40. The method of any one of claims 1-3, 6 or 8, wherein the sample comprises a tissue, or component thereof, obtained from said subject.

41. The method of claim 40, wherein said tissue is selected from the group consisting of breast tissue, connective tissue, lymphatic tissue, tissue obtained from a
30 biopsy and tissue obtained from a lump biopsy.

42. The method of claim 40, wherein the tissue is breast tissue or a component thereof.

43. The method of claim 42, wherein said component of said breast tissue comprises breast tissue cells.

5 44. The method of claim 43, wherein said breast tissue cells are circulating breast tumor cells.

45. The method of any one of claims 1-3 or 6-8, wherein said subject is a human subject.

10

46. A kit for predicting whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, may be used to treat a subject having breast cancer, the kit comprising

15 reagents for determining the level of expression of a biomarker selected from the group of biomarkers listed in Table 1; and

instructions for use of the kit to predict whether eribulin, an analog thereof, or a pharmaceutically acceptable salt thereof, may be used to treat a subject having breast cancer.

20 47. The kit of claim 46, wherein the pharmaceutically acceptable salt of eribulin is eribulin mesylate.

48. The kit of claim 46, wherein the reagent for determining the level of expression of the biomarker is a probe for identifying a null mutation in the biomarker.

25

49. The kit of claim 46, wherein the reagent for determining the level of expression of the biomarker is a probe for amplifying and/or detecting the biomarker.

30 50. The kit of claim 46, wherein the reagent for determining the level of expression of the biomarker is an antibody.

51. The kit of claim 46, further comprising reagents for obtaining a biological sample from a subject.

52. The kit of claim 46, further comprising a control sample.

5

Sequence_Listing.txt
SEQUENCE LISTING

<110> Eisai R&D Management Co., Ltd.et al.

<120> METHODS AND COMPOSITIONS FOR PREDICTING RESPONSE TO ERIBULIN

<130> 117824-12320

<140> NEW APPLICATION

<141> Concurrently Herewith

<150> 61/454,426

<151> 2011-03-18

<160> 80

<170> PatentIn version 3.5

<210> 1

<211> 2129

<212> DNA

<213> Homo sapiens

<400> 1

tcctatccac cctccactcc cctgtccctt ggtgactcat ccctgagctt cccaaggaag	60
ccccaccct ctgcccttc ctccgcctt ccatgagtgg aaaatccacc tccgccccct	120
atagcaggcc agcccccttc ctcccagtc tccgaccca tccccagcc gaccagtttc	180
ctctccagga ccaggagca atcacagctg ccccgacctt ggcttctct gctgggtggg	240
attgggggct gggccccaa atgggccctt ggcttcccc ttctctggg caggggacag	300
agagacacag gctcggggag caggactgac ttctcttgt cccggaatga gcatgcctgc	360
ccttgcaag caggttggg tctcacgcag aggaaacaa aagcaataag agggagggaa	420
ggcagagcaa ccaatcaagg gcagggtgag actcaaacg agcgggctcc ctggggagcc	480
agacagaggc tgggggtgat ggcggagcta cagcagctgc aggagttga gatccccact	540

Sequence_Listing.txt

ggccgggagg ctctgagggg caaccacagt gccctgctgc gggtcgctga ctactgcgag 600
gacaactatg tgcaggccac agacaagcgg aaggcgctgg aggagacat ggccttact 660
accagggcac tggccagcgt ggcctaccag gtgggcaacc tggccgggca cactctgcgc 720
atgttgacc tgcagggggc cgccctgcgg caggtggaag cccgtgtaag cacgctgggc 780
cagatggtga acatgcatat ggagaagggt gccgaagg agatcggcac cttagccact 840
gtccagcggc tgcccccg ccagaaggtc atgccccag agaacctacc ccctctacg 900
ccctactgca ggagaccct caacttggc tgctggacg acattggcca tgggatcaag 960
gacctcagca cgagctgtc aagaacagg accctgtctc gaaagagcat caaggccct 1020
gccacaccg cctccggcac ctgggggaga ccacccgga tcccgagcc agtcacctg 1080
ccggtgtgtc ccgacggcag actctccgc gcctctctg cgtcttcct ggctcggcc 1140
ggcagcgccg aagggtcgg tggggcccc acgccaagg ggcaggcagc acctccagcc 1200
ccacctctc ccagctcct ggaccacct cctccaccag cagccgtcga ggtgtccag 1260
cggcctcca cgctggagga gttgtccca cccccaccg acgaagagct gccctgcca 1320
ctggacctgc ctctctcc accctggat ggagatgaat tggggtgcc tcaccccca 1380
ccaggattg ggcctgatga gccagctgg gtgcctgcct catactgga gaaagtgtg 1440
acactgtacc catacaccag ccagaaggac aatgagctct ccttctctga gggcactgtc 1500
atctgttca ctgccgcta ctccgatggc tggtcgagg gcgtcagtc agaggggact 1560
ggattctcc ctgggaacta tgtggagccc agctgtgac agcccagggc tctctggca 1620
gctgatgtct gcactgagt ggttcatga gcccgaagc aaaaccagct ccagtcacag 1680
ctggactggg tctgccacc tctgggctg tgagctgtgt tctgtcttc ctccatcgg 1740
agggagaagg ggtctggg agagagaatt tatccagagg cctgtgcag atggggaaga 1800

Sequence_Listing.txt

gctggaaacc aagaagtttg tcaacagagg acccctactc catgcaggac agggctctct 1860
gctgcaagtc ccaactttga ataaaacaga tgatgtcttg tgactgcccc acagagataa 1920
ggggccagga gggattgaaa ggcatcccag ttctaaggct gctgctaatt acagcccca 1980
acctcaacc caccagctga cctagaagca gcatcttccc atttctcag taccacaaa 2040
gtgcagcca cattggaccc cagacacccc tctgcagcca ttgactgcaa ctgttcttt 2100
tgccattga aaaaaaaaaa aaaaaaaaaa 2129

<210> 2

<211> 366

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Glu Leu Gln Gln Leu Gln Glu Phe Glu Ile Pro Thr Gly Arg

1 5 10 15

Glu Ala Leu Arg Gly Asn His Ser Ala Leu Leu Arg Val Ala Asp Tyr

20 25 30

Cys Glu Asp Asn Tyr Val Gln Ala Thr Asp Lys Arg Lys Ala Leu Glu

35 40 45

Glu Thr Met Ala Phe Thr Thr Gln Ala Leu Ala Ser Val Ala Tyr Gln

50 55 60

Val Gly Asn Leu Ala Gly His Thr Leu Arg Met Leu Asp Leu Gln Gly

65 70 75 80

Ala Ala Leu Arg Gln Val Glu Ala Arg Val Ser Thr Leu Gly Gln Met

85 90 95

Sequence_Listing.txt

Val Asn Met His Met Glu Lys Val Ala Arg Arg Glu Ile Gly Thr Leu
100 105 110

Ala Thr Val Gln Arg Leu Pro Pro Gly Gln Lys Val Ile Ala Pro Glu
115 120 125

Asn Leu Pro Pro Leu Thr Pro Tyr Cys Arg Arg Pro Leu Asn Phe Gly
130 135 140

Cys Leu Asp Asp Ile Gly His Gly Ile Lys Asp Leu Ser Thr Gln Leu
145 150 155 160

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

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

His Leu Pro Val Val Pro Asp Gly Arg Leu Ser Ala Ala Ser Ser Ala
195 200 205

Ser Ser Leu Ala Ser Ala Gly Ser Ala Glu Gly Val Gly Gly Ala Pro
210 215 220

Thr Pro Lys Gly Gln Ala Ala Pro Pro Ala Pro Pro Leu Pro Ser Ser
225 230 235 240

Leu Asp Pro Pro Pro Pro Pro Ala Ala Val Glu Val Phe Gln Arg Pro
245 250 255

Pro Thr Leu Glu Glu Leu Ser Pro Pro Pro Pro Asp Glu Glu Leu Pro

Sequence_Listing.txt

260 265 270

Leu Pro Leu Asp Leu Pro Pro Pro Pro Pro Leu Asp Gly Asp Glu Leu
275 280 285

Gly Leu Pro Pro Pro Pro Pro Gly Phe Gly Pro Asp Glu Pro Ser Trp
290 295 300

Val Pro Ala Ser Tyr Leu Glu Lys Val Val Thr Leu Tyr Pro Tyr Thr
305 310 315 320

Ser Gln Lys Asp Asn Glu Leu Ser Phe Ser Glu Gly Thr Val Ile Cys
325 330 335

Val Thr Arg Arg Tyr Ser Asp Gly Trp Cys Glu Gly Val Ser Ser Glu
340 345 350

Gly Thr Gly Phe Phe Pro Gly Asn Tyr Val Glu Pro Ser Cys
355 360 365

<210> 3

<211> 742

<212> DNA

<213> Homo sapiens

<400> 3

tccagggtca cacaactgga acccatctcc aggaacaaac agctggaacc catctccgt 60

tgaaggga aa ctgccagatt ttgttaagat tcttctcct gggagcctgt gttggaagag 120

atggtgatgg gcctgggcgt ttgtgttg gtcttcgtgc tgggtctggg tctgaccca 180

ccgaccctgg ctgaggataa ctccaggtag acacacttc tgaccagca ctatgatgcc 240

aaaccacagg gccgggatga cagatactgt gaaagcatca tgaggagacg gggcctgacc 300

Sequence_Listing.txt

tcacctgca aagacatcaa cacatttatt catggcaaca agcgcagcat caaggccatc 360
 tgtgaaaaca agaattgaaa ccctcacaga gaaaacctaa gaataagcaa gtcttcttc 420
 caggtcacca ctgcaagct acatggagggt tccccctggc ctccatgcca gtaccgagcc 480
 acagcgggggt tcagaaacgt tgtgttgct tgtgaaaatg gcttacctgt ccacttgat 540
 cagtcaattt tccgtcgtcc gtaaccagcg ggccccctgg caagtgcctg ctctgctgc 600
 ctgccttcc atttccctc tgcaccaga acagtgggtg caacattcat tgccaagggc 660
 ccaaagaaag agctacctgg accttttgt ttctgttga caacatgtt aataaataaa 720
 aatgtcttga tatcagtaag aa 742

<210> 4

<211> 147

<212> PRT

<213> Homo sapiens

<400> 4

Met Val Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu
 1 5 10 15

Gly Leu Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His
 20 25 30

Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg
 35 40 45

Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys
 50 55 60

Asp Ile Asn Thr Phe Ile His Gly Asn Lys Arg Ser Ile Lys Ala Ile
 65 70 75 80

Sequence_Listing.txt

Cys Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser
85 90 95

Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro
100 105 110

Trp Pro Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val
115 120 125

Val Ala Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe
130 135 140

Arg Arg Pro
145

<210> 5
<211> 8935
<212> DNA
<213> Homo sapiens

<400> 5
gccaaagcct ggagaagtgg aatctcgtca gcgccgctcc ctgcgcggga ctgcgcgaac 60
ggcactgagc atgctcagtt gccggagccc gttctggctt caagtaggaa gctagtgcgc 120
tgaaccgca tctgatctgg gcgctccggg aagggcgaga ctggagcaga gccgctgggc 180
gccggagccg aggcgagcgc cgcgcgcacc actggttga gttgctgtgg gtgagctgct 240
gtggtctgta gccaagcatg ctgtggtcgg atctgccag ccgtggaaca gaaacatttg 300
ctggatggaa aatccataaa agaaagctcc tgtgaaaagc tgaggctgac aataatttaa 360
gcaaaatcag atcgatctct ttgggctgcc tgacctcctt gggtgcttgc tattaattaa 420

Sequence_Listing.txt

cagactttgt ggggaaaaaa aggagcttgc ctctgagct ttgtacaaa gacctgggaa 480

aactaacct ctcagctttt cctgaggact tgggaactgc cgaggcctct gccaatgtgt 540

tgactgtgc tatgggtca ctgtgtcca ggcagctcat attcaaatt ataacctatt 600

tcctgcacca ttctgacgc ctggtgatcc atgtcagaag tacttcagc tgactcaggt 660

gttgacacct tggcagtgt tatggccagc agcggaaacta cagacgtcac aaatcggaac 720

agcccagcca caccacaaa caccctaac ctccgatct cccacaatga actgttgaac 780

gctgaaataa aacacacaga aaccaagaac agcacacctc ccaaatgcag gaaaaaatat 840

gcactaacta acatccaggc ggccatgggc ctctcggatc cagctgcaca gccctgtctg 900

ggaaatggct ctccaacat caagctgggtg aaaaatgggg agaaccagct ccgtaaggct 960

gcagagcaag ggcagcagga cccaacaaa aacctgagcc ccactgcagt catcaacata 1020

actctgaga agttagaggg taaagagccc caccacagg attcctcgag ctgtgagatt 1080

ttacctccc agcccaggag aactaagagc ttctaataatt actatgcaga tctggaaacc 1140

tcagccagag aactagagca gaaccgaggc aatcacatg ggactgcgga agagaaatcc 1200

cagccagtc agggccaggc ctccaccatc attgggaatg gcgatttgc gctgcagaaa 1260

ccaaacagac ccagtcag ccctgaagac ggccaagtag ccacagtgc atccagccca 1320

gaaaccaaga aggatcatcc gaaaacagg gcaaaaaccg actgtgact gcaccggatc 1380

cagaacctgg caccgagcga tgaggagtcc agctggacaa cgttgtcca agacagtgcc 1440

tcaccagct ccccgatga aacagatata tggagtgatc actcattca gactgatcca 1500

gatttgccgc ctggctggaa aagagtcagt gacattgcc ggacctatta ttggcacatc 1560

ccaacaggaa cgactcagt ggaacggccc gtcctcatcc cagcagatct ccagggttct 1620

aggaaagggt cacttagtgc tgtaacgcca tctccaccc cagagaacga ggatttgc 1680

Sequence_Listing.txt

gcagccactg ttaacccgga cccagttta aaagagttg aaggagcaac cctacgctat 1740

gcaccttga aactcagaaa tgccccacac cctgatgatg atgattcttg tagtatcaac 1800

agtgaccag aagccaagtg tttgctgtg cgtctctgg gatgggtaga gatggcagaa 1860

gaggacctg cccccggtaa aagtagtgtt gcggtaaca actgcatcag gcaactttcc 1920

tactgcaaaa atgacatccg agacacagtc gggatttggg gagaggggaa agacatgtac 1980

ctgatcctgg agaatacat gctcagcctg gtggaccca tggaccgag cgtgctgcac 2040

tcgcagccca tcgtcagcat ccgcgtgtgg ggcgtgggcc gcgacaatgg ccgggatttt 2100

gcttatgtag caagagataa agatacaaga atttgaaat gtcattgtt tcgatgtgac 2160

acaccagcaa aagccattgc cacaagtctc cagagatct gctcaagat tatggctgaa 2220

cggaagaatg ccaaagcgtt ggctgcagc tccttacagg aaagggccaa tgtgaacctc 2280

gatgtccctt tgaagattt tccaacacca aagactgagc tggccagaa gttccacgtg 2340

cagtacttgg gcatgttacc ttagacaaa ccagtcggaa tggatatatt gaacagtgcc 2400

atagaaaatc ttatgacctc atccaacaag gaggactggc tgcagttaa catgaacgtg 2460

gctgatgcca ctgtgactgt catcagttaa aagaatgaag aggaagtctt agtggaatgt 2520

cgtgtgcgat tcctgtcctt catgggtgtt gggaaggacg tccacacatt tgccttcac 2580

atggacacgg ggaaccagcg cttgagtgc cacgtttct ggtgcgagcc taatgctggt 2640

aacgtgtctg aggcggtgca ggccgcctgc atgttacgat atcagaagtg cttggtagcc 2700

aggccgcctt ctcaaaaagt tcgaccacct ccaccgccag cagattcagt aaccagaaga 2760

gtcacaacca atgtaaaacg aggggtctta tccctcattg acactttgaa acagaaacgc 2820

cctgtcaccg aaatgccata gctgcacatg caaaaggact cggctattta cctgaagatt 2880

gactagctac actaaagaaa atgaactccg ccatccgacc ttccatccag ttgctgatgc 2940

Sequence_Listing.txt

tttgtcttca gagaatttac ccttaaccaa gcagtgtagt acaagcatgt tctctcgtct 3000

tgccaccatc atgtgatatg aaaagaagca tgaataattt ttttgctgt aagttacatc 3060

atgcgcagtg gaaggctctt tcttattgt aaatatttg aacattactt aactcacac 3120

acacacagag aagagtgtag ccccccct cctagtgaac taacgctgcg tccttggaat 3180

gaatgatgcg tgagtagt tctctgtct ctggctgga cctgtcaca gcaaccttta 3240

agtcttacag cactttgcc tgtttcaac attggagtag gcactgcata gcagatacca 3300

ttgaattgct gtaaaaatag gatggcgagt ttgtgttta attttcata aaattgaacc 3360

tgttggtga caaaattggc tgtggcatc agtatagaaa ccaactggca gcttccctg 3420

acaagctctt tgacacatgg acaccatttc atgtctacag ctgttgtagg gatgttgaa 3480

aaaaatgaaa ctcaaaatt gatgaaaaac taaattcgag gaattaaat cgaacaaaac 3540

atagccttc tttccgatg gtttcaaac tgattattt taaaagagat taataaaatc 3600

ataatgcatt ttgggtggga catattcaa acttctgcct tatattgtac ggtgcagcta 3660

gagaattata gttcactatg gccattctct acataaacat taagatgaaa tactcctcat 3720

cagccttca tccttagttt gagaattagc tgatgcaa ttgaagtg aggaaatc 3780

attgatatt ctatcatgca cgattattt agattctac caccgtgtga ttttgctag 3840

tccatgtgct agaggtaaac gttctgctgg aattctgcat ccagctctat cccctctga 3900

tgcttttgc ccagaaagct gtctgtccat catgtattgt ccatggcaac aaattacatt 3960

aggtgaacc ttccttgat ttatgtatt taatattaga attgttgga ctcaactaga 4020

tatattttt aatttatatt tttccattt tacttgaag attgaaatg ttcatacctg 4080

agcaaagtct acacaggagt aatggactgt ttaacaagt tcccaaaaca gcattttcct 4140

gctcctcgt atgtaggtag gaaacttagc tgaaagaca taaaattta gactctcgtt 4200

Sequence_Listing.txt

gacattgtcg tttaaaagg aagttgctaa ggcgatcaat ctcaatatta gtctgttta 4260

cttcttcta atgtcaaaat taacatttac aacatccaat tataaaagta atgctttatg 4320

tttatacact gctatgtact tgtcaaaatg gttccacat tctatcaca tctgagcctt 4380

accaggtaga gaaggtaga aatacacttt agaagtaaaa atatgaagta ccgagaggct 4440

aaaccactg gcctaagatc tcaccaaagt tcatgaaaac caggactagg acccacggct 4500

cccaaagccc gttctgtcg tgtgtgtcg cctccatac cgtcaggaag agcctttcca 4560

gaatgattct gggcatatac taagaagagc aggtatggaa agatctattg tcagggaatc 4620

ttagaattcc ctacacgagt gggagaaaaga tgtccaaatt ccttacgcag tggattcat 4680

gatgggtccc tatctaagtc caggactgtt ttctacagc gtgcctcaaa agtgtgttag 4740

agggcaggat tctacattca cagcctgttc catctacgag attttccaga tgctactgt 4800

ggtagacatt cctaactcat ggtacttagc caccagagat catgatggaa tgagtgggtg 4860

gctttctac ctgccattcc ctcaaatc atgaggggtg ggggacaggg ggaccggaat 4920

tgtcttagca cccaatgtt atgacaaaac tatgtactt tagaaacgca gtctgtttt 4980

caccaattga catactactg atctgaagta accagtcca tcataagaaa ttactgcatt 5040

aagaaaatcc ttgctgtgcc cttgaaaag ctgttcagaa atcatttaca gtgatcttc 5100

atctcggtcg ctgtatgaa acattttagt gtgataaatt tcaaaattct aaacaaatta 5160

cccacttta tattggaaat ctctaccaga actccctctt catTTTTTaa ggcatacatt 5220

tgctgtttt caagatcaag aattctgagc tagctttaag tagcaaactg atttatatgt 5280

gcaattatag gatgcattaa gatgaatgat agcctttaca tattgaaaac ttgcagacg 5340

tttgTTTTg aaaaatggcat tgtatagtaa atgcaaatta atttgtaaa attatgttaa 5400

agagtatgtt cagacacttt ctgccatggc caaaaagtat gtagaaagt atgtgtgtat 5460

Sequence_Listing.txt

ttgtttgtaa aaggatgcc aatgtttacc tgatatctta gtgacacttc agttatctat 5520

gcattcttta gatctgtgat tcggtaaaca ggcagccatg ttcacgatgc cttctatgtc 5580

ttaccatatt ttaattaac ctgttaaata cagcttaaaa tattttatt ttattattc 5640

tattttact gaaatatact gcattattgt gttaatgtat tatctttcct ggatattatc 5700

tcccagtgt tccagatcta agtaactca gtgaactata cattgcctaa aaagtgggtt 5760

tgtaatgatt tgtagtcaca ttctattgg gatgtgtaga agaaaaggca aaatgcttaa 5820

agttcctttt atttttaaa agcagctaga tagacacaga ctgccacct catacatctg 5880

ctccttgcca acatcaaggg gaacgactag ccaacatgcc tatggctaaa aactttcctt 5940

tgcagactaa agcactgctt ggtgcttctg ttcttacct ttcacaacat gtgtgatttc 6000

atctaagaga tatafacatg tacacatgcc cttgtttcc acctggatac aagatcactc 6060

atagctaatt aggaccattg tttttgttc atctgtcttg ttgcatgaag ggacattaga 6120

cccattcca taaaataag ttcttggtga taaactgtgg cactgctact tcttttaaa 6180

tccactttat gatttcaaga tggacacttg taagatgact cgacacaagg ccattgcctg 6240

gaagccccag agctttcctc tgtttgatg gcccgttcat gtcccaggca ttgcaacaca 6300

aactcctcaa gattcacca caacatgaca agcattttcc taactgatat tagcacaatt 6360

taactaataa gccccttcgc tctctagtgt gccaggctta acctaatata catctaacgt 6420

gtgtgccaca cggccagtag aaagttaac ttcagcttca gggcaaagat acccactcac 6480

accgtgtcaa cgcaagcagt agttcctggc ctccagagca gcttacttc cctgaaagaa 6540

cgctttgttt tctttatgc ccttttcctg ttgaccactt ttacacattt aaatgtaatt 6600

tgttgtgaga ataaatttag ctgcataaaa cgttcggctc atttatctga catcttagtc 6660

acatatacaa ggaatagaaa tagaaactcg gtgtctctag ttattttaa attattctta 6720

Sequence_Listing.txt

cctcagactt ctagaaaac actttagtaa tggagcattt tgcttgatt agttactaca 6780
 tatttcgcc tgtaagaac taggaagtaa ctcaaattt tgagtaatca ccctgtactt 6840
 atttggtgat caggaaggcc agctggcctt ccggacatag aagcctattt agtcaccaac 6900
 tcgagtcttt tgtaagcggc ctgctagga ttggtatatt ttagcacgaa gaagtttatt 6960
 acttccttta agaacctgac atcaaagaat aaagaataga ggtgtacaca cactaaatcc 7020
 aaaatgaaag gtaactagag aaatcagttg aatctggttt agcttaactg ttaggcgcag 7080
 gaaggcagat aaacagaatt taaagtatgt ccccgctttt tgttcatctt gcacttcac 7140
 agtggtttct ctctagtcag taacaaaatt tcattatggt ttcaggcatt atatggtggt 7200
 aaataatttc agattaataaa tgtgtttgct attggagtat ctgaatacta gtaatttcatt 7260
 tatttagaat ttgcagcac tttatctca agaagaagtc caagaatgta aaatgccaaa 7320
 tgaaacatgt cagtggaatc aatatttccc ttcatagaa ttccctcata ttgctttttt 7380
 ttttttctt cagacagagg agtcttactc tggagtgcag tgggtgaatt tcagctcacc 7440
 acaacctcca cctccaagt tcaagcaatt ctgcctcag cctctgagt agctgggatt 7500
 acaggcatgc accgccacgc ctggccaatt tgtatattt tagtagagac agggtttcgc 7560
 cacgttgccc aggcgtgtct cgaactcctg acctcaggtg atccgcccgc cccaacctcc 7620
 caaagtatgt gagccaccac gtccggcctc atattgcttt tatccaaaat tottttcctt 7680
 ttccactcta ccaaagtatt taaataatcc tgccttcat agaagattct caaagaagaa 7740
 aactgcagtg taattaatga atggtttaat tcagaatctt cataacttc taaagagaaa 7800
 aataatttag tgccaaatgc atgtaggag ataataatg taagtggcaa caaattgtga 7860
 cttcacatgc tactgtagag atcagaaaat tatcctaaac tattcataa caatgagaca 7920
 acatcacaga aaatacactt gaaaataaaa atcctaagac cagctacttc tggacaatgg 7980

Sequence_Listing.txt

aatacttttc agtctggtat ggtggagggc ccgaaaagga taagggttc ttatgataca 8040
 caatgggatt cttactgaa caatatgta aattaagctg caccgccttc cttgaggcat 8100
 ggactaccct aaccaaccag atagaaatct ggggtgggata agaggatgag ccacacgcta 8160
 taattttagg gcaaggagat agtggttgat ttcaaaaatc agcaaaataa gctgagcact 8220
 ttatatcttt ctgtacaaga gtgataacat gaagaattct tcttcagga tttaaatac 8280
 aataagcctg gticaactat aaaaagtctt gtttccttc ttcattgaca ctttttttt 8340
 ttttttttt ttttgaggc aaggctcac tctgctccc aggctggagt gcagtggggc 8400
 aatattggct cactgcaacc tgcacctct ggactcaaga gatcctcgta cctcagcctc 8460
 ctaagtagct gggactacag gcgtgtcca ccacaccag ctaattttg tatttttgt 8520
 agagatgggg tttgggggt tcgcatgtt gtccaggctc gtctggaact ccggtgctca 8580
 agtggcgtgc ccacctcagc ctcccaaact gctgagatta cagatgtgag ccactgcacc 8640
 cagcccactg acacgtttta ctgataaatg taaatctaag ctaaaataaa aataatgtat 8700
 taccgtata atacaattca ccattctctt ttctcacttc aagtaagaaa gtaaaaatag 8760
 aatacagag ctgaagtaga cctaagtatt catctgaag aagataatat tctaaaaatc 8820
 atgccacctg aattgagcat ttaggaattt atgtaacatt tctatacaac tgaattgcaa 8880
 aaataaaact ttaaattcaa actttaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 8935

<210> 6

<211> 736

<212> PRT

<213> Homo sapiens

<400> 6

Met Ser Glu Val Leu Pro Ala Asp Ser Gly Val Asp Thr Leu Ala Val

1 5 10 15

Sequence_Listing.txt

Phe Met Ala Ser Ser Gly Thr Thr Asp Val Thr Asn Arg Asn Ser Pro
20 25 30

Ala Thr Pro Pro Asn Thr Leu Asn Leu Arg Ser Ser His Asn Glu Leu
35 40 45

Leu Asn Ala Glu Ile Lys His Thr Glu Thr Lys Asn Ser Thr Pro Pro
50 55 60

Lys Cys Arg Lys Lys Tyr Ala Leu Thr Asn Ile Gln Ala Ala Met Gly
65 70 75 80

Leu Ser Asp Pro Ala Ala Gln Pro Leu Leu Gly Asn Gly Ser Ala Asn
85 90 95

Ile Lys Leu Val Lys Asn Gly Glu Asn Gln Leu Arg Lys Ala Ala Glu
100 105 110

Gln Gly Gln Gln Asp Pro Asn Lys Asn Leu Ser Pro Thr Ala Val Ile
115 120 125

Asn Ile Thr Ser Glu Lys Leu Glu Gly Lys Glu Pro His Pro Gln Asp
130 135 140

Ser Ser Ser Cys Glu Ile Leu Pro Ser Gln Pro Arg Arg Thr Lys Ser
145 150 155 160

Phe Leu Asn Tyr Tyr Ala Asp Leu Glu Thr Ser Ala Arg Glu Leu Glu
165 170 175

Gln Asn Arg Gly Asn His His Gly Thr Ala Glu Glu Lys Ser Gln Pro

Sequence_Listing.txt

180 185 190

Val Gln Gly Gln Ala Ser Thr Ile Ile Gly Asn Gly Asp Leu Leu Leu
195 200 205

Gln Lys Pro Asn Arg Pro Gln Ser Ser Pro Glu Asp Gly Gln Val Ala
210 215 220

Thr Val Ser Ser Ser Pro Glu Thr Lys Lys Asp His Pro Lys Thr Gly
225 230 235 240

Ala Lys Thr Asp Cys Ala Leu His Arg Ile Gln Asn Leu Ala Pro Ser
245 250 255

Asp Glu Glu Ser Ser Trp Thr Thr Leu Ser Gln Asp Ser Ala Ser Pro
260 265 270

Ser Ser Pro Asp Glu Thr Asp Ile Trp Ser Asp His Ser Phe Gln Thr
275 280 285

Asp Pro Asp Leu Pro Pro Gly Trp Lys Arg Val Ser Asp Ile Ala Gly
290 295 300

Thr Tyr Tyr Trp His Ile Pro Thr Gly Thr Thr Gln Trp Glu Arg Pro
305 310 315 320

Val Ser Ile Pro Ala Asp Leu Gln Gly Ser Arg Lys Gly Ser Leu Ser
325 330 335

Ser Val Thr Pro Ser Pro Thr Pro Glu Asn Glu Asp Leu His Ala Ala
340 345 350

Sequence_Listing.txt

Thr Val Asn Pro Asp Pro Ser Leu Lys Glu Phe Glu Gly Ala Thr Leu
355 360 365

Arg Tyr Ala Ser Leu Lys Leu Arg Asn Ala Pro His Pro Asp Asp Asp
370 375 380

Asp Ser Cys Ser Ile Asn Ser Asp Pro Glu Ala Lys Cys Phe Ala Val
385 390 395 400

Arg Ser Leu Gly Trp Val Glu Met Ala Glu Glu Asp Leu Ala Pro Gly
405 410 415

Lys Ser Ser Val Ala Val Asn Asn Cys Ile Arg Gln Leu Ser Tyr Cys
420 425 430

Lys Asn Asp Ile Arg Asp Thr Val Gly Ile Trp Gly Glu Gly Lys Asp
435 440 445

Met Tyr Leu Ile Leu Glu Asn Asp Met Leu Ser Leu Val Asp Pro Met
450 455 460

Asp Arg Ser Val Leu His Ser Gln Pro Ile Val Ser Ile Arg Val Trp
465 470 475 480

Gly Val Gly Arg Asp Asn Gly Arg Asp Phe Ala Tyr Val Ala Arg Asp
485 490 495

Lys Asp Thr Arg Ile Leu Lys Cys His Val Phe Arg Cys Asp Thr Pro
500 505 510

Ala Lys Ala Ile Ala Thr Ser Leu His Glu Ile Cys Ser Lys Ile Met

Sequence_Listing.txt

515 520 525

Ala Glu Arg Lys Asn Ala Lys Ala Leu Ala Cys Ser Ser Leu Gln Glu
530 535 540

Arg Ala Asn Val Asn Leu Asp Val Pro Leu Gln Asp Phe Pro Thr Pro
545 550 555 560

Lys Thr Glu Leu Val Gln Lys Phe His Val Gln Tyr Leu Gly Met Leu
565 570 575

Pro Val Asp Lys Pro Val Gly Met Asp Ile Leu Asn Ser Ala Ile Glu
580 585 590

Asn Leu Met Thr Ser Ser Asn Lys Glu Asp Trp Leu Ser Val Asn Met
595 600 605

Asn Val Ala Asp Ala Thr Val Thr Val Ile Ser Glu Lys Asn Glu Glu
610 615 620

Glu Val Leu Val Glu Cys Arg Val Arg Phe Leu Ser Phe Met Gly Val
625 630 635 640

Gly Lys Asp Val His Thr Phe Ala Phe Ile Met Asp Thr Gly Asn Gln
645 650 655

Arg Phe Glu Cys His Val Phe Trp Cys Glu Pro Asn Ala Gly Asn Val
660 665 670

Ser Glu Ala Val Gln Ala Ala Cys Met Leu Arg Tyr Gln Lys Cys Leu
675 680 685

Sequence_Listing.txt

Val Ala Arg Pro Pro Ser Gln Lys Val Arg Pro Pro Pro Pro Ala
690 695 700

Asp Ser Val Thr Arg Arg Val Thr Thr Asn Val Lys Arg Gly Val Leu
705 710 715 720

Ser Leu Ile Asp Thr Leu Lys Gln Lys Arg Pro Val Thr Glu Met Pro
725 730 735

<210> 7

<211> 562

<212> DNA

<213> Homo sapiens

<400> 7

ctggaattga ggctgagcca aagaccccag ggccgtctca gtctcataaa aggggatcag 60

gcaggaggag ttgggagaa acctgagaag ggctgattt gcagcatcat gatgggcctc 120

tcctggcct ctgctgtgct cctggcctcc ctctgagtc tccacctgg aactgccaca 180

cgtgggagtg acatatcaa gacctgctgc ttccaataca gccacaagcc cttccctgg 240

acctgggtgc gaagctatga attcaccagt aacagctgct cccagcgggc tgtgatattc 300

actacaaaa gaggcaagaa agtctgtacc catccaagga aaaaatgggt gcaaaaatac 360

attctttac tgaaaactcc gaaacaattg tgactcagct gaattttcat ccgaggacgc 420

ttggaccccg ctctggctc tgcagccctc tggggagcct gcggaatctt ttctgaaggc 480

tacatggacc cgctggggag gagaggggtg ttctcccag agttacttta ataaaggttg 540

ttcatagagt tgactgttc at 562

<210> 8

<211> 94

Sequence_Listing.txt

<212> PRT

<213> Homo sapiens

<400> 8

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

Ser Leu His Leu Gly Thr Ala Thr Arg Gly Ser Asp Ile Ser Lys Thr
20 25 30

Cys Cys Phe Gln Tyr Ser His Lys Pro Leu Pro Trp Thr Trp Val Arg
35 40 45

Ser Tyr Glu Phe Thr Ser Asn Ser Cys Ser Gln Arg Ala Val Ile Phe
50 55 60

Thr Thr Lys Arg Gly Lys Lys Val Cys Thr His Pro Arg Lys Lys Trp
65 70 75 80

Val Gln Lys Tyr Ile Ser Leu Leu Lys Thr Pro Lys Gln Leu
85 90

<210> 9

<211> 1697

<212> DNA

<213> Homo sapiens

<400> 9

gaggcgtaag ccaggcgtgt taaagccggt cggaactgct ccggagggca cgggctccgt 60
aggcaccaac tgcaaggacc cctccccctg cgggcgctcc catggcacag ttcgcgttcg 120
agagtgacct gcactcgctg cttcagctgg atgcacccat cccaatgca cccctgcgc 180
gctggcagcg caaagccaag gaagccgcag gcccgcccc ctcacccatg cgggccgcca 240

Sequence_Listing.txt

accgatccca cagcgccggc aggactccgg gccgaactcc tggcaaatcc agttccaagg 300

ttcagaccac tcctagcaaa cctggcgggtg accgctatat ccccatcgc agtgctgccc 360

agatggaggt ggccagcttc ctctgagca aggagaacca gcctgaaaac agccagacgc 420

ccaccaagaa ggaacatcag aaagcctggg ctttgaacct gaacggtttt gatgtagagg 480

aagccaagat ccttcggctc agtgaaaaac caaaaatgc gccagagggt tatcagaaca 540

gactgaaagt actctacagc caaaaggcca ctctggctc cagccggaag acctgccgtt 600

acattccttc cctgccagac cgtatcctgg atgcgcctga aatccgaaat gactattacc 660

tgaaccttgt ggattggagt tctgggaatg tactggccgt ggcactggac aacagtgtgt 720

acctgtggag tgcaagctct ggtgacatcc tgcagctttt gcaaattggag cagcctgggg 780

aatatatctc ctctgtggcc tggatcaaag agggcaacta ctggctgtg ggcaccagca 840

gtgctgaggt gcagctatgg gatgtgcagc agcagaaaac gcttcgaaat atgaccagtc 900

actctgcccg agtgggctcc ctaagctgga acagctatat cctgtccagt gggtcacgtt 960

ctggccacat ccaccacat gatgttcggg tagcagaaca ccatgtggcc aactgagtg 1020

gccacagcca ggaagtgtgt gggctgcgct gggccccaga tggacgacat ttggccagtg 1080

gtgtaatga taacttggtc aatgtgtggc ctagtctcc tggagagggt ggctgggttc 1140

ctctgcagac attcaccag catcaagggg ctgtcaaggc cgtagcatgg tgtccctggc 1200

agtccaatgt cctggcaaca ggagggggca ccagtgatcg acacattcgc atctggaatg 1260

tgtgtctggt ggctgtctg agtgccgtgg atgccattc ccagggtgtc tccatcctct 1320

ggtctcccca ttacaaggag ctcatctcag gccatggctt tgcacagaac cagctagtta 1380

tttgaagta cccaacctg gccaaagggtg ctgaactcaa aggtcacaca tcccgggtcc 1440

tgagtctgac catgagccca gatggggcca cagtggcatc cgcagcagca gatgagacct 1500

Sequence_Listing.txt

tgaggctatg ggcgtgtttt gagttggacc ctgcgcggcg gcgggagcgg gagaaggcca 1560
 gtgcagccaa aagcagcctc atccaccaag gcatccgctg aagaccaacc catcacctca 1620
 gttgtttttt atttttctaa taaagtcatg tctcccttca tgtttttttt taaaaaaaaa 1680
 aaaaaaaaaa aaaaaaa 1697

<210> 10
 <211> 499
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Ala Gln Phe Ala Phe Glu Ser Asp Leu His Ser Leu Leu Gln Leu
 1 5 10 15

Asp Ala Pro Ile Pro Asn Ala Pro Pro Ala Arg Trp Gln Arg Lys Ala
 20 25 30

Lys Glu Ala Ala Gly Pro Ala Pro Ser Pro Met Arg Ala Ala Asn Arg
 35 40 45

Ser His Ser Ala Gly Arg Thr Pro Gly Arg Thr Pro Gly Lys Ser Ser
 50 55 60

Ser Lys Val Gln Thr Thr Pro Ser Lys Pro Gly Gly Asp Arg Tyr Ile
 65 70 75 80

Pro His Arg Ser Ala Ala Gln Met Glu Val Ala Ser Phe Leu Leu Ser
 85 90 95

Lys Glu Asn Gln Pro Glu Asn Ser Gln Thr Pro Thr Lys Lys Glu His
 100 105 110

Sequence_Listing.txt

Gln Lys Ala Trp Ala Leu Asn Leu Asn Gly Phe Asp Val Glu Glu Ala
115 120 125

Lys Ile Leu Arg Leu Ser Gly Lys Pro Gln Asn Ala Pro Glu Gly Tyr
130 135 140

Gln Asn Arg Leu Lys Val Leu Tyr Ser Gln Lys Ala Thr Pro Gly Ser
145 150 155 160

Ser Arg Lys Thr Cys Arg Tyr Ile Pro Ser Leu Pro Asp Arg Ile Leu
165 170 175

Asp Ala Pro Glu Ile Arg Asn Asp Tyr Tyr Leu Asn Leu Val Asp Trp
180 185 190

Ser Ser Gly Asn Val Leu Ala Val Ala Leu Asp Asn Ser Val Tyr Leu
195 200 205

Trp Ser Ala Ser Ser Gly Asp Ile Leu Gln Leu Leu Gln Met Glu Gln
210 215 220

Pro Gly Glu Tyr Ile Ser Ser Val Ala Trp Ile Lys Glu Gly Asn Tyr
225 230 235 240

Leu Ala Val Gly Thr Ser Ser Ala Glu Val Gln Leu Trp Asp Val Gln
245 250 255

Gln Gln Lys Arg Leu Arg Asn Met Thr Ser His Ser Ala Arg Val Gly
260 265 270

Ser Leu Ser Trp Asn Ser Tyr Ile Leu Ser Ser Gly Ser Arg Ser Gly

Sequence_Listing.txt

275 280 285

His Ile His His His Asp Val Arg Val Ala Glu His His Val Ala Thr
290 295 300

Leu Ser Gly His Ser Gln Glu Val Cys Gly Leu Arg Trp Ala Pro Asp
305 310 315 320

Gly Arg His Leu Ala Ser Gly Gly Asn Asp Asn Leu Val Asn Val Trp
325 330 335

Pro Ser Ala Pro Gly Glu Gly Gly Trp Val Pro Leu Gln Thr Phe Thr
340 345 350

Gln His Gln Gly Ala Val Lys Ala Val Ala Trp Cys Pro Trp Gln Ser
355 360 365

Asn Val Leu Ala Thr Gly Gly Gly Thr Ser Asp Arg His Ile Arg Ile
370 375 380

Trp Asn Val Cys Ser Gly Ala Cys Leu Ser Ala Val Asp Ala His Ser
385 390 395 400

Gln Val Cys Ser Ile Leu Trp Ser Pro His Tyr Lys Glu Leu Ile Ser
405 410 415

Gly His Gly Phe Ala Gln Asn Gln Leu Val Ile Trp Lys Tyr Pro Thr
420 425 430

Met Ala Lys Val Ala Glu Leu Lys Gly His Thr Ser Arg Val Leu Ser
435 440 445

Sequence_Listing.txt

Leu Thr Met Ser Pro Asp Gly Ala Thr Val Ala Ser Ala Ala Ala Asp
450 455 460

Glu Thr Leu Arg Leu Trp Arg Cys Phe Glu Leu Asp Pro Ala Arg Arg
465 470 475 480

Arg Glu Arg Glu Lys Ala Ser Ala Ala Lys Ser Ser Leu Ile His Gln
485 490 495

Gly Ile Arg

<210> 11
<211> 5478
<212> DNA
<213> Homo sapiens

<400> 11
gcccacggg cgagcttcta gtcggcgatt gaaggatgcg agtgctcctt aagggcctcc 60
gccccgtgag ttcggttgtag actaggaagg agctagtggga ctagagccag ggtaagggga 120
tctgctagaa gttggtcttc cgccaggact agagtttctt cgcggtaaca gcctccgtgg 180
cctccggagg accatgtcat tagactttgg cagtgtggca ctaccagtgc aaaatgaaga 240
tgaagagtat gacgaagagg actatgaaag agagaaagag ttgcagcagt tactcacaga 300
ccttcccat gacatgtctg atgacgacct ctctctcca gagctccagt attcggactg 360
cagcgaggat ggcacagacg gacaaccaca tcatcctgag caattggaga tgagctggaa 420
tgagcaaatg ctgccaaat ctcaaagtgat aaatggctat aatgaaattc agagtttata 480
tgctggagaa aaatgtggta atgtctggga agaaaataga agtaaaactg aagaccgaca 540
tctgtgtac catcctgaag aaggtggaga tgaaggtgga agtgggtata gtctccaag 600

Sequence_Listing.txt

taaatgtgaa cagactgatt tatatcacct tctgaaaac tttaggcat ataccaatgg 660
 tcagaagcag gaatttaata accaagcaac caatgtaatt aaattttcag atcctcaatg 720
 gaaccatttt caggggtcca gtgtcaagg ttggaaccg tataataaag tgacatataa 780
 accttatcag tcttctgcc agaataatgg ctcaccagcc caggagataa caggaagtga 840
 cacattcgaa ggctgcaac aacaatttt aggagctaag gagaactctg cagaaaatat 900
 gcagattatt caactcagg ttctaaca agcaaaagag agacaactgg agaacttaat 960
 tgaaaagtta aatgaaagt aacgtcaat tcgatatctg aatcaccagc ttgtaataat 1020
 aaaagatgaa aaggatgggt tgactctcag ccttcgagaa tcacagaaac tcttcagaa 1080
 tggaaaagaa agagagatac agctgaagc tcaataaaa gcactggaga ctcagataca 1140
 agcattaaaa gtcaatgaag aacagatgat caagaagtc agaacaactg aaatggctct 1200
 ggaaagcttg aagcagcagc tggtagacct tcatcattct gaatcacttc aacgagctag 1260
 agaacagcat gagagcattg ttatggcct cacaagaag tacgaagagc aagtattgtc 1320
 cttacaaaag aatttgatg ccacagtcac cgcacttaa gaacaggaag acatttgctc 1380
 tcgtctgaaa gatcacgtga aacaactgga aaggaatcaa gaagcaatca agttagaaaa 1440
 gactgagatc attaataagt tgacaagaag tctagaggag agtcaaaagc agtgtgcca 1500
 cttgttcag tccgggtcag tacaagaggt ggctcagcta cagttccagc tgcagcaagc 1560
 acagaaggca catgctatga gtgcaaacat gaacaaggct ttgcaagaag aattaacaga 1620
 actaaaagat gaaatttctc tctatgaatc tgcgcaaaa ctaggaatac atccaagtga 1680
 ctcagaagga gaattaaata tagaactcac tgaatcgtat gtggatttgg gtattaaaaa 1740
 ggtcaactgg aaaaaatcca aagttaccag cattgtacaa gaagaagacc caaatgaaga 1800
 gcttcaaaa gatgagttca ttctgaagtt aaaggcagaa gtacagcgtt tgctgggtag 1860

Sequence_Listing.txt

caactcaatg aagcgtcatc tgggtgtctca gttacaaaat gacctcaaag actgtcataa 1920
gaaaattgaa gatctccacc aagtgaagaa ggatgaaaaa agcattgagg ttgagactaa 1980
aacagatacc tcagaaaaac caaagaatca attatggcct gagtcttcta ctctgatgt 2040
gtcagagat gatattctgc tgcttaaaaa tgaaattcaa gttttacaac aacaaaatca 2100
ggaacttaa gaaactgaag gaaaactgag aaatacaaat caagacttat gtaatcaaat 2160
gagacaaatg gtacaagatt ttgaccatga caaacaagaa gctgtggata ggtgtgaaag 2220
gacttatcag cagcaccatg aagccatgaa aactcaaata cgtgaaagcc tattagcaaa 2280
gcatgctttg gagaagcagc agctctttga ggcttatgag agaactcatt tgcaactgag 2340
gtctgagttg gataagttga ataaggaggt gactgctgtg caggaatgtt acctagaagt 2400
gtgcagagag aaggataatc tagaattgac tctcaggaag accactgaaa aggagcaaca 2460
gactcaggag aagatcaaag aaaaactcat tcaacagctt gaaaaggagt ggcagtctaa 2520
gctggatcaa actataaagg caatgaaaaa gaagacctta gattgtggca gccaaactga 2580
ccaagtaacc accagtgatg ttatttcaa gaaagagatg gcaattatga tagaagagca 2640
gaagtgcaca atccagcaaa acttagaaca agagaaggac atagccatca agggggctat 2700
gaagaaactc gaaattgaat tggaactcaa acattgtgaa aatattacca aacaggtaga 2760
aatagctgtg caaatgctc atcagcgatg gctgggagaa ctaccagagc tggcagagta 2820
tcaagcactt gtgaaggcag aacagaaaaa gtgggaagaa cagcatgagg tctctgtgaa 2880
caaaaggata tcatttgctg ttctgaagc taaagagaaa tggaagagtg agcttgaaaa 2940
tatgaggaaa aatatacttc ctggaaagga attggaagag aagattcatt ctctcagaa 3000
ggaacttgag ttaaagaacg aagaagtccc tgtggtcatc agggctgagt tagctaaggc 3060
tcggagttaa tggaacaaag aaaagcaaga agaatccac agaatccaag aacaaaatga 3120

Sequence_Listing.txt

gcaagattac cggcaatftt tagatgatca ccgaaataaa attaatgagg tgcttgcggc 3180
agctaaagaa gactttatga aacaaaaaac tgaactactt cttcagaagg agacagaatt 3240
acaaacttgt ctgaccaga gtcgtagaga atggactatg caggaagcca agcggatcca 3300
actggaaatc tatcagtatg aggaagacat cctgactgta cttgggggtc tttaagtga 3360
taccctaaag gagcacatca gtgattctga ggacaagcag cttttggaaa tcatgtcgac 3420
ttgttctca aaatggatgt ctgtgcaata tttgaaaaa cttaaagggt gcatacagaa 3480
agcatttcaa gatacacttc ctctgctgt agaaaacgct gaccagaat ggaaaaagag 3540
aaatatggcc gagctcicta aggattctgc cagccagggc actggccaag gagaccctgg 3600
acctgctgct ggacaccatg ctgagccctt ggccctacaa gcaacagaag cagaagctga 3660
agagaataat aaagtgtgtg aagaattaat agaagaaaac aacgacatga agaataaatt 3720
ggaagaattg caaacacttt gtaaacacc accaagggtca ttgtcagcag gggccattga 3780
aaatgcttgc ctgccatgca gtgggggagc cttggaagaa cttctggtggc agtacattaa 3840
agctgtaaaa aaaattaaat gtgacatgct tcgttatatt caggagagta aggaacgagc 3900
tgcagaaatg gtaaaagcag aggtactgcg agaacgtcaa gaaaccgccc gaaagatgcg 3960
caaataattt ttgatttggc tccaacagat ttgcaggat gatggaaaag aaggggctga 4020
gaaaaagatt atgaatgctg ctgcaaaact tgctacaatg gcaaaattac tggaacacc 4080
tatttctagt aagtcccaa gcaaaactac acagtcagca ctgcccctaa cttcagagat 4140
gctgattgca gttaaaaaat caaaaagaaa tgatgtgaat cagaaaatac catgttgtat 4200
tgaaagcaaa tcaaatagtg taaacacat caccagaact ctgtgcaac aagctcccaa 4260
gaggagggca gctgttaact taaaaggct gtagagaac tcagagcatc agagcataaa 4320
gcatgtggga tcaaagaga cacatttga attccagttt ggggatggta gttgcaagca 4380

Sequence_Listing.txt

cctaaacagt ttgccaagga atgtttctcc tgagtttggt ccttgtgaag gtgaaggagg 4440
 ctttggttg cacaagaaga aagacctact cagtataat ggttctgaat cactccgca 4500
 ttacgtgca tacccttctc ttggaacctt aggaaataaa cctcaccta gatgtacccc 4560
 tggctctct gaatcaggat gcatgcataa aaccttctgc gattctaag aaagacttg 4620
 tttaaagta tataaatgca atccactaat ggaaagtga aatgctgcat ctgagaaaag 4680
 tcaaggttg gatgttcagg aacctccagt aaaagatgga ggggacctta gtgactgctt 4740
 gggctggcct tccagcagtg caacctatc cttgacagt cgtgaagcat cattgtaca 4800
 tggtaggcca caaggaactt tggaataacc aagtgaatct gttaatcca aacagtttct 4860
 accatccggt tatcttctag atacagagga aagtaatatg attgtcaaa caatgaaatg 4920
 tcagcgttat caaactccat acctgtcaga agaaaccacg tattggagc caggaaagat 4980
 cagtgtgaat tgtggacacc catctcgtca taaggctgat agattaaagt cagattcaa 5040
 aaaactgagc agtacattac catcttcagt gtgtcagcag cctcaagaa aattaattgt 5100
 tccgtatct agccaacaag atagtggctt tgatagccca ttgttaatc tagactaatt 5160
 atgttacagt atttaagaag aatcattaat atattaacaa aaatggaagg gaagacctca 5220
 tactgaaaaa aattgtgagc cctgcctctt ttgagatgtt ttaataacat ctgttatata 5280
 agtaaagcat tcttctaaaa ttgcttgaga tatttatgtt gccttaatat tccaaaggcc 5340
 tgatggtgta tgtataatct gcttttgtgt ggtgcttatt ttggtttct aaaccatcta 5400
 ttttatact tataaattga ctactctgc agtgtaaact tatttaaata aactgcata 5460
 tggctgtaa aaaaaaaaaa 5478

<210> 12
 <211> 1654

Sequence_Listing.txt

<212> PRT

<213> Homo sapiens

<400> 12

Met Ser Leu Asp Phe Gly Ser Val Ala Leu Pro Val Gln Asn Glu Asp
1 5 10 15

Glu Glu Tyr Asp Glu Glu Asp Tyr Glu Arg Glu Lys Glu Leu Gln Gln
20 25 30

Leu Leu Thr Asp Leu Pro His Asp Met Leu Asp Asp Asp Leu Ser Ser
35 40 45

Pro Glu Leu Gln Tyr Ser Asp Cys Ser Glu Asp Gly Thr Asp Gly Gln
50 55 60

Pro His His Pro Glu Gln Leu Glu Met Ser Trp Asn Glu Gln Met Leu
65 70 75 80

Pro Lys Ser Gln Ser Val Asn Gly Tyr Asn Glu Ile Gln Ser Leu Tyr
85 90 95

Ala Gly Glu Lys Cys Gly Asn Val Trp Glu Glu Asn Arg Ser Lys Thr
100 105 110

Glu Asp Arg His Pro Val Tyr His Pro Glu Glu Gly Gly Asp Glu Gly
115 120 125

Gly Ser Gly Tyr Ser Pro Pro Ser Lys Cys Glu Gln Thr Asp Leu Tyr
130 135 140

His Leu Pro Glu Asn Phe Arg Pro Tyr Thr Asn Gly Gln Lys Gln Glu
145 150 155 160

Sequence_Listing.txt

Phe Asn Asn Gln Ala Thr Asn Val Ile Lys Phe Ser Asp Pro Gln Trp
165 170 175

Asn His Phe Gln Gly Pro Ser Cys Gln Gly Leu Glu Pro Tyr Asn Lys
180 185 190

Val Thr Tyr Lys Pro Tyr Gln Ser Ser Ala Gln Asn Asn Gly Ser Pro
195 200 205

Ala Gln Glu Ile Thr Gly Ser Asp Thr Phe Glu Gly Leu Gln Gln Gln
210 215 220

Phe Leu Gly Ala Asn Glu Asn Ser Ala Glu Asn Met Gln Ile Ile Gln
225 230 235 240

Leu Gln Val Leu Asn Lys Ala Lys Glu Arg Gln Leu Glu Asn Leu Ile
245 250 255

Glu Lys Leu Asn Glu Ser Glu Arg Gln Ile Arg Tyr Leu Asn His Gln
260 265 270

Leu Val Ile Ile Lys Asp Glu Lys Asp Gly Leu Thr Leu Ser Leu Arg
275 280 285

Glu Ser Gln Lys Leu Phe Gln Asn Gly Lys Glu Arg Glu Ile Gln Leu
290 295 300

Glu Ala Gln Ile Lys Ala Leu Glu Thr Gln Ile Gln Ala Leu Lys Val
305 310 315 320

Sequence_Listing.txt

Asn Glu Glu Gln Met Ile Lys Lys Ser Arg Thr Thr Glu Met Ala Leu
325 330 335

Glu Ser Leu Lys Gln Gln Leu Val Asp Leu His His Ser Glu Ser Leu
340 345 350

Gln Arg Ala Arg Glu Gln His Glu Ser Ile Val Met Gly Leu Thr Lys
355 360 365

Lys Tyr Glu Glu Gln Val Leu Ser Leu Gln Lys Asn Leu Asp Ala Thr
370 375 380

Val Thr Ala Leu Lys Glu Gln Glu Asp Ile Cys Ser Arg Leu Lys Asp
385 390 395 400

His Val Lys Gln Leu Glu Arg Asn Gln Glu Ala Ile Lys Leu Glu Lys
405 410 415

Thr Glu Ile Ile Asn Lys Leu Thr Arg Ser Leu Glu Glu Ser Gln Lys
420 425 430

Gln Cys Ala His Leu Leu Gln Ser Gly Ser Val Gln Glu Val Ala Gln
435 440 445

Leu Gln Phe Gln Leu Gln Gln Ala Gln Lys Ala His Ala Met Ser Ala
450 455 460

Asn Met Asn Lys Ala Leu Gln Glu Glu Leu Thr Glu Leu Lys Asp Glu
465 470 475 480

Ile Ser Leu Tyr Glu Ser Ala Ala Lys Leu Gly Ile His Pro Ser Asp
485 490 495

Sequence_Listing.txt

Ser Glu Gly Glu Leu Asn Ile Glu Leu Thr Glu Ser Tyr Val Asp Leu
500 505 510

Gly Ile Lys Lys Val Asn Trp Lys Lys Ser Lys Val Thr Ser Ile Val
515 520 525

Gln Glu Glu Asp Pro Asn Glu Glu Leu Ser Lys Asp Glu Phe Ile Leu
530 535 540

Lys Leu Lys Ala Glu Val Gln Arg Leu Leu Gly Ser Asn Ser Met Lys
545 550 555 560

Arg His Leu Val Ser Gln Leu Gln Asn Asp Leu Lys Asp Cys His Lys
565 570 575

Lys Ile Glu Asp Leu His Gln Val Lys Lys Asp Glu Lys Ser Ile Glu
580 585 590

Val Glu Thr Lys Thr Asp Thr Ser Glu Lys Pro Lys Asn Gln Leu Trp
595 600 605

Pro Glu Ser Ser Thr Ser Asp Val Val Arg Asp Asp Ile Leu Leu Leu
610 615 620

Lys Asn Glu Ile Gln Val Leu Gln Gln Gln Asn Gln Glu Leu Lys Glu
625 630 635 640

Thr Glu Gly Lys Leu Arg Asn Thr Asn Gln Asp Leu Cys Asn Gln Met
645 650 655

Sequence_Listing.txt

Arg Gln Met Val Gln Asp Phe Asp His Asp Lys Gln Glu Ala Val Asp
660 665 670

Arg Cys Glu Arg Thr Tyr Gln Gln His His Glu Ala Met Lys Thr Gln
675 680 685

Ile Arg Glu Ser Leu Leu Ala Lys His Ala Leu Glu Lys Gln Gln Leu
690 695 700

Phe Glu Ala Tyr Glu Arg Thr His Leu Gln Leu Arg Ser Glu Leu Asp
705 710 715 720

Lys Leu Asn Lys Glu Val Thr Ala Val Gln Glu Cys Tyr Leu Glu Val
725 730 735

Cys Arg Glu Lys Asp Asn Leu Glu Leu Thr Leu Arg Lys Thr Thr Glu
740 745 750

Lys Glu Gln Gln Thr Gln Glu Lys Ile Lys Glu Lys Leu Ile Gln Gln
755 760 765

Leu Glu Lys Glu Trp Gln Ser Lys Leu Asp Gln Thr Ile Lys Ala Met
770 775 780

Lys Lys Lys Thr Leu Asp Cys Gly Ser Gln Thr Asp Gln Val Thr Thr
785 790 795 800

Ser Asp Val Ile Ser Lys Lys Glu Met Ala Ile Met Ile Glu Glu Gln
805 810 815

Lys Cys Thr Ile Gln Gln Asn Leu Glu Gln Glu Lys Asp Ile Ala Ile
820 825 830

Sequence_Listing.txt

Lys Gly Ala Met Lys Lys Leu Glu Ile Glu Leu Glu Leu Lys His Cys
835 840 845

Glu Asn Ile Thr Lys Gln Val Glu Ile Ala Val Gln Asn Ala His Gln
850 855 860

Arg Trp Leu Gly Glu Leu Pro Glu Leu Ala Glu Tyr Gln Ala Leu Val
865 870 875 880

Lys Ala Glu Gln Lys Lys Trp Glu Glu Gln His Glu Val Ser Val Asn
885 890 895

Lys Arg Ile Ser Phe Ala Val Ser Glu Ala Lys Glu Lys Trp Lys Ser
900 905 910

Glu Leu Glu Asn Met Arg Lys Asn Ile Leu Pro Gly Lys Glu Leu Glu
915 920 925

Glu Lys Ile His Ser Leu Gln Lys Glu Leu Glu Leu Lys Asn Glu Glu
930 935 940

Val Pro Val Val Ile Arg Ala Glu Leu Ala Lys Ala Arg Ser Glu Trp
945 950 955 960

Asn Lys Glu Lys Gln Glu Glu Ile His Arg Ile Gln Glu Gln Asn Glu
965 970 975

Gln Asp Tyr Arg Gln Phe Leu Asp Asp His Arg Asn Lys Ile Asn Glu
980 985 990

Sequence_Listing.txt

Val Leu Ala Ala Ala Lys Glu Asp Phe Met Lys Gln Lys Thr Glu Leu
 995 1000 1005

Leu Leu Gln Lys Glu Thr Glu Leu Gln Thr Cys Leu Asp Gln Ser
 1010 1015 1020

Arg Arg Glu Trp Thr Met Gln Glu Ala Lys Arg Ile Gln Leu Glu
 1025 1030 1035

Ile Tyr Gln Tyr Glu Glu Asp Ile Leu Thr Val Leu Gly Val Leu
 1040 1045 1050

Leu Ser Asp Thr Gln Lys Glu His Ile Ser Asp Ser Glu Asp Lys
 1055 1060 1065

Gln Leu Leu Glu Ile Met Ser Thr Cys Ser Ser Lys Trp Met Ser
 1070 1075 1080

Val Gln Tyr Phe Glu Lys Leu Lys Gly Cys Ile Gln Lys Ala Phe
 1085 1090 1095

Gln Asp Thr Leu Pro Leu Leu Val Glu Asn Ala Asp Pro Glu Trp
 1100 1105 1110

Lys Lys Arg Asn Met Ala Glu Leu Ser Lys Asp Ser Ala Ser Gln
 1115 1120 1125

Gly Thr Gly Gln Gly Asp Pro Gly Pro Ala Ala Gly His His Ala
 1130 1135 1140

Gln Pro Leu Ala Leu Gln Ala Thr Glu Ala Glu Ala Glu Glu Asn
 1145 1150 1155

Sequence_Listing.txt

Asn Lys Val Val Glu Glu Leu Ile Glu Glu Asn Asn Asp Met Lys
1160 1165 1170

Asn Lys Leu Glu Glu Leu Gln Thr Leu Cys Lys Thr Pro Pro Arg
1175 1180 1185

Ser Leu Ser Ala Gly Ala Ile Glu Asn Ala Cys Leu Pro Cys Ser
1190 1195 1200

Gly Gly Ala Leu Glu Glu Leu Arg Gly Gln Tyr Ile Lys Ala Val
1205 1210 1215

Lys Lys Ile Lys Cys Asp Met Leu Arg Tyr Ile Gln Glu Ser Lys
1220 1225 1230

Glu Arg Ala Ala Glu Met Val Lys Ala Glu Val Leu Arg Glu Arg
1235 1240 1245

Gln Glu Thr Ala Arg Lys Met Arg Lys Tyr Tyr Leu Ile Cys Leu
1250 1255 1260

Gln Gln Ile Leu Gln Asp Asp Gly Lys Glu Gly Ala Glu Lys Lys
1265 1270 1275

Ile Met Asn Ala Ala Ser Lys Leu Ala Thr Met Ala Lys Leu Leu
1280 1285 1290

Glu Thr Pro Ile Ser Ser Lys Ser Gln Ser Lys Thr Thr Gln Ser
1295 1300 1305

Sequence_Listing.txt

Ala Leu Pro Leu Thr Ser Glu Met Leu Ile Ala Val Lys Lys Ser
1310 1315 1320

Lys Arg Asn Asp Val Asn Gln Lys Ile Pro Cys Cys Ile Glu Ser
1325 1330 1335

Lys Ser Asn Ser Val Asn Thr Ile Thr Arg Thr Leu Cys Glu Gln
1340 1345 1350

Ala Pro Lys Arg Arg Ala Ala Cys Asn Leu Gln Arg Leu Leu Glu
1355 1360 1365

Asn Ser Glu His Gln Ser Ile Lys His Val Gly Ser Lys Glu Thr
1370 1375 1380

His Leu Glu Phe Gln Phe Gly Asp Gly Ser Cys Lys His Leu Asn
1385 1390 1395

Ser Leu Pro Arg Asn Val Ser Pro Glu Phe Val Pro Cys Glu Gly
1400 1405 1410

Glu Gly Gly Phe Gly Leu His Lys Lys Lys Asp Leu Leu Ser Asp
1415 1420 1425

Asn Gly Ser Glu Ser Leu Pro His Ser Ala Ala Tyr Pro Phe Leu
1430 1435 1440

Gly Thr Leu Gly Asn Lys Pro Ser Pro Arg Cys Thr Pro Gly Pro
1445 1450 1455

Ser Glu Ser Gly Cys Met His Ile Thr Phe Arg Asp Ser Asn Glu
1460 1465 1470

Sequence_Listing.txt

Arg Leu Gly Leu Lys Val Tyr Lys Cys Asn Pro Leu Met Glu Ser
1475 1480 1485

Glu Asn Ala Ala Ser Glu Lys Ser Gln Gly Leu Asp Val Gln Glu
1490 1495 1500

Pro Pro Val Lys Asp Gly Gly Asp Leu Ser Asp Cys Leu Gly Trp
1505 1510 1515

Pro Ser Ser Ser Ala Thr Leu Ser Phe Asp Ser Arg Glu Ala Ser
1520 1525 1530

Phe Val His Gly Arg Pro Gln Gly Thr Leu Glu Ile Pro Ser Glu
1535 1540 1545

Ser Val Lys Ser Lys Gln Phe Ser Pro Ser Gly Tyr Leu Ser Asp
1550 1555 1560

Thr Glu Glu Ser Asn Met Ile Cys Gln Thr Met Lys Cys Gln Arg
1565 1570 1575

Tyr Gln Thr Pro Tyr Leu Ser Glu Glu Thr Thr Tyr Leu Glu Pro
1580 1585 1590

Gly Lys Ile Ser Val Asn Cys Gly His Pro Ser Arg His Lys Ala
1595 1600 1605

Asp Arg Leu Lys Ser Asp Phe Lys Lys Leu Ser Ser Thr Leu Pro
1610 1615 1620

Sequence_Listing.txt

Ser Ser Val Cys Gln Gln Pro Ser Arg Lys Leu Ile Val Pro Leu
1625 1630 1635

Ser Ser Gln Gln Asp Ser Gly Phe Asp Ser Pro Phe Val Asn Leu
1640 1645 1650

Asp

<210> 13
<211> 1260
<212> DNA
<213> Homo sapiens

<400> 13
ggccggcggg aagactccgt tacccagcga gcgaggcggc ggcgagggc cagcggactc 60
catttcccg cggtcgcgg tgggagcgcc ggaagccgc cccaccctc attgtgcggc 120
tctactaaa cggaaggggc ggggagaggc cgcgttcagt cgggtcccgg cagcggctgc 180
agcgtctcg tcttctcgg ctctcggtc cctctcctt tcgtttccgg aaacatggcc 240
tccggtgtgg ctgtcttga tgggttcac aaggtgtca acgacatgaa ggtgcgtaag 300
tctcaacgc cagaggaggt gaagaagcgc aagaaggcgg tgctcttctg cctgagttag 360
gacaagaaga acatcatcct ggaggagggc aaggagatcc tggtgggcga tggggccag 420
actgtcgacg acccctacgc cacctttgc aagatgtgc cagataagga ctgccgctat 480
gccctctatg atgcaacctg tgagaccaag gagagcaaga aggaggatct ggtgtttatc 540
ttctggggcc ccgagtctgc gccccttaag agcaaatga ttatgccag ctccaaggac 600
gccatcaaga agaagctgac agggatcaag catgaattgc aagcaaactg ctacgaggag 660
gtcaaggacc gctgcacctt ggcagagaag ctggggggca gtgccgtcat ctccctggag 720

Sequence_Listing.txt

ggcaagcctt tgtgagcccc ttctggcccc ctgctggag catctggcag cccacacct 780
 gcccttgggg gttgaggct gccccctcc tgccagaccg gaggggctgg ggggatccca 840
 gcagggggag ggcaatccct tcacccagc tgccaaacag acccccacc ccctggattt 900
 tccttctccc tccatccctt gacggtctg gccttccaa actgctttg atctttgat 960
 tcctctggg ctgaagcaga ccaagttccc ccaggcacc ccagtgtgg gggagcctgt 1020
 attttttta acaacatccc cattccccac ctggtctcc cccttccat gctgccaact 1080
 tctaaccgca atagtactc tgtgctgtc tgttagtgc tgtgtataaa tggaatgtg 1140
 tggagatgac ccttccctgt gccggctggt tcctctccct ttcccctgg tcacggctac 1200
 tcatggaagc aggaccagta agggaccttc gattaaaaaa aaaaaagaca ataataaaaa 1260

<210> 14
 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Ser Gly Val Ala Val Ser Asp Gly Val Ile Lys Val Phe Asn
 1 5 10 15

Asp Met Lys Val Arg Lys Ser Ser Thr Pro Glu Glu Val Lys Lys Arg
 20 25 30

Lys Lys Ala Val Leu Phe Cys Leu Ser Glu Asp Lys Lys Asn Ile Ile
 35 40 45

Leu Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Gln Thr Val
 50 55 60

Asp Asp Pro Tyr Ala Thr Phe Val Lys Met Leu Pro Asp Lys Asp Cys

Sequence_Listing.txt

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

<210> 15
 <211> 633
 <212> DNA
 <213> Homo sapiens

<400> 15
 atgcgcgcaa gagagcggga agccgagctg ggcgagaagt aggggagggc ggtgctccgc 60
 cgcggtggcg gttgctatcg ctgcgcagaa cctactcagg cagccagctg agaagagttg 120
 agggaaagtg ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 180
 catcgccctt tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct ggtgtttgca 240
 ctgtgacag cagtatgctg tcttgccgac ggggccctta ttaccggaa gcttctgttc 300

Sequence_Listing.txt

```

aatcccagcg gtccttacca gaaaaagcct gtgcatgaaa aaaaagaagt ttgtaattt    360
tatattactt ttagtttga tactaagtat taaacatatt tctgtattct tccacatatt    420
ttctgcagtt attttaactc agtataggag ctagaggaag agattccga agtctgcacc    480
ccgcgcagag cactactgta acttccaagg gagcgctggg agcagcggga tcgggttttc    540
cggcaccgag gcctgggtgg caggaagaa tggccggga tccgcctcag ggatcttga    600
atctctttac tgctggctg gccggcagct ccg                                633

```

<210> 16
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
 1 5 10 15

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

Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
 35 40 45

Phe Asn Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys
 50 55 60

Glu Val Leu
 65

<210> 17
 <211> 9169

Sequence_Listing.txt

<212> DNA

<213> Homo sapiens

<400> 17

```

gatgacgctg cggcttctgg tggccgcgct ctgcgccggg atcctggcag aggcgccccg    60
agtgcgagcc cagcacaggg agagagtgac ctgcacgcgc ctttacgccg ctgacattgt    120
gttcttactg gatggctcct catccattgg cgcagcaat ttccgcgagg tccgcagctt    180
tctgaaggg ctggtgctgc ctttctctgg agcagccagt gcacagggtg tgcgctttgc    240
cacagtgcag tacagcgatg acccacggac agagttcggc ctggaatcac ttggctctgg    300
gggtgatgtg atccgcgcc a tccgtgagct tagctacaag gggggcaaca ctgcacaggg    360
ggctgcaatt ctccatgtgg ctgacatgt cttctgccc cagctggccc gacctggtgt    420
cccaaggctc tgcatctga tcacagacgg gaagtcccag gacctggtgg acacagctgc    480
ccaaaggctg aaggggcagg gggtaagct attgctgtg gggatcaaga atgctgacct    540
tgaggagctg aagcgagttg cctcacagcc caccagtgc ttcttctct tctcaatga    600
cttcagcctc ttgaggacac tactgcccct cgtttcccgg agagtgtgca cgactgctgg    660
tggcgtgcct gtgacccgac ctccgatga ctgcacctct gctccacgag acctggtgct    720
gtctgagcca agcagccaat ccttgagagt acagtggaca gcggccagtg gccctgtgac    780
tggctacaag gtccagtaca ctctctgac ggggctggga cagccactgc cgagtgagcg    840
gcaggagggtg aacgtcccag ctggtgagac cagtgtgcgg ctgcggggtc tccggccact    900
gaccgagtac caagtgactg tgattgccct ctacgccaac agcatcgggg aggctgtgag    960
cgggacagct cggaccactg ccctagaagg gccggaactg accatccaga ataccacagc   1020
ccacagcctc ctggtggcct ggcggagtgt gccagggtgc actggctacc gtgtgacatg   1080
gcgggtcctc agtgggtggc ccacacagca gcaggagctg ggccctgggc agggttcagt   1140

```

Sequence_Listing.txt

gttgctgcgt gacttgagc ctggcacgga ctatgaggtg accgtgagca ccctatttgg 1200
 ccgcagtggt gggcccgcca ctccctgat ggctcgact gacgctctg ttgagcagac 1260
 cctgcgcccg gtcatcctgg gcccacatc catcctcctt tcctggaact tggtgctga 1320
 ggcccgtggc taccggttgg aatggcgggc tgagactggc ttggagccac cgcagaaggt 1380
 ggtactgccc tctgatgtga cccgtacca gttgatggg ctgcagccgg gcactgagta 1440
 ccgcctcaca ctctacactc tgctggaggg ccacgaggtg gccaccctg caaccgtggt 1500
 tccactgga ccagagctgc ctgtgagccc tgaacagac ctgcaagcca ccgagctgcc 1560
 cgggcagcgg gtgcgagtg cctggagccc agtccctggt gccaccagt accgcatcat 1620
 tgtgcgcagc acccaggggg ttgagcggac cctggtgctt cctgggagtc agacagcatt 1680
 cgacttggat gacgttcagg ctgggcttag ctacactgtg cgggtgtctg ctgagtggg 1740
 tccccgtgag ggcagtgcc a gtgctcac tgtccgccc gagccgaaa ctccacttc 1800
 gttccagggt ctgcgggttg tgggtcaga tgcaacgga gtgaggggtg cctggggacc 1860
 cgtccctgga gccagtggat ttccgattag ctggagcaca ggcagtggc cggagtccag 1920
 ccagacactg ccccagact ctactgccac agacatcaca gggctgcagc ctggaaccac 1980
 ctaccagggt gctgtgtcgg tactgcgagg cagagaggag ggccctgctg cagtcatcgt 2040
 ggctcgaacg gaccactgg gccagttag gacggtccat gtgactcagg ccagcagctc 2100
 atctgtcacc attacctgga ccagggttcc tggcgccaca ggatacaggg ttccctggca 2160
 ctgagccac ggcccagaga aatcccagtt ggtttctggg gaggccacgg tggctgagct 2220
 ggatggactg gagccagata ctgagtatac ggtgcatgtg agggccatg tggctggcgt 2280
 ggatgggccc cctgcctctg tgggtgtgag gactgccct gagcctgtgg gtcgtgtgtc 2340
 gaggctgcag atcctcaatg ctccagcga cgttctacgg atcacctggg taggggtcac 2400

Sequence_Listing.txt

tggagccaca gcttacagac tggcctgggg ccggagtga ggcggcccca tgaggcacca 2460
 gatactccca ggaacacag actctgcaga gatccgggg ctcgaagggt gagtcagcta 2520
 ctcaagtcca gtgactgcac ttgtcgggga ccgcgagggc acacctgtct ccattgttgt 2580
 cactacgccg cctgaggctc cgccagccct ggggacgctt cacgtggtgc agcgcgggga 2640
 gcactcgtg aggcctgcgt gggagccggt gccagagcg cagggttcc ttctgcactg 2700
 gcaacctgag ggtggccagg aacagtcccg ggtcctgggg cccgagctca gcagctatca 2760
 cctggacggg ctggagccag cgacacagta ccgctgagg ctgagtgtcc tagggccagc 2820
 tggagaaggg ccctctgcag aggtgactgc gcgcactgag tcacctctg ttccaagcat 2880
 tgaactacgt gtggtggaca cctgatcga ctcggtgact ttggcctgga ctccagtgtc 2940
 cagggcatcc agctacatcc tatcctggcg gccactcaga ggccctggcc aggaagtgcc 3000
 tgggtccccg cagacacttc cagggatctc aagctcccag cgggtgacag ggctagagcc 3060
 tggcgtctct tacatctct cctgacgcc tgtcctggat ggtgtgcggg gtctgaggc 3120
 atctgtcaca cagacgccag tgtgccccg tggcctggcg gatgtggtgt tctaccaca 3180
 tgccactcaa gacaatgtc accgtgcgga ggctacgagg agggctctgg agcgtctggt 3240
 gttggcactt gggcctcttg ggccacaggc agttcagggt ggctgtgtgt ctacagtca 3300
 tcggccctcc ccactgttcc cactgaatgg ctccatgac ctggcatta tctgcaaag 3360
 gatccgtgac atgccctaca tggaccaag tgggaacaac ctgggcacag ccgtggtcac 3420
 agctcacaga tacatgttg caccagatgc tctggggcg cgccagcacg taccaggggt 3480
 gatggtctg ctagtggatg aacccttgag aggtgacata ttcagcccca tccgtgaggc 3540
 ccaggcttct gggcttaatg tggatggtt gggaatggct ggagcggacc cagagcagct 3600
 gcgtcgcttg gcgcgggta tggactctgt ccagaccttc ttgccgtgg atgatgggcc 3660

Sequence_Listing.txt

aagcctggac caggcagtca gtggtctggc cacagccctg tgtcaggcat ccttcactac 3720

tcagccccgg ccagagccct gccagtgta ttgtccaaag ggccagaagg gggaacctgg 3780

agagatgggc ctgagaggac aagtggggc tcttggcgac cctggcctcc cgggcaggac 3840

cgggtctccc ggcccccagg ggccccctgg aagtgccact gccaagggcg agaggggctt 3900

ccctggagca gatgggcgtc caggcagccc tggccgcgcc gggaatcctg ggaccctgg 3960

agccctggc ctaaagggtc ctccagggtt gcctggccct cgtggggacc cgggagagcg 4020

aggacctga ggcccaaagg gggagccggg ggctcccgga caagtcacg gagtgaagg 4080

acctgggctt cctgggcgga aaggggacct tggacctcg ggccccctg gacctcgtg 4140

accactgggg gaccaggac cccgtggccc ccaggggctt cctggaacag ccatgaagg 4200

tgacaaaggc gatcgtggg agcggggctc ccctggacca ggtgaaggcg gcattgctc 4260

tggggagcct gggctgccg gtcttcccg aagccctgga cccaaggcc ccgttgccc 4320

ccctggaaag aaaggagaaa aaggtagctc tgaggatgga gctccaggcc tcccaggaca 4380

acctgggtct ccgggtgagc agggcccacg gggacctct ggagctattg gcccaaagg 4440

tgaccggggc ttccagggc ccctgggtga ggtggagag aagggcgaac gtggaccccc 4500

agggccagcg ggtcccggt ggctgccagg ggttgctgga cgtcctggag ccaagggctc 4560

tgaagggcca ccaggacca ctggccgcca aggagagaag ggggagcctg gtcgccctg 4620

ggacctgca gtggtgggac ctgctgttc tggacccaaa ggagaaaagg gagatgtgg 4680

gcccgtggg ccagaggag ctaccggagt ccaaggggaa cggggccac ccggcttgg 4740

tttctctgga gacctggcc ccaagggaga ccctggagac cggggtcca ttggccttac 4800

tggcagagca ggacccccag gtgactcagg gcctcctgga gagaaggag accctgggcg 4860

gcctggcccc ccaggacctg ttggccccg aggacgagat ggtgaagtg gagagaaagg 4920

Sequence_Listing.txt

tgacgagggt cctccgggtg acccgggttt gcctggaaaa gcaggcgagc gtggccttcg 4980

gggggcacct ggagttcggg ggctgtggg tgaagggga gaccaggag atcctggaga 5040

ggatggacga aatggcagcc ctggatcatc tggaccaag ggtgaccgtg gggagccggg 5100

tccccagga ccccggggac ggctggtaga cacaggacct ggagccagag agaagggaga 5160

gcctggggac cgcggaag agggctctc agggcccaag ggtgatcctg gcctccctgg 5220

agccctggg gaaaggggca ttgaagggtt tcggggacc ccaggccac agggggacc 5280

agggtgccga ggccagcag gagaaaagg tgaccgggt cccctgggc tggatggccg 5340

gagcggactg gatgggaaac caggagccgc tgggcccctt gggccgaatg gtgctcagg 5400

caaagctggg gaccagga gagacgggt tccaggcctc cgtggagaac agggcctccc 5460

tggcccctt ggtcccctg gattaccgg aaagccaggc gaggatggca aacctggcct 5520

gaatgaaaa aacggagaac ctggggacc tggagaagac gggaggaagg gagagaaagg 5580

agattcaggc gcctctggga gagaaggctg tgatggccc aagggtgagc gtggagctcc 5640

tggatcctt ggacccagg ggctccagg cctccagg ccagtgggc ctctggcca 5700

gggtttcct ggtgtccag gaggcagg cccaagggt gaccgtggg agactggatc 5760

caaaggggag cagggcctc ctggagagc tggcctgca ggagagcctg gaagtgtgcc 5820

gaatgtgat cggtgtctg aaactgtct catcaaggca tctgcctgc gggagatcgt 5880

ggagacctg gatgagagct ctggtagct cctgcctgt cccgaacggc gtcgaggccc 5940

caagggggac tcaggcgaac agggccccc aggaaggag ggcccatcg gctttcctg 6000

agaacgcggg ctgaaggcg accgtggaga ccctggcct caggggccac ctggtctggc 6060

cctggggag aggggcccc cgggccttc cggccttgc ggggagcctg gaaagcctg 6120

tattccggg ctccaggca gggctgggg tgtgggagag gcaggaaggc caggagagag 6180

Sequence_Listing.txt

gggagaacgg ggagagaaag gagaacgtgg agaacagggc agagatggcc ctctggact 6240
 ccctggaacc cctgggcccc ccggaccccc tggccccaag gtgtctgtgg atgagccagg 6300
 tcctggactc tctggagaac agggaccccc tggactcaag ggtgctaagg gggagccggg 6360
 cagcaatggt gaccaaggtc ccaaaggaga caggggtgtg ccaggcatca aaggagaccg 6420
 gggagagcct ggaccgaggg gtcaggacgg caaccgggt ctaccaggag agcgtggtat 6480
 ggctgggcct gaagggaagc cgggtctgca gggccaaga gggccccctg gccagtggg 6540
 tggcatgga gacctggac cacctggtgc cccgggtctt gctggccctg caggacccca 6600
 aggacctct gccctgaagg gggagcctgg agagacagga cctccaggac ggggcctgac 6660
 tggacctact ggagctgtgg gacttctgg accccccggc ccttcaggcc ttgtgggtcc 6720
 acaggggtct ccaggttgc ctggacaagt gggggagaca gggaagccgg gagccccagg 6780
 tcgagatggt gccagtggaa aagatggaga cagagggagc cctggtgtgc cagggtcacc 6840
 aggtctgcct gggcctgtc gacctaaagg agaacctggc cccacggggg cccctggaca 6900
 ggctgtgtc gggctccctg gagcaaagg agagaaggga gcccctggag gccttgctgg 6960
 agacctggtg ggtgagccgg gagccaaagg tgaccgagga ctgccagggc cgcgaggcga 7020
 gaagggtgaa gctggccgtg caggggagcc cggagaccct ggggaagatg gtcagaaagg 7080
 ggctccagga ccaaagggt tcaagggtga cccaggagtc ggggtcccgg gctcccctgg 7140
 gcctcctggc cctcagggt tgaagggaga tctgggctc cctggcctgc ccggtgctcc 7200
 tgggtgtgtt ggggtcccgg gtcagacagg cctcgagga gagatgggtc agccaggccc 7260
 tagtgagag cggggtctgg caggcccccc agggagagaa ggaatcccag gaccctggg 7320
 gccacctgga ccaccggggc cagtgggacc acctggggcc tctggactca aaggagacaa 7380
 gggagaccct ggagtagggc tgctggggc ccgaggcgag cgtggggagc caggcatccg 7440

Sequence_Listing.txt

ggggtgaagat ggccgccccg gccaggaggg accccgagga ctcacggggc cccctggcag 7500
 caggggagag cgtggggaga aggggtgatgt tgggagtga ggactaaagg gtgacaagg 7560
 agactcagct gtgatcctgg ggcctccagg cccacggggg gccaaagggg acatgggtga 7620
 acgagggcct cggggcttgg atggtgacaa aggacctcg ggagacaatg gggaccttg 7680
 tgacaagggc agcaaggag agcctggtga caagggctca gccgggttc caggactcg 7740
 tggactcctg ggaccccagg gtcaacctgg tgcagcagg atccctggtg acccgggatc 7800
 cccaggaaag gatggagtgc ctggtatccg aggagaaaaa ggagatgtg gcttcatgg 7860
 tccccggggc ctcaagggtg aacggggagt gaaggagcc tgtggcctg atggagagaa 7920
 gggagacaag ggagaagctg gtccccagg ccgccccggg ctggcaggac acaaaggaga 7980
 gatgggggag cctggtgtgc cggggccatc gggggcccct ggcaaggagg gcctgatcg 8040
 tccaagggt gaccgaggct ttgacggga gccaggcccc aagggtgacc agggcgagaa 8100
 aggggagcgg ggaaccccag gaattggggg ctcccaggc cccagtggaa atgatggctc 8160
 tgctggtccc ccaggggcac ctggcagtgt tggcccaga ggccccgaag gacttcagg 8220
 ccagaagggt gagcgaggtc cccccgaga gagagtggg ggggctcctg gggccctgg 8280
 agctcctggc gagagagggg agcaggggag gccagggcct gccggtcctc gaggcgagaa 8340
 gggagaagct gcactgacgg aggatgacat ccggggcttt gtgcgccaag agatgagtca 8400
 gcactgtgcc tgccagggcc agttcatgc atctggatca cgacctcc ctagttatgc 8460
 tgcagacact gccggctccc agtccatgc tgtgcctgt ctccgctct ctcagcaga 8520
 ggaggaagag cgggtacccc ctgaggatga tgagtactct gaatactcc agtattctgt 8580
 ggaggagtac caggacctg aagctcctg ggatagtga gacctgtt cctgccact 8640
 ggatagggc tctgcactg cctacacct gcgctgttac catcgggctg tgacaggcag 8700

Sequence_Listing.txt

cacagaggcc tgcaccctt ttgtctatgg tggctgtgga gggaatgcca accgttttgg 8760
gacccgtgag gcctgcgagc gccgctgccc acccgggtg gtccagagcc aggggacagg 8820
tactgccag gactgaggcc cagataatga gctgagattc agcatcccct ggaggagtgc 8880
gggtctcagc agaacccac tgcctctccc ctgtgtgcta gaggtgtgtg tgcacgtgag 8940
cgtgcgtgtg cacgtccgtt attcagtga ctgtgtcccg tgggtctagc ctccccct 9000
gtggacaaac cccattgtg gctcctgcca cctggcaga tgactcactg tgggggggtg 9060
gctgtgggca gtgagcggat gtgactggcg tctgaccgc ccttgacct aagcctgtga 9120
tgacatggtg ctgattctgg ggggcattaa agctgctgtt taaaaggc 9169

<210> 18
<211> 2944
<212> PRT
<213> Homo sapiens

<400> 18
Met Thr Leu Arg Leu Leu Val Ala Ala Leu Cys Ala Gly Ile Leu Ala
1 5 10 15

Glu Ala Pro Arg Val Arg Ala Gln His Arg Glu Arg Val Thr Cys Thr
20 25 30

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

Ile Gly Arg Ser Asn Phe Arg Glu Val Arg Ser Phe Leu Glu Gly Leu
50 55 60

Val Leu Pro Phe Ser Gly Ala Ala Ser Ala Gln Gly Val Arg Phe Ala
65 70 75 80

Sequence_Listing.txt

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

Leu Gly Ser Gly Gly Asp Val Ile Arg Ala Ile Arg Glu Leu Ser Tyr
100 105 110

Lys Gly Gly Asn Thr Arg Thr Gly Ala Ala Ile Leu His Val Ala Asp
115 120 125

His Val Phe Leu Pro Gln Leu Ala Arg Pro Gly Val Pro Lys Val Cys
130 135 140

Ile Leu Ile Thr Asp Gly Lys Ser Gln Asp Leu Val Asp Thr Ala Ala
145 150 155 160

Gln Arg Leu Lys Gly Gln Gly Val Lys Leu Phe Ala Val Gly Ile Lys
165 170 175

Asn Ala Asp Pro Glu Glu Leu Lys Arg Val Ala Ser Gln Pro Thr Ser
180 185 190

Asp Phe Phe Phe Phe Val Asn Asp Phe Ser Ile Leu Arg Thr Leu Leu
195 200 205

Pro Leu Val Ser Arg Arg Val Cys Thr Thr Ala Gly Gly Val Pro Val
210 215 220

Thr Arg Pro Pro Asp Asp Ser Thr Ser Ala Pro Arg Asp Leu Val Leu
225 230 235 240

Ser Glu Pro Ser Ser Gln Ser Leu Arg Val Gln Trp Thr Ala Ala Ser

Sequence_Listing.txt

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

Sequence_Listing.txt

Val Glu Gln Thr Leu Arg Pro Val Ile Leu Gly Pro Thr Ser Ile Leu
420 425 430

Leu Ser Trp Asn Leu Val Pro Glu Ala Arg Gly Tyr Arg Leu Glu Trp
435 440 445

Arg Arg Glu Thr Gly Leu Glu Pro Pro Gln Lys Val Val Leu Pro Ser
450 455 460

Asp Val Thr Arg Tyr Gln Leu Asp Gly Leu Gln Pro Gly Thr Glu Tyr
465 470 475 480

Arg Leu Thr Leu Tyr Thr Leu Leu Glu Gly His Glu Val Ala Thr Pro
485 490 495

Ala Thr Val Val Pro Thr Gly Pro Glu Leu Pro Val Ser Pro Val Thr
500 505 510

Asp Leu Gln Ala Thr Glu Leu Pro Gly Gln Arg Val Arg Val Ser Trp
515 520 525

Ser Pro Val Pro Gly Ala Thr Gln Tyr Arg Ile Ile Val Arg Ser Thr
530 535 540

Gln Gly Val Glu Arg Thr Leu Val Leu Pro Gly Ser Gln Thr Ala Phe
545 550 555 560

Asp Leu Asp Asp Val Gln Ala Gly Leu Ser Tyr Thr Val Arg Val Ser
565 570 575

Ala Arg Val Gly Pro Arg Glu Gly Ser Ala Ser Val Leu Thr Val Arg

Sequence_Listing.txt

580 585 590

Arg Glu Pro Glu Thr Pro Leu Ala Val Pro Gly Leu Arg Val Val Val
595 600 605

Ser Asp Ala Thr Arg Val Arg Val Ala Trp Gly Pro Val Pro Gly Ala
610 615 620

Ser Gly Phe Arg Ile Ser Trp Ser Thr Gly Ser Gly Pro Glu Ser Ser
625 630 635 640

Gln Thr Leu Pro Pro Asp Ser Thr Ala Thr Asp Ile Thr Gly Leu Gln
645 650 655

Pro Gly Thr Thr Tyr Gln Val Ala Val Ser Val Leu Arg Gly Arg Glu
660 665 670

Glu Gly Pro Ala Ala Val Ile Val Ala Arg Thr Asp Pro Leu Gly Pro
675 680 685

Val Arg Thr Val His Val Thr Gln Ala Ser Ser Ser Ser Val Thr Ile
690 695 700

Thr Trp Thr Arg Val Pro Gly Ala Thr Gly Tyr Arg Val Ser Trp His
705 710 715 720

Ser Ala His Gly Pro Glu Lys Ser Gln Leu Val Ser Gly Glu Ala Thr
725 730 735

Val Ala Glu Leu Asp Gly Leu Glu Pro Asp Thr Glu Tyr Thr Val His
740 745 750

Sequence_Listing.txt

Val Arg Ala His Val Ala Gly Val Asp Gly Pro Pro Ala Ser Val Val
755 760 765

Val Arg Thr Ala Pro Glu Pro Val Gly Arg Val Ser Arg Leu Gln Ile
770 775 780

Leu Asn Ala Ser Ser Asp Val Leu Arg Ile Thr Trp Val Gly Val Thr
785 790 795 800

Gly Ala Thr Ala Tyr Arg Leu Ala Trp Gly Arg Ser Glu Gly Gly Pro
805 810 815

Met Arg His Gln Ile Leu Pro Gly Asn Thr Asp Ser Ala Glu Ile Arg
820 825 830

Gly Leu Glu Gly Gly Val Ser Tyr Ser Val Arg Val Thr Ala Leu Val
835 840 845

Gly Asp Arg Glu Gly Thr Pro Val Ser Ile Val Val Thr Thr Pro Pro
850 855 860

Glu Ala Pro Pro Ala Leu Gly Thr Leu His Val Val Gln Arg Gly Glu
865 870 875 880

His Ser Leu Arg Leu Arg Trp Glu Pro Val Pro Arg Ala Gln Gly Phe
885 890 895

Leu Leu His Trp Gln Pro Glu Gly Gly Gln Glu Gln Ser Arg Val Leu
900 905 910

Gly Pro Glu Leu Ser Ser Tyr His Leu Asp Gly Leu Glu Pro Ala Thr

Sequence_Listing.txt

915 920 925

Gln Tyr Arg Val Arg Leu Ser Val Leu Gly Pro Ala Gly Glu Gly Pro
930 935 940

Ser Ala Glu Val Thr Ala Arg Thr Glu Ser Pro Arg Val Pro Ser Ile
945 950 955 960

Glu Leu Arg Val Val Asp Thr Ser Ile Asp Ser Val Thr Leu Ala Trp
965 970 975

Thr Pro Val Ser Arg Ala Ser Ser Tyr Ile Leu Ser Trp Arg Pro Leu
980 985 990

Arg Gly Pro Gly Gln Glu Val Pro Gly Ser Pro Gln Thr Leu Pro Gly
995 1000 1005

Ile Ser Ser Ser Gln Arg Val Thr Gly Leu Glu Pro Gly Val Ser
1010 1015 1020

Tyr Ile Phe Ser Leu Thr Pro Val Leu Asp Gly Val Arg Gly Pro
1025 1030 1035

Glu Ala Ser Val Thr Gln Thr Pro Val Cys Pro Arg Gly Leu Ala
1040 1045 1050

Asp Val Val Phe Leu Pro His Ala Thr Gln Asp Asn Ala His Arg
1055 1060 1065

Ala Glu Ala Thr Arg Arg Val Leu Glu Arg Leu Val Leu Ala Leu
1070 1075 1080

Sequence_Listing.txt

Gly Pro Leu Gly Pro Gln Ala Val Gln Val Gly Leu Leu Ser Tyr
1085 1090 1095

Ser His Arg Pro Ser Pro Leu Phe Pro Leu Asn Gly Ser His Asp
1100 1105 1110

Leu Gly Ile Ile Leu Gln Arg Ile Arg Asp Met Pro Tyr Met Asp
1115 1120 1125

Pro Ser Gly Asn Asn Leu Gly Thr Ala Val Val Thr Ala His Arg
1130 1135 1140

Tyr Met Leu Ala Pro Asp Ala Pro Gly Arg Arg Gln His Val Pro
1145 1150 1155

Gly Val Met Val Leu Leu Val Asp Glu Pro Leu Arg Gly Asp Ile
1160 1165 1170

Phe Ser Pro Ile Arg Glu Ala Gln Ala Ser Gly Leu Asn Val Val
1175 1180 1185

Met Leu Gly Met Ala Gly Ala Asp Pro Glu Gln Leu Arg Arg Leu
1190 1195 1200

Ala Pro Gly Met Asp Ser Val Gln Thr Phe Phe Ala Val Asp Asp
1205 1210 1215

Gly Pro Ser Leu Asp Gln Ala Val Ser Gly Leu Ala Thr Ala Leu
1220 1225 1230

Cys Gln Ala Ser Phe Thr Thr Gln Pro Arg Pro Glu Pro Cys Pro

Sequence_Listing.txt

1235	1240	1245
Val Tyr Cys Pro Lys Gly Gln	Lys Gly Glu Pro Gly	Glu Met Gly
1250	1255	1260
Leu Arg Gly Gln Val Gly Pro	Pro Gly Asp Pro Gly	Leu Pro Gly
1265	1270	1275
Arg Thr Gly Ala Pro Gly Pro	Gln Gly Pro Pro Gly	Ser Ala Thr
1280	1285	1290
Ala Lys Gly Glu Arg Gly Phe	Pro Gly Ala Asp Gly	Arg Pro Gly
1295	1300	1305
Ser Pro Gly Arg Ala Gly Asn	Pro Gly Thr Pro Gly	Ala Pro Gly
1310	1315	1320
Leu Lys Gly Ser Pro Gly Leu	Pro Gly Pro Arg Gly	Asp Pro Gly
1325	1330	1335
Glu Arg Gly Pro Arg Gly Pro	Lys Gly Glu Pro Gly	Ala Pro Gly
1340	1345	1350
Gln Val Ile Gly Gly Glu Gly	Pro Gly Leu Pro Gly	Arg Lys Gly
1355	1360	1365
Asp Pro Gly Pro Ser Gly Pro	Pro Gly Pro Arg Gly	Pro Leu Gly
1370	1375	1380
Asp Pro Gly Pro Arg Gly Pro	Pro Gly Leu Pro Gly	Thr Ala Met
1385	1390	1395

Sequence_Listing.txt

Lys Gly Asp Lys Gly Asp Arg Gly Glu Arg Gly Pro Pro Gly Pro
1400 1405 1410

Gly Glu Gly Gly Ile Ala Pro Gly Glu Pro Gly Leu Pro Gly Leu
1415 1420 1425

Pro Gly Ser Pro Gly Pro Gln Gly Pro Val Gly Pro Pro Gly Lys
1430 1435 1440

Lys Gly Glu Lys Gly Asp Ser Glu Asp Gly Ala Pro Gly Leu Pro
1445 1450 1455

Gly Gln Pro Gly Ser Pro Gly Glu Gln Gly Pro Arg Gly Pro Pro
1460 1465 1470

Gly Ala Ile Gly Pro Lys Gly Asp Arg Gly Phe Pro Gly Pro Leu
1475 1480 1485

Gly Glu Ala Gly Glu Lys Gly Glu Arg Gly Pro Pro Gly Pro Ala
1490 1495 1500

Gly Ser Arg Gly Leu Pro Gly Val Ala Gly Arg Pro Gly Ala Lys
1505 1510 1515

Gly Pro Glu Gly Pro Pro Gly Pro Thr Gly Arg Gln Gly Glu Lys
1520 1525 1530

Gly Glu Pro Gly Arg Pro Gly Asp Pro Ala Val Val Gly Pro Ala
1535 1540 1545

Val Ala Gly Pro Lys Gly Glu Lys Gly Asp Val Gly Pro Ala Gly

Sequence_Listing.txt

1550 1555 1560

Pro Arg Gly Ala Thr Gly Val Gln Gly Glu Arg Gly Pro Pro Gly
1565 1570 1575

Leu Val Leu Pro Gly Asp Pro Gly Pro Lys Gly Asp Pro Gly Asp
1580 1585 1590

Arg Gly Pro Ile Gly Leu Thr Gly Arg Ala Gly Pro Pro Gly Asp
1595 1600 1605

Ser Gly Pro Pro Gly Glu Lys Gly Asp Pro Gly Arg Pro Gly Pro
1610 1615 1620

Pro Gly Pro Val Gly Pro Arg Gly Arg Asp Gly Glu Val Gly Glu
1625 1630 1635

Lys Gly Asp Glu Gly Pro Pro Gly Asp Pro Gly Leu Pro Gly Lys
1640 1645 1650

Ala Gly Glu Arg Gly Leu Arg Gly Ala Pro Gly Val Arg Gly Pro
1655 1660 1665

Val Gly Glu Lys Gly Asp Gln Gly Asp Pro Gly Glu Asp Gly Arg
1670 1675 1680

Asn Gly Ser Pro Gly Ser Ser Gly Pro Lys Gly Asp Arg Gly Glu
1685 1690 1695

Pro Gly Pro Pro Gly Pro Pro Gly Arg Leu Val Asp Thr Gly Pro
1700 1705 1710

Sequence_Listing.txt

Gly Ala Arg Glu Lys Gly Glu Pro Gly Asp Arg Gly Gln Glu Gly
1715 1720 1725

Pro Arg Gly Pro Lys Gly Asp Pro Gly Leu Pro Gly Ala Pro Gly
1730 1735 1740

Glu Arg Gly Ile Glu Gly Phe Arg Gly Pro Pro Gly Pro Gln Gly
1745 1750 1755

Asp Pro Gly Val Arg Gly Pro Ala Gly Glu Lys Gly Asp Arg Gly
1760 1765 1770

Pro Pro Gly Leu Asp Gly Arg Ser Gly Leu Asp Gly Lys Pro Gly
1775 1780 1785

Ala Ala Gly Pro Ser Gly Pro Asn Gly Ala Ala Gly Lys Ala Gly
1790 1795 1800

Asp Pro Gly Arg Asp Gly Leu Pro Gly Leu Arg Gly Glu Gln Gly
1805 1810 1815

Leu Pro Gly Pro Ser Gly Pro Pro Gly Leu Pro Gly Lys Pro Gly
1820 1825 1830

Glu Asp Gly Lys Pro Gly Leu Asn Gly Lys Asn Gly Glu Pro Gly
1835 1840 1845

Asp Pro Gly Glu Asp Gly Arg Lys Gly Glu Lys Gly Asp Ser Gly
1850 1855 1860

Ala Ser Gly Arg Glu Gly Arg Asp Gly Pro Lys Gly Glu Arg Gly

Sequence_Listing.txt

1865	1870	1875
Ala Pro	Gly Ile Leu Gly Pro	Gln Gly Pro Pro Gly Leu Pro Gly
1880	1885	1890
Pro Val	Gly Pro Pro Gly Gln	Gly Phe Pro Gly Val Pro Gly Gly
1895	1900	1905
Thr Gly	Pro Lys Gly Asp Arg	Gly Glu Thr Gly Ser Lys Gly Glu
1910	1915	1920
Gln Gly	Leu Pro Gly Glu Arg	Gly Leu Arg Gly Glu Pro Gly Ser
1925	1930	1935
Val Pro	Asn Val Asp Arg Leu	Leu Glu Thr Ala Gly Ile Lys Ala
1940	1945	1950
Ser Ala	Leu Arg Glu Ile Val	Glu Thr Trp Asp Glu Ser Ser Gly
1955	1960	1965
Ser Phe	Leu Pro Val Pro Glu	Arg Arg Arg Gly Pro Lys Gly Asp
1970	1975	1980
Ser Gly	Glu Gln Gly Pro Pro	Gly Lys Glu Gly Pro Ile Gly Phe
1985	1990	1995
Pro Gly	Glu Arg Gly Leu Lys	Gly Asp Arg Gly Asp Pro Gly Pro
2000	2005	2010
Gln Gly	Pro Pro Gly Leu Ala	Leu Gly Glu Arg Gly Pro Pro Gly
2015	2020	2025

Sequence_Listing.txt

Pro Ser Gly Leu Ala Gly Glu Pro Gly Lys Pro Gly Ile Pro Gly
2030 2035 2040

Leu Pro Gly Arg Ala Gly Gly Val Gly Glu Ala Gly Arg Pro Gly
2045 2050 2055

Glu Arg Gly Glu Arg Gly Glu Lys Gly Glu Arg Gly Glu Gln Gly
2060 2065 2070

Arg Asp Gly Pro Pro Gly Leu Pro Gly Thr Pro Gly Pro Pro Gly
2075 2080 2085

Pro Pro Gly Pro Lys Val Ser Val Asp Glu Pro Gly Pro Gly Leu
2090 2095 2100

Ser Gly Glu Gln Gly Pro Pro Gly Leu Lys Gly Ala Lys Gly Glu
2105 2110 2115

Pro Gly Ser Asn Gly Asp Gln Gly Pro Lys Gly Asp Arg Gly Val
2120 2125 2130

Pro Gly Ile Lys Gly Asp Arg Gly Glu Pro Gly Pro Arg Gly Gln
2135 2140 2145

Asp Gly Asn Pro Gly Leu Pro Gly Glu Arg Gly Met Ala Gly Pro
2150 2155 2160

Glu Gly Lys Pro Gly Leu Gln Gly Pro Arg Gly Pro Pro Gly Pro
2165 2170 2175

Val Gly Gly His Gly Asp Pro Gly Pro Pro Gly Ala Pro Gly Leu

Sequence_Listing.txt

2180

2185

2190

Ala Gly Pro Ala Gly Pro Gln Gly Pro Ser Gly Leu Lys Gly Glu
2195 2200 2205

Pro Gly Glu Thr Gly Pro Pro Gly Arg Gly Leu Thr Gly Pro Thr
2210 2215 2220

Gly Ala Val Gly Leu Pro Gly Pro Pro Gly Pro Ser Gly Leu Val
2225 2230 2235

Gly Pro Gln Gly Ser Pro Gly Leu Pro Gly Gln Val Gly Glu Thr
2240 2245 2250

Gly Lys Pro Gly Ala Pro Gly Arg Asp Gly Ala Ser Gly Lys Asp
2255 2260 2265

Gly Asp Arg Gly Ser Pro Gly Val Pro Gly Ser Pro Gly Leu Pro
2270 2275 2280

Gly Pro Val Gly Pro Lys Gly Glu Pro Gly Pro Thr Gly Ala Pro
2285 2290 2295

Gly Gln Ala Val Val Gly Leu Pro Gly Ala Lys Gly Glu Lys Gly
2300 2305 2310

Ala Pro Gly Gly Leu Ala Gly Asp Leu Val Gly Glu Pro Gly Ala
2315 2320 2325

Lys Gly Asp Arg Gly Leu Pro Gly Pro Arg Gly Glu Lys Gly Glu
2330 2335 2340

Sequence_Listing.txt

Ala Gly Arg Ala Gly Glu Pro Gly Asp Pro Gly Glu Asp Gly Gln
2345 2350 2355

Lys Gly Ala Pro Gly Pro Lys Gly Phe Lys Gly Asp Pro Gly Val
2360 2365 2370

Gly Val Pro Gly Ser Pro Gly Pro Pro Gly Pro Pro Gly Val Lys
2375 2380 2385

Gly Asp Leu Gly Leu Pro Gly Leu Pro Gly Ala Pro Gly Val Val
2390 2395 2400

Gly Phe Pro Gly Gln Thr Gly Pro Arg Gly Glu Met Gly Gln Pro
2405 2410 2415

Gly Pro Ser Gly Glu Arg Gly Leu Ala Gly Pro Pro Gly Arg Glu
2420 2425 2430

Gly Ile Pro Gly Pro Leu Gly Pro Pro Gly Pro Pro Gly Ser Val
2435 2440 2445

Gly Pro Pro Gly Ala Ser Gly Leu Lys Gly Asp Lys Gly Asp Pro
2450 2455 2460

Gly Val Gly Leu Pro Gly Pro Arg Gly Glu Arg Gly Glu Pro Gly
2465 2470 2475

Ile Arg Gly Glu Asp Gly Arg Pro Gly Gln Glu Gly Pro Arg Gly
2480 2485 2490

Leu Thr Gly Pro Pro Gly Ser Arg Gly Glu Arg Gly Glu Lys Gly

Sequence_Listing.txt

2495 2500 2505

Asp Val Gly Ser Ala Gly Leu Lys Gly Asp Lys Gly Asp Ser Ala
2510 2515 2520

Val Ile Leu Gly Pro Pro Gly Pro Arg Gly Ala Lys Gly Asp Met
2525 2530 2535

Gly Glu Arg Gly Pro Arg Gly Leu Asp Gly Asp Lys Gly Pro Arg
2540 2545 2550

Gly Asp Asn Gly Asp Pro Gly Asp Lys Gly Ser Lys Gly Glu Pro
2555 2560 2565

Gly Asp Lys Gly Ser Ala Gly Leu Pro Gly Leu Arg Gly Leu Leu
2570 2575 2580

Gly Pro Gln Gly Gln Pro Gly Ala Ala Gly Ile Pro Gly Asp Pro
2585 2590 2595

Gly Ser Pro Gly Lys Asp Gly Val Pro Gly Ile Arg Gly Glu Lys
2600 2605 2610

Gly Asp Val Gly Phe Met Gly Pro Arg Gly Leu Lys Gly Glu Arg
2615 2620 2625

Gly Val Lys Gly Ala Cys Gly Leu Asp Gly Glu Lys Gly Asp Lys
2630 2635 2640

Gly Glu Ala Gly Pro Pro Gly Arg Pro Gly Leu Ala Gly His Lys
2645 2650 2655

Sequence_Listing.txt

Gly Glu Met Gly Glu Pro Gly Val Pro Gly Gln Ser Gly Ala Pro
2660 2665 2670

Gly Lys Glu Gly Leu Ile Gly Pro Lys Gly Asp Arg Gly Phe Asp
2675 2680 2685

Gly Gln Pro Gly Pro Lys Gly Asp Gln Gly Glu Lys Gly Glu Arg
2690 2695 2700

Gly Thr Pro Gly Ile Gly Gly Phe Pro Gly Pro Ser Gly Asn Asp
2705 2710 2715

Gly Ser Ala Gly Pro Pro Gly Pro Pro Gly Ser Val Gly Pro Arg
2720 2725 2730

Gly Pro Glu Gly Leu Gln Gly Gln Lys Gly Glu Arg Gly Pro Pro
2735 2740 2745

Gly Glu Arg Val Val Gly Ala Pro Gly Val Pro Gly Ala Pro Gly
2750 2755 2760

Glu Arg Gly Glu Gln Gly Arg Pro Gly Pro Ala Gly Pro Arg Gly
2765 2770 2775

Glu Lys Gly Glu Ala Ala Leu Thr Glu Asp Asp Ile Arg Gly Phe
2780 2785 2790

Val Arg Gln Glu Met Ser Gln His Cys Ala Cys Gln Gly Gln Phe
2795 2800 2805

Ile Ala Ser Gly Ser Arg Pro Leu Pro Ser Tyr Ala Ala Asp Thr

Sequence_Listing.txt

2810 2815 2820

Ala Gly Ser Gln Leu His Ala Val Pro Val Leu Arg Val Ser His
2825 2830 2835

Ala Glu Glu Glu Glu Arg Val Pro Pro Glu Asp Asp Glu Tyr Ser
2840 2845 2850

Glu Tyr Ser Glu Tyr Ser Val Glu Glu Tyr Gln Asp Pro Glu Ala
2855 2860 2865

Pro Trp Asp Ser Asp Asp Pro Cys Ser Leu Pro Leu Asp Glu Gly
2870 2875 2880

Ser Cys Thr Ala Tyr Thr Leu Arg Trp Tyr His Arg Ala Val Thr
2885 2890 2895

Gly Ser Thr Glu Ala Cys His Pro Phe Val Tyr Gly Gly Cys Gly
2900 2905 2910

Gly Asn Ala Asn Arg Phe Gly Thr Arg Glu Ala Cys Glu Arg Arg
2915 2920 2925

Cys Pro Pro Arg Val Val Gln Ser Gln Gly Thr Gly Thr Ala Gln
2930 2935 2940

Asp

<210> 19
<211> 2988
<212> DNA

Sequence_Listing.txt

<213> Homo sapiens

<400> 19

```

agaagaaggg gagaggaggt tgtgtgggac aagggtgctc tgacagaagg atgccacagc    60
tgagcctgtc ctgctgggc cttggccaa tggcagcatc cccgtggctg ctctgctgc    120
tggttggggc ctctggctc ctggcccgca tcctggcctg gacctatacc ttctatgaca    180
actgctgccg cctccggtgt ttcccgcaac ccccgaaacg gaattgggtc ttgggtcacc    240
tgggcctgat tcacagctcg gaggaaggtc tcctatacac acaaagcctg gcatgcacct    300
tcggtgatat gtgctgtgg tgggtggggc cctggcacgc aatcgtccgc atcttcacc    360
ccacctacat caagcctgtg ctcttgctc cagctgcat tgtaccaaag gacaaggctt    420
tctacagctt cctgaagccc tggctggggg atgggctcct gctgagtgt ggtgaaaagt    480
ggagccgcca cgtcggatg ctgacgctg ccttcattt caacatcctg aagccctata    540
tgaagatfff caatgagagt gtgaacatca tgcatgcaa gtggcagctc ctggcctcag    600
agggtagtgc cgtctggac atgtttgagc acatcagcct catgacctg gacagtctgc    660
agaaatgtgt cttcagcttt gacagccatt gccaggagaa gcccagtga tatttgccg    720
ccatcttga gctcagtgc ctttgacaa aaagacacca gcagatcctc ctgtacatag    780
acttctgta ttatctacc cctgatggg agcgtttccg cagggcctgc cgctggtgc    840
acgacttcac agatgccgtc atccaggagc ggcgccgcac cctccctagc cagggtgtg    900
atgacttctt ccaagccaag gccaaatcca agactttgga cttcattgat gtactcctgc    960
tgagcaagga tgaagatggg aagaagtgt ccgatgagga cataagagca gaagctgaca   1020
cctttatgtt tgagggccat gacaccacag ccagtgtct ctctgggtc ctgtaccacc   1080
ttgcaaagca cccggaatac caggagcgt gtcggcagga ggtgcaagag cttctgaagg   1140
accgtgagcc taaagagatt gaatgggacg acctggccca gctgcccttc ctgacctgt   1200

```

Sequence_Listing.txt

gcattaagga gagcctgagg ctgcatcccc cagtcctgc cgtctctgc tgcgcaccc 1260

aagacattgt gctcccagac ggccgggtca tcccaaagg cattatctgc ctcatcagt 1320

ttttggaac ccatcacaac ccagccgtgt ggccggaccc tgaggtctat gaccccttc 1380

gcttgaccc aaagaacatc aaggagaggt cacctctggc tttattccc ttctcagcag 1440

ggcccaggaa ctgcatcggg caggcggtcg cgatggcgga gatgaagggtg gtcctggggc 1500

tcacgctgct gcgcttcgc gtcctgcctg accacaccga gcccgcagg aagccggagc 1560

tggctctgcg cgcagagggc ggactttggc tgcgggtgga gccctgagc tgagtctgc 1620

agagaccac tctgaccca ctaaaatgac cctgattca taaaagtga ggcctagaat 1680

taccctaaga cctgttcca cagtcctgta ttcatccta gatatctact caaaataatt 1740

gagacaagtg ttcaaacaga aagacgcttg tgcgtgaatg ttcatggcag ccctattcac 1800

agtagccaaa cgatgaaaac aacccaagc tatatttac cagatgaaag gataaacaaa 1860

atatggtcca tccatacaat ggagtattac acagccataa aaaggaatga agcagtgatc 1920

cccactacac tgtggatgaa ccttgaatgc atgatactga atgaaagaca tcagatgcaa 1980

aaggtcacat agtctactgt cctttatat gaaattcca gaacaggcca atctgaagag 2040

atgtatagtg gattggtggc tticagcagc tctggggagg tgggactgag gagcgactgc 2100

taatcaggat ggggttcct cctgggatgg tgaaaatgt ccggacctag atagtatga 2160

aggtagcacg acactgtgag tgcactaaat gctattgaat tggacacttt agaattggtg 2220

aaatagtgat tttatgtga attctaccta aacatgctat tacagctcat atatacttt 2280

ttcatctgga ttctcaciaa aagaatatgt tctgagcatc ttccatgat attaaatcat 2340

cttaggaaac attattttgt gttctcaaa atgtgcatgt taagtattca aatcagcttt 2400

aaatttttaa aaatatgtaa ttttagaaaa taatttaaaa ggttttgtt cagtttgtaa 2460

Sequence_Listing.txt

gatttcttt ctggcacttt aatggcttga ggtatcatta tcagttacaa attgagttat 2520
 tcttcatcaa atgacttttg gagtagagat ttattttta tagcaataga tgcacagata 2580
 ttctgtaag atacaggtgt ggtagacac tttctagaa caggcatgcc ctgcaaactc 2640
 cacagacact gactgtttt gtcctattaa gaagtagacc actgagaagg gagaaggtga 2700
 cattttagct ttcccaggta aaagtgggtt tcatcctcac accaatttta tggactggac 2760
 gttaactctc ttgctcaagg tcactctgag tggaagagtg gggataaatc tggttcgttt 2820
 ggcacagag gccatgactt ttctaccac agaagtaatt ttcaaagtaa gtctctgccc 2880
 taggcacatc agatcacctg gggaccactc cagagtgagt agacaagact ttgacagggg 2940
 tgcctaattt tttttttt ttgagatgga gtctcgctct gttgccca 2988

<210> 20
 <211> 520
 <212> PRT
 <213> Homo sapiens

<400> 20
 Met Pro Gln Leu Ser Leu Ser Ser Leu Gly Leu Trp Pro Met Ala Ala
 1 5 10 15

Ser Pro Trp Leu Leu Leu Leu Leu Val Gly Ala Ser Trp Leu Leu Ala
 20 25 30

Arg Ile Leu Ala Trp Thr Tyr Thr Phe Tyr Asp Asn Cys Cys Arg Leu
 35 40 45

Arg Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe Leu Gly His Leu
 50 55 60

Sequence_Listing.txt

Gly Leu Ile His Ser Ser Glu Glu Gly Leu Leu Tyr Thr Gln Ser Leu
65 70 75 80

Ala Cys Thr Phe Gly Asp Met Cys Cys Trp Trp Val Gly Pro Trp His
 85 90 95

Ala Ile Val Arg Ile Phe His Pro Thr Tyr Ile Lys Pro Val Leu Phe
 100 105 110

Ala Pro Ala Ala Ile Val Pro Lys Asp Lys Val Phe Tyr Ser Phe Leu
 115 120 125

Lys Pro Trp Leu Gly Asp Gly Leu Leu Leu Ser Ala Gly Glu Lys Trp
 130 135 140

Ser Arg His Arg Arg Met Leu Thr Pro Ala Phe His Phe Asn Ile Leu
145 150 155 160

Lys Pro Tyr Met Lys Ile Phe Asn Glu Ser Val Asn Ile Met His Ala
 165 170 175

Lys Trp Gln Leu Leu Ala Ser Glu Gly Ser Ala Arg Leu Asp Met Phe
 180 185 190

Glu His Ile Ser Leu Met Thr Leu Asp Ser Leu Gln Lys Cys Val Phe
 195 200 205

Ser Phe Asp Ser His Cys Gln Glu Lys Pro Ser Glu Tyr Ile Ala Ala
 210 215 220

Ile Leu Glu Leu Ser Ala Leu Val Thr Lys Arg His Gln Gln Ile Leu
225 230 235 240

Sequence_Listing.txt

Leu Tyr Ile Asp Phe Leu Tyr Tyr Leu Thr Pro Asp Gly Gln Arg Phe
245 250 255

Arg Arg Ala Cys Arg Leu Val His Asp Phe Thr Asp Ala Val Ile Gln
260 265 270

Glu Arg Arg Arg Thr Leu Pro Ser Gln Gly Val Asp Asp Phe Leu Gln
275 280 285

Ala Lys Ala Lys Ser Lys Thr Leu Asp Phe Ile Asp Val Leu Leu Leu
290 295 300

Ser Lys Asp Glu Asp Gly Lys Lys Leu Ser Asp Glu Asp Ile Arg Ala
305 310 315 320

Glu Ala Asp Thr Phe Met Phe Glu Gly His Asp Thr Thr Ala Ser Gly
325 330 335

Leu Ser Trp Val Leu Tyr His Leu Ala Lys His Pro Glu Tyr Gln Glu
340 345 350

Arg Cys Arg Gln Glu Val Gln Glu Leu Leu Lys Asp Arg Glu Pro Lys
355 360 365

Glu Ile Glu Trp Asp Asp Leu Ala Gln Leu Pro Phe Leu Thr Met Cys
370 375 380

Ile Lys Glu Ser Leu Arg Leu His Pro Pro Val Pro Ala Val Ser Arg
385 390 395 400

Sequence_Listing.txt

Cys Cys Thr Gln Asp Ile Val Leu Pro Asp Gly Arg Val Ile Pro Lys
 405 410 415

Gly Ile Ile Cys Leu Ile Ser Val Phe Gly Thr His His Asn Pro Ala
 420 425 430

Val Trp Pro Asp Pro Glu Val Tyr Asp Pro Phe Arg Phe Asp Pro Lys
 435 440 445

Asn Ile Lys Glu Arg Ser Pro Leu Ala Phe Ile Pro Phe Ser Ala Gly
 450 455 460

Pro Arg Asn Cys Ile Gly Gln Ala Phe Ala Met Ala Glu Met Lys Val
 465 470 475 480

Val Leu Gly Leu Thr Leu Leu Arg Phe Arg Val Leu Pro Asp His Thr
 485 490 495

Glu Pro Arg Arg Lys Pro Glu Leu Val Leu Arg Ala Glu Gly Gly Leu
 500 505 510

Trp Leu Arg Val Glu Pro Leu Ser
 515 520

<210> 21

<211> 6914

<212> DNA

<213> Homo sapiens

<400> 21

gcggccgccg cccagccagg tgcaaaatgc cgtgtcattg ggagactccg cagccggagc 60

attagattac agctcgacgg agctcgggaa gggcggcggg ggtggaagat gaggagaagc 120

Sequence_Listing.txt

ccctgttctc ggaacgccgg ctgacaagcg ggttgagcgc agccggggcg gggaccacgc 180
ctagcccact ggagcagccg ggggtggccc gtccccctt aagagcaact gctctaagcc 240
aggagccaga gattcgagcc ggccctgccc agccagccct ctccagcgag gggaccacaca 300
agcggcgccct cggccctccc gacctttccg agccctcttt gcgccttggg cgcacggggc 360
cctacacgcg ccaagcatgc tgagggtctt catcctctat gccgagaacg tccacacacc 420
cgacaccgac atcagcgatg cctactgctc gcgggtgttt gcaggggtga agaagagaac 480
caaagtcac aagaacagcg tgaacctgt atggaatgag ggatttgaat gggacctcaa 540
gggcatcccc ctggaccagg gctctgagct tcatgtggg gtcaaagacc atgagacgat 600
ggggaggaac aggttcttg ggaagccaa ggtccactc cgagaggtcc tcgccacccc 660
tagtctgtcc gccagcttca atgccccct gctggacacc aagaagcagc ccacaggggc 720
ctcgctggtc ctgcagggt cctacacacc gctgcctgga gctgtgcccc tgttcccgcc 780
ccctactcct ctggagccct ccccgactct gcctgacctg gatgtagtgg cagacacagg 840
aggagaggaa gacacagagg accagggact cactggagat gaggcggagc cattctgga 900
tcaaagcgga ggccggggg ctcccaccac cccaaggaaa ctacctcac gtctccgcc 960
ccactacccc gggatcaaaa gaaagcgaag tgcgcctaca tctagaaagc tgctgtcaga 1020
caaaccgcag gatttcaga tcagggtcca ggtgatcgag gggcgccagc tgccgggggt 1080
gaacatcaag cctgtgtca aggttaccgc tgcagggcag accaagcgga cgcggatcca 1140
caagggaac agcccactct tcaatgagac tctttcttc aactgtttg acttctctgg 1200
ggagctgttt gatgagccca tctttatcac ggtggtagac tctgttctc tcaggacaga 1260
tgctctctc ggggagttcc ggatggacgt gggcaccatt tacagagagc cccggcacgc 1320
ctatctcagg aagtggctgc tgctctcaga cctgatgac ttctctgctg gggccagagg 1380

Sequence_Listing.txt

ctacctgaaa acaagccttt gtgtgctggg gcctggggac gaagcgctc tggagagaaa 1440
agacccctct gaagacaagg aggacattga aagcaacctg ctccggccca caggcgtagc 1500
cctgcgagga gccacttct gcctgaaggt ctccggggc gaggactgc cgcagatgga 1560
cgatgccgtg atggacaacg tgaacagat cttggcttc gagagtaaca agaagaactt 1620
ggtggacccc ttgtggagg tcagcttgc ggggaaaatg ctgtgcagca agatcttga 1680
gaagacggcc aaccctcagt ggaaccagaa catcacactg cctgccatgt ttccctccat 1740
gtgcgaaaaa atgaggattc gtatcataga ctgggaccgc ctgactcaca atgacatcgt 1800
ggctaccacc tacctgagta tgcgaaaat ctctgccct ggaggagaaa tagaagagga 1860
gcctgcaggt gctgtcaagc cttcgaaagc ctgacttg gatgactacc tgggcttct 1920
ccccactttt gggccctgct acatcaacct ctatggcagt cccagagagt tcacaggctt 1980
cccagacccc tacacagagc tcaacacagg caagggggaa ggtgtggctt atcgtggccg 2040
gcttctgctc tccttgaga ccaagctggt ggagcacagt gaacagaagg tggaggacct 2100
tctgcggat gacatcctc gggtgagaa gtaccttagg aggcgcaagt actccctgtt 2160
tgcggcctc tactcagca ccatgctgca ggatgtggat gatgcatcc agtttgaggt 2220
cagcatcggg aactacggga acaagttcga catgacctgc ctgccgtgg cctccaccac 2280
tcagtacagc cgtgcagtct ttgacgggtg ccactactac tacctaccct ggggtaacgt 2340
gaaacctgtg gtgtgtgtgt catctactg ggaggacatc agccatagaa tcgagactca 2400
gaaccagctg ctgggattg ctgaccggct ggaagctggc ctggagcagg tccacctggc 2460
cctgaaggcg cagtgtcca cggaggacgt ggactcgtg gtggctcagc tgacggatga 2520
gctcatcgca ggctgcagcc agcctctggg tgacatccat gagacaccct ctgccacca 2580
cctggaccag tacctgtacc agctgcgcac ccatcacctg agccaaatca ctgaggctgc 2640

Sequence_Listing.txt

cctggccctg aagctcggcc acagtgcgct cctgcagct ctggagcagg cggaggactg 2700

gctcctgcgt ctgcgtgcc tggcagagga gccccagaac agcctgccgg acatcgtcat 2760

ctggatgctg cagggagaca agcgtgtggc ataccagcgg gtgcccggcc accaagtctt 2820

cttctcccg cggggtgcc actactgtgg caagaattgt ggaagctac agacaatctt 2880

tctgaaatat ccgatggaga aggtgcctgg cccccgatg ccagtgcaga tacgggtcaa 2940

gctgtggttt gggctctcag tggatgagaa ggagtcaac cagtttgctg aggggaagct 3000

gtctgtctt gctgaaacct atgagaacga gactaagttg gccctgttg ggaactgggg 3060

cacaacgggc ctacctacc ccaagtttc tgacgtcacg ggcaagatca agctaccaa 3120

ggacagcttc cggccctcg cggctggac ctgggctgga gattggtcg tgtgtccga 3180

gaagactctg ctccatgaca tggacgccgg tcacctgagc ttcgtggaag aggtgttga 3240

gaaccagacc cggcttccg gaggccagt gatctacatg agtgacaact acaccgatgt 3300

gaacggggag aaggtgttc ccaaggatga cattgagtgc cactgggct ggaagtggga 3360

agatgaggaa tggccacag acctcaaccg ggctgtgat gagcaaggct gggagtatag 3420

catcaccatc cccccggagc ggaagccgaa gactgggtc cctgtgaga agatgtacta 3480

cacacaccga cggcggcgct gggtcgcct gcgcaggagg gatctcagcc aaatggaagc 3540

actgaaaagg cacaggcagg cggaggcgga gggcgagggc tgggagtacg cctctctttt 3600

tggctggaag ttccacctg agtaccgcaa gacagatgcc ttccgccgc gccgtggcg 3660

ccgtgcgatg gagccactgg agaagacggg gcctgcagct gtgttgccc ttgagggggc 3720

cctggcggc gtgatggatg acaagagtga agattccatg tccgtctcca cttgagctt 3780

cgggtgtaac agaccacga ttctctcat attcgactat gggaaccgct accatctacg 3840

ctgtacatg taccaggccc gggacctggc tgcgatggac aaggactctt ttctgatcc 3900

Sequence_Listing.txt

ctatgccatc gtctccttcc tgcaccagag ccagaagacg gtggtggtga agaaccacct 3960

taaccccacc tgggaccaga cgctcatctt ctacgagatc gagatctttg gcgagccggc 4020

cacagttgct gagcaaccgc ccagcattgt ggtggagctg tacgaccatg acacttatgg 4080

tgagacgag ttatgggtc gctgcatctg tcaaccgagt ctggaacgga tgccacggct 4140

ggcctgggtc ccactgacga ggggcagcca gccgtcgggg gagctgctgg cctcttttga 4200

gctcatccag agagagaagc cggccatcca ccatattcct ggttttgagg tgcaggagac 4260

atcaaggatc ctggtatgagt ctgaggacac agacctgccc taccaccac cccagaggga 4320

ggccaacatc tacatgggtc ctgagaacat caagccagcg ctccagcgtc ccgccatcga 4380

gatcctggca tggggcctgc ggaacatgaa gagttaccag ctggccaaca tctctcccc 4440

cagcctcgtg gtagagtgtg ggggccagac ggtgcagtcc tgtgtcatca ggaacctccg 4500

gaagaacccc aactttgaca tctgaccct ctcatggaa gtgatgctgc ccagggagga 4560

gctctactgc cccccatca ccgtcaaggt catcgataac cgccagtttg gccgccggcc 4620

tgtggtgggc cagtgtacca tccgtccct ggagagcttc ctgtgtgacc cctactcggc 4680

ggagagtcca tccccacagg gtggcccaga cgatgtgagc ctactcagtc ctggggaaga 4740

cggtctatc gacattgatg acaaggagcc cctcatcccc atccaggagg aagagttcat 4800

cgattggtgg agcaaattct ttgcctccat aggggagagg gaaaagtgcg gctcctacct 4860

ggagaaggat ttgacaccc tgaaggctta tgacacacag ctggagaatg tggaggcctt 4920

tgagggcctg tctgactttt gtaacacctt caagctgtac cggggcaaga cgcaggagga 4980

gacagaagat ccactctgtg ttggtgaatt taagggcctc ttcaaaattt atcccctccc 5040

agaagacca gccatcccca tgccccaag acagttccac cagctggccg cccagggacc 5100

ccaggagtgc ttggtccgta tctacattgt ccgagcattt ggctgcagc ccaaggaccc 5160

Sequence_Listing.txt

caatggaaag tgtgatcctt acatcaagat ctccataggg aagaaatcag tgagtgacca 5220

ggataactac atcccctgca cgtcggagcc cgtatttga aagatgttcg agctgacctg 5280

cactctgcct ctggagaagg acctaaagat cactctctat gactatgacc tcctctccaa 5340

ggacgaaaag atcggtgaga cggtcgtcga cctggagaac aggctgctgt ccaagtttgg 5400

ggctcgtgt ggactccac agacctactg tgtctctgga ccgaaccagt ggcgggacca 5460

gctccgcccc tccagctcc tcacctctt ctgccagcag catagagtca aggcacctgt 5520

gtaccggaca gaccgtgtaa tgtttcagga taaagaatat tcattgaag agatagaggc 5580

tggcaggatc ccaaaccac acctggggcc agtggaggag cgtctggctc tgcattgtct 5640

tcagcagcag ggccctgtcc cggagcacgt ggagtcacgg cccctctaca gccccctgca 5700

gccagacatc gagcagggga agctgcagat gtgggtcgac ctatttccga aggccctggg 5760

gcggcctgga cctccctca acatcacccc acggagagcc agaaggtttt tctgcgttg 5820

tattatctgg aataccagag atgtgatcct ggatgacctg agcctcacgg gggagaagat 5880

gagcgacatt tatgtgaaag gttggatgat tggctttgaa gaacacaagc aaaagacaga 5940

cgtgcattat cgttccctgg gaggtgaagg caactcaac tggaggttca ttttccctt 6000

cgactacctg ccagctgagc aagctgtac cattgccaag aaggatgcct tctggaggct 6060

ggacaagact gagagcaaaa tccagcacg agtgggttgc cagatctggg acaatgacaa 6120

gttctccttt gatgattttc tgggtccct gcagctcgat ctcaaccgca tgccaagcc 6180

agccaagaca gccaagaagt gctccttgga ccagctggat gatgctttcc acccagaatg 6240

gtttgtgtcc cttttgagc agaaaacagt gaagggctgg tggccctgtg tagcagaaga 6300

gggtgagaag aaaatactgg cgggcaagct ggaaatgacc ttggagattg tagcagagag 6360

tgagcatgag gagcggcctg ctggccaggg ccgggatgag cccaacatga accctaagct 6420

Sequence_Listing.txt

tgaggacca aggcgccccg acacctcctt cctgtggtt acctcccat acaagaccat 6480
 gaagttcatc ctgtggcggc gttccggtg ggccatcatc ctctcatca tcctcttcat 6540
 cctgctgctg ttctggcca tcttcatcta cgccttccc aactatgctg ccatgaagct 6600
 ggtaagccc ttcagctgag gactctctg ccctgtagaa ggggccgtgg ggtcccctcc 6660
 agcatgggac tggcctgcct cctccgcca gctcggcgag ctctccaga cctcctaggc 6720
 ctgattgtcc tgccaggggtg ggcagacaga cagatggacc ggcccacact cccagagttg 6780
 ctaacatgga gctctgagat caccacctt ccatcattt ctctcccc aaccaacgc 6840
 tttttgat cagctcagac atatttcagt ataaaacagt tggaaccaca aaaaaaaaaa 6900
 aaaaaaaaaa aaaa 6914

<210> 22
 <211> 2080
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Leu Arg Val Phe Ile Leu Tyr Ala Glu Asn Val His Thr Pro Asp
 1 5 10 15

Thr Asp Ile Ser Asp Ala Tyr Cys Ser Ala Val Phe Ala Gly Val Lys
 20 25 30

Lys Arg Thr Lys Val Ile Lys Asn Ser Val Asn Pro Val Trp Asn Glu
 35 40 45

Gly Phe Glu Trp Asp Leu Lys Gly Ile Pro Leu Asp Gln Gly Ser Glu
 50 55 60

Leu His Val Val Val Lys Asp His Glu Thr Met Gly Arg Asn Arg Phe

Sequence_Listing.txt

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

Sequence_Listing.txt

Val Lys Val Thr Ala Ala Gly Gln Thr Lys Arg Thr Arg Ile His Lys
245 250 255

Gly Asn Ser Pro Leu Phe Asn Glu Thr Leu Phe Phe Asn Leu Phe Asp
260 265 270

Ser Pro Gly Glu Leu Phe Asp Glu Pro Ile Phe Ile Thr Val Val Asp
275 280 285

Ser Arg Ser Leu Arg Thr Asp Ala Leu Leu Gly Glu Phe Arg Met Asp
290 295 300

Val Gly Thr Ile Tyr Arg Glu Pro Arg His Ala Tyr Leu Arg Lys Trp
305 310 315 320

Leu Leu Leu Ser Asp Pro Asp Asp Phe Ser Ala Gly Ala Arg Gly Tyr
325 330 335

Leu Lys Thr Ser Leu Cys Val Leu Gly Pro Gly Asp Glu Ala Pro Leu
340 345 350

Glu Arg Lys Asp Pro Ser Glu Asp Lys Glu Asp Ile Glu Ser Asn Leu
355 360 365

Leu Arg Pro Thr Gly Val Ala Leu Arg Gly Ala His Phe Cys Leu Lys
370 375 380

Val Phe Arg Ala Glu Asp Leu Pro Gln Met Asp Asp Ala Val Met Asp
385 390 395 400

Asn Val Lys Gln Ile Phe Gly Phe Glu Ser Asn Lys Lys Asn Leu Val

Sequence_Listing.txt

405	410	415
Asp Pro Phe Val Glu Val Ser Phe Ala Gly Lys Met Leu Cys Ser Lys		
420	425	430
Ile Leu Glu Lys Thr Ala Asn Pro Gln Trp Asn Gln Asn Ile Thr Leu		
435	440	445
Pro Ala Met Phe Pro Ser Met Cys Glu Lys Met Arg Ile Arg Ile Ile		
450	455	460
Asp Trp Asp Arg Leu Thr His Asn Asp Ile Val Ala Thr Thr Tyr Leu		
465	470	475 480
Ser Met Ser Lys Ile Ser Ala Pro Gly Gly Glu Ile Glu Glu Glu Pro		
485	490	495
Ala Gly Ala Val Lys Pro Ser Lys Ala Ser Asp Leu Asp Asp Tyr Leu		
500	505	510
Gly Phe Leu Pro Thr Phe Gly Pro Cys Tyr Ile Asn Leu Tyr Gly Ser		
515	520	525
Pro Arg Glu Phe Thr Gly Phe Pro Asp Pro Tyr Thr Glu Leu Asn Thr		
530	535	540
Gly Lys Gly Glu Gly Val Ala Tyr Arg Gly Arg Leu Leu Leu Ser Leu		
545	550	555 560
Glu Thr Lys Leu Val Glu His Ser Glu Gln Lys Val Glu Asp Leu Pro		
565	570	575

Sequence_Listing.txt

Ala Asp Asp Ile Leu Arg Val Glu Lys Tyr Leu Arg Arg Arg Lys Tyr
580 585 590

Ser Leu Phe Ala Ala Phe Tyr Ser Ala Thr Met Leu Gln Asp Val Asp
595 600 605

Asp Ala Ile Gln Phe Glu Val Ser Ile Gly Asn Tyr Gly Asn Lys Phe
610 615 620

Asp Met Thr Cys Leu Pro Leu Ala Ser Thr Thr Gln Tyr Ser Arg Ala
625 630 635 640

Val Phe Asp Gly Cys His Tyr Tyr Tyr Leu Pro Trp Gly Asn Val Lys
645 650 655

Pro Val Val Val Leu Ser Ser Tyr Trp Glu Asp Ile Ser His Arg Ile
660 665 670

Glu Thr Gln Asn Gln Leu Leu Gly Ile Ala Asp Arg Leu Glu Ala Gly
675 680 685

Leu Glu Gln Val His Leu Ala Leu Lys Ala Gln Cys Ser Thr Glu Asp
690 695 700

Val Asp Ser Leu Val Ala Gln Leu Thr Asp Glu Leu Ile Ala Gly Cys
705 710 715 720

Ser Gln Pro Leu Gly Asp Ile His Glu Thr Pro Ser Ala Thr His Leu
725 730 735

Asp Gln Tyr Leu Tyr Gln Leu Arg Thr His His Leu Ser Gln Ile Thr

Sequence_Listing.txt

740 745 750

Glu Ala Ala Leu Ala Leu Lys Leu Gly His Ser Glu Leu Pro Ala Ala
755 760 765

Leu Glu Gln Ala Glu Asp Trp Leu Leu Arg Leu Arg Ala Leu Ala Glu
770 775 780

Glu Pro Gln Asn Ser Leu Pro Asp Ile Val Ile Trp Met Leu Gln Gly
785 790 795 800

Asp Lys Arg Val Ala Tyr Gln Arg Val Pro Ala His Gln Val Leu Phe
805 810 815

Ser Arg Arg Gly Ala Asn Tyr Cys Gly Lys Asn Cys Gly Lys Leu Gln
820 825 830

Thr Ile Phe Leu Lys Tyr Pro Met Glu Lys Val Pro Gly Ala Arg Met
835 840 845

Pro Val Gln Ile Arg Val Lys Leu Trp Phe Gly Leu Ser Val Asp Glu
850 855 860

Lys Glu Phe Asn Gln Phe Ala Glu Gly Lys Leu Ser Val Phe Ala Glu
865 870 875 880

Thr Tyr Glu Asn Glu Thr Lys Leu Ala Leu Val Gly Asn Trp Gly Thr
885 890 895

Thr Gly Leu Thr Tyr Pro Lys Phe Ser Asp Val Thr Gly Lys Ile Lys
900 905 910

Sequence_Listing.txt

Leu Pro Lys Asp Ser Phe Arg Pro Ser Ala Gly Trp Thr Trp Ala Gly
915 920 925

Asp Trp Phe Val Cys Pro Glu Lys Thr Leu Leu His Asp Met Asp Ala
930 935 940

Gly His Leu Ser Phe Val Glu Glu Val Phe Glu Asn Gln Thr Arg Leu
945 950 955 960

Pro Gly Gly Gln Trp Ile Tyr Met Ser Asp Asn Tyr Thr Asp Val Asn
965 970 975

Gly Glu Lys Val Leu Pro Lys Asp Asp Ile Glu Cys Pro Leu Gly Trp
980 985 990

Lys Trp Glu Asp Glu Glu Trp Ser Thr Asp Leu Asn Arg Ala Val Asp
995 1000 1005

Glu Gln Gly Trp Glu Tyr Ser Ile Thr Ile Pro Pro Glu Arg Lys
1010 1015 1020

Pro Lys His Trp Val Pro Ala Glu Lys Met Tyr Tyr Thr His Arg
1025 1030 1035

Arg Arg Arg Trp Val Arg Leu Arg Arg Arg Asp Leu Ser Gln Met
1040 1045 1050

Glu Ala Leu Lys Arg His Arg Gln Ala Glu Ala Glu Gly Glu Gly
1055 1060 1065

Trp Glu Tyr Ala Ser Leu Phe Gly Trp Lys Phe His Leu Glu Tyr

Sequence_Listing.txt

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

Sequence_Listing.txt

Tyr Gly Ala Asp Glu Phe Met Gly Arg Cys Ile Cys Gln Pro Ser
1235 1240 1245

Leu Glu Arg Met Pro Arg Leu Ala Trp Phe Pro Leu Thr Arg Gly
1250 1255 1260

Ser Gln Pro Ser Gly Glu Leu Leu Ala Ser Phe Glu Leu Ile Gln
1265 1270 1275

Arg Glu Lys Pro Ala Ile His His Ile Pro Gly Phe Glu Val Gln
1280 1285 1290

Glu Thr Ser Arg Ile Leu Asp Glu Ser Glu Asp Thr Asp Leu Pro
1295 1300 1305

Tyr Pro Pro Pro Gln Arg Glu Ala Asn Ile Tyr Met Val Pro Gln
1310 1315 1320

Asn Ile Lys Pro Ala Leu Gln Arg Thr Ala Ile Glu Ile Leu Ala
1325 1330 1335

Trp Gly Leu Arg Asn Met Lys Ser Tyr Gln Leu Ala Asn Ile Ser
1340 1345 1350

Ser Pro Ser Leu Val Val Glu Cys Gly Gly Gln Thr Val Gln Ser
1355 1360 1365

Cys Val Ile Arg Asn Leu Arg Lys Asn Pro Asn Phe Asp Ile Cys
1370 1375 1380

Thr Leu Phe Met Glu Val Met Leu Pro Arg Glu Glu Leu Tyr Cys

Sequence_Listing.txt

1385	1390	1395
Pro Pro Ile Thr Val Lys Val Ile Asp Asn Arg Gln Phe Gly Arg		
1400	1405	1410
Arg Pro Val Val Gly Gln Cys Thr Ile Arg Ser Leu Glu Ser Phe		
1415	1420	1425
Leu Cys Asp Pro Tyr Ser Ala Glu Ser Pro Ser Pro Gln Gly Gly		
1430	1435	1440
Pro Asp Asp Val Ser Leu Leu Ser Pro Gly Glu Asp Val Leu Ile		
1445	1450	1455
Asp Ile Asp Asp Lys Glu Pro Leu Ile Pro Ile Gln Glu Glu Glu		
1460	1465	1470
Phe Ile Asp Trp Trp Ser Lys Phe Phe Ala Ser Ile Gly Glu Arg		
1475	1480	1485
Glu Lys Cys Gly Ser Tyr Leu Glu Lys Asp Phe Asp Thr Leu Lys		
1490	1495	1500
Val Tyr Asp Thr Gln Leu Glu Asn Val Glu Ala Phe Glu Gly Leu		
1505	1510	1515
Ser Asp Phe Cys Asn Thr Phe Lys Leu Tyr Arg Gly Lys Thr Gln		
1520	1525	1530
Glu Glu Thr Glu Asp Pro Ser Val Ile Gly Glu Phe Lys Gly Leu		
1535	1540	1545

Sequence_Listing.txt

Phe Lys Ile Tyr Pro Leu Pro Glu Asp Pro Ala Ile Pro Met Pro
1550 1555 1560

Pro Arg Gln Phe His Gln Leu Ala Ala Gln Gly Pro Gln Glu Cys
1565 1570 1575

Leu Val Arg Ile Tyr Ile Val Arg Ala Phe Gly Leu Gln Pro Lys
1580 1585 1590

Asp Pro Asn Gly Lys Cys Asp Pro Tyr Ile Lys Ile Ser Ile Gly
1595 1600 1605

Lys Lys Ser Val Ser Asp Gln Asp Asn Tyr Ile Pro Cys Thr Leu
1610 1615 1620

Glu Pro Val Phe Gly Lys Met Phe Glu Leu Thr Cys Thr Leu Pro
1625 1630 1635

Leu Glu Lys Asp Leu Lys Ile Thr Leu Tyr Asp Tyr Asp Leu Leu
1640 1645 1650

Ser Lys Asp Glu Lys Ile Gly Glu Thr Val Val Asp Leu Glu Asn
1655 1660 1665

Arg Leu Leu Ser Lys Phe Gly Ala Arg Cys Gly Leu Pro Gln Thr
1670 1675 1680

Tyr Cys Val Ser Gly Pro Asn Gln Trp Arg Asp Gln Leu Arg Pro
1685 1690 1695

Ser Gln Leu Leu His Leu Phe Cys Gln Gln His Arg Val Lys Ala

Sequence_Listing.txt

1700	1705	1710
Pro Val Tyr Arg Thr Asp Arg	Val Met Phe Gln Asp	Lys Glu Tyr
1715	1720	1725
Ser Ile Glu Glu Ile Glu Ala	Gly Arg Ile Pro Asn	Pro His Leu
1730	1735	1740
Gly Pro Val Glu Glu Arg Leu	Ala Leu His Val Leu	Gln Gln Gln
1745	1750	1755
Gly Leu Val Pro Glu His Val	Glu Ser Arg Pro Leu	Tyr Ser Pro
1760	1765	1770
Leu Gln Pro Asp Ile Glu Gln	Gly Lys Leu Gln Met	Trp Val Asp
1775	1780	1785
Leu Phe Pro Lys Ala Leu Gly	Arg Pro Gly Pro Pro	Phe Asn Ile
1790	1795	1800
Thr Pro Arg Arg Ala Arg Arg	Phe Phe Leu Arg Cys	Ile Ile Trp
1805	1810	1815
Asn Thr Arg Asp Val Ile Leu	Asp Asp Leu Ser Leu	Thr Gly Glu
1820	1825	1830
Lys Met Ser Asp Ile Tyr Val	Lys Gly Trp Met Ile	Gly Phe Glu
1835	1840	1845
Glu His Lys Gln Lys Thr Asp	Val His Tyr Arg Ser	Leu Gly Gly
1850	1855	1860

Sequence_Listing.txt

Glu Gly Asn Phe Asn Trp Arg Phe Ile Phe Pro Phe Asp Tyr Leu
1865 1870 1875

Pro Ala Glu Gln Val Cys Thr Ile Ala Lys Lys Asp Ala Phe Trp
1880 1885 1890

Arg Leu Asp Lys Thr Glu Ser Lys Ile Pro Ala Arg Val Val Phe
1895 1900 1905

Gln Ile Trp Asp Asn Asp Lys Phe Ser Phe Asp Asp Phe Leu Gly
1910 1915 1920

Ser Leu Gln Leu Asp Leu Asn Arg Met Pro Lys Pro Ala Lys Thr
1925 1930 1935

Ala Lys Lys Cys Ser Leu Asp Gln Leu Asp Asp Ala Phe His Pro
1940 1945 1950

Glu Trp Phe Val Ser Leu Phe Glu Gln Lys Thr Val Lys Gly Trp
1955 1960 1965

Trp Pro Cys Val Ala Glu Glu Gly Glu Lys Lys Ile Leu Ala Gly
1970 1975 1980

Lys Leu Glu Met Thr Leu Glu Ile Val Ala Glu Ser Glu His Glu
1985 1990 1995

Glu Arg Pro Ala Gly Gln Gly Arg Asp Glu Pro Asn Met Asn Pro
2000 2005 2010

Lys Leu Glu Asp Pro Arg Arg Pro Asp Thr Ser Phe Leu Trp Phe

Sequence_Listing.txt

2015	2020	2025	
Thr Ser Pro Tyr Lys Thr Met Lys Phe Ile Leu Trp Arg Arg Phe			
2030	2035	2040	
Arg Trp Ala Ile Ile Leu Phe Ile Ile Leu Phe Ile Leu Leu Leu			
2045	2050	2055	
Phe Leu Ala Ile Phe Ile Tyr Ala Phe Pro Asn Tyr Ala Ala Met			
2060	2065	2070	
Lys Leu Val Lys Pro Phe Ser			
2075	2080		

<210> 23
 <211> 2974
 <212> DNA
 <213> Homo sapiens

<400> 23

agaagccccg cagccgccgc gcggagaaca gcgacagccg agcgcccggg ccgcctgtct	60
gccggtgggt ctgcctgcc gcgcagcaga cccggggcgg ccgcgggagc ccgcgccccg	120
cccgcgcgc cctgcggg acccaccgc agcggagggc tgagcccgcc ggcggctccc	180
cggagctcac ccacctccgc gcgccggagc gcaggcaaaa ggggaggaaa ggctcctctc	240
tttagtcacc actctgccc tctcaagaa ttgtttaac aaagcgctga ggaaagagaa	300
cgtctcttg aattcttag taggggcgga gtcgtgtgt gccctgcgt gccacctcg	360
ctacactgcc ctccgcgacg acccctgacc agccggggtc acgtccggga gacgggatca	420
tgaagcgctc ggtagccgtc tggctcttg tcgggctcag cctcggtgt cccagttcg	480
gcaaagggtga tatttgtat cccaatccat gtgaaaatgg aggtatctgt ttgccaggat	540

Sequence_Listing.txt

tggctgatgg ttcttttcc tgtgagtg cagatggctt cacagacccc aactgttcta 600
 gtgttggtga ggttgcatca gatgaagaag aaccaacttc agcagggtccc tgcactccta 660
 atccatgccca taatggagga acctgtgaaa taagtgaagc ataccgaggg gatacattca 720
 taggctatgt ttgtaaatgt ccccgaggat ttaatgggat tcaactgtcag cacaacataa 780
 atgaatgcga agttgagcct tgcaaaaatg gtggaatatg tacagatctt gttgctaact 840
 attcctgtga gtgcccaggc gaatttatgg gaagaaattg tcaatacaaa tgctcaggcc 900
 cactgggaat tgaaggtgga attatatcaa accagcaaat cacagcttcc tctactcacc 960
 gagctctttt tggactccaa aaatggtatc cctactatgc acgtcttaat aagaaggggc 1020
 ttataaatgc gtggacagct gcagaaaatg acagatggcc gtggattcag ataaatttgc 1080
 aaaggaaaat gagagttact ggtgtgatta cccaaggagc caagaggatt ggaagcccag 1140
 agtatataaa atcctacaaa attgcctaca gtaatgatgg aaagacttgg gcaatgtaca 1200
 aagtgaaggg caccaatgaa gacatggtgt ttcgtggaaa cattgataac aacactccat 1260
 atgctaactc ttacacccc ccataaaaag ctcatgatgt aagactctat cccaagttt 1320
 gtcgaagaca ttgcactttg cgaatggaac ttcttggtcg tgaactgtcg ggttgtctcg 1380
 agcctctggg tatgaaatca ggacatatac aagactatca gatcactgcc tccagcatct 1440
 tcagaacgct caacatggac atgttcaact gggaaccaag gaaagctcgg ctggacaagc 1500
 aaggcaaagt gaatgcctgg acctctggcc acaatgacca gtcacaatgg ttacagggtg 1560
 atctcttgtt tccaaccaa gtgactggca tcattacaca aggagctaaa gattttggtc 1620
 atgtacagtt tgttggtcc tacaaactgg ctacagcaa tgatggagaa cactggactg 1680
 tataccagga tgaaaagcaa agaaaagata aggttttcca gggaaatttt gacaatgaca 1740
 ctacagaaa aaatgtatc gacctccca tctatgcag acacataaga atccttcctt 1800

Sequence_Listing.txt

ggtcctggta cgggaggatc acattgcggt cagagctgct gggctgcaca gaggaggaat 1860
 gaggggaggc tacattcac aacctcttc cctattccc taaaagtatc tccatggaat 1920
 gaactgtgca aaatctgtag gaaactgaat ggTTTTTT tttttcat gaaaaagtgc 1980
 tcaaattatg gtaggcaact aacgggtgtt ttaaggggt ctaagcctgc ctttcaatg 2040
 attaatttg attttattt atccgtcaaa tctcttaagt aacaacacat taagtgtgaa 2100
 ttactttct ctcatgttt cctgaattat tcgcatgggt agaaatata tagggaaaga 2160
 aagtagcctt cttttatag caagagtaaa aaagtccaa agtcatcaaa taagagcaag 2220
 agtgataga gctttacaa tcaatactca cctaattctg ataaaaggaa tactgcaatg 2280
 ttagcaataa gtttttct tctgtaatga ctctacgtta tcctgttcc ctgtgcctac 2340
 caaacactgt caatgttat tacaaaattt taaagaagaa tatgtaacat gcagtactga 2400
 tattataatt ctcatttac ttcatattt tctaataaga gattatgtga cttcttttc 2460
 ttttagttt attctacatt ctaaatattg tatattacct gaataattca attttttct 2520
 aattgaattt cctattagtt gactaaaaga agtgtcatgt ttactcatat atgtagaaca 2580
 tgactgccta tcagtagatt gatctgtatt taatatctgt taattaaatc tgcagtttta 2640
 ttttgaagg aagccataac tatttaattt ccaaataatt gcttcataaa gaatcccata 2700
 ctctcagttt gcacaaaaga acaaaaaata tatatgtctc tttaaattta aatcttcatt 2760
 tagatggtaa ttacatatcc ttatatctac tttaaaaaat cggcttattt gtttatttta 2820
 taaaaaattt agcaaagaaa tattaatata gtgctgcata gtttgccaa gcatactcat 2880
 cattctttg ttcagctcca catttctgt gaaactaaca tcttattgag atttgaaact 2940
 ggtggtagtt tcccaggaag gcacagggtg agtt 2974

Sequence_Listing.txt

<210> 24

<211> 480

<212> PRT

<213> Homo sapiens

<400> 24

Met Lys Arg Ser Val Ala Val Trp Leu Leu Val Gly Leu Ser Leu Gly

1 5 10 15

Val Pro Gln Phe Gly Lys Gly Asp Ile Cys Asp Pro Asn Pro Cys Glu

20 25 30

Asn Gly Gly Ile Cys Leu Pro Gly Leu Ala Asp Gly Ser Phe Ser Cys

35 40 45

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

50 55 60

Val Ala Ser Asp Glu Glu Glu Pro Thr Ser Ala Gly Pro Cys Thr Pro

65 70 75 80

Asn Pro Cys His Asn Gly Gly Thr Cys Glu Ile Ser Glu Ala Tyr Arg

85 90 95

Gly Asp Thr Phe Ile Gly Tyr Val Cys Lys Cys Pro Arg Gly Phe Asn

100 105 110

Gly Ile His Cys Gln His Asn Ile Asn Glu Cys Glu Val Glu Pro Cys

115 120 125

Lys Asn Gly Gly Ile Cys Thr Asp Leu Val Ala Asn Tyr Ser Cys Glu

130 135 140

Sequence_Listing.txt

Cys Pro Gly Glu Phe Met Gly Arg Asn Cys Gln Tyr Lys Cys Ser Gly
145 150 155 160

Pro Leu Gly Ile Glu Gly Gly Ile Ile Ser Asn Gln Gln Ile Thr Ala
 165 170 175

Ser Ser Thr His Arg Ala Leu Phe Gly Leu Gln Lys Trp Tyr Pro Tyr
 180 185 190

Tyr Ala Arg Leu Asn Lys Lys Gly Leu Ile Asn Ala Trp Thr Ala Ala
 195 200 205

Glu Asn Asp Arg Trp Pro Trp Ile Gln Ile Asn Leu Gln Arg Lys Met
 210 215 220

Arg Val Thr Gly Val Ile Thr Gln Gly Ala Lys Arg Ile Gly Ser Pro
225 230 235 240

Glu Tyr Ile Lys Ser Tyr Lys Ile Ala Tyr Ser Asn Asp Gly Lys Thr
 245 250 255

Trp Ala Met Tyr Lys Val Lys Gly Thr Asn Glu Asp Met Val Phe Arg
 260 265 270

Gly Asn Ile Asp Asn Asn Thr Pro Tyr Ala Asn Ser Phe Thr Pro Pro
 275 280 285

Ile Lys Ala Gln Tyr Val Arg Leu Tyr Pro Gln Val Cys Arg Arg His
 290 295 300

Cys Thr Leu Arg Met Glu Leu Leu Gly Cys Glu Leu Ser Gly Cys Ser
305 310 315 320

Sequence_Listing.txt

Glu Pro Leu Gly Met Lys Ser Gly His Ile Gln Asp Tyr Gln Ile Thr
325 330 335

Ala Ser Ser Ile Phe Arg Thr Leu Asn Met Asp Met Phe Thr Trp Glu
340 345 350

Pro Arg Lys Ala Arg Leu Asp Lys Gln Gly Lys Val Asn Ala Trp Thr
355 360 365

Ser Gly His Asn Asp Gln Ser Gln Trp Leu Gln Val Asp Leu Leu Val
370 375 380

Pro Thr Lys Val Thr Gly Ile Ile Thr Gln Gly Ala Lys Asp Phe Gly
385 390 395 400

His Val Gln Phe Val Gly Ser Tyr Lys Leu Ala Tyr Ser Asn Asp Gly
405 410 415

Glu His Trp Thr Val Tyr Gln Asp Glu Lys Gln Arg Lys Asp Lys Val
420 425 430

Phe Gln Gly Asn Phe Asp Asn Asp Thr His Arg Lys Asn Val Ile Asp
435 440 445

Pro Pro Ile Tyr Ala Arg His Ile Arg Ile Leu Pro Trp Ser Trp Tyr
450 455 460

Gly Arg Ile Thr Leu Arg Ser Glu Leu Leu Gly Cys Thr Glu Glu Glu
465 470 475 480

Sequence_Listing.txt

<210> 25

<211> 1368

<212> DNA

<213> Homo sapiens

<400> 25

```
gtggctccag gccggaagag ggagctctga ggggcgggcc ggctggcgtc ccctttccgg    60
ccggtcccca tggaggcgct ggggaagctg aagcagttcg atgcctaccc caagactttg    120
gaggacttcc gggtaagac ctgcgggggc gccaccgtga ccattgtcag tggccttctc    180
atgctgttac tgttcctgtc cgagctgcag tattacctca ccacggaggt gcatcctgag    240
ctctacgtgg acaagtcgcg gggagataaa ctgaagatca acatcgatgt actttttccg    300
cacatgcctt gtgcctatct gagtattgat gccatggatg tggccggaga acagcagctg    360
gatgtggaac acaacctgtt caagcaacga ctagataaag atggcatccc cgtgagctca    420
gaggctgagc ggcatgagct tgggaaagtc gaggtgacgg tgtttgacct tgactccctg    480
gacctgatc gctgtgagag ctgctatggt gctgaggcag aagatatcaa gtgctgtaac    540
acctgtgaag atgtgcggga ggcatatcgc cgtagaggct gggccttcaa gaaccagat    600
actattgagc agtgccggcg agagggttc agccagaaga tgcaggagca gaagaatgaa    660
ggctgccagg tgtatggctt ctggaagtc aataaggtag ccggaactt ccactttgcc    720
cctgggaaga gcttcagca gtcccatgtg cacgtccatg actgcagag ctttgcctt    780
gacaacatca acatgacca ctacatccag cacctgtcat ttggggagga ctatccaggc    840
attgtgaacc ccctggacca caccaatgtc actgcgcccc aagcctccat gatgttcag    900
tactttgtga aggtggtgcc cactgtgtac atgaaggtag acggagaggt actgaggaca    960
aatcagttct ctgtgaccag acatgagaag gttgccaatg ggctgttggg cgaccaaggc   1020
cttcccgag tcttcgtct ctatgagctc tcgcccatga tggtaagct gacggagaag   1080
```

Sequence_Listing.txt

cacaggtcct tcaccactt cctgacaggt gtgtgcgcca tcattggggg catgttcaca 1140

gtggctggac tcatcgattc gctcatctac cactcagcac gagccatcca gaagaaaatt 1200

gatctagggg agacaacgta gtcaccctcg gtgcttcttc tgtctctctt ttctccctgg 1260

cctgtggttg tccccagcc tctgccaccc tccacctctt cggtcagccc cagccccagg 1320

ttgataaatc tattgattga ttgtgatagt aaaaaaaaaa aaaaaaaaaa 1368

<210> 26

<211> 383

<212> PRT

<213> Homo sapiens

<400> 26

Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp Ala Tyr Pro Lys Thr

1 5 10 15

Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly Ala Thr Val Thr Ile

20 25 30

Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu Ser Glu Leu Gln Tyr

35 40 45

Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr Val Asp Lys Ser Arg

50 55 60

Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu Phe Pro His Met Pro

65 70 75 80

Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val Ala Gly Glu Gln Gln

85 90 95

Leu Asp Val Glu His Asn Leu Phe Lys Gln Arg Leu Asp Lys Asp Gly

Sequence_Listing.txt

100 105 110

Ile Pro Val Ser Ser Glu Ala Glu Arg His Glu Leu Gly Lys Val Glu
115 120 125

Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro Asp Arg Cys Glu Ser
130 135 140

Cys Tyr Gly Ala Glu Ala Glu Asp Ile Lys Cys Cys Asn Thr Cys Glu
145 150 155 160

Asp Val Arg Glu Ala Tyr Arg Arg Arg Gly Trp Ala Phe Lys Asn Pro
165 170 175

Asp Thr Ile Glu Gln Cys Arg Arg Glu Gly Phe Ser Gln Lys Met Gln
180 185 190

Glu Gln Lys Asn Glu Gly Cys Gln Val Tyr Gly Phe Leu Glu Val Asn
195 200 205

Lys Val Ala Gly Asn Phe His Phe Ala Pro Gly Lys Ser Phe Gln Gln
210 215 220

Ser His Val His Val His Asp Leu Gln Ser Phe Gly Leu Asp Asn Ile
225 230 235 240

Asn Met Thr His Tyr Ile Gln His Leu Ser Phe Gly Glu Asp Tyr Pro
245 250 255

Gly Ile Val Asn Pro Leu Asp His Thr Asn Val Thr Ala Pro Gln Ala
260 265 270

Sequence_Listing.txt

Ser Met Met Phe Gln Tyr Phe Val Lys Val Val Pro Thr Val Tyr Met
275 280 285

Lys Val Asp Gly Glu Val Leu Arg Thr Asn Gln Phe Ser Val Thr Arg
290 295 300

His Glu Lys Val Ala Asn Gly Leu Leu Gly Asp Gln Gly Leu Pro Gly
305 310 315 320

Val Phe Val Leu Tyr Glu Leu Ser Pro Met Met Val Lys Leu Thr Glu
325 330 335

Lys His Arg Ser Phe Thr His Phe Leu Thr Gly Val Cys Ala Ile Ile
340 345 350

Gly Gly Met Phe Thr Val Ala Gly Leu Ile Asp Ser Leu Ile Tyr His
355 360 365

Ser Ala Arg Ala Ile Gln Lys Lys Ile Asp Leu Gly Lys Thr Thr
370 375 380

<210> 27
<211> 2483
<212> DNA
<213> Homo sapiens

<400> 27
agttgattgc aggtcctcct ggggccagaa gggcgctcgg gaggccaggt tctggggatc 60
ccctccatcc agaagaacca cctgctcact ctgtcccttc gcctgctgct gggaccatgg 120
gggctggggc cagtgtgag gagaagcact ccaggagct ggaaaagaag ctgaaagagg 180
acgctgagaa ggatgctga accgtgaagc tgcgtcttct gggcgccggg gagtccggga 240

Sequence_Listing.txt

agagcaccat cgtaagcag atgaagatta tccaccagga cgggtactcg ctggaagagt 300
 gcctcgagtt tatgccatc atctacggca acacgttgca gtccatcctg gccatcgtac 360
 gcgccatgac cacactcaac atccagtacg gagactctgc acgccaggac gacgcccgga 420
 agctgatgca catggcagac actatcgagg agggcacgat gccaaggag atgtcggaca 480
 tcatccagcg gctgtggaag gactccggta tccaggcctg tttgagcgc gcctcggagt 540
 accagctcaa cgactcggcg ggctactacc tctccgacct ggagcgctg gtaaccccgg 600
 gctacgtgcc caccgagcag gacgtgctgc gctcgcgagt caagaccact ggcatcatcg 660
 agacgcagtt ctcttcaag gatctcaact tccgatgtt cgatgtgggc gggcagcgct 720
 cggagcgcaa gaagtggatc cactgcttcg agggcgtgac ctgcatcatc ttcacgcgg 780
 cgtgagcgc ctacgacatg gtgctagtgg aggacgacga agtgaaccgc atgcacgaga 840
 gcctgcacct gttcaacagc atctgaacc accgctactt cgccacgacg tccatcgtgc 900
 tcttccttaa caagaaggac gtcttctcg agaagatcaa gaaggcgac ctacgcatct 960
 gtttcccgga ctacgatgga cccaacacct acgaggacgc cggcaactac atcaagggtc 1020
 agttcctga gctcaacatg cggcgcgacg tgaaggagat ctattccac atgacgtgcg 1080
 ccaccgacac gcagaacgtc aaatttgtct tcgacgctgt caccgacatc atcatcaagg 1140
 agaacctcaa agactgtggc ctcttctgag gccagggcct gtgctgcagt cggggacaag 1200
 gagctccgt ctggcaaggc cggggcaca tttgcactcc cctcagctag acgcacagac 1260
 tcagcaataa accttgcac caggctccag ctgtccttc ttggtggagg acttaattat 1320
 cacaagtcac gggcatttat taagtccca gtgctgggtt gggcatgaag tgggaagatg 1380
 gccctccca ggaagaagta cctggcctga caaggtgggg cactcttggg ggtatgggac 1440
 caactcatgg cttttcacgg gagttagga gagaggagct gtggaaaata ttactggga 1500

Sequence_Listing.txt

```

cagtcttga tcaagaggga gtttgaggt ggaggctcat tctggcaggg accgtagtgt 1560
ctaccagccc cagaaacatg ggcttatggc cacaggagtt cagtgaggca agagcagggg 1620
aggagagacg tggacagggtg cccaaagcca gtcggagggc ctgggctttc tcagaagggtg 1680
atggagagtc ttggaagccc tcgaggcagg aacataattg cagggctggg attaggggtga 1740
gggaagtgag gcacactcac ctgggtgca acatttaagg cgatgccaaa aaatttagta 1800
accaaggtaa ataatttag gataatattt ttaaaaatca aatgaatgca aaaccccaca 1860
atgaatgaaa tatcaaaatc caacagagga tcaaacagag gcatgctaag atatattggg 1920
gcttgaagca aagggaaaac tatttgttc tatatgttg tagggatttt ttgccagttt 1980
taaaaataca tgatcataa agtttactat ctacgccact tgccggtgta tagtttggtg 2040
gtgttaagta cattcataat gttgtacaac caccgcaact gttcatctcc agaactcctt 2100
tctcttgta aaactgtaac tctgtacca tgaaaaaata accccccatt cctgccttcc 2160
cccggtcctt ggcatccacc atttacttt ccatctctat gaatgtgact gctctaagtg 2220
cctcagatgt gtgggtccat gaagtcttg tcttttgca actggcttat ttacttagc 2280
atcatgtctt caaggtttat tcatgtgtag catatggcag aatctccttc cttttaagg 2340
ttgaataata ttccattgta tatattccac acttgttta ttattcatc tattgatgaa 2400
tggttacatc tgccttttg ctattgtgaa taatgctgct atgaacatgg ggtgtacaaat 2460
ctctcaaaaa aaaaaaaaaa aaa 2483

```

<210> 28

<211> 350

<212> PRT

<213> Homo sapiens

<400> 28

Sequence_Listing.txt

Met Gly Ala Gly Ala Ser Ala Glu Glu Lys His Ser Arg Glu Leu Glu
1 5 10 15

Lys Lys Leu Lys Glu Asp Ala Glu Lys Asp Ala Arg Thr Val Lys Leu
20 25 30

Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln
35 40 45

Met Lys Ile Ile His Gln Asp Gly Tyr Ser Leu Glu Glu Cys Leu Glu
50 55 60

Phe Ile Ala Ile Ile Tyr Gly Asn Thr Leu Gln Ser Ile Leu Ala Ile
65 70 75 80

Val Arg Ala Met Thr Thr Leu Asn Ile Gln Tyr Gly Asp Ser Ala Arg
85 90 95

Gln Asp Asp Ala Arg Lys Leu Met His Met Ala Asp Thr Ile Glu Glu
100 105 110

Gly Thr Met Pro Lys Glu Met Ser Asp Ile Ile Gln Arg Leu Trp Lys
115 120 125

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

Asn Asp Ser Ala Gly Tyr Tyr Leu Ser Asp Leu Glu Arg Leu Val Thr
145 150 155 160

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

Sequence_Listing.txt

Thr Thr Gly Ile Ile Glu Thr Gln Phe Ser Phe Lys Asp Leu Asn Phe
180 185 190

Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys Lys Trp Ile
195 200 205

His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Ile Ala Ala Leu Ser
210 215 220

Ala Tyr Asp Met Val Leu Val Glu Asp Asp Glu Val Asn Arg Met His
225 230 235 240

Glu Ser Leu His Leu Phe Asn Ser Ile Cys Asn His Arg Tyr Phe Ala
245 250 255

Thr Thr Ser Ile Val Leu Phe Leu Asn Lys Lys Asp Val Phe Phe Glu
260 265 270

Lys Ile Lys Lys Ala His Leu Ser Ile Cys Phe Pro Asp Tyr Asp Gly
275 280 285

Pro Asn Thr Tyr Glu Asp Ala Gly Asn Tyr Ile Lys Val Gln Phe Leu
290 295 300

Glu Leu Asn Met Arg Arg Asp Val Lys Glu Ile Tyr Ser His Met Thr
305 310 315 320

Cys Ala Thr Asp Thr Gln Asn Val Lys Phe Val Phe Asp Ala Val Thr
325 330 335

Sequence_Listing.txt

Asp Ile Ile Ile Lys Glu Asn Leu Lys Asp Cys Gly Leu Phe
 340 345 350

<210> 29

<211> 4337

<212> DNA

<213> Homo sapiens

<400> 29

```

cgtcatttta ggggaagca gaggacctca gtgctgaaca tgctaaggag gttggacaaa    60
atcagggttca gaggtcaca gagagatgac ttctcgatc tagcggagtc tccaaatgcc    120
tcggacaccg aatgcagcga cgaaatcccc ctgaaggtag cgcgagacct gccccgggac    180
agcgaggagc tgagggaccc tgctgttcca gggacctca tcatggccac aggagtccag    240
gactttaacc ggacagagtt tgatcgactg aatgagatca aaggcacct ggaaattgcc    300
ttattgaaa aacatttctt acaggaggag ctccggaagc tgcgagaaga aaccaacgcg    360
gagatgtctc ggcaggagct ggaccgcgag cggcagcggc ggatggagct ggagcagaag    420
gtgcaggagg tgctgaaggc cagaaccgag gagcagatgg ctacgagcc cccaaaaggg    480
caggcccagg ccagcaatgg agcagagcgc cggagccagg ggctgtctc gcgcctgcag    540
aagtgttct acgagcgggt cggggagtag gtggaggact tccggtcca gcccgaggag    600
aacactgtgg agacagagga acccctgagc gccgcaggt taactgaaa tatgagacgg    660
ctcaagcgcg gtccaagcc ggtcactaac ttgtgaaga acctctctc ctatccgac    720
tggtactccg tctacacgtc tgccattgcc ttaccgtgt acatgaatgc cgtgtggcat    780
ggctgggcca tccattgtt ctatttcta gcaattctga gggtatccct caattacctc    840
atcgccaggg ggtggcgat acagtggagc atcgtgccc aagtgtctga gcccgaggaa    900
cctccaaagg aagacctgac tgtgtctgag aagttccagc tgggtctgga cgtcgcccag    960

```

Sequence_Listing.txt

aaagcccaga accttttcgg gaagatggct gacatcctgg agaagatcaa gaacttggtc 1020
 atgtgggtcc agccggagat cacacagaag ctgtatgtgg cgctctgggc tgccttcctg 1080
 gcctcctgct tcttccccta ccgcctgggtg gggcttgccg tgggactcta tgctggatc 1140
 aagttcttcc tcattgattt catctttaa cgctgcccga ggctgcgcgc caagtacgac 1200
 acgccctata tcacttgag gagtctcccc accgaccgc agctcaagga gcgctccagc 1260
 gccgcagtct cacgcaggct gcagacgacc tcgtcacgga gctacgtacc cagcgcaccg 1320
 gccggcctgg gtaaagagga ggacgccgt cgctccaca gcaccaagaa gggcaatttc 1380
 cagagatct tcaatctgac agaaaacgag cgtccgctgg cgggtgcca gaatggctgg 1440
 cgctgctgcc tcatcaacag ggaccggaag atgccacgg actacatcag gaacggggtg 1500
 ctctacgtca cggagaatta ctgtgcttc gaaagctcca aatctgggtc ctcaaagagg 1560
 aacaaagta tcaagtagt ggacatcacg gacatccaga agtacaagg cctgtctgtc 1620
 ctcccaggct caggcatggg gattgccgtg tcgacgcat ccaccagaa accgctcgtg 1680
 ttgtgtcca tgggtcacag ggaataggcc ttgagacca ttctcagcca gtacatcaag 1740
 atcacctcag cggcagcgtc tggcggggac agctagtatt gacttgcca ggacgttgct 1800
 ggaattttct ttttctttt cttttcttt tttttttt acgatttgg agtggaaca 1860
 attggacatc ctcatgagct ttgcaataa ttctcctgga cctgtgggtc tattgtgtg 1920
 acctctcgt ttatcgacc aagaaggggc cagggctcac agggacgggg gtgccctct 1980
 cccacagggc acgtcagggt cctctgagg ccaccgcag actgggggag ggggcagagg 2040
 ccctcggggg cccgtggaga agacacacag gacccctggc cctgcccttc tccgttcag 2100
 cctggacaga gaaaccttc cagccacccc aagaggttct cgcaaccttg tgcctcgtc 2160
 tccagaggcc agaagctcgt ccaccacaa agccatagct gaagagtgcg gggcccttc 2220

Sequence_Listing.txt

tcctggggac agaaagatgt cgtcaaggag ggacatgggg gccttcacc aaccaccgag 2280
 aaacgggcct ggcggccctc ctctcttta catgagaccc tcctgtggca ttgcccctg 2340
 gtgccgggct ggggccgggc gcagtgaccc tgctgcgct ccacactgc tccacgggaa 2400
 cagagagggg gagaagggcc caccctcgc ctgccctcag tgtcttggg ggcacctcc 2460
 ttgctggcct ccagggcgct cagcaccgcg tctgtaagg cctgcctgct gctctcgcc 2520
 tgacacgccg gccaggaggt ctgtagctgg ggaccagtaa gggcacagga tggtcaggt 2580
 aaaagcacat cttctcaca cttgtctt tggaagggcc aggagaacat ccgcgaaggc 2640
 tgttgagggt gctccgagca ctgtggcatg tctggcacat ggccccagg ctgcggttc 2700
 ctgggttggg tgggggagga agtggggagg agtgtccgg gacctggg gcccaggctg 2760
 cagccgcctt tgggcatcc gagaggctct ggcagcccct gtgcttagg gagcaaccgt 2820
 gagccgagcc cagaggcctg ggcctgcact gcctgcagcc gacatgcgac agcgttcct 2880
 cccccgctg cctagccggt gccgtccgg gcacagaccc cccagcccc cgccctgccc 2940
 caggaagcc tgggctccc ggaacaagg tggcattgt ggaggagcg cccgcaggcc 3000
 tggctcgtg gggccgctg cgctgggctg aaggaggga aaggcggctt gggcctcctg 3060
 gaaggagggt gccacccgc gggcctgcgt gtctgctgg gcgatcccg cagctccctc 3120
 agctgtcct gagtccctg ggtgtcgtg agattgtgt ttttgaaga aacagaagat 3180
 tctattttt acagcgagca agctggttt ctatttttg tatcctttt cagatgtaat 3240
 tttatctt gctccgatcc tcatttgctg gtgtgggtga gggatccggc ggcattggct 3300
 ggttcaccc ccttcacgag gggccgcaga gtcacacgct ggtgccggg gtgcttggg 3360
 gggagctcg ccgatcacca gattaagcac atgtcctatc ccaggcggg gagcggagcc 3420
 cccgtggctc tggactgcgc ggacgtggc gtcaggatga ccacacggcg gccttcccg 3480

Sequence_Listing.txt

```

aatggggaca gaacccgctc tgagccgtgg gtctggctcc ttagggggac tggctctctt 3540
gggtgcaccag gggaggggga catatcccag tgaacccac cttggcgctt gaggcaacac 3600
aggggtgggca ctgacccacc cccaggggag gctgcagagg cagtggcgc agacaatggc 3660
cacacctctc tcccagggc ccggcagtcg ccaaggatgg gtccggggcc tcggggccaa 3720
tgagcgctc ttctaggtg ctgggattca gtcccaaac acagcgggag gggtccttg 3780
ggcagatggg gcttaccag cgtcgggtgg ttagttcga gtccctttg tggagaaagg 3840
gagatgaaaa ctgaccacgt gccagggtg gccgaagccc ccaggagggg ccacattcgg 3900
ggagcggggg gtcgggggag ggccaccgac tggctctgt gccagcacag gccctcct 3960
ggaagtctc gggagcggag cgcggatcg cacgggctt gggctcccc tggagagaag 4020
ctgtagttt taccaaattg tgtacatctg ggcagatgt taatttctg tactaatcac 4080
tgaactagac gaatgttaa tttttatgt ctgaagcctg agtctatgt ggatctgta 4140
ataatcattg ccagtgtgac tttgttcaa caaaggatt gtactgtatt aagaaccgat 4200
gaaaaaaaa ctcctgtaac attttttaa gaaaacttg ttttttaa gaaaaagtat 4260
tgtataaatt ataatttta tttaaataa cctaaaatgc ttgtgctaa ggctcaaaaa 4320
aaaaaaaaa aaaaaaa 4337

```

<210> 30

<211> 578

<212> PRT

<213> Homo sapiens

<400> 30

Met Leu Arg Arg Leu Asp Lys Ile Arg Phe Arg Gly His Lys Arg Asp

1 5 10 15

Asp Phe Leu Asp Leu Ala Glu Ser Pro Asn Ala Ser Asp Thr Glu Cys

Sequence_Listing.txt

20 25 30

Ser Asp Glu Ile Pro Leu Lys Val Pro Arg Thr Ser Pro Arg Asp Ser
35 40 45

Glu Glu Leu Arg Asp Pro Ala Gly Pro Gly Thr Leu Ile Met Ala Thr
50 55 60

Gly Val Gln Asp Phe Asn Arg Thr Glu Phe Asp Arg Leu Asn Glu Ile
65 70 75 80

Lys Gly His Leu Glu Ile Ala Leu Leu Glu Lys His Phe Leu Gln Glu
85 90 95

Glu Leu Arg Lys Leu Arg Glu Glu Thr Asn Ala Glu Met Leu Arg Gln
100 105 110

Glu Leu Asp Arg Glu Arg Gln Arg Arg Met Glu Leu Glu Gln Lys Val
115 120 125

Gln Glu Val Leu Lys Ala Arg Thr Glu Glu Gln Met Ala Gln Gln Pro
130 135 140

Pro Lys Gly Gln Ala Gln Ala Ser Asn Gly Ala Glu Arg Arg Ser Gln
145 150 155 160

Gly Leu Ser Ser Arg Leu Gln Lys Trp Phe Tyr Glu Arg Phe Gly Glu
165 170 175

Tyr Val Glu Asp Phe Arg Phe Gln Pro Glu Glu Asn Thr Val Glu Thr
180 185 190

Sequence_Listing.txt

Glu Glu Pro Leu Ser Ala Arg Arg Leu Thr Glu Asn Met Arg Arg Leu
195 200 205

Lys Arg Gly Ala Lys Pro Val Thr Asn Phe Val Lys Asn Leu Ser Ala
210 215 220

Leu Ser Asp Trp Tyr Ser Val Tyr Thr Ser Ala Ile Ala Phe Thr Val
225 230 235 240

Tyr Met Asn Ala Val Trp His Gly Trp Ala Ile Pro Leu Phe Leu Phe
245 250 255

Leu Ala Ile Leu Arg Leu Ser Leu Asn Tyr Leu Ile Ala Arg Gly Trp
260 265 270

Arg Ile Gln Trp Ser Ile Val Pro Glu Val Ser Glu Pro Val Glu Pro
275 280 285

Pro Lys Glu Asp Leu Thr Val Ser Glu Lys Phe Gln Leu Val Leu Asp
290 295 300

Val Ala Gln Lys Ala Gln Asn Leu Phe Gly Lys Met Ala Asp Ile Leu
305 310 315 320

Glu Lys Ile Lys Asn Leu Phe Met Trp Val Gln Pro Glu Ile Thr Gln
325 330 335

Lys Leu Tyr Val Ala Leu Trp Ala Ala Phe Leu Ala Ser Cys Phe Phe
340 345 350

Pro Tyr Arg Leu Val Gly Leu Ala Val Gly Leu Tyr Ala Gly Ile Lys

Sequence_Listing.txt

355 360 365

Phe Phe Leu Ile Asp Phe Ile Phe Lys Arg Cys Pro Arg Leu Arg Ala
370 375 380

Lys Tyr Asp Thr Pro Tyr Ile Ile Trp Arg Ser Leu Pro Thr Asp Pro
385 390 395 400

Gln Leu Lys Glu Arg Ser Ser Ala Ala Val Ser Arg Arg Leu Gln Thr
405 410 415

Thr Ser Ser Arg Ser Tyr Val Pro Ser Ala Pro Ala Gly Leu Gly Lys
420 425 430

Glu Glu Asp Ala Gly Arg Phe His Ser Thr Lys Lys Gly Asn Phe His
435 440 445

Glu Ile Phe Asn Leu Thr Glu Asn Glu Arg Pro Leu Ala Val Cys Glu
450 455 460

Asn Gly Trp Arg Cys Cys Leu Ile Asn Arg Asp Arg Lys Met Pro Thr
465 470 475 480

Asp Tyr Ile Arg Asn Gly Val Leu Tyr Val Thr Glu Asn Tyr Leu Cys
485 490 495

Phe Glu Ser Ser Lys Ser Gly Ser Ser Lys Arg Asn Lys Val Ile Lys
500 505 510

Leu Val Asp Ile Thr Asp Ile Gln Lys Tyr Lys Val Leu Ser Val Leu
515 520 525

Sequence_Listing.txt

Pro Gly Ser Gly Met Gly Ile Ala Val Ser Thr Pro Ser Thr Gln Lys
530 535 540

Pro Leu Val Phe Gly Ala Met Val His Arg Asp Glu Ala Phe Glu Thr
545 550 555 560

Ile Leu Ser Gln Tyr Ile Lys Ile Thr Ser Ala Ala Ala Ser Gly Gly
565 570 575

Asp Ser

<210> 31
<211> 2005
<212> DNA
<213> Homo sapiens

<400> 31
tttctctca gggggcagca ggaagtgagg agaaagggt gggatgggag gcgggagcgg 60
atgggagggga atggggttta tcaagtcctc ggcgagctgc ccaacgggca gcagctggcg 120
caagtagcct agctggagag gctcacccca ggaaggaggg aggccaccga cctactgggc 180
cgacggactc ccacacagtt cctgagctgg tgccaggcag gtgacacctc ctgcagcccc 240
cagcatgcgg gcaggcccag gccccaccgt tacattggcc ctggtgctgg cgggtgcatg 300
ggccatggag ctcaagccca cagcaccacc catcttact ggccggccct ttgtggtagc 360
gtgggacgtg cccacacagg actgtggccc acgcctcaag gtgccactgg acctgaatgc 420
ctttgatgtg caggcctcac ctaatgaggg tttgtgaac cagaatatta ccattctta 480
ccgcgaccgt ctaggcctgt atccacgctt cgattctgcc ggaaggctctg tgcattggtg 540
tgtgccacag aatgtcagcc tttgggcaca ccggaagatg ctgcagaaac gtgtggagca 600

Sequence_Listing.txt

ctacattcgg acacaggagt ctgcggggct ggcggtcatc gactgggagg actggcgacc 660

tgtgtgggtg cgcaactggc aggacaaaga tgtgtatcgc cggttatcac gccagctagt 720

ggccagtcgt caccctgact ggccctcaga ccgcatagtc aaacaggcac aatatgagtt 780

tgagttcgca gcacagcagt tcatgtcga gacactcgt tatgtcaagg cagtgcggcc 840

ccggcacctc tggggcttct acctcttcc tgactgctac aatcatgatt atgtgcagaa 900

ctgggagagc tacacaggcc gctgccctga tgtgaggtg gcccgcaatg accagctggc 960

ctggctgtgg gctgagagca cggccctctt cccgtctgtc tacctggacg agacactgc 1020

ttctcccgcatggccga acttgtgag ctccgtgtt caggaggccc ttcgtgtggc 1080

tcgcaccac catgccaacc atgcactccc agtctacgtc ttcacacgac ccacctacag 1140

ccgcaggctc acggggctta gtgagatgga cctcatctct accattggcg agagtgcggc 1200

cctgggcgca gctggtgtca tcctctgggg tgacgcgggg tacaccacaa gcacggagac 1260

ctgccagtac ctcaaagatt acctgacag gctgctggtc cctacgtgg tcaatgtgc 1320

ctgggccacc caatattgca gccgggcca gtgccatggc catgggcgct gtgtgcgccg 1380

caacccagtc gccagtacct tctgcatct cagcaccaac agttccgcc tagtgcttg 1440

ccatgcacct ggtgaacccc agctgcgacc tggggggag ctgagttggg ccgacattga 1500

ccacctgcag acacacttc gctgccagt ctactgggc tggagtgtg agcaatgcca 1560

gtgggacat aggagggcag ctggagggtc cagcgaggcc tgggctgggt cccacctac 1620

cagtctctg gctctggcag cctggcctt tacctggacc ttgtaggggt ctctgccta 1680

gctgcctagc aagctggcct ctaccacaag ggctctctta ggcattagg accctgcagg 1740

gggtggacaa actggagtc gtgagtgga gagccccag gaagcccagg agggcatcca 1800

taccagctcg cccccctg ttctaagggg gaggggaagt cctgggagg ccccttctct 1860

Sequence_Listing.txt

ccctgccaga ggggaaggag ggtacagctg ggctggggag gacctgaccc tactcccttg 1920

ccctagatag ttattattta ttattatit gggtctctt ttgtaaatta aacataaaac 1980

aattgcttct ctgcttgat ttgt 2005

<210> 32

<211> 473

<212> PRT

<213> Homo sapiens

<400> 32

Met Arg Ala Gly Pro Gly Pro Thr Val Thr Leu Ala Leu Val Leu Ala

1 5 10 15

Val Ser Trp Ala Met Glu Leu Lys Pro Thr Ala Pro Pro Ile Phe Thr

20 25 30

Gly Arg Pro Phe Val Val Ala Trp Asp Val Pro Thr Gln Asp Cys Gly

35 40 45

Pro Arg Leu Lys Val Pro Leu Asp Leu Asn Ala Phe Asp Val Gln Ala

50 55 60

Ser Pro Asn Glu Gly Phe Val Asn Gln Asn Ile Thr Ile Phe Tyr Arg

65 70 75 80

Asp Arg Leu Gly Leu Tyr Pro Arg Phe Asp Ser Ala Gly Arg Ser Val

85 90 95

His Gly Gly Val Pro Gln Asn Val Ser Leu Trp Ala His Arg Lys Met

100 105 110

Sequence_Listing.txt

Leu Gln Lys Arg Val Glu His Tyr Ile Arg Thr Gln Glu Ser Ala Gly
115 120 125

Leu Ala Val Ile Asp Trp Glu Asp Trp Arg Pro Val Trp Val Arg Asn
130 135 140

Trp Gln Asp Lys Asp Val Tyr Arg Arg Leu Ser Arg Gln Leu Val Ala
145 150 155 160

Ser Arg His Pro Asp Trp Pro Pro Asp Arg Ile Val Lys Gln Ala Gln
165 170 175

Tyr Glu Phe Glu Phe Ala Ala Gln Gln Phe Met Leu Glu Thr Leu Arg
180 185 190

Tyr Val Lys Ala Val Arg Pro Arg His Leu Trp Gly Phe Tyr Leu Phe
195 200 205

Pro Asp Cys Tyr Asn His Asp Tyr Val Gln Asn Trp Glu Ser Tyr Thr
210 215 220

Gly Arg Cys Pro Asp Val Glu Val Ala Arg Asn Asp Gln Leu Ala Trp
225 230 235 240

Leu Trp Ala Glu Ser Thr Ala Leu Phe Pro Ser Val Tyr Leu Asp Glu
245 250 255

Thr Leu Ala Ser Ser Arg His Gly Arg Asn Phe Val Ser Phe Arg Val
260 265 270

Gln Glu Ala Leu Arg Val Ala Arg Thr His His Ala Asn His Ala Leu
275 280 285

Sequence_Listing.txt

Pro Val Tyr Val Phe Thr Arg Pro Thr Tyr Ser Arg Arg Leu Thr Gly
290 295 300

Leu Ser Glu Met Asp Leu Ile Ser Thr Ile Gly Glu Ser Ala Ala Leu
305 310 315 320

Gly Ala Ala Gly Val Ile Leu Trp Gly Asp Ala Gly Tyr Thr Thr Ser
325 330 335

Thr Glu Thr Cys Gln Tyr Leu Lys Asp Tyr Leu Thr Arg Leu Leu Val
340 345 350

Pro Tyr Val Val Asn Val Ser Trp Ala Thr Gln Tyr Cys Ser Arg Ala
355 360 365

Gln Cys His Gly His Gly Arg Cys Val Arg Arg Asn Pro Ser Ala Ser
370 375 380

Thr Phe Leu His Leu Ser Thr Asn Ser Phe Arg Leu Val Pro Gly His
385 390 395 400

Ala Pro Gly Glu Pro Gln Leu Arg Pro Val Gly Glu Leu Ser Trp Ala
405 410 415

Asp Ile Asp His Leu Gln Thr His Phe Arg Cys Gln Cys Tyr Leu Gly
420 425 430

Trp Ser Gly Glu Gln Cys Gln Trp Asp His Arg Gln Ala Ala Gly Gly
435 440 445

Sequence_Listing.txt

Ala Ser Glu Ala Trp Ala Gly Ser His Leu Thr Ser Leu Leu Ala Leu
450 455 460

Ala Ala Leu Ala Phe Thr Trp Thr Leu
465 470

<210> 33
<211> 1629
<212> DNA
<213> Homo sapiens

<400> 33
acacatcagg ggcttgctct tgcaaaacca aaccacaaga cagacttgca aaagaaggca 60
tgcacagctc agcactgctc tgttgccctgg tcctcctgac tggggtgagg gccagcccag 120
gccagggcac ccagctgag aacagctgca cccacttccc aggcaacctg cctaacaatgc 180
ttcgagatct ccgagatgcc ttcagcagag tgaagacttt cttcaaagt aaggatcagc 240
tggacaactt gttgttaaag gagtccttgc tggaggactt taagggttac ctgggttgcc 300
aagcctgtgc tgagatgac cagttttacc tggaggaggt gatgccccaa gctgagaacc 360
aagaccaga catcaaggcg catgtgaact ccttggggga gaacctgaag accctcaggc 420
tgaggctacg gcgctgtcat cgatttcttc cctgtgaaaa caagagcaag gccgtggagc 480
aggtaagaa tgcctttaat aagctccaag agaaaggcat ctacaaagcc atgagtgagt 540
ttgacatctt catcaactac atagaagcct acatgacaat gaagatacga aactgagaca 600
tcagggtggc gactctatag actctaggac ataaattaga ggtctccaaa atcggatctg 660
gggctctggg atagctgacc cagccccttg agaaacctta ttgtacctct cttatagaat 720
atttattacc tctgatacct caacccccat ttctatttat ttactgagct tctctgtgaa 780
cgatttagaa agaagcccaa tattataatt ttttcaata ttattattt tcacctgttt 840

Sequence_Listing.txt

ttaagctgtt tccatagggt gacacactat ggtatttgag tgtttaaga taaattataa 900
 gttacataag ggaggaaaaa aaatgttctt tggggagcca acagaagctt ccattccaag 960
 cctgaccacg cttctagct gttgagctgt ttccctgac ctccctctaa ttatcttgt 1020
 ctctgggctt ggggcttct aactgctaca aatactctta ggaagagaaa ccaggagacc 1080
 ccttgatga ttaattcacc ttccagtgc tcggagggat tcccctaacc tcattcccca 1140
 accacttcat tctgaaagc tggggcagc ttgtattta taacaacctt aatttggtt 1200
 taggccgggc gcggtggctc acgcctgtta tccagcact ttgggaggct gaggcgggtg 1260
 gatcacttga ggtcaggagt tctaaccag cctggtaac atggtgaaac cccgtctcta 1320
 ctaaaaatac aaaaattagc cgggcatggt ggcgcgcacc tgtaatccca gctacttggg 1380
 aggctgaggc aagagaattg cttgaaccca ggagatggaa gttgcagtga gctgatatca 1440
 tgcccctgta ctccagctg ggtgacagag caagactctg tctcaaaaaa taaaataaaa 1500
 aataaatttg gttctaatag aactcagttt taactagaat ttattcaatt cctctgggaa 1560
 tgttacattg ttgtctgic ttcatagcag attttaattt tgaataaata aatgtatctt 1620
 attcacatc 1629

<210> 34
 <211> 178
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met His Ser Ser Ala Leu Leu Cys Cys Leu Val Leu Leu Thr Gly Val
 1 5 10 15

Arg Ala Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His
 20 25 30

Sequence_Listing.txt

Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe
35 40 45

Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu
50 55 60

Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
65 70 75 80

Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
85 90 95

Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu
100 105 110

Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg
115 120 125

Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn
130 135 140

Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu
145 150 155 160

Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile
165 170 175

Arg Asn

<210> 35

Sequence_Listing.txt

<211> 2970

<212> DNA

<213> Homo sapiens

<400> 35

```

agtgacgcca gggggcgggg ccagcggcgc ggtcgggtga gaggccgcg cggcaggtcc    60
acctgggctt gcgaaggcac agattccccg tccacagctc acgaccagat gcaccagcag    120
gagtcacat cgaggacgtc ctccgggcac tcccacgacc agtgaccagg agttaaactt    180
tgggatgtgc ccgtgatgtt ggaccacaag gacttagagg ccgaaatcca cccctgaaa    240
aatgaagaaa gaaaatcgca ggaaaatctg ggaaatccat caaaaaatga ggataacgtg    300
aaaagcgcgc ctccacagtc ccggctctcc cggtgccgag cggcggcggt ttttcttca    360
ttgtttctct gccttttgt ggtgttcgtc gtctcattcg tcatcccgta tccagaccgg    420
ccggcgtcac agcgaatgtg gaggatagac tacagtgccg ctgttatcta tgactttctg    480
gctgtggatg atataaacgg ggacaggatc caagatgttc ttttcttta taaaaacacc    540
aacagcagca acaatttcag ccgatcctgt gtggacgaag gcttttctc tccctgcacc    600
tttgacgtc ctgtgtcggg ggccaacggc agcacgctct gggagagacc tgtggcccaa    660
gacgtggccc tcgtggagtg tgctgtgcc cagccaagag gcagtgaggc acctctgcc    720
tgcatcctgg tgggcagacc cagtcttctc attgcagtca actgtttcac aggggaaacc    780
ctgtggaacc acagcagcag ctccagcggg aatgcgtcca tctgagccc tctgctgcag    840
gtgcctgatg tggacggcga tggggcccca gacctgctgg ttctaccca ggagcgggag    900
gaggttagt gccacctcta ctccgcagc accgggcacc agattggcct cagaggcagc    960
cttggtgtgg acggggaaag tggcttctc ctccacgtca ccaggacagg tgcccactac   1020
atcctcttc cctgcgcaag ctccctctgc ggctgctctg tgaagggtct ctacgagaag   1080
gtgaccggga gcggcggccc gttcaagagt gaccgcact gggagagcat gctcaatgcc   1140

```

Sequence_Listing.txt

accacccgca ggatgcttcc ccacagctct ggagcagtgc gctacctgat gcatgtccca 1200
gggaacgccg gtgcagatgt gcttctgtg ggctcagagg ccttcgtgct gctggacggg 1260
caggagctga cgctcgctg gacacccaag gcagcccatg tctgagaaa acccatcttc 1320
ggccgctaca aaccagacac cttggctgta gccgttgaaa acggaactgg caccgacaga 1380
cagatcctgt ttctggacct tggcactgga gccgtcctgt gtagcctagc cctcccagac 1440
ctccctgggg gtccactgtc cgccagcctg ccgaccgcag accaccgctc agccttcttc 1500
ttctggggcc tccacgagct ggggagcacc agcgagacgg agaccgggga ggcccggcac 1560
agcctgtaca tgtccaccc caccctgccg cgcgtgctgc tggagctggc caatgtctct 1620
accacattg tcgccttga cgccgtcctg ttgagccaa gccgccacgc cgctacatc 1680
cttctgacag gcccggcaga ctgagaggca cccggcctgg tctctgtgat caagcacaag 1740
gtgcgggacc ttgtcccaag cagcaggggtg gtccgcctgg gtgaggggtg gccagacagt 1800
gaccaagcca tcagggaccg gtctccccg ctgcgttacc agagttaggc gtagaggcac 1860
gccagccaga gcctgtggag agactccgcc tctgacact aaacgtcctg ggaagtgggc 1920
ccttccctgg gtctctgcac tgactcccc actcctgacc ctggtgatgg tcgccactgg 1980
gcagcagcag ccttaccagt cctccatgat cacaccagg gacctgcatg ggtgagggga 2040
caccctgggc ctctctcccg cccagcatcc tccctgagtc cccacacagg gcctcactct 2100
gcaccccacc agggctccgc tcacaccagg cagccttcat agtggctcct ctggccacct 2160
tgggcagagc tgggtcatgc agcaccat ccttaccgg tgccctctcc ttgccagctt 2220
ctccccaggc cagagcggcc atcgcgtaga aagaaccagg gtgtccccgg gacaggccgt 2280
ccccacccc atcctgtaga agtccattcc cctttccct cctgtgctct gtccccaaag 2340
gagtcatgga actcagggtg ctgggcctca acgggaacct gagacagctc cagcttcgca 2400

Sequence_Listing.txt

```

gcccttccg gagctacagg gggatcctct agcatggggg gtgtgacttg gttccttga 2460
ccaggctctg tgaggaagcc tggagcaagg gtctcccca gcaggatggg tggggcctgc 2520
tctggagctg agcccggtgc cgctcacagg tgccttagt ggtgttcag ctgtctactg 2580
gctgcatgtg ctgtgaatat cccaaggaac tggctgtgga atgcgtgtt gggtcagtct 2640
gtgccctctc agtagacact ggagctgctc tgccttgaa gaggccccgt gcccaggca 2700
tggcaagcgc ctgcctctcc cttccggtg ctacacgcc cagccgtgc caccgatgc 2760
aggactcacc tctgtgcctt gctgctcctg aggccaagg gcagccatgg tgctctgtac 2820
tgctcgggcc gccagggtca cagagcctga gttcgtagc caaagcagcc tgatgacca 2880
cccaccaagg aagaaagcag aataaacatt ttgcactgc ctgaaaaacc ccggtggtca 2940
ggcgtgagcc taaaaaaaaa aaaaaaaaaa 2970

```

<210> 36
 <211> 552
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Leu Asp His Lys Asp Leu Glu Ala Glu Ile His Pro Leu Lys Asn
 1 5 10 15

Glu Glu Arg Lys Ser Gln Glu Asn Leu Gly Asn Pro Ser Lys Asn Glu
 20 25 30

Asp Asn Val Lys Ser Ala Pro Pro Gln Ser Arg Leu Ser Arg Cys Arg
 35 40 45

Ala Ala Ala Phe Phe Leu Ser Leu Phe Leu Cys Leu Phe Val Val Phe
 50 55 60

Sequence_Listing.txt

Val Val Ser Phe Val Ile Pro Cys Pro Asp Arg Pro Ala Ser Gln Arg
65 70 75 80

Met Trp Arg Ile Asp Tyr Ser Ala Ala Val Ile Tyr Asp Phe Leu Ala
 85 90 95

Val Asp Asp Ile Asn Gly Asp Arg Ile Gln Asp Val Leu Phe Leu Tyr
 100 105 110

Lys Asn Thr Asn Ser Ser Asn Asn Phe Ser Arg Ser Cys Val Asp Glu
 115 120 125

Gly Phe Ser Ser Pro Cys Thr Phe Ala Ala Ala Val Ser Gly Ala Asn
 130 135 140

Gly Ser Thr Leu Trp Glu Arg Pro Val Ala Gln Asp Val Ala Leu Val
145 150 155 160

Glu Cys Ala Val Pro Gln Pro Arg Gly Ser Glu Ala Pro Ser Ala Cys
 165 170 175

Ile Leu Val Gly Arg Pro Ser Ser Phe Ile Ala Val Asn Leu Phe Thr
 180 185 190

Gly Glu Thr Leu Trp Asn His Ser Ser Ser Phe Ser Gly Asn Ala Ser
 195 200 205

Ile Leu Ser Pro Leu Leu Gln Val Pro Asp Val Asp Gly Asp Gly Ala
 210 215 220

Sequence_Listing.txt

Pro Asp Leu Leu Val Leu Thr Gln Glu Arg Glu Glu Val Ser Gly His
225 230 235 240

Leu Tyr Ser Gly Ser Thr Gly His Gln Ile Gly Leu Arg Gly Ser Leu
 245 250 255

Gly Val Asp Gly Glu Ser Gly Phe Leu Leu His Val Thr Arg Thr Gly
 260 265 270

Ala His Tyr Ile Leu Phe Pro Cys Ala Ser Ser Leu Cys Gly Cys Ser
 275 280 285

Val Lys Gly Leu Tyr Glu Lys Val Thr Gly Ser Gly Gly Pro Phe Lys
 290 295 300

Ser Asp Pro His Trp Glu Ser Met Leu Asn Ala Thr Thr Arg Arg Met
305 310 315 320

Leu Ser His Ser Ser Gly Ala Val Arg Tyr Leu Met His Val Pro Gly
 325 330 335

Asn Ala Gly Ala Asp Val Leu Leu Val Gly Ser Glu Ala Phe Val Leu
 340 345 350

Leu Asp Gly Gln Glu Leu Thr Pro Arg Trp Thr Pro Lys Ala Ala His
 355 360 365

Val Leu Arg Lys Pro Ile Phe Gly Arg Tyr Lys Pro Asp Thr Leu Ala
 370 375 380

Val Ala Val Glu Asn Gly Thr Gly Thr Asp Arg Gln Ile Leu Phe Leu
385 390 395 400

Sequence_Listing.txt

Asp Leu Gly Thr Gly Ala Val Leu Cys Ser Leu Ala Leu Pro Ser Leu
405 410 415

Pro Gly Gly Pro Leu Ser Ala Ser Leu Pro Thr Ala Asp His Arg Ser
420 425 430

Ala Phe Phe Phe Trp Gly Leu His Glu Leu Gly Ser Thr Ser Glu Thr
435 440 445

Glu Thr Gly Glu Ala Arg His Ser Leu Tyr Met Phe His Pro Thr Leu
450 455 460

Pro Arg Val Leu Leu Glu Leu Ala Asn Val Ser Thr His Ile Val Ala
465 470 475 480

Phe Asp Ala Val Leu Phe Glu Pro Ser Arg His Ala Ala Tyr Ile Leu
485 490 495

Leu Thr Gly Pro Ala Asp Ser Glu Ala Pro Gly Leu Val Ser Val Ile
500 505 510

Lys His Lys Val Arg Asp Leu Val Pro Ser Ser Arg Val Val Arg Leu
515 520 525

Gly Glu Gly Gly Pro Asp Ser Asp Gln Ala Ile Arg Asp Arg Phe Ser
530 535 540

Arg Leu Arg Tyr Gln Ser Glu Ala
545 550

Sequence_Listing.txt

<210> 37

<211> 3675

<212> DNA

<213> Homo sapiens

<400> 37

```

tagacctcag cttcctctgt caccatgggt cgggctcggc tgggcccggc ggtcgccatg    60
gtaactgggg cgggtcgcag ggtcctggca ggctgggcgc atgcgcgcgg ggactacaag    120
ccgcgccgcg ctgccgtgg cccctcagca accctcgaca tggcgctgag gcggccaccg    180
cgactccggc tctgcgtcg gctgcctgac ttctcctgc tgcgtcttt caggggctgc    240
ctgatagggg ctgtaaatct caaatccagc aatcgaacc cagtgggtaca ggaattgaa    300
agtgtggaac tgtctgcat cattacggat tcgcagacaa gtgacccag gatcgagtgg    360
aagaaaattc aagatgaaca aaccacatat gtgtttttg acaacaaaat tcaggagagac    420
ttggcgggtc gtgcagaaat actggggaag acatccctga agatctggaa tgtgacacgg    480
agagactcag ccccttatcg ctgtgaggtc gttgctcgaa atgaccgcaa ggaaattgat    540
gagattgtga tcgagttaac tgtgaagtg aagccagtga cccctgtctg tagagtccg    600
aaggctgtac cagtaggcaa gatggcaaca ctgcactgcc aggagagtga gggccacccc    660
cggcctcact acagctggta tcgcaatgat gtaccactgc ccacggattc cagagccaat    720
cccagatttc gcaattctt ttccactta aactctgaaa caggcacttt ggtgttact    780
gctgttcaca aggacgactc tgggcagtac tactgcattg ctccaatga cgcagggtca    840
gccagggtgt aggagcagga gatggaagtc tatgacctga acattggcgg aattattggg    900
ggggttctgg ttgtccttc tgtactggcc ctgatcacgt tgggcatctg ctgtgcatac    960
agacgtggct acttcatcaa caataaacag gatggagaaa gttacaagaa cccagggaaa   1020
ccagatggag ttaactacat ccgcactgac gaggagggcg acttcagaca caagtcatcg   1080

```

Sequence_Listing.txt

tttgtgatct gagacccgcg gtgtggctga gagcgcacag agcgcacgtg cacatacctc 1140

tgctagaaac tctgtcaag gcagcgagag ctgatgcact cggacagagc tagacactca 1200

ttcagaagct ttcgttttg gccaaagttg accactactc ttcttactct aacaagccac 1260

atgaatagaa gaatttctct caagatggac ccggtaaata taaccacaag gaagcgaaac 1320

tgggtgcgtt cactgagttg ggttcctaata ctgtttctgg cctgattccc gcatgagtat 1380

tagggtgatc ttaaagagtt tgctcacgta aacgcccgtg ctgggccctg tgaagccagc 1440

atgttcacca ctggtcgttc agcagccacg acagcaccat gtgagatggc gaggtggctg 1500

gacagcacca gcagcgcatc ccggcgggaa cccagaaaag gcttcttaca cagcagcctt 1560

acttcatcgg cccacagaca ccaccgcagt ttctctttaa aggcctctgt gatcgggtgtt 1620

gcagtgacca ttgtggagaa gctttttgga tcagcatttt gtaaaaacaa ccaaaatcag 1680

gaaggtaaat tgggtgctgg aagagggatc ttgcctgagg aacctgctt gtccaacagg 1740

gtgtcaggat ttaaggaaaa ccttcgtctt aggctaagtc tgaaatggta ctgaaatatg 1800

ctttctatg ggtctgttt atttataaa attttacatc taaattttg ctaaggatgt 1860

attttgatta ttgaaaagaa aatttctatt taaactgtaa atatattgtc atacaatgtt 1920

aaataaccta ttttttaaa aaagtcaac ttaaggtaga agttccaagc tactagtgtt 1980

aaattggaaa atatcaataa ttaagagtat ttacccaag gaatcctctc atggaagttt 2040

actgtgatgt tcctttctc acacaagttt tagcctttt cacaagggaa ctcatactgt 2100

ctacacatca gaccatagtt gcttaggaaa cctttaaaaa ttccagttaa gcaatgttga 2160

aatcagttg catctctca aaagaaacct ctcaggttag ctttgaactg cctcttctg 2220

agatgactag gacagtctgt acccagaggc caccagaag cctcagatg tacatacaca 2280

gatgccagtc agctcctggg gttgcgccag gcgccccgc tctagctcac tgttgctcg 2340

Sequence_Listing.txt

ctgtctgcc a ggaggccctg ccatccttgg gccctggcag tggctgtgtc ccagtgtgct 2400

ttactcacgt ggcccttgct tcatccagca cagctctcag gtgggcactg cagggacact 2460

ggtgtcttcc atgtagcgtc ccagctttgg gctcctgtaa cagacctctt ttgggttatg 2520

gatggctcac aaaatagggc ccccaatgct atttttttt ttaagtgtg ttaattatt 2580

tgtaagatt gtctaaggcc aaaggcaatt gcgaaatcaa gtctgtcaag tacaataaca 2640

ttttaaaag aaaatggatc ccactgttcc tcttgccac agagaaagca ccagacgcc 2700

acaggctctg tcgcatttca aaacaaacca tgatggagtg gcggccagtc cagcctttta 2760

aagaacgtca ggtggagcag ccaggtgaaa gccctggcgg ggaggaaagt gaaacgcctg 2820

aatcaaaagc agttttctaa tttgacttt aaatttttca tccgccggag acactgtctc 2880

cattgtggg gggacattag caacatcact cagaagcctg tgttttcaa gacaggtgt 2940

tctcagctc acatgccctg ccgtgctgga ctcaggactg aagtgtgtga aagcaaggag 3000

ctgtctgagaa ggagcactcc actgtgtgcc tggagaatgg ctctactac tcacctgtc 3060

tttcagctc cagtgtctg ggtttttat actttgacag cttttttta attgcataca 3120

tgagactgtg ttgactttt ttagttatgt gaaacacttt gccgcaggcc gcctggcaga 3180

ggcaggaaat gtccagcag tggctcagt ctcctgggtg tctgtgcat ggcatcctgg 3240

atgcttagca tgcaagtcc ctccatcatt gccaccttg tagagaggga tggctccca 3300

ccctcagcgt tggggattca cgctccagcc tccttctgg ttgtcatagt gatagggtag 3360

ccttattgcc cctctctt ataccctaaa acctctaca ctagtccat gggaaccagg 3420

tctgaaaaag tagagagaag tgaaagtaga gtctgggaag tagctgccta taactgagac 3480

tagacggaaa aggaatactc gtgtatttta agatatgaat gtgactcaag actcgaggcc 3540

gatacagggc tgtattctg cctttggatg gatgtgtctg tacacagatg ctacagactt 3600

Sequence_Listing.txt

gtactaacac accgtaattt ggcatttggt taacctcatt tataaaagct tcaaaaaaac 3660

ccaaaaaaac ccaaa 3675

<210> 38

<211> 355

<212> PRT

<213> Homo sapiens

<400> 38

Met Val Pro Ala Arg Leu Gly Pro Ala Val Ala Met Val Thr Gly Ala

1 5 10 15

Gly Arg Arg Val Leu Ala Gly Trp Ala His Ala Arg Gly Asp Tyr Lys

20 25 30

Pro Arg Arg Ala Ala Ala Gly Pro Ser Ala Thr Leu Asp Met Ala Leu

35 40 45

Arg Arg Pro Pro Arg Leu Arg Leu Cys Ala Arg Leu Pro Asp Phe Phe

50 55 60

Leu Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly Ala Val Asn Leu Lys

65 70 75 80

Ser Ser Asn Arg Thr Pro Val Val Gln Glu Phe Glu Ser Val Glu Leu

85 90 95

Ser Cys Ile Ile Thr Asp Ser Gln Thr Ser Asp Pro Arg Ile Glu Trp

100 105 110

Lys Lys Ile Gln Asp Glu Gln Thr Thr Tyr Val Phe Phe Asp Asn Lys

115 120 125

Sequence_Listing.txt

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

Leu Lys Ile Trp Asn Val Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys
145 150 155 160

Glu Val Val Ala Arg Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile
165 170 175

Glu Leu Thr Val Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro
180 185 190

Lys Ala Val Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser
195 200 205

Glu Gly His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro
210 215 220

Leu Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
225 230 235 240

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His Lys
245 250 255

Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala Gly Ser
260 265 270

Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu Asn Ile Gly
275 280 285

Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val Leu Ala Leu Ile

Sequence_Listing.txt

290 295 300

Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly Tyr Phe Ile Asn Asn
305 310 315 320

Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro Gly Lys Pro Asp Gly Val
325 330 335

Asn Tyr Ile Arg Thr Asp Glu Glu Gly Asp Phe Arg His Lys Ser Ser
340 345 350

Phe Val Ile
355

<210> 39

<211> 2581

<212> DNA

<213> Homo sapiens

<400> 39

agtgagcgac acagagcggg ccgccaccgc cgagcagccc tccggcagtc tccgcgtccg 60

ttaagcccg cgggtcctccg cgaatcggcg gtgggtccgg cagccgaatg cagccccgca 120

gcgagcggcc ggccggcagg acgcagagcc cggagcacgg cagcccgggg cccggggccc 180

aggcgccgcc gcctccaccg ccgcagccgc cggccccga ggcagagcgc acgcggcccc 240

ggcaggctcg gcccgcagcc cccatggagg gagccgtgca gctgctgagc cgcgagggcc 300

acagcgtggc ccacaactcc aagcggcact accacgatgc ctctgtggcc atgagccgca 360

tgcgccagcg cggcctcctg tgcgacatcg tctgcacgt ggctgccaag gagatccgtg 420

cgcacaaagt ggtgctggcc tctgcagcc cctacttcca cgccatgttc acaaagaga 480

tgagcgagag ccgccagacc cacgtgacgc tgcacgacat cgaccctcag gccttgacc 540

Sequence_Listing.txt

agctggtgca gttgcctac acggctgaga ttgtggtggg cgagggcaat gtgcagactc 600
 tgctcccagc cgccagtctc ctgcagctga atggcgctccg agacgcttgc tgcaagtttc 660
 tactgagtca gctcgacccc tccaactgcc tgggtatccg gggctttgcc gatgcgcact 720
 cctgcagcga cctgctcaag gccgcccaca ggtacgtgct gcagcacttc gtggacgtgg 780
 ccaagaccga ggagtttatg ctgctgcccc tgaacagggt tctggaactg gtctctagcg 840
 acagcctgaa ctgacctca gaggaggagg tctaccgagc cgtcctgagc tgggtgaaac 900
 acgacgtgga cgcccgagg cagcatgtcc cacggctcat gaagtgtgtg cggctgccct 960
 tgctgagccg cgacttctg ctgggccacg tggatgccga gagcctggtg aggcaccacc 1020
 ctgactgcaa ggacctctc atcgaggccc tgaagtcca cctgctgcct gagcagaggg 1080
 gcgtcctagg caccagccgc acacgtcccc ggcgtgcga gggggccggg cctgtgcttt 1140
 ttgctgtggg cggcgggagc ctgttgcca tccacggaga ctgtgaggcc tacgacacgc 1200
 gcaccgaccg ctggcacgtg gtggcctcca tgtccacgcg ccggggcccg gtgggagtgg 1260
 ctgcggtggg gaaccggctc tatgtgtgg gcggctatga tgggacctca gacctggcta 1320
 ccgtggagtc ctacgacccc gtgactaaca cgtggcagcc ggagggtgcc atgggcacaa 1380
 ggcaagctg cctgggtgtg gccgccttgc atggactcct gtactcggcc ggcggctatg 1440
 acggggcctc ctgctgaac agtctgaac gctacgacc cctgaccgga acgtggacgt 1500
 ccgtcgtgc catgagcacc cggaggcgct atgtgcgagt ggccacgct gatgggaacc 1560
 tgtatgctgt gggcggctac gacagctcct cacacctggc cactgtggag aagtatgagc 1620
 cccaggtgaa cgtgtggtcg cccgtggcgt ccatgctgag ccgacgcagc tcagcgggcg 1680
 tggccgtgct ggagggtgcc ctgtacgtgg cagggggcaa cgacggcacc agctgcctca 1740
 actcggtaga gagatacagt ccaaggctg gagcctggga aagcgtggcg cccatgaata 1800

Sequence_Listing.txt

tccgcaggag cacgcatgac ctggtggcca tggacggatg gttgtacgcc gtggggggta 1860
 acgacggtag ctccagcctc aactccatcg agaagtacaa cccgaggacc aacaagtggg 1920
 tggccgcac ctgcatgttc acccggcgca gcagtgtggg tgtggcggtg ctggagctgc 1980
 tcaatttccc gccgccaacc tccccgacgc tgtccgtgtc ctccaccagc ctctgaccca 2040
 cctaccacca gaggcctgca gccctccaca tgccttaagg ggaccgtggc ccccaccagg 2100
 gagctcctgc gccatccgtt cagctctctg catccattcc ttcatgtctt tatttagttg 2160
 ttatttatt tagttattta tcttatttat tgaggggtga ggagtgccac ggctgcccg 2220
 ttacaccttt agcgtctggt cctcctgcgt gtctccct ccactgcctg catggggggc 2280
 gcgggggagtg accaggcggg ggcctcaccg cccagggcc gtgcctgct cagacctgc 2340
 aggcgtgga gcaagaggcc ctgggtctct ccaagcagct gcagaccca gctgaattt 2400
 tgcacatggc ggggtcccgg gaagggtggg gagcagttgt ccttctgtc gtcgtctgcc 2460
 gtgtgccatc ttctctgga ctgttagtgg gtgcacacgc gtgcactggg accccacaca 2520
 gcaatacgag tccaacttaa taaacacatt tctggggttc ctcaaaaaaa aaaaaaaaaa 2580
 a 2581

<210> 40
 <211> 642
 <212> PRT
 <213> Homo sapiens

<400> 40
 Met Gln Pro Arg Ser Glu Arg Pro Ala Gly Arg Thr Gln Ser Pro Glu
 1 5 10 15

His Gly Ser Pro Gly Pro Gly Pro Glu Ala Pro Pro Pro Pro Pro
 20 25 30

Sequence_Listing.txt

Gln Pro Pro Ala Pro Glu Ala Glu Arg Thr Arg Pro Arg Gln Ala Arg
35 40 45

Pro Ala Ala Pro Met Glu Gly Ala Val Gln Leu Leu Ser Arg Glu Gly
50 55 60

His Ser Val Ala His Asn Ser Lys Arg His Tyr His Asp Ala Phe Val
65 70 75 80

Ala Met Ser Arg Met Arg Gln Arg Gly Leu Leu Cys Asp Ile Val Leu
85 90 95

His Val Ala Ala Lys Glu Ile Arg Ala His Lys Val Val Leu Ala Ser
100 105 110

Cys Ser Pro Tyr Phe His Ala Met Phe Thr Asn Glu Met Ser Glu Ser
115 120 125

Arg Gln Thr His Val Thr Leu His Asp Ile Asp Pro Gln Ala Leu Asp
130 135 140

Gln Leu Val Gln Phe Ala Tyr Thr Ala Glu Ile Val Val Gly Glu Gly
145 150 155 160

Asn Val Gln Thr Leu Leu Pro Ala Ala Ser Leu Leu Gln Leu Asn Gly
165 170 175

Val Arg Asp Ala Cys Cys Lys Phe Leu Leu Ser Gln Leu Asp Pro Ser
180 185 190

Sequence_Listing.txt

Asn Cys Leu Gly Ile Arg Gly Phe Ala Asp Ala His Ser Cys Ser Asp
195 200 205

Leu Leu Lys Ala Ala His Arg Tyr Val Leu Gln His Phe Val Asp Val
210 215 220

Ala Lys Thr Glu Glu Phe Met Leu Leu Pro Leu Lys Gln Val Leu Glu
225 230 235 240

Leu Val Ser Ser Asp Ser Leu Asn Val Pro Ser Glu Glu Glu Val Tyr
245 250 255

Arg Ala Val Leu Ser Trp Val Lys His Asp Val Asp Ala Arg Arg Gln
260 265 270

His Val Pro Arg Leu Met Lys Cys Val Arg Leu Pro Leu Leu Ser Arg
275 280 285

Asp Phe Leu Leu Gly His Val Asp Ala Glu Ser Leu Val Arg His His
290 295 300

Pro Asp Cys Lys Asp Leu Leu Ile Glu Ala Leu Lys Phe His Leu Leu
305 310 315 320

Pro Glu Gln Arg Gly Val Leu Gly Thr Ser Arg Thr Arg Pro Arg Arg
325 330 335

Cys Glu Gly Ala Gly Pro Val Leu Phe Ala Val Gly Gly Gly Ser Leu
340 345 350

Phe Ala Ile His Gly Asp Cys Glu Ala Tyr Asp Thr Arg Thr Asp Arg
355 360 365

Sequence_Listing.txt

Trp His Val Val Ala Ser Met Ser Thr Arg Arg Ala Arg Val Gly Val
370 375 380

Ala Ala Val Gly Asn Arg Leu Tyr Ala Val Gly Gly Tyr Asp Gly Thr
385 390 395 400

Ser Asp Leu Ala Thr Val Glu Ser Tyr Asp Pro Val Thr Asn Thr Trp
405 410 415

Gln Pro Glu Val Ser Met Gly Thr Arg Arg Ser Cys Leu Gly Val Ala
420 425 430

Ala Leu His Gly Leu Leu Tyr Ser Ala Gly Gly Tyr Asp Gly Ala Ser
435 440 445

Cys Leu Asn Ser Ala Glu Arg Tyr Asp Pro Leu Thr Gly Thr Trp Thr
450 455 460

Ser Val Ala Ala Met Ser Thr Arg Arg Arg Tyr Val Arg Val Ala Thr
465 470 475 480

Leu Asp Gly Asn Leu Tyr Ala Val Gly Gly Tyr Asp Ser Ser Ser His
485 490 495

Leu Ala Thr Val Glu Lys Tyr Glu Pro Gln Val Asn Val Trp Ser Pro
500 505 510

Val Ala Ser Met Leu Ser Arg Arg Ser Ser Ala Gly Val Ala Val Leu
515 520 525

Sequence_Listing.txt

Glu Gly Ala Leu Tyr Val Ala Gly Gly Asn Asp Gly Thr Ser Cys Leu
530 535 540

Asn Ser Val Glu Arg Tyr Ser Pro Lys Ala Gly Ala Trp Glu Ser Val
545 550 555 560

Ala Pro Met Asn Ile Arg Arg Ser Thr His Asp Leu Val Ala Met Asp
565 570 575

Gly Trp Leu Tyr Ala Val Gly Gly Asn Asp Gly Ser Ser Ser Leu Asn
580 585 590

Ser Ile Glu Lys Tyr Asn Pro Arg Thr Asn Lys Trp Val Ala Ala Ser
595 600 605

Cys Met Phe Thr Arg Arg Ser Ser Val Gly Val Ala Val Leu Glu Leu
610 615 620

Leu Asn Phe Pro Pro Pro Ser Ser Pro Thr Leu Ser Val Ser Ser Thr
625 630 635 640

Ser Leu

<210> 41

<211> 1897

<212> DNA

<213> Homo sapiens

<400> 41

actcttcgtc atcacctctc ctattcgctt ggacaagctc atgtttgcag gagcaccatg 60

tcttgctcgt ctgcgcctc ctctccagg gctggaggca gcagctcagc caggggtgtct 120

Sequence_Listing.txt

gctggtggaa gcagcttcag cagtgaagc agatgtggtc tggggggcag ctcgcccag 180
ggcttccgag gaggagccag cagctgcagc ctgagtggg ggtctagcg tgctttggg 240
ggcagcttg gagggggctt tgtagctgc tcagtagggg gtggtttgg gggagctca 300
ggctctggga caggatttg tgggggtct agcttggcg gggctctgg atttgcagg 360
ggttctggat tctgtgggag ttctagattc agcagtgtg ctactggagg ctctacagc 420
tatggtggtg gtatgggagg tgggttggc gatggggggc tttctctgg aggggaaaag 480
caaaccatgc agaacctcaa tgaccgttg gccaattacc tagacaaggc cagagccctg 540
gaggaggcta acactgatct ggagaacaaa atcaaggagt ggtatgaca atatggcct 600
gggtctggag acgttggatc gggaagagat tatagcaaat actattcaat aattgaagat 660
ctcagaaacc agatcattgc tgccactgt gaaaatgctg ggatcattt gcacattgac 720
aatgccagat tggctctga tgactcaga ctgaagtatg agaacgagct gtgtctccg 780
cagagcgtgg aggctgacat caatggcctg cggaagtcc tggatgacct gactatgacc 840
cgctctgacc tggagatgca gattgagagt ttaccgagg agctagccta cctgaggaag 900
aaccacgagg aggaaatgaa gaatatgcaa ggaagctctg gaggggagg gaccgtagaa 960
atgaatgctg cgccagggac cgacctgacc aaattactga atgacatgag ggcgagtag 1020
gaggagctgg ctgagcaaaa ccgccgagag gctgaggagc ggttaacaa gcagagcgca 1080
tcactacaag cacaatctc cactgatgt ggggcagcca ctctgcaa gaatgagata 1140
acagaactaa aacgtaccct gcaagccctg gaaattgagc ttactccca actggccatg 1200
aaaagctccc tggagggaac cctggctgac acagaagctg gctacgtggc tcagctgtca 1260
gaaattcaaa cgcagatcag tgccctggag gaggagatct gccagatctg ggtgagact 1320
aatgccaga acgcagagta caagcaattg ctggacatca agacacgcct ggaggtggag 1380

Sequence_Listing.txt

atcgagacct accgccgcct gctcgatgga gagggagggtg gttctagttt tgcagaattt 1440
 ggtggtagaa actcaggatc tgtaaacaatg ggatccaggg atctggtatc tggtgactca 1500
 agatctggaa gctgttctgg tcaaggacga gattcaagca agactagagt gactaagact 1560
 atcgtagagg agttgggtgga tggcaagggt gtcctgtctc aagtcagcag tatttctgag 1620
 gtgaaagtta aataaggaac ttccagatca acaaaagtgt ctttcaaaga aaaaaaaatc 1680
 aagaaggaca caagcgaaga aatggcatca atctaggcat ctttctggat aatttcagga 1740
 aaagcttcag tccagaaatg gatgactagc caacttttct gcatcttctt atttcctcat 1800
 tagaatgctc ttgaaatagc tgaattaaca actttgcttt aattgttct atgcttcaat 1860
 aaatttactt ttgcaagtta aaaaaaaaaa aaaaaaa 1897

<210> 42
 <211> 525
 <212> PRT
 <213> Homo sapiens

<400> 42
 Met Ser Cys Ser Ser Arg Ala Ser Ser Ser Arg Ala Gly Gly Ser Ser
 1 5 10 15

Ser Ala Arg Val Ser Ala Gly Gly Ser Ser Phe Ser Ser Gly Ser Arg
 20 25 30

Cys Gly Leu Gly Gly Ser Ser Ala Gln Gly Phe Arg Gly Gly Ala Ser
 35 40 45

Ser Cys Ser Leu Ser Gly Gly Ser Ser Gly Ala Phe Gly Gly Ser Phe
 50 55 60

Gly Gly Gly Phe Gly Ser Cys Ser Val Gly Gly Gly Phe Gly Gly Ala

Sequence_Listing.txt

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

Sequence_Listing.txt

Arg Gln Ser Val Glu Ala Asp Ile Asn Gly Leu Arg Lys Val Leu Asp
245 250 255

Asp Leu Thr Met Thr Arg Ser Asp Leu Glu Met Gln Ile Glu Ser Phe
260 265 270

Thr Glu Glu Leu Ala Tyr Leu Arg Lys Asn His Glu Glu Glu Met Lys
275 280 285

Asn Met Gln Gly Ser Ser Gly Gly Glu Val Thr Val Glu Met Asn Ala
290 295 300

Ala Pro Gly Thr Asp Leu Thr Lys Leu Leu Asn Asp Met Arg Ala Gln
305 310 315 320

Tyr Glu Glu Leu Ala Glu Gln Asn Arg Arg Glu Ala Glu Glu Arg Phe
325 330 335

Asn Lys Gln Ser Ala Ser Leu Gln Ala Gln Ile Ser Thr Asp Ala Gly
340 345 350

Ala Ala Thr Ser Ala Lys Asn Glu Ile Thr Glu Leu Lys Arg Thr Leu
355 360 365

Gln Ala Leu Glu Ile Glu Leu Gln Ser Gln Leu Ala Met Lys Ser Ser
370 375 380

Leu Glu Gly Thr Leu Ala Asp Thr Glu Ala Gly Tyr Val Ala Gln Leu
385 390 395 400

Ser Glu Ile Gln Thr Gln Ile Ser Ala Leu Glu Glu Glu Ile Cys Gln

Sequence_Listing.txt

405

410

415

Ile Trp Gly Glu Thr Lys Cys Gln Asn Ala Glu Tyr Lys Gln Leu Leu
420 425 430

Asp Ile Lys Thr Arg Leu Glu Val Glu Ile Glu Thr Tyr Arg Arg Leu
435 440 445

Leu Asp Gly Glu Gly Gly Gly Ser Ser Phe Ala Glu Phe Gly Gly Arg
450 455 460

Asn Ser Gly Ser Val Asn Met Gly Ser Arg Asp Leu Val Ser Gly Asp
465 470 475 480

Ser Arg Ser Gly Ser Cys Ser Gly Gln Gly Arg Asp Ser Ser Lys Thr
485 490 495

Arg Val Thr Lys Thr Ile Val Glu Glu Leu Val Asp Gly Lys Val Val
500 505 510

Ser Ser Gln Val Ser Ser Ile Ser Glu Val Lys Val Lys
515 520 525

<210> 43

<211> 1283

<212> DNA

<213> Homo sapiens

<400> 43

attctaaccg caaggagtag cggaggggag gtcgtgatgg cggcgccgga ggcggaggtt 60

ctgtcctcag ccgcagtccc tgatttgag tggtatgaga agtccgaaga aactcacgcc 120

tccagatag aactactga gacaagctct acgcaggaac ctctcaacgc ttcggaggcc 180

Sequence_Listing.txt

```

tttgcccaa gagactgcat ggtaccagt gtgtttctg ggctgtgag ccaggaaggc 240
tgctgtcagt ttactgtga acttctaaag cataatcatgt atcaacgcc aacagtcct 300
ctgccctatg aacagcttaa gcactttac cgaaaacctt cccccaggc agaggagatg 360
ctgaagaaga aacctcgggc caccactgag gtgagcagca ggaaatgcc acaagccctg 420
gcagaactgg agagtgtcct cagccacctg gaggacttct ttgcacggac actagtaccg 480
cgagtgtga ttctccttg gggcaatgcc ctaagcccca aggagttcta tgaactcgac 540
ttgtctctg tggcccccta cagcgtggac cagagcctga gcacagcagc ttgttgccg 600
cgtctctcc gagccatatt catggctgat gcctttagcg agcttcaggc tctccactc 660
atgggcaccg tcgtcatggc acaggacac cgcaactgtg gagaagattg gttcgacc 720
aagctcaact atcgagtgc cagccggggc cataaactga ctgtgacct gtcagtggc 780
agacctcca tccgaaccac ggctgggaa gactacattt ggttcaggc accagtgaca 840
tttaaaggct tccgagtg aatgagtgt tctaatcct aaaaacacaa tggctgaatt 900
atcttctcc atgtggcgt gaatcaccca tctggttg agctagagt gcttctggt 960
gagagaggaa gcaactctc ttctggtgt ctgcctccc tcagattcc tgataggctg 1020
atggcatgtg gctgtgactg tgaactaat cattgtgaa caacatctt ttgaatcaaa 1080
ggttgattt cccagagggg gctgggtcag gcatttctat taggagttg aaagcaaaaa 1140
tgggtccata gacactctat ggaggtgtc cttctgctc ttgctgtgt ctttcagaa 1200
ttttaccag gaacataatg tggatgtgac ttatgaactt aaatataaaa taaatagatt 1260
cttattatat ttctgaaa aaa 1283

```

<210> 44
<211> 274

Sequence_Listing.txt

<212> PRT

<213> Homo sapiens

<400> 44

Met Ala Ala Pro Glu Ala Glu Val Leu Ser Ser Ala Ala Val Pro Asp

1 5 10 15

Leu Glu Trp Tyr Glu Lys Ser Glu Glu Thr His Ala Ser Gln Ile Glu

20 25 30

Leu Leu Glu Thr Ser Ser Thr Gln Glu Pro Leu Asn Ala Ser Glu Ala

35 40 45

Phe Cys Pro Arg Asp Cys Met Val Pro Val Val Phe Pro Gly Pro Val

50 55 60

Ser Gln Glu Gly Cys Cys Gln Phe Thr Cys Glu Leu Leu Lys His Ile

65 70 75 80

Met Tyr Gln Arg Gln Gln Leu Pro Leu Pro Tyr Glu Gln Leu Lys His

85 90 95

Phe Tyr Arg Lys Pro Ser Pro Gln Ala Glu Glu Met Leu Lys Lys Lys

100 105 110

Pro Arg Ala Thr Thr Glu Val Ser Ser Arg Lys Cys Gln Gln Ala Leu

115 120 125

Ala Glu Leu Glu Ser Val Leu Ser His Leu Glu Asp Phe Phe Ala Arg

130 135 140

Thr Leu Val Pro Arg Val Leu Ile Leu Leu Gly Gly Asn Ala Leu Ser

145 150 155 160

Sequence_Listing.txt

Pro Lys Glu Phe Tyr Glu Leu Asp Leu Ser Leu Leu Ala Pro Tyr Ser
165 170 175

Val Asp Gln Ser Leu Ser Thr Ala Ala Cys Leu Arg Arg Leu Phe Arg
180 185 190

Ala Ile Phe Met Ala Asp Ala Phe Ser Glu Leu Gln Ala Pro Pro Leu
195 200 205

Met Gly Thr Val Val Met Ala Gln Gly His Arg Asn Cys Gly Glu Asp
210 215 220

Trp Phe Arg Pro Lys Leu Asn Tyr Arg Val Pro Ser Arg Gly His Lys
225 230 235 240

Leu Thr Val Thr Leu Ser Cys Gly Arg Pro Ser Ile Arg Thr Thr Ala
245 250 255

Trp Glu Asp Tyr Ile Trp Phe Gln Ala Pro Val Thr Phe Lys Gly Phe
260 265 270

Arg Glu

<210> 45

<211> 2297

<212> DNA

<213> Homo sapiens

<400> 45

aaccacaaaa cccgccaggc cggtcggga gctgcggagc atccgctgcg gtctcgccg 60

Sequence_Listing.txt

agacccccgc gcggattcgc cggtccttcc cgcgggcgcg acagagctgt cctcgcacct 120
 ggatggcagc aggggcgcgc gggtcctctc gacgccagag agaaatctca tcactgtgc 180
 agccttcta aagcaaacta agaccagagg gaggattatc cttgacctt gaagaccaa 240
 actaaactga aatttaaat gtcttcggg ggagaaggga gctgactta cactttgta 300
 ataattgct tcctgacact aaggctgtct gctagtcaga attgcctcaa aaagagtcta 360
 gaagatgtg tcattgacat ccagtcactt ctttctaagg gaatcagagg caatgagccc 420
 gtatatactt caactcaaga agactgcatt aattcttgc gtcaacaaa aaacataatca 480
 ggggacaaag catgtaactt gatgatcttc gacactcgaa aaacagctag acaaccaaac 540
 tgctacctat tttctgtcc caacgaggaa gccgtccat tgaaccagc aaaaggactt 600
 atgagtaca ggataattac agattttcca tcttgacca gaaattgcc aagccaagag 660
 ttacccagg aagattctct ctacatggc caattttcac aagcagtcac tcccctagcc 720
 catcatcaca cagattatc aaagcccacc gatctctcat ggagagacac actttctcag 780
 aagttggat cctcagatca ctggagaaa ctatttaaga tggatgaagc aagtgccag 840
 ctctgtctt ataaggaaaa aggccattct cagagttcac aatttcctc tgatcaagaa 900
 atagctatc tgcgtcctga aaatgtgagt gcgtcccag ctacggtggc agttgcttct 960
 ccacatacca cctgggtac tcaaagccc gccacccttc taccaccaa tgcttcagt 1020
 acaccttctg ggacttcca gccacagctg gccaccacag ctccacctgt aaccactgtc 1080
 acttctcagc ctcccagac cctcatttct acagtttta cacgggctgc ggctacactc 1140
 caagcaatgg ctacaacagc agttctgact accaccttc aggcacctac ggactcgaaa 1200
 ggcagcttag aaaccatacc gtttacagaa atctccaacc taacttgaa cacagggaat 1260
 gtgtataacc ctactgcact ttctatgtca aatgtggagt ctccactat gaataaaact 1320

Sequence_Listing.txt

gcttcctggg aaggtaggga ggccagttca ggcagttcct cccagggcag tgttcagaa 1380
aatcagtagc gccttcatt tgaaaaatgg ctcttalcg ggtccctgct ctttggtgtc 1440
ctgttcctgg tgataggcct cgtcctcctg ggtagaatcc tctcggaatc actccgcagg 1500
aaacgttact caagactgga ttattgatc aatgggatct atgtggacat ctaaggatgg 1560
aactcgggtg ctcttaatc atttagtaac cagaagccca aatgcaatga gtttctgctg 1620
acttgctagt ctagcagga ggttgatatt tgaagacagg aaaatgcccc ctctgcttt 1680
ccttttttt tttggagac agagtctgc ttgttgccc aggctggagt gcagtagcac 1740
gatctcggct ctcaccgcaa cctccgtctc ctgggttcaa gcgattctcc tgccacagcc 1800
tcctaagtat ctgggattac aggcatgtc caccacacct gggatgattt tgtatttta 1860
gtagagacgg gggttcacca tgttggtcag gctgggtcga aactcctgac ctatgatcc 1920
accctcctcg gcctcccaaa gtgctgggat tacaggcatg agccaccaca gctggcccc 1980
ttctgttta tgttggttt ttgagaagga atgaagtggg aaccaaatta ggtaatttg 2040
ggtaatctgt ctctaaaata tttagtaaaa acaaagctct atgtaaagta ataaagtata 2100
attgcatat aaattcaaa attcaactgg ctcttatgca aagaaacagg ttaggacatc 2160
taggttccaa ttattcaca ttcttggtc cagataaaat caactgttta tatcaatttc 2220
taatggattt gctttcttt ttatatggat tccttataaa ctattccag atgtagttcc 2280
ttccaattaa atatttg 2297

<210> 46

<211> 431

<212> PRT

<213> Homo sapiens

<400> 46

Met Phe Phe Gly Gly Glu Gly Ser Leu Thr Tyr Thr Leu Val Ile Ile

Sequence_Listing.txt

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

Sequence_Listing.txt

Gly Ser Ser Asp His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser
180 185 190

Ala Gln Leu Leu Ala Tyr Lys Glu Lys Gly His Ser Gln Ser Ser Gln
195 200 205

Phe Ser Ser Asp Gln Glu Ile Ala His Leu Leu Pro Glu Asn Val Ser
210 215 220

Ala Leu Pro Ala Thr Val Ala Val Ala Ser Pro His Thr Thr Ser Ala
225 230 235 240

Thr Pro Lys Pro Ala Thr Leu Leu Pro Thr Asn Ala Ser Val Thr Pro
245 250 255

Ser Gly Thr Ser Gln Pro Gln Leu Ala Thr Thr Ala Pro Pro Val Thr
260 265 270

Thr Val Thr Ser Gln Pro Pro Thr Thr Leu Ile Ser Thr Val Phe Thr
275 280 285

Arg Ala Ala Ala Thr Leu Gln Ala Met Ala Thr Thr Ala Val Leu Thr
290 295 300

Thr Thr Phe Gln Ala Pro Thr Asp Ser Lys Gly Ser Leu Glu Thr Ile
305 310 315 320

Pro Phe Thr Glu Ile Ser Asn Leu Thr Leu Asn Thr Gly Asn Val Tyr
325 330 335

Asn Pro Thr Ala Leu Ser Met Ser Asn Val Glu Ser Ser Thr Met Asn

Sequence_Listing.txt

340 345 350

Lys Thr Ala Ser Trp Glu Gly Arg Glu Ala Ser Pro Gly Ser Ser Ser
355 360 365

Gln Gly Ser Val Pro Glu Asn Gln Tyr Gly Leu Pro Phe Glu Lys Trp
370 375 380

Leu Leu Ile Gly Ser Leu Leu Phe Gly Val Leu Phe Leu Val Ile Gly
385 390 395 400

Leu Val Leu Leu Gly Arg Ile Leu Ser Glu Ser Leu Arg Arg Lys Arg
405 410 415

Tyr Ser Arg Leu Asp Tyr Leu Ile Asn Gly Ile Tyr Val Asp Ile
420 425 430

<210> 47

<211> 1336

<212> DNA

<213> Homo sapiens

<400> 47

gcgagggtggg gtaggcgggc aaggcgggcg ccgagggttg caaaggctcg cagcggccag 60

aaacccggct ccgagcggcg gcggcccggc ttccgtgcc cgtgagctaa ggacggtccg 120

ctccctctag ccagctccga atcctgatcc aggcgggggc caggggcccc tcgctcccc 180

tctgaggacc gaagatgagc ttctcttca gcagccgctc ttctaaaaca ttcaaaccaa 240

agaagaatat ccctgaagga tctcatcagt atgaactctt aaaacatgca gaagcaactc 300

taggaagtgg gaatctgaga caagctgtta tgtgcctga gggagaggat ctcaatgaat 360

ggattgctgt gaacactgtg gatttctta accagatcaa catgttatat ggaactatta 420

Sequence_Listing.txt

cagaattctg cactgaagca agctgtccag tcatgtctgc aggtccgaga tatgaatac 480
actgggcaga tggactaat attaaaaagc caatcaaatg ttctgcacca aaatacattg 540
actattgat gacttgggtt caagatcagc ttgatgatga aactctttt ccttctaaga 600
ttggtgtccc atttccaaa aactttatgt ctgtggcaaa gactattcta aagcgtctgt 660
tcagggttta tgccatatt taccaccagc actttgattc tgtgatgcag ctgcaagagg 720
agggccacct caacacctcc ttaagcact ttatttctt tgttcaggag ttaacttga 780
ttgataggcg tgagctggca cctctcaag aattaataga gaaacttga tcaaaagaca 840
gataaatgtt tctttagaa cacagttacc ccttgcctc atctattgct agaactatct 900
cattgctatc tgttatagac tagtgataca aactttaaga aaacaggata aaaagatacc 960
cattgcctgt gtctactgat aaaattatcc caaaggtagg ttggtgtgat agttccgag 1020
taagacctta aggacacagc caaatctaa gtactgtgtg accactctg ttgtatcac 1080
atagcatatc ttggtgttaa tatgtgatgg ttaacctga gctataaat ttactatta 1140
ttctttact catttactca gtcatttct tacaagaaa tgattgaac tgttttaggt 1200
gacagcacia tggacattaa gaattccat caataattt tgaataagt tccagaacia 1260
atttctaata aacacaatca gattggttt attctttat ttacgaata aaaaatgtat 1320
tttcagtaa aaaaaa 1336

<210> 48
<211> 216
<212> PRT
<213> Homo sapiens

<400> 48
Met Ser Phe Leu Phe Ser Ser Arg Ser Ser Lys Thr Phe Lys Pro Lys
1 5 10 15

Sequence_Listing.txt

Lys Asn Ile Pro Glu Gly Ser His Gln Tyr Glu Leu Leu Lys His Ala
20 25 30

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

Glu Gly Glu Asp Leu Asn Glu Trp Ile Ala Val Asn Thr Val Asp Phe
50 55 60

Phe Asn Gln Ile Asn Met Leu Tyr Gly Thr Ile Thr Glu Phe Cys Thr
65 70 75 80

Glu Ala Ser Cys Pro Val Met Ser Ala Gly Pro Arg Tyr Glu Tyr His
85 90 95

Trp Ala Asp Gly Thr Asn Ile Lys Lys Pro Ile Lys Cys Ser Ala Pro
100 105 110

Lys Tyr Ile Asp Tyr Leu Met Thr Trp Val Gln Asp Gln Leu Asp Asp
115 120 125

Glu Thr Leu Phe Pro Ser Lys Ile Gly Val Pro Phe Pro Lys Asn Phe
130 135 140

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

His Ile Tyr His Gln His Phe Asp Ser Val Met Gln Leu Gln Glu Glu
165 170 175

Sequence_Listing.txt

Ala His Leu Asn Thr Ser Phe Lys His Phe Ile Phe Phe Val Gln Glu
180 185 190

Phe Asn Leu Ile Asp Arg Arg Glu Leu Ala Pro Leu Gln Glu Leu Ile
195 200 205

Glu Lys Leu Gly Ser Lys Asp Arg
210 215

<210> 49
<211> 5381
<212> DNA
<213> Homo sapiens

<400> 49
attgagaggc caccgggaaa ccattgagaa gccccggagg accggcctga gcggaggcgg 60
agactagagc ggccgcccgc acgacccgcc ttcaggcgta cgacgaccgc ggccccgggg 120
ctctgagtgg ccaaagcggc ggcactttct gcgtggcccc ggaaggacat agagcggaag 180
gcgggagaaa gaagtagccg gcaggcggag gcagcccag ggggcggttg catgtgtgcc 240
agacgttcgt agcccactga gcttctcac gccggctgtc gcagcgcta gccccaccg 300
gcggcctctc ctgcgttcc ggggccgtgg cgagctagt cgctgcgtg ccggcccatc 360
cgcgcgctt gcagctgtcc ttgcgtcggc cagcgccag acagttctg cagcgcttac 420
cgctggcct ctgggttccg cggcgcaccg gagggcagca tgcgcggcg gcggcacagc 480
gacgagaacg acggtgggca gcctcacaaa aggagaaaga cctctgatgc aatgaaact 540
gaagatcatt tggaatctt aatatgaaa gtaggagaaa agagtgcctg ctcttggag 600
agcaacctag aaggcttggc tgggttttg gaagctgac ttctaacta caagagcaag 660
atcttaaggc ttcttgtac agttgcacgc ctattacctg agaagctgac aattatata 720

Sequence_Listing.txt

acattagtgtg gactactgaa tgccaggaat tacaattttg gtggagaatt ttagaagcc 780

atgattcgtc aacttaaaga atcattgaaa gcaaacaatt ataataagc cgtgtatttg 840

gtccgttttt tatctgatct tgtgaattgt catgtgattg ccgccccatc aatgggtgct 900

atgtttgaaa attttgaag cgtaactcag gaagaagatg tacctcaggt gcgacgagat 960

tggtatgtgt atgcatttct gtacattttg ccttgggttg gaaaggagtt gtacgaaaag 1020

aaagatgcag agatggaccg catctttgcc aacctgaaa gctatcttaa aagacgccaa 1080

aagactcatg taccatgtt acaggtatgg actgctgata aaccacatcc acaagaagag 1140

tatttagatt gctgtgggc ccagattcag aaattgaaaa aggatcgctg gcaggaacgg 1200

cacatcctaa gacctatct tgccttgac agcatcctgt gtgaagcact gcagcacaat 1260

ctgcctcctt ttacaccacc tctcacact gaagattcag tgtaccaat gccaaaggtc 1320

atcttcagaa tgttgatta cacagatgat cccgaggggc ctgtcatgcc agggagtcac 1380

tcagtggaaa gatttgaat agaagagaat cttactgca tcattaagtc cactggaag 1440

gaaaggaaga ctgtgtctgc acagttatgt agctatccag ggaagaacaa gatccccttg 1500

aactaccaca tagttgaggt gatctttgca gagctgttc aactccagc accccctcac 1560

attgatgtga tttacacaac actcctcatt gaactgtgca aactcaacc tggctctcta 1620

ccccaagttc ttgcacaggc aactgaaatg ctatacatgc gtttgacac aatgaacact 1680

acctgtgtag acaggtttat taattggttt tctcatcacc taagtaactt ccagttccgt 1740

tggagctggg aagattggc agattgtctt agtcaagatc ctgaaagtcc caaacgaag 1800

tttgaagag aagtctaga aaaatgtatg aggtgtctt accatcagcg tatattagat 1860

attgttcctc ctacctctc agctctgtgt cctgcaaacc caacctgcat ttacaagtat 1920

ggagatgaaa gtagcaattc tcttctgga cattctgttg ccctctgttt agctgttgcc 1980

Sequence_Listing.txt

tttaaaagta aggcaaccaa tgatgaaatc ttcagcattc tgaaagatgt accaaatcct 2040
aaccaggatg atgacgacga tgaaggattc agttttaacc cattgaaaat agaagctttt 2100
gtacagactc tgctacactt ggcagccaaa tcattcagcc actccttcag tgctcttgca 2160
aagtttcag aagcttcaa aaccctagct gaaagtgatg aaggaaagtt acatgtgcta 2220
agagttatgt ttgaggtctg gaggaacat ccacagatga ttgctgtact agtggataag 2280
atgattcgta cacaaatagt tgattgtgct gccgtagcaa attggatctt ctcttcagaa 2340
ctatctctg actttaccag attgtttgtt tgggaaattt tgcactctac aattcgtaag 2400
atgaacaaac atgtcctgaa gatccagaaa gagctggaag aagctaaaga gaaacttgct 2460
aggcaacaca aacggcggaag tgatgatgac gacagaagca gtgacaggaa agacgggggt 2520
cttgaggaac aaatagaacg acttcaggaa aaagtggaat ctgctcagag tgaacaaaag 2580
aatcttttc tegtatat ttagcggtt atcatgatct tgaccgagca cctagtacga 2640
tgcgaaactg atgggaccag tgtattaaca ccatggtata agaactgtat agagaggctg 2700
cagcagatct tcttacagca tcaccaaata atccagcagt acatggtgac cctggagaac 2760
cttctctca ctgctgaatt agaccctcat atctggccg tgttcagca gttctgtgcc 2820
ctgcaggcct aagggtcatt tttcctcat gtcaagggtt ttttgatat cttaaaataa 2880
ttgtcttat ttttgatgg ttgaatgct tgcttcttg tagtatcctt tcacttcta 2940
aaggaaacaa aggggaagag gacagtgaat gaacatggca ttacttttaa ttgccctgaa 3000
aagcaaatac ttctaacgg cagtaatgtg actatgacca tgatatatta tatatgtgac 3060
agatacaaat tctctgigat cagtttgta ttttttct ccttaaggca caaaataatt 3120
ggttgaggt atgtgaaaca cttaggtca acctacata gtatatagaa ctgatgggtt 3180
taccagcta ccagtagca taactttca cagctcgggg atgaattaac atggctgaaa 3240

Sequence_Listing.txt

taaaactaaa agtatgggtt ttaaactttg gcatttcacg atttatcatc tcactctact 3300
 ctaaaactgg tggtttcta ctgaagggtg tcgccatttg aaattttatc ttcaaagtat 3360
 ttttaagtag tatctttaag acatgacttg ttagtaataa aagtgttact agttggaaga 3420
 gtgacttca aatttgtctt aatgtaaac accctgggaat cttcaagtt attttgaaat 3480
 ttaaaccacc gtcgtggggg ggaacgcaga catcctcagt aatccttaa gttccccag 3540
 gtgattccag gtttggtcac cattatcta gagcatctac tcacttcctc tagccttggg 3600
 gttattgtc caaggcttg tagtgagtta cagaatacta aagtggatgt agaagtggc 3660
 agattgactg aaactatacc ctgaattaga tgtgagttta gattttgtt atatggaacc 3720
 tgatccaaaa aactacgaag tcctgagctt gtttctgta tagtactgat gctgaaataa 3780
 gatgacagca gtttgtaaaa taatacacia atatgaggaa ttgtctgaca ttccaaattt 3840
 cgaggatttt tagacttttt tcattaaacc ttgaaaaaa attaccagta atcctacaac 3900
 tactggtagt gttgtgtgc atttgcacaa aataggtata atttttctt attacatccc 3960
 aagttatga tgcattaaag gttttgcata ttttgatata ttttgcttt ggtttaccat 4020
 acattttagt ggctacagaa ttagtctgc ttaataaatg ggaattccta gaatgtttaa 4080
 ataccatact atttaagaca aaatacaaaa tatccagaaa aatccagggt gcgtggctgg 4140
 ttagtaaagg actaaaaccc aggttcttg cttaaatttt tcgtttatac tgtttatctt 4200
 tccattgct taagcacagc acaaactatg taattatata taattacagt tgacccttga 4260
 acaacatggg ttgaactgt gtgagtctcc ttacacacag gtttcttcc acccctgaga 4320
 tggcaagacc agcccctgt cttcctcagc ctgctcaacg tgaagatgat gaggatgaag 4380
 accttatga tgatccactt ctactatta aatagtaa atatttttt cttatgattt 4440
 tattttctt tcctagctt cataagaata tagcatatgg gctgggcgca gtggctcag 4500

Sequence_Listing.txt

cctgtaatcc cagcactttg ggaggctgag gcgggcggat cacaaggtca ggagattgag 4560
 accatcctgg ctaacacagt gaaaccctgt ctctactaaa aacacaaaaa ctagccagg 4620
 cgtggtggta catggctgta gtcccagcta cttgggaggc tgagacagga gaatcgcttg 4680
 aacctgggag gtggagggtt cagttagcca agattgtgcc actgcactcc agcctgggtg 4740
 atggagcgag gctctgtctc aaaaaagaaa aaaaatata agcatataac atacaaaatg 4800
 agtttatcaa ctgtttgta ttgtaagtc agcagtgggc tattggtggt taagttttg 4860
 gggagtcaaa agttacatgc aaattttta ctgtcgggg tgcagcatc cctaacccca 4920
 tgttgtcaa gggcaactg tagtttaaaa tgactcctgt ctcaaaaaac caaaggataa 4980
 ccttaaggg attgtaact ttgactcaaa actgctttgt aatctttca caatgtactg 5040
 aaaagtgtg ctagttaagt ttgatccaca ttctagagaa attgtaggt ttaatttct 5100
 ttctcttg tctctctc atgtataatg gttgcttta acagctgttc gctgatgtg 5160
 tctgctctg tccagctca gcagctttag tgatggaaa aattgaacta ggaattgagt 5220
 ttgaagaaa taaagggtga agagcaaaca ttcaacagtt gctgtccca gtaatgaagt 5280
 tcatacagac aaaagatggc atgtcactgt acatcatacc ttgcaataaa tattctgtta 5340
 aattgtgctg gtgcaattta acatgcttt gtcaaagtaa a 5381

<210> 50

<211> 790

<212> PRT

<213> Homo sapiens

<400> 50

Met Ser Arg Arg His Ser Asp Glu Asn Asp Gly Gly Gln Pro His

1 5 10 15

Lys Arg Arg Lys Thr Ser Asp Ala Asn Glu Thr Glu Asp His Leu Glu

Sequence_Listing.txt

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

Sequence_Listing.txt

Asp Arg Ile Phe Ala Asn Thr Glu Ser Tyr Leu Lys Arg Arg Gln Lys
195 200 205

Thr His Val Pro Met Leu Gln Val Trp Thr Ala Asp Lys Pro His Pro
210 215 220

Gln Glu Glu Tyr Leu Asp Cys Leu Trp Ala Gln Ile Gln Lys Leu Lys
225 230 235 240

Lys Asp Arg Trp Gln Glu Arg His Ile Leu Arg Pro Tyr Leu Ala Phe
245 250 255

Asp Ser Ile Leu Cys Glu Ala Leu Gln His Asn Leu Pro Pro Phe Thr
260 265 270

Pro Pro Pro His Thr Glu Asp Ser Val Tyr Pro Met Pro Arg Val Ile
275 280 285

Phe Arg Met Phe Asp Tyr Thr Asp Asp Pro Glu Gly Pro Val Met Pro
290 295 300

Gly Ser His Ser Val Glu Arg Phe Val Ile Glu Glu Asn Leu His Cys
305 310 315 320

Ile Ile Lys Ser His Trp Lys Glu Arg Lys Thr Cys Ala Ala Gln Leu
325 330 335

Val Ser Tyr Pro Gly Lys Asn Lys Ile Pro Leu Asn Tyr His Ile Val
340 345 350

Glu Val Ile Phe Ala Glu Leu Phe Gln Leu Pro Ala Pro Pro His Ile

Sequence_Listing.txt

355 360 365

Asp Val Met Tyr Thr Thr Leu Leu Ile Glu Leu Cys Lys Leu Gln Pro
370 375 380

Gly Ser Leu Pro Gln Val Leu Ala Gln Ala Thr Glu Met Leu Tyr Met
385 390 395 400

Arg Leu Asp Thr Met Asn Thr Thr Cys Val Asp Arg Phe Ile Asn Trp
405 410 415

Phe Ser His His Leu Ser Asn Phe Gln Phe Arg Trp Ser Trp Glu Asp
420 425 430

Trp Ser Asp Cys Leu Ser Gln Asp Pro Glu Ser Pro Lys Pro Lys Phe
435 440 445

Val Arg Glu Val Leu Glu Lys Cys Met Arg Leu Ser Tyr His Gln Arg
450 455 460

Ile Leu Asp Ile Val Pro Pro Thr Phe Ser Ala Leu Cys Pro Ala Asn
465 470 475 480

Pro Thr Cys Ile Tyr Lys Tyr Gly Asp Glu Ser Ser Asn Ser Leu Pro
485 490 495

Gly His Ser Val Ala Leu Cys Leu Ala Val Ala Phe Lys Ser Lys Ala
500 505 510

Thr Asn Asp Glu Ile Phe Ser Ile Leu Lys Asp Val Pro Asn Pro Asn
515 520 525

Sequence_Listing.txt

Gln Asp Asp Asp Asp Asp Glu Gly Phe Ser Phe Asn Pro Leu Lys Ile
530 535 540

Glu Val Phe Val Gln Thr Leu Leu His Leu Ala Ala Lys Ser Phe Ser
545 550 555 560

His Ser Phe Ser Ala Leu Ala Lys Phe His Glu Val Phe Lys Thr Leu
565 570 575

Ala Glu Ser Asp Glu Gly Lys Leu His Val Leu Arg Val Met Phe Glu
580 585 590

Val Trp Arg Asn His Pro Gln Met Ile Ala Val Leu Val Asp Lys Met
595 600 605

Ile Arg Thr Gln Ile Val Asp Cys Ala Ala Val Ala Asn Trp Ile Phe
610 615 620

Ser Ser Glu Leu Ser Arg Asp Phe Thr Arg Leu Phe Val Trp Glu Ile
625 630 635 640

Leu His Ser Thr Ile Arg Lys Met Asn Lys His Val Leu Lys Ile Gln
645 650 655

Lys Glu Leu Glu Glu Ala Lys Glu Lys Leu Ala Arg Gln His Lys Arg
660 665 670

Arg Ser Asp Asp Asp Asp Arg Ser Ser Asp Arg Lys Asp Gly Val Leu
675 680 685

Glu Glu Gln Ile Glu Arg Leu Gln Glu Lys Val Glu Ser Ala Gln Ser

Sequence_Listing.txt

690 695 700

Glu Gln Lys Asn Leu Phe Leu Val Ile Phe Gln Arg Phe Ile Met Ile
705 710 715 720

Leu Thr Glu His Leu Val Arg Cys Glu Thr Asp Gly Thr Ser Val Leu
725 730 735

Thr Pro Trp Tyr Lys Asn Cys Ile Glu Arg Leu Gln Gln Ile Phe Leu
740 745 750

Gln His His Gln Ile Ile Gln Gln Tyr Met Val Thr Leu Glu Asn Leu
755 760 765

Leu Phe Thr Ala Glu Leu Asp Pro His Ile Leu Ala Val Phe Gln Gln
770 775 780

Phe Cys Ala Leu Gln Ala
785 790

<210> 51
<211> 818
<212> DNA
<213> Homo sapiens

<400> 51
agtcctgtgt ccgggccccg aggcacagcc agggcaccag gtggagcacc agctacgcgt 60
ggcgcagcgc agcgtcccta gcaccgagcc tccgcagcc gccgagatgc tgcgaacaga 120
gagctgccgc cccaggctgc ccgccggaca ggtggccgcg gcgtccccgc tctgctgct 180
gctgctgctg ctgcctggt gcgcgggcgc ctgccgaggt gctccaatat tacctcaagg 240
attacagcct gaacaacagc tacagttgtg gaatgagata gatgatactt gtctgtcttt 300

Sequence_Listing.txt

```
tctgtccatt gattctcagc ctcaggcatc caacgcactg gaggagcttt gctttatgat    360
tatgggaatg ctaccaaagc ctcaggaaca agatgaaaaa gataatacta aaaggttctt    420
atttcattat tcgaagacac agaagttggg caagtcaa atgtgtgtcgt cagttgtgca    480
tccgttgctg cagctcgttc ctcacctgca tgagagaaga atgaagagat tcagagtgga    540
cgaagaattc caaagtcctt ttgcaagtca aagtcgagga tattttttat tcaggccacg    600
gaatggaaga aggtcagcag ggttcattta aaatggatgc cagctaattt tccacagagc    660
aatgctatgg aatacaaaat gtactgacat ttgttttct tctgaaaaaa atccttgcta    720
aatgtactct gttgaaaatc cctgtgttgt caatgttctc agttgtaaca atgttgtaaa    780
tgttcaattt gttgaaaatt aaaaaatcta aaaataaa                                818
```

```
<210> 52
<211> 174
<212> PRT
<213> Homo sapiens
```

```
<400> 52
Met Leu Arg Thr Glu Ser Cys Arg Pro Arg Ser Pro Ala Gly Gln Val
1      5      10      15
```

```
Ala Ala Ala Ser Pro Leu Leu Leu Leu Leu Leu Leu Ala Trp Cys
20      25      30
```

```
Ala Gly Ala Cys Arg Gly Ala Pro Ile Leu Pro Gln Gly Leu Gln Pro
35      40      45
```

```
Glu Gln Gln Leu Gln Leu Trp Asn Glu Ile Asp Asp Thr Cys Ser Ser
50      55      60
```

Sequence_Listing.txt

Phe Leu Ser Ile Asp Ser Gln Pro Gln Ala Ser Asn Ala Leu Glu Glu
65 70 75 80

Leu Cys Phe Met Ile Met Gly Met Leu Pro Lys Pro Gln Glu Gln Asp
85 90 95

Glu Lys Asp Asn Thr Lys Arg Phe Leu Phe His Tyr Ser Lys Thr Gln
100 105 110

Lys Leu Gly Lys Ser Asn Val Val Ser Ser Val Val His Pro Leu Leu
115 120 125

Gln Leu Val Pro His Leu His Glu Arg Arg Met Lys Arg Phe Arg Val
130 135 140

Asp Glu Glu Phe Gln Ser Pro Phe Ala Ser Gln Ser Arg Gly Tyr Phe
145 150 155 160

Leu Phe Arg Pro Arg Asn Gly Arg Arg Ser Ala Gly Phe Ile
165 170

<210> 53

<211> 5849

<212> DNA

<213> Homo sapiens

<400> 53

gcgttccttg cggcccggcc gacctcgcgg gcttgggcct gggcgggcac cgacggagcg 60

gccctggctg cagcctcccg gcgccagcga agacaggctg agatgcggct gctcctgctc 120

gtgccgctgc tgctggctcc agcggccggg tcctcggctc ccaaggtgag gcggcagagt 180

gacacctggg gacctggag ccagtggagc ccctgcagcc ggacctgtgg aggggggtgc 240

Sequence_Listing.txt

agcttccggg agcgccctg ctactcccag aggagagatg gaggctccag ctgctgggc 300

ccgccccga gccaccgctc ttgtgcacg gagagctgcc ccgacggcgc ccgggacttc 360

cgggccgagc agtgcgcga gttcgacga gcggagtcc aggggcggcg gtatcggtg 420

ctgccctact acagcgcgcc aaacaagtgt gaactgaact gcattccaa gggggagaac 480

ttctactaca agcacaggga ggtgtggt gatgggacgc cctgcgagcc tggcaagagg 540

gatgtctgtg tggatggcag ctgccgggtt gtcggctgtg atcacgagct ggactcgtcc 600

aagcaggagg acaagtgtct gcggtgtggg ggtgacggca cgacctgcta ccccgctgca 660

ggcaccttg acgctaata cctcagccga gctgtgaaga atgttcgtgg ggaatactac 720

ctcaatgggc actggacat cgaggcggcc cgggccctgc cagcagccag caccatcctg 780

cattacgagc ggggtgctga gggggacctg gccctgagc gactccatgc ccggggcccc 840

acctcggagc ccctggtcat cgagctcatc agccaggagc ccaaccccg tgtgcactat 900

gagtaccacc tgccccgcg ccgcccagc cccggctca gctggagcca cggctcatgg 960

agtactgca gcgcggagtg tggcggaggc caccagtccc gcctggtgtt ctgcaccatc 1020

gacctgagg cctaccccga ccacatgtc cagcgcagc cacggccagc tgaccggcgt 1080

tcctgcaatc ttacccttg cccggagacc aagcgtgga aggcagggcc atgggcaccc 1140

tgctcagcct cctgtggagg aggtcccag tccgctccg tgtactcat ctgctgac 1200

ggggccggca tccaggaggc cgtggaggag gctgagtgt cgggctgcc tgggaagccc 1260

cctgccatc aggcctgtaa cctgcagcgc tgtcagcct ggagcccga gccctgggga 1320

gagtgtctg tcagtgtgg cgtggcgc cggaagcga gcgttactg ccggggtgaa 1380

aggggtctt tgcctcatc cgcagcgtc tcctggaag accggccacc tctgactgag 1440

ccctgtgtc atgaggactg cccctctc agtgaccagg cctggcatgt tggcacctgg 1500

Sequence_Listing.txt

ggtctatgct ccaagagctg cagctcgggc actcggaggc gacaggatcat ctgtgccatt 1560
 gggccgcccc gccactgcgg gagcctgcag cactccaagc ctgtggatgt ggagccttgt 1620
 aacacgcagc cctgtcatct cccccaggag gtccccagca tgcaggatgt gcacaccct 1680
 gccagcaacc cctggatgcc gtggggccct caggagtcct ctgcctcaga ctccagaggc 1740
 cagtgggtggg cagcccagga acacccctca gccaggggtg accacagggg agaacgaggt 1800
 gaccccaggg gcgaccaagg caccacctg tcagccctgg gcccgcctcc ctctctgcag 1860
 cagcccccat accagcaacc cctgcggtcg ggctcagggc cccacgactg cagacacagt 1920
 cctcacgggt gctgccccga tggccacacg gcattctcg ggctcagt gcaaggctgc 1980
 cctggggccc cctgtcagca gagcaggtag ggtgtctgcc ctgacagggt atctgtcgt 2040
 gaggggcccc atcacgttg ctgcacaaag tcgtatgtg gtgacagcac cgggggcatg 2100
 cccaggtaaa gggcagtggc ttctacagtc cacaacacc accagcccc ggcccagcag 2160
 aatgagccca gtgagtgcg gggctcccag ttggctgtt gctatgaaa cgtggccact 2220
 gcagccggtc ctctgggga aggtgtgtg ggccagccca gccatgccta cccgtgcgg 2280
 tgctgtctgc ccagtcccc tggctctgc gcagactggg ctgcccgtg gtactctgt 2340
 gcctctgtg gccaatgaa ccgtctctg tatggcggt gccatggaa tgccaataac 2400
 ttgcctcg agcaagagt catgagcagc tgccaggat ctctccatg gcccgtcgt 2460
 cccagcctg gggctctg aaggagcacc cacacgatg gtggcggcag cagtcctga 2520
 ggcgagcagg aaccagcca gcacaggaca ggggccgcg tgacagaaaa gccctggcct 2580
 tctggtgtc tctggcgga agaccaacag cctgggccag gggaggcccc ccacaccag 2640
 gccttggag aatggccatg ggggcaggag ctgggtcca gggccctg actgggtga 2700
 gatccggat caccagcgc accctccac agctcctct acaggattag ctggcaggt 2760

Sequence_Listing.txt

gtggagccct cgttggtgca ggcagccctg gggcagttgg tgcggctctc ctgctcagac 2820

gacactgccc cggaatccca ggctgcctgg cagaaagatg gccagcccat ctctctgac 2880

aggcacaggc tgcagttcga cggatccctg atcatccacc ccctgcaggc agaggacgcg 2940

ggcacctaca gctgtggcag caccgggcca ggccgcgact ccagaagat ccaacttcgc 3000

atcatagggg gtgacatggc cgtgctgtct gaggtgagc tgagccgctt ccctcagccc 3060

agggaccag ctgaggactt tggccaagcg ggggctgctg ggcccctggg ggccatcccc 3120

tcttcacacc cacagcctgc aaacaggctg cgtttggacc agaaccagcc ccgggtggtg 3180

gatgccagtc caggccagcg gatccgcatg acctgccgtg ccgaaggctt cccgccccca 3240

gccatcgagt ggcagagaga tgggcagcct gtctcttctc ccagacacca gctgcagcct 3300

gatggctccc tggcattag ccgagtggct gtagaagatg gcggcttcta cacctgtgtc 3360

gctttcaatg ggcaggaccg agaccagcga tgggtccagc tcagagtctt gggggagctg 3420

acaatctcag gactgcccc tactgtgaca gtgccagagg gtgatacggc caggctattg 3480

tgtgtggtag caggagaaag tgtgaacatc aggtggtcca ggaacgggct acctgtgcag 3540

gctgatggcc accgtgtcca ccagtcccca gatggcacgc tgctcattta caacttcgag 3600

gccagggatg agggctccta cacgtgcagt gcctaccagg ggagccaggc agtcagccgc 3660

agcaccgagg tgaaggtgt ctcaccagca ccaccgccc agcccaggga ccctggcagg 3720

gactgcgtcg accagccaga gctggccaac tgtgattga tctgcaggc ccagctttgt 3780

ggcaatgagt attactccag ctctgtgtgt gccagctgtt cacgtttcca gcctcacgct 3840

cagcccatct ggcagtaggg atgaaggcta gtccagccc cagtccaaaa tagttcatag 3900

ggctagggag aaaggaagat ggactcttg ctctctct ctggctggca aaggagtta 3960

tctctggaa tacattagct cttcaaaaa ccaccaggt gtttagcctc aacggcagcc 4020

Sequence_Listing.txt

agttaccagc ttctctctgt agccttcagc agtggttgca tctctgacat aaccacaggc 4080

tgctgttttc aagaagagca atctgtttgg ataagaaaaa cctttacttt acagcttccc 4140

tttataattt gttacacagg aatagttaaa tgcatttggt tgtttgtttt ttgagacaga 4200

gtttcactct tgttgcccag gctggagggc aatggcgcgga tctcagctca ctgcaacctc 4260

cgtctcctgg gtcttgatt ctctgtgtc agccttctga gtagctagga ttacagatgc 4320

ctatcaccat gcctgggtaa ttttgtatt ttagttgag atgggggttc accatgttgg 4380

ccaggctggg ctggaacttc tgacctcaga tgatctgcc gcctcagcct cccaaagtgc 4440

tgggattaca ggcatgagcc accacgccc gccatcaatg catttttttt atttttttt 4500

tgagacagag ttgcgactt ctgcccagg ctggagtaca atgggtcgat ctgggtcac 4560

tgcaacctcc acctctggg ttcaagcgt tctccagcct cagcctcctg agtagctggg 4620

attacaggta tgtgccacca tgcttgcta attttgtatt ttagtagag acgggggttc 4680

tccatgttgg tcagactggt ctggaactcc cgacctcagg taatccgccc gcctcgccct 4740

cccaaatgc tgggattaga ggtgtgagcc actgtgccc gccatcaat gtgttttaaa 4800

gctagctgtc agggttccac ttaatttaaa gctgggcagg gagatgtgta atgattcaa 4860

agttaacacc tgtttgttt ctaaagggca tgccaagtcc tgctgtatca gggaagtatt 4920

ctgtgctaaa atcagcgatg gttcattgct ctagtctctc tcacccttct aggcagtga 4980

tcagttagct ctaaactgg tgagagggt taacagcata acctgttg gcaaatgga 5040

atagatgtta agacctcaaa tagggatttg ggaatgaaaca gctgcagtta gcactgttat 5100

ctgagcatga aagaactgga aacgctcctt acgtcgagat gttggacctt gaagccctcc 5160

tgaggccaac atgcaaatct ggctgtgacg gttcatctga cacctgtgta aagctgacca 5220

gcctgctctg tacagtgaca atgaggagcc cctctcttcc ttaagtagga atctgtgaag 5280

Sequence_Listing.txt

caaaatgttt gctgccaaag acaaatcaga ctgtcagtca ttaaaaacag cattagcagg 5340
atgaggatag caatggggaa gggttgtggg caatgcagta acagggaaat ggcttcagaa 5400
atggttgag ttgaagaca acattctca tcttcagga ctctaattc ctgatgcta 5460
aaagaagagg catggattct atgagcttc aagtccttt ccactttaac ctctacaaa 5520
tcttcagag gactgcctag tagcaaaggt tattcctgga cacaggaaag acgggcatta 5580
cagggaccaa agctctgaaa ggtgactttt attaccaaca cactggctgg aaaagggaca 5640
aaccacatca cgggtgagtg atacttctca gtcttctcta ctattcaac aaaggaaatg 5700
tgggctgggg cagaggtctt ttctattta atactggaaa aatattgaag agcatccatg 5760
ttcacttatg gctggttttg ctatagaaat tggaaaataa aggccacttt ttgaaatcc 5820
ccagtttaat taaaaaaaaa aaaaaaaaaa 5849

<210> 54
<211> 1251
<212> PRT
<213> Homo sapiens

<400> 54
Met Arg Leu Leu Leu Val Pro Leu Leu Leu Ala Pro Ala Pro Gly
1 5 10 15

Ser Ser Ala Pro Lys Val Arg Arg Gln Ser Asp Thr Trp Gly Pro Trp
20 25 30

Ser Gln Trp Ser Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Ser Phe
35 40 45

Arg Glu Arg Pro Cys Tyr Ser Gln Arg Arg Asp Gly Gly Ser Ser Cys
50 55 60

Sequence_Listing.txt

Val Gly Pro Ala Arg Ser His Arg Ser Cys Arg Thr Glu Ser Cys Pro
65 70 75 80

Asp Gly Ala Arg Asp Phe Arg Ala Glu Gln Cys Ala Glu Phe Asp Gly
 85 90 95

Ala Glu Phe Gln Gly Arg Arg Tyr Arg Trp Leu Pro Tyr Tyr Ser Ala
 100 105 110

Pro Asn Lys Cys Glu Leu Asn Cys Ile Pro Lys Gly Glu Asn Phe Tyr
 115 120 125

Tyr Lys His Arg Glu Ala Val Val Asp Gly Thr Pro Cys Glu Pro Gly
 130 135 140

Lys Arg Asp Val Cys Val Asp Gly Ser Cys Arg Val Val Gly Cys Asp
145 150 155 160

His Glu Leu Asp Ser Ser Lys Gln Glu Asp Lys Cys Leu Arg Cys Gly
 165 170 175

Gly Asp Gly Thr Thr Cys Tyr Pro Val Ala Gly Thr Phe Asp Ala Asn
 180 185 190

Asp Leu Ser Arg Ala Val Lys Asn Val Arg Gly Glu Tyr Tyr Leu Asn
 195 200 205

Gly His Trp Thr Ile Glu Ala Ala Arg Ala Leu Pro Ala Ala Ser Thr
 210 215 220

Ile Leu His Tyr Glu Arg Gly Ala Glu Gly Asp Leu Ala Pro Glu Arg

Sequence_Listing.txt

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

Sequence_Listing.txt

Ser Pro Glu Pro Trp Gly Glu Cys Ser Val Ser Cys Gly Val Gly Val
405 410 415

Arg Lys Arg Ser Val Thr Cys Arg Gly Glu Arg Gly Ser Leu Leu His
420 425 430

Thr Ala Ala Cys Ser Leu Glu Asp Arg Pro Pro Leu Thr Glu Pro Cys
435 440 445

Val His Glu Asp Cys Pro Leu Leu Ser Asp Gln Ala Trp His Val Gly
450 455 460

Thr Trp Gly Leu Cys Ser Lys Ser Cys Ser Ser Gly Thr Arg Arg Arg
465 470 475 480

Gln Val Ile Cys Ala Ile Gly Pro Pro Ser His Cys Gly Ser Leu Gln
485 490 495

His Ser Lys Pro Val Asp Val Glu Pro Cys Asn Thr Gln Pro Cys His
500 505 510

Leu Pro Gln Glu Val Pro Ser Met Gln Asp Val His Thr Pro Ala Ser
515 520 525

Asn Pro Trp Met Pro Leu Gly Pro Gln Glu Ser Pro Ala Ser Asp Ser
530 535 540

Arg Gly Gln Trp Trp Ala Ala Gln Glu His Pro Ser Ala Arg Gly Asp
545 550 555 560

His Arg Gly Glu Arg Gly Asp Pro Arg Gly Asp Gln Gly Thr His Leu

565

570

575

Ser Ala Leu Gly Pro Ala Pro Ser Leu Gln Gln Pro Pro Tyr Gln Gln
580 585 590

Pro Leu Arg Ser Gly Ser Gly Pro His Asp Cys Arg His Ser Pro His
595 600 605

Gly Cys Cys Pro Asp Gly His Thr Ala Ser Leu Gly Pro Gln Trp Gln
610 615 620

Gly Cys Pro Gly Ala Pro Cys Gln Gln Ser Arg Tyr Gly Cys Cys Pro
625 630 635 640

Asp Arg Val Ser Val Ala Glu Gly Pro His His Ala Gly Cys Thr Lys
645 650 655

Ser Tyr Gly Gly Asp Ser Thr Gly Gly Met Pro Arg Ser Arg Ala Val
660 665 670

Ala Ser Thr Val His Asn Thr His Gln Pro Gln Ala Gln Gln Asn Glu
675 680 685

Pro Ser Glu Cys Arg Gly Ser Gln Phe Gly Cys Cys Tyr Asp Asn Val
690 695 700

Ala Thr Ala Ala Gly Pro Leu Gly Glu Gly Cys Val Gly Gln Pro Ser
705 710 715 720

His Ala Tyr Pro Val Arg Cys Leu Leu Pro Ser Ala His Gly Ser Cys
725 730 735

Sequence_Listing.txt

Ala Asp Trp Ala Ala Arg Trp Tyr Phe Val Ala Ser Val Gly Gln Cys
740 745 750

Asn Arg Phe Trp Tyr Gly Gly Cys His Gly Asn Ala Asn Asn Phe Ala
755 760 765

Ser Glu Gln Glu Cys Met Ser Ser Cys Gln Gly Ser Leu His Gly Pro
770 775 780

Arg Arg Pro Gln Pro Gly Ala Ser Gly Arg Ser Thr His Thr Asp Gly
785 790 795 800

Gly Gly Ser Ser Pro Ala Gly Glu Gln Glu Pro Ser Gln His Arg Thr
805 810 815

Gly Ala Ala Val Gln Arg Lys Pro Trp Pro Ser Gly Gly Leu Trp Arg
820 825 830

Gln Asp Gln Gln Pro Gly Pro Gly Glu Ala Pro His Thr Gln Ala Phe
835 840 845

Gly Glu Trp Pro Trp Gly Gln Glu Leu Gly Ser Arg Ala Pro Gly Leu
850 855 860

Gly Gly Asp Ala Gly Ser Pro Ala Pro Pro Phe His Ser Ser Ser Tyr
865 870 875 880

Arg Ile Ser Leu Ala Gly Val Glu Pro Ser Leu Val Gln Ala Ala Leu
885 890 895

Gly Gln Leu Val Arg Leu Ser Cys Ser Asp Asp Thr Ala Pro Glu Ser

Sequence_Listing.txt

900 905 910

Gln Ala Ala Trp Gln Lys Asp Gly Gln Pro Ile Ser Ser Asp Arg His
915 920 925

Arg Leu Gln Phe Asp Gly Ser Leu Ile Ile His Pro Leu Gln Ala Glu
930 935 940

Asp Ala Gly Thr Tyr Ser Cys Gly Ser Thr Arg Pro Gly Arg Asp Ser
945 950 955 960

Gln Lys Ile Gln Leu Arg Ile Ile Gly Gly Asp Met Ala Val Leu Ser
965 970 975

Glu Ala Glu Leu Ser Arg Phe Pro Gln Pro Arg Asp Pro Ala Gln Asp
980 985 990

Phe Gly Gln Ala Gly Ala Ala Gly Pro Leu Gly Ala Ile Pro Ser Ser
995 1000 1005

His Pro Gln Pro Ala Asn Arg Leu Arg Leu Asp Gln Asn Gln Pro
1010 1015 1020

Arg Val Val Asp Ala Ser Pro Gly Gln Arg Ile Arg Met Thr Cys
1025 1030 1035

Arg Ala Glu Gly Phe Pro Pro Pro Ala Ile Glu Trp Gln Arg Asp
1040 1045 1050

Gly Gln Pro Val Ser Ser Pro Arg His Gln Leu Gln Pro Asp Gly
1055 1060 1065

Sequence_Listing.txt

Ser Leu Val Ile Ser Arg Val Ala Val Glu Asp Gly Gly Phe Tyr
1070 1075 1080

Thr Cys Val Ala Phe Asn Gly Gln Asp Arg Asp Gln Arg Trp Val
1085 1090 1095

Gln Leu Arg Val Leu Gly Glu Leu Thr Ile Ser Gly Leu Pro Pro
1100 1105 1110

Thr Val Thr Val Pro Glu Gly Asp Thr Ala Arg Leu Leu Cys Val
1115 1120 1125

Val Ala Gly Glu Ser Val Asn Ile Arg Trp Ser Arg Asn Gly Leu
1130 1135 1140

Pro Val Gln Ala Asp Gly His Arg Val His Gln Ser Pro Asp Gly
1145 1150 1155

Thr Leu Leu Ile Tyr Asn Leu Arg Ala Arg Asp Glu Gly Ser Tyr
1160 1165 1170

Thr Cys Ser Ala Tyr Gln Gly Ser Gln Ala Val Ser Arg Ser Thr
1175 1180 1185

Glu Val Lys Val Val Ser Pro Ala Pro Thr Ala Gln Pro Arg Asp
1190 1195 1200

Pro Gly Arg Asp Cys Val Asp Gln Pro Glu Leu Ala Asn Cys Asp
1205 1210 1215

Leu Ile Leu Gln Ala Gln Leu Cys Gly Asn Glu Tyr Tyr Ser Ser

Sequence_Listing.txt

1220 1225 1230

Phe Cys Cys Ala Ser Cys Ser Arg Phe Gln Pro His Ala Gln Pro
1235 1240 1245

Ile Trp Gln
1250

<210> 55
<211> 3851
<212> DNA
<213> Homo sapiens

<400> 55
cgcaaagccg ccgggctgct gcgccagag ccagccggag ccggagccgg agcccgaact 60
gcagctccag cccagccgt gcggagccgc agcccaggcc ggggccggcg gcggctcatg 120
gacagcgggg cgggcgccg gcgctgccg gaggcggccc tctgattct ggggcctccc 180
aggatggagc acctgaggca cagcccaggc cctggggggc aacggctact gctgccctcc 240
atgtctctag cactgtctct cctgtggct ccatcccag gccacgccac tcgggtagtg 300
tacaaggtag cgagggaaca gccaccaac accctcattg ggagcctcgc agccgactat 360
ggttttccag atgtggggca cctgtacaag ctagaggtag gtgccccgta ccttcgctg 420
gatggcaaga caggtagcat ttaccacc gagacctca tcgaccgtga ggggctccgt 480
gaatgccaga accagctccc tggtagccc tgcacctgg agtttgaggt atctatcaca 540
gacctgtgc agaatggcag cccccggctg ctagagggcc agatagaagt acaagacatc 600
aatgacaaca caccgaactt cgctcacca gtcatcactc tggccatccc tgagaacacc 660
aacatcggct cactctccc catcccgctg gttcagacc gtgatgctgg tccaacggt 720
gtggcatcct atgagctgca ggctgggcct gaggcccagg agctatttgg gctgcaggtg 780

Sequence_Listing.txt

gcagaggacc aggaggagaa gcaaccacag ctcatgtga tgggaacct ggaccgtgag 840
cgctgggact cctatgacct caccatcaag gtcaggatg gcggcagccc cccacgcgcc 900
agcagtgtcc tgctgcgtgt caccgtgctt gacaccaatg acaacgcccc caagtttgag 960
cggccctcct atgaggccga actatctgag aatagcccca taggccactc ggtcatccag 1020
gtgaaggcca atgactcaga ccaagggtcc aatgcagaaa tcgaatacac attccaccag 1080
gcgcccgaag ttgtgaggcg tcttctcga ctggacagga aactggact tatcactgtt 1140
cagggcccg tgaccgtga ggacctaac accctgcgt tctcagtgt tgtaaggac 1200
cgaggacca accccaagag tccccgtgcc caggtggtg tgaccgtgaa ggacatgaat 1260
gacaatgtcc ccaccattga gatccggggc atagggttag tgactcatca agatgggatg 1320
gctaacatct cagaggatgt ggcagaggag acagctgtg ccttggtgca ggtgtctgac 1380
cgagatgagg gagagaatgc agctgtcacc tgtgtggtg caggtgatgt gcccttcag 1440
ctgcgccagg ccagtgtgac aggcagtgt agcaagaaga agtatttcct gcagactacc 1500
accccgttag actacgagaa ggtcaaagac tacaccattg agattgtggc tgtggactct 1560
ggcaaccccc cactctccag cactaactcc ctcaagggtc aggtggtgga cgtcaatgac 1620
aacgcacctg tcttactca gagtgtcact gaggtgcct tcccgaaaa caacaagcct 1680
ggtgaagtga ttgtgagat cactgccagt gatgtgact ctggctctaa tgctgagctg 1740
gtttactctc tggagcctga gccggctgt aaggcctct tcaccatctc acccgagact 1800
ggagagatcc aggtgaagac atctctggat cggaacagc gggagagcta tgagttgaag 1860
gtggtggcag ctgaccgggg cagtccatgc ctccaggga cagccactgt cctgtcaat 1920
gtgctggact gcaatgaaa tgacccaaa ttatgtctga gtggctaaa cttctcagt 1980
atggagaaca tgccagcact gagtccagt ggcatggtga ctgtcattga tggagacaag 2040

Sequence_Listing.txt

ggggagaatg cccagggtgca gctctcagtg gagcaggaca acgggtgactt tgttatccag 2100
 aatggcacag gcaccatcct atccagcctg agctttgatc gagagcaaca aagcacctac 2160
 accttcagc tgaaggcagt ggaagggtgc gtccacctc gctcagctta cgttggtgtc 2220
 accatcaatg tgcgggacga gaatgacaac gcacctata tctgcccc ttctaacacc 2280
 tctacaagc tgcagcccc ccagacacgt ctggtgaga cggtcagcca ggtggcagcc 2340
 gaggactttg actctggtgt caatgctgag ctgatctaca gattgcagg tggcaaccct 2400
 tatggactct tccagattgg gtcacattca ggtgccatca ccctggagaa ggagattgag 2460
 cggcgccacc atgggctaca ccgctgggtg gtaagggtca gtagccgagg caagcccca 2520
 cgctatggca cagccttggc ccatcttat gtaatgaga ctctggccaa ccgacgctg 2580
 ctggagacc tctgggcca cagcctggac acgcccgtgg atattgacat tctggggat 2640
 ccagaatatg agcgctcaa gcagcgtggc aacattctct ttggtgtgtt ggctggtgtg 2700
 gtggccgtgg cctgtctcat cgcctggcg gttctgtgc gctactgcag acagcgggag 2760
 gccaaaagtg gttaccaggc tggtaagaag gagaccaagg acctgtatgc cccaagccc 2820
 atgggaagg cctcaaggg aaacaaaagc aaaggcaaga agagcaagtc ccaaagccc 2880
 gtaagccag tggaggacga ggaaggaggc gggctgcaga agtccctcaa gttcaacctg 2940
 atgagcagt cccctgggga cagtccccgc atccacctgc cctcaacta cccaccaggc 3000
 agccctgacc tgggcccga ctatgctct aactccccac tgccttccat ccagctgcag 3060
 cccagtcac cctcagctc caagaagcac cagggtgtac aggacctgcc acctgcaaac 3120
 acattcgttg gcaccgggga caccacgtcc acgggctctg agcagtactc cgactacagc 3180
 taccgacca acccccca ataccacagc aagcaggtag gccagccctt tcagctcagc 3240
 acaccacag cctaccaca cccctaccac ggagccatct ggaccgaggt gtgggagtga 3300

Sequence_Listing.txt

tggagcaggt ttactgtgcc tgcccggtt gggggccagc ctgagccagc agtgggaggt 3360
 ggggccttag tgctcaccg ggcacacgga ttaggctgag tgaagattaa gggagggtgt 3420
 gctctgtggt ctctccctg cctctcccc actggggaga gacctgtgat ttgccaagtc 3480
 cctggaccct ggaccagcta ctgggcctta tgggttgggg gtggtaggca ggtgagcgta 3540
 agtggggagg gaaatggga agaagtctac tccaaaccta ggtctctatg tcagaccaga 3600
 cctagggtct tctctaggag ggaaacaggg agacctgggg tctgtggat aactgagtgg 3660
 ggagtctgcc aggggagggc acctcccat tgtgccttct gtgtgtattg tgcattaacc 3720
 tttctcac cactaggctt ctggggctgg gtccacatg ccttgacc tgacaataaa 3780
 gttctctatt ttggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3840
 aaaaaaaaaa a 3851

<210> 56
 <211> 1060
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Asp Ser Gly Ala Gly Gly Arg Arg Cys Pro Glu Ala Ala Leu Leu
 1 5 10 15

Ile Leu Gly Pro Pro Arg Met Glu His Leu Arg His Ser Pro Gly Pro
 20 25 30

Gly Gly Gln Arg Leu Leu Leu Pro Ser Met Leu Leu Ala Leu Leu Leu
 35 40 45

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

Sequence_Listing.txt

Pro Glu Glu Gln Pro Pro Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp
65 70 75 80

Tyr Gly Phe Pro Asp Val Gly His Leu Tyr Lys Leu Glu Val Gly Ala
 85 90 95

Pro Tyr Leu Arg Val Asp Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu
 100 105 110

Thr Ser Ile Asp Arg Glu Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro
 115 120 125

Gly Asp Pro Cys Ile Leu Glu Phe Glu Val Ser Ile Thr Asp Leu Val
 130 135 140

Gln Asn Gly Ser Pro Arg Leu Leu Glu Gly Gln Ile Glu Val Gln Asp
145 150 155 160

Ile Asn Asp Asn Thr Pro Asn Phe Ala Ser Pro Val Ile Thr Leu Ala
 165 170 175

Ile Pro Glu Asn Thr Asn Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala
 180 185 190

Ser Asp Arg Asp Ala Gly Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln
 195 200 205

Ala Gly Pro Glu Ala Gln Glu Leu Phe Gly Leu Gln Val Ala Glu Asp
 210 215 220

Sequence_Listing.txt

Gln Glu Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu Asp Arg
225 230 235 240

Glu Arg Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp Gly Gly
245 250 255

Ser Pro Pro Arg Ala Ser Ser Ala Leu Leu Arg Val Thr Val Leu Asp
260 265 270

Thr Asn Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu Ala Glu
275 280 285

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

Asn Asp Ser Asp Gln Gly Ala Asn Ala Glu Ile Glu Tyr Thr Phe His
305 310 315 320

Gln Ala Pro Glu Val Val Arg Arg Leu Leu Arg Leu Asp Arg Asn Thr
325 330 335

Gly Leu Ile Thr Val Gln Gly Pro Val Asp Arg Glu Asp Leu Ser Thr
340 345 350

Leu Arg Phe Ser Val Leu Ala Lys Asp Arg Gly Thr Asn Pro Lys Ser
355 360 365

Ala Arg Ala Gln Val Val Val Thr Val Lys Asp Met Asn Asp Asn Ala
370 375 380

Pro Thr Ile Glu Ile Arg Gly Ile Gly Leu Val Thr His Gln Asp Gly
385 390 395 400

Sequence_Listing.txt

Met Ala Asn Ile Ser Glu Asp Val Ala Glu Glu Thr Ala Val Ala Leu
405 410 415

Val Gln Val Ser Asp Arg Asp Glu Gly Glu Asn Ala Ala Val Thr Cys
420 425 430

Val Val Ala Gly Asp Val Pro Phe Gln Leu Arg Gln Ala Ser Glu Thr
435 440 445

Gly Ser Asp Ser Lys Lys Lys Tyr Phe Leu Gln Thr Thr Thr Pro Leu
450 455 460

Asp Tyr Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val Ala Val Asp
465 470 475 480

Ser Gly Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys Val Gln Val
485 490 495

Val Asp Val Asn Asp Asn Ala Pro Val Phe Thr Gln Ser Val Thr Glu
500 505 510

Val Ala Phe Pro Glu Asn Asn Lys Pro Gly Glu Val Ile Ala Glu Ile
515 520 525

Thr Ala Ser Asp Ala Asp Ser Gly Ser Asn Ala Glu Leu Val Tyr Ser
530 535 540

Leu Glu Pro Glu Pro Ala Ala Lys Gly Leu Phe Thr Ile Ser Pro Glu
545 550 555 560

Sequence_Listing.txt

Thr Gly Glu Ile Gln Val Lys Thr Ser Leu Asp Arg Glu Gln Arg Glu
565 570 575

Ser Tyr Glu Leu Lys Val Val Ala Ala Asp Arg Gly Ser Pro Ser Leu
580 585 590

Gln Gly Thr Ala Thr Val Leu Val Asn Val Leu Asp Cys Asn Asp Asn
595 600 605

Asp Pro Lys Phe Met Leu Ser Gly Tyr Asn Phe Ser Val Met Glu Asn
610 615 620

Met Pro Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp Gly Asp
625 630 635 640

Lys Gly Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp Asn Gly
645 650 655

Asp Phe Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser Leu Ser
660 665 670

Phe Asp Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys Ala Val
675 680 685

Asp Gly Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr Ile Asn
690 695 700

Val Leu Asp Glu Asn Asp Asn Ala Pro Tyr Ile Thr Ala Pro Ser Asn
705 710 715 720

Thr Ser His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu Thr Val
725 730 735

Sequence_Listing.txt

Ser Gln Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala Glu Leu
740 745 750

Ile Tyr Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln Ile Gly
755 760 765

Ser His Ser Gly Ala Ile Thr Leu Glu Lys Glu Ile Glu Arg Arg His
770 775 780

His Gly Leu His Arg Leu Val Val Lys Val Ser Asp Arg Gly Lys Pro
785 790 795 800

Pro Arg Tyr Gly Thr Ala Leu Val His Leu Tyr Val Asn Glu Thr Leu
805 810 815

Ala Asn Arg Thr Leu Leu Glu Thr Leu Leu Gly His Ser Leu Asp Thr
820 825 830

Pro Leu Asp Ile Asp Ile Ala Gly Asp Pro Glu Tyr Glu Arg Ser Lys
835 840 845

Gln Arg Gly Asn Ile Leu Phe Gly Val Val Ala Gly Val Val Ala Val
850 855 860

Ala Leu Leu Ile Ala Leu Ala Val Leu Val Arg Tyr Cys Arg Gln Arg
865 870 875 880

Glu Ala Lys Ser Gly Tyr Gln Ala Gly Lys Lys Glu Thr Lys Asp Leu
885 890 895

Sequence_Listing.txt

Tyr Ala Pro Lys Pro Ser Gly Lys Ala Ser Lys Gly Asn Lys Ser Lys
 900 905 910

Gly Lys Lys Ser Lys Ser Pro Lys Pro Val Lys Pro Val Glu Asp Glu
 915 920 925

Asp Glu Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met Ser Asp
 930 935 940

Ala Pro Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr Pro Pro
 945 950 955 960

Gly Ser Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro Leu Pro
 965 970 975

Ser Ile Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys His Gln
 980 985 990

Val Val Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr Gly Asp
 995 1000 1005

Thr Thr Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr Arg
 1010 1015 1020

Thr Asn Pro Pro Lys Tyr Pro Ser Lys Gln Val Gly Gln Pro Phe
 1025 1030 1035

Gln Leu Ser Thr Pro Gln Pro Leu Pro His Pro Tyr His Gly Ala
 1040 1045 1050

Ile Trp Thr Glu Val Trp Glu
 1055 1060

Sequence_Listing.txt

<210> 57
 <211> 3393
 <212> DNA
 <213> Homo sapiens

<400> 57
 cctgcctgcc tccctgcgca cccgcagcct cccccgctgc ctccctaggg ctcccctcgg 60
 gccgccagcg cccatttttc attccctaga tagagatact ttgcgcgcac acacatacat 120
 acgcgcgcaa aaaggaaaaa aaaaaaaaaa agcccaccct ccagcctcgc tgcaaagaga 180
 aaaccggagc agccgcagct cgcagctcgc agctcgcagc ccgcagcccg cagaggacgc 240
 ccagagcggc gagcgggagg gcagacggac cgacggactc gcgccgcgtc cacctgtcgg 300
 ccggggccag ccgagcgcgc agcggggcacg ccgcgcgcgc ggagcagccg tgcccgccgc 360
 ccggggcccg cgccaggggc cacacgtcc cgcccccta cccggcccg gcgggagttt 420
 gcaccttcc ctgccgggt gctcagctg ccgttgcaa gccaaattg gaaaaagttt 480
 ttgggggag acttgggcct tgagggtccc agctccgcgc ttccgattt tgggggcctt 540
 tccagaaaat gttgaaaaa agctaagccg gcgggcagag gaaaacgcct gtagccggcg 600
 agtgaagacg aaccatcgac tgccgtgttc ctttctctt tggaggttg agtcccctgg 660
 gcgccccac acggctagac gcctcggctg gttcgcgacg cagcccccg gccgtggatg 720
 ctactcggg ctgggatcc gccaggtag cggcctcga cccaggtcct gcgccaggt 780
 cctcccctgc ccccagcga cggagccggg gccgggggag gcggcgcccg ggggccatgc 840
 gggtagccg cggctgcaga ggctgagcg cctgatgcc gcggaccga gccgagcca 900
 cccccctcc cagccccca ccctggcgc gggggcggcg cgctcatct acgcgtccgg 960
 ggcccccg gcggggccc ggagtcggca tgaatcgct ctgggcgctc ttctgtctc 1020

Sequence_Listing.txt

tctgtctcta cctgcgtctg gtcagcgccg aggggggaccc cattcccgag gagctttatg 1080
 agatgtctgag tgaccactcg atccgctcct ttgatgatct ccaacgcctg ctgcacggag 1140
 accccggaga ggaagatggg gccgagttgg acctgaacat gaccgcctcc cactctggag 1200
 gcgagctgga gagcttggct cgtggaagaa ggagcctggg ttccctgacc attgtgagc 1260
 cggccatgat cgccgagtc aagacgcgca ccgaggtgtt cgagatctcc cggcgccctca 1320
 tagaccgcac caacgccaac ttctggtgt ggccgccctg tgtggagggt cagcgctgct 1380
 ccggctgctg caacaaccgc aacgtgcagt gccgccccac ccaggtgcag ctgcgacctg 1440
 tccaggtgag aaagatcgag attgtgcgga agaagccaat ctttaagaag gccacggtga 1500
 cgttgaaga ccacctggca tgcaagtgtg agacagtggc agctgcacgg cctgtgaccc 1560
 gaagcccggtt gggttcccag gagcagcgag caaaacgcc ccaaactcgg gtgaccattc 1620
 ggacggtgag agtcgcccgg cccccaagg gcaagcaccg gaaattcaag cacacgcatg 1680
 acaagacggc actgaaggag acccttgag cctaggggca tcggcaggag agtgtgtggg 1740
 caggggtatt taatatggtt ttgtctgtat tgccccatg gggtccttgg agtgataata 1800
 ttgtttccct cgtccgtctg tctcgatgcc tgattcggac ggccaatggt gcttcccca 1860
 cccctccacg tgcctgcca ccttccatc agcgggtctc ctcccagcgg cctccggcgt 1920
 ctgcccagc agtcaagaa gaaaaagaag gactgaactc catcgccatc ttcttcctt 1980
 aactccaaga acttgggata agagtgtgag agagactgat ggggtcgctc ttgggggaa 2040
 acgggtcctt tccctgcac ctggcctggg ccacacctga gcgctgtgga ctgtcctgag 2100
 gagccctgag gacctctcag catagcctgc ctgatccctg aaccctggc cagctctgag 2160
 gggaggcacc tccaggcagg ccaggctgcc tcggactcca tggctaagac cacagacggg 2220
 cacacagact ggagaaaacc cctccacgg tgcccaaaca ccagtcacct cgtctccctg 2280

Sequence_Listing.txt

gtgcctctgt gcacagtggc ttcttttctg ttctgtttg aagacgtgga ctctcttgg 2340

tgggtgtggc cagcacacca agtggctggg tgcctctca ggtgggtag agatggagt 2400

tgctgttag gtggctgtag atggtgacct gggatcccc tgcctctgc cacccttcc 2460

tccccacact ccactctgat tcacctctc ctctggttcc ttcatctct ctacctccac 2520

cctgcatttt cctctgtcc tggccctca gtctgtcca ccaaggggct ctgaacccc 2580

ttattaaggc ccagatgat ccagtcact cctcttagg gcagaagact agaggccagg 2640

gcagcaaggg acctgtcat catattcaa ccagccacg actgccatgt aagggtgtgc 2700

aggggtgtga ctgcacaagg acattgtatg caggagcac tgtcacatc atagataaag 2760

ctgatttga tatttattat gacaattct ggcagatga ggtaaagagg aaaaggatcc 2820

tttctaat tcacacaaag actcctgtg gactggctgt gccctgatg cagcctgtgg 2880

cttgagtggt ccaaatagga gggagactgt ggtaggggca gggaggcaac actgctgtcc 2940

acatgacctc catttccaa agtctctgc tccagcaact gccctccag gtgggtgtgg 3000

gacacctggg agaaggctc caaggagggt tgcagccctc ttgccgcac ccctccctgc 3060

ttgcacactt ccccatctt gatcctctg agctccacct ctggtggctc ctctaggaa 3120

accagctctg gggctgggaa tgggggagag aagggaagaa atccccaaga cccctgggg 3180

tgggatctga gctccacct ccttccac ctactgcact tccccctc cgccttcca 3240

aaacctgctt ccttcagttt gtaaagtcgg tgattataat ttgggggct ttcttttat 3300

ttttaaatg taaaatttat ttatattccg tatttaaagt tgtaaaaaaa aataaccaca 3360

aaacaaaacc aaatgaaaaa aaaaaaaaaa aaa 3393

<210> 58

<211> 241

<212> PRT

Sequence_Listing.txt

<213> Homo sapiens

<400> 58

Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg

1 5 10 15

Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met

20 25 30

Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu

35 40 45

His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met

50 55 60

Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg

65 70 75 80

Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu

85 90 95

Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp

100 105 110

Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln

115 120 125

Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr

130 135 140

Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg

145 150 155 160

Sequence_Listing.txt

Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
165 170 175

Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser
180 185 190

Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
195 200 205

Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg
210 215 220

Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly
225 230 235 240

Ala

<210> 59
<211> 1149
<212> DNA
<213> Homo sapiens

<400> 59
aacaagggag gtgctgcagt tggcggtcgg gctagagaag agaggcgctt gcgcttgcca 60
gctgggcttg tgagtggggc tgccgagagg gcaggcgtgg ggcgaggcca aaggactgaa 120
cccgcaggag cgtcacgggc gccggggcgg ctgccgacgg cgggactggg tttctatca 180
gatgtccac gtaataatgc tggagttaag aagttccat tatTTgctc caaaccagaa 240
gactctgttc cctgtatata gaataggagt aatattgaa aacaactggc tgatgtttaa 300
aactgaagat tgtcatgatt gttatccta atcccaatgc tgaagtaaga ttgtottgga 360

Sequence_Listing.txt

```

aatactaagt tggggaatc caaatctatt tctggaacca tgaaaatttt gctagttttt 420
gactttgaca atacaatcat agatgacaat agtgacactt ggattgtaca atgtgctccc 480
aacaaaaagc ttctattga actacgtgat tcttatcgaa aaggattttg gacagaattt 540
atgggcagag tctttaagta ttggggagat aagggtgtaa gagaacatga aatgaaaaga 600
gcagtgacat cattgccttt cactccaggg atggtggaac tcttcaactt tataagaaag 660
aataaggata aatttgactg cattattatt tcagattcaa attcggctct catagattgg 720
gttttagaag ctgccagttt tcatgacata ttgataaag tgtttacaaa tccagcagct 780
tttaatagca atgggtcatct cactgttgaa aattatcata ctattcttg caatagatgc 840
ccaaagaatc ttgcaaaaaa ggtagttttg atagaatttg tagataaaca gttacaacag 900
ggagtgaatt atacacaaat tgtttatatt ggtgatgggt gaaatgatgt ctgtccagtc 960
acctttttaa agaatgatga tgttgccatg ccacggaaag gatatacctt acagaaaact 1020
cttccagaa tgtctcaaaa tcttgagcct atggaatatt ctgtgtagt ttgtcctca 1080
ggtgttgata taatttctca ttacaattt ctaataaagg attaatatgt cagcaaaaaa 1140
aaaaaaaaa                                     1149

```

<210> 60
 <211> 241
 <212> PRT
 <213> Homo sapiens

<400> 60
 Met Lys Ile Leu Leu Val Phe Asp Phe Asp Asn Thr Ile Ile Asp Asp
 1 5 10 15

Asn Ser Asp Thr Trp Ile Val Gln Cys Ala Pro Asn Lys Lys Leu Pro
 20 25 30

Sequence_Listing.txt

Ile Glu Leu Arg Asp Ser Tyr Arg Lys Gly Phe Trp Thr Glu Phe Met
35 40 45

Gly Arg Val Phe Lys Tyr Leu Gly Asp Lys Gly Val Arg Glu His Glu
50 55 60

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

Leu Phe Asn Phe Ile Arg Lys Asn Lys Asp Lys Phe Asp Cys Ile Ile
85 90 95

Ile Ser Asp Ser Asn Ser Val Phe Ile Asp Trp Val Leu Glu Ala Ala
100 105 110

Ser Phe His Asp Ile Phe Asp Lys Val Phe Thr Asn Pro Ala Ala Phe
115 120 125

Asn Ser Asn Gly His Leu Thr Val Glu Asn Tyr His Thr His Ser Cys
130 135 140

Asn Arg Cys Pro Lys Asn Leu Cys Lys Lys Val Val Leu Ile Glu Phe
145 150 155 160

Val Asp Lys Gln Leu Gln Gln Gly Val Asn Tyr Thr Gln Ile Val Tyr
165 170 175

Ile Gly Asp Gly Gly Asn Asp Val Cys Pro Val Thr Phe Leu Lys Asn
180 185 190

Sequence_Listing.txt

Asp Asp Val Ala Met Pro Arg Lys Gly Tyr Thr Leu Gln Lys Thr Leu
195 200 205

Ser Arg Met Ser Gln Asn Leu Glu Pro Met Glu Tyr Ser Val Val Val
210 215 220

Trp Ser Ser Gly Val Asp Ile Ile Ser His Leu Gln Phe Leu Ile Lys
225 230 235 240

Asp

<210> 61
<211> 678
<212> DNA
<213> Homo sapiens

<400> 61
ctgcccaaa gaagactaca atctccaggg aaacctgggg cgtctcgcgc aaacgtccat 60
aactgaaagt agctaaggca cccagccgg aggaagtgag ctctctggg gcgtggtgt 120
tcgtgatcct tgcattgtt acttagggc aaggctggg tctgccccg cagacccttg 180
ggacgacccg gcccagcgc agctatgaac ctggagcgag tgtccaatga ggagaaattg 240
aacctgtgcc ggaagtacta cctggggggg ttgctttcc tgcctttct ctggttggtc 300
aacattctct ggttctccg agaggcctc ctgtcccag cctacacaga acagagccaa 360
atcaaaggct atgtctggcg ctgagctgtg ggcttcctt tctgggtgat agtctcacc 420
tcctggatca ccatctcca gatctaccg ccccgctggg gtgcccttg ggactacctc 480
tcctcacca taccctggg caccctga caactctgc acatactgg gccctgcta 540
ttctcccagg acaggctct taaagcagag gagcctgtcc tgggagcccc ttctcaaact 600

Sequence_Listing.txt

cctaagactt gtttcatgt cccacgttct ctgctgacat cccccaataa aggaccctaa 660

ctttcaaaaa aaaaaaaaa 678

<210> 62

<211> 101

<212> PRT

<213> Homo sapiens

<400> 62

Met Asn Leu Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg

1 5 10 15

Lys Tyr Tyr Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val

20 25 30

Asn Ile Phe Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr

35 40 45

Glu Gln Ser Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe

50 55 60

Leu Phe Trp Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile

65 70 75 80

Tyr Arg Pro Arg Trp Gly Ala Leu Gly Asp Tyr Leu Ser Phe Thr Ile

85 90 95

Pro Leu Gly Thr Pro

100

<210> 63

<211> 5556

<212> DNA

Sequence_Listing.txt

<213> Homo sapiens

<400> 63

```

tttctcgctc gctcccgttc cccggacgcg gcggatgagc cggccccgct ggggaaggct    60
ccgggcgggc gcgggaggcc gggaggaggc tgcgtgctcg gggctggggc tgcgagcggg    120
gtgattttgt attaaatga ggaggaggaa gaagaggcac ccacagcggc agcggcgggc    180
gcggcgggcag cagcagcagg agcagcggcg gagagggctg cagcccgggc ggacgcgcgg    240
agccgagcgg ggcacggcgg cggcagcgac agcggccggg atgagtcaac taataattta    300
atgggggcag agacggcagc gaggggtaga gctagcgagg gagagagcga gagaagcagc    360
cccgccggg gactcgctc cactctcac cacacacaca aacacacaca cacctctccc    420
tgtgccacc agcaacacc ggcctctca caacaacaac agccggggc gccctctatc    480
ctgcccggg gccagccga aagccaggc gactctagag gacgtgccc gccccctct    540
ttcatttcg gaaactcct atcagtttt tcggggttc tgggttctt tccccaaa    600
gtcctagtgc cattgtgtg ctcgtgttt acctcggact ctggacgagt gagagcttgg    660
cgacttttg gggggaggg gcggggagtt tgcgtgccc taggcggtg aggtggctg    720
gggtgccttc tgatctct cctctcccc ctccccga acctctctc tctcacttg    780
ctgggacccc agacgtcac agccccgct caatgggcag ggagagggc cttgcggctg    840
ttgtcagcga gggcagaatc aaaagtggca tttagtgcc ttccggggc tttctcgcg    900
accccctgcc cccaccctc gctgtcccc gctagatgcc ctcgtgggg gtgcgaggct    960
gtggggaaaa gttaaggtt tgtaatat agtcgcgatt gttggcgagg ggggtgggg    1020
tgattggaag ggaggcgagg tggcctccc aatgcgcgtt attcggggtt attgaagaat    1080
aatattgcaa gtgacagcca gaagtagact ttctgtctc acaccgaaga acccgagtga    1140
gcaggaggga gggagagacg cgaagagacc tttttcctt ttggagacc ttgtccgag    1200

```

Sequence_Listing.txt

tgatTTTT tTTTaaga gaatcctcag tcaccacgtc gtttccccag caccatcaca 1260
 gtgtacagct cataacgggt ttgctttgt ttTtacgatt tcccccaac gaatcacttg 1320
 tcagatcaat tTatcttct tcttctccc tgcttccac tctccctcc tcccatcgc 1380
 aaacctgtt cctgagggt agacattta caaaccccta tatgtgggt tTcgaattgt 1440
 gatTTTTt tTaaaccct tTctcatggc tactcttcta gacgtttatt tctgcccttc 1500
 ccccgcttag gggggcgggg gtaggggaaa ggaaaataat acaatttcag gggaagtcgc 1560
 ctTcaggtct gctgctttt tattTTTT tTTTaatta aaaaaaaaaa ggacatagaa 1620
 aacatcagtc tTgaacttct ctTcaagaac ccgggctgca aaggaaatct ctttgtttt 1680
 tgttattat gtgctgTcaa gtttTgaagt ggtgatcttT agacagtgc tgagtatgga 1740
 tcattTgaac gaggcaactc aggggaaaga acattcagaa atgtctaaca atgtgagtga 1800
 tccgaagggt ccaccagcca agattgcccg cctggagcag aacgggagcc cgctaggaag 1860
 aggaaggctt gggagTcag gtgcaaaaat gcagggagtT cctTaaaac actcgggcca 1920
 tctgatgaaa accaaccTta ggaaaggaac catgctgcca gtttctgtg tggTggaaca 1980
 tTatgaaaac gccattgaat atgattgcaa ggaggagcat gcagaattTg TcTggTgag 2040
 aaaggatatg cttTcaacc agctgatcga aatggcattg ctgtctctag gttattcaca 2100
 tagctctgct gcccaggcca aagggtaat ccaggTtTga aagtTgaatc cagtccact 2160
 gtcttacgtg acagatgccc ctgatgctac agtagcagat atgctTcaag atgtgtatca 2220
 tTggtTcaca tTgaaaattc agttacacag ttgccccaaa ctagaagact Tgcctcccga 2280
 acaatggTcg cacaccacag Tgaggaatgc tctgaaggac ttactgaaag atatgaatca 2340
 gagTtcattg gccaaggagt gcccccttc acagagtatg atttctcca ttgtgaacag 2400
 tacttactat gcaaatgtct cagcagcaaa atgtcaagaa tTtTgaaggT ggtacaaaca 2460

Sequence_Listing.txt

tttcaagaag acaaaagata tgatggtga aatggatagt ctttctgagc tatcccagca 2520
 aggcgccaat catgtcaatt ttggccagca accagttcca gggaacacag ccgagcagcc 2580
 tccatcccct ggcgagctct cccatggcag ccagccctct gtccggacac ctcttccaaa 2640
 cctgcaccct gggctcgtat caacacctat cagtctctaa ttggtcaacc agcagctggt 2700
 gatggctcag ctgctgaacc agcagtatgc agtgaataga ctttagccc agcagtcctt 2760
 aaaccaacaa tacttgaacc accctcccc tgcagtaga tctatgaata agcctttgga 2820
 gcaacagggt tcgaccaaca cagagggtgc ttccgaaatc taccagtggg tacgcgatga 2880
 actgaaacga gcaggaatct cccaggcggt attgcacgt gtggctttta acagaactca 2940
 gggcttgctt tcagaaatcc tccgaaagga agaggacccc aagactgcat ccagtcctt 3000
 gctggtaaac cttcgggcta tgcagaattt cttgcagtta ccggaagctg aaagagaccg 3060
 aatataccag gacgaaaggg aaaggagctt gaatgctgcc tcggccatgg gtctgcccc 3120
 cctcatcagc acaccacca gccgtctcc ccaggtgaaa acagctacta ttgccactga 3180
 aaggaatggg aaaccagaga acaataccat gaacattaat gcttccattt atgatgagat 3240
 tcagcaggaa atgaagcgtg ctaaagtgc tcaagcactg ttgcaaagg ttgcagcaac 3300
 caaaagccag ggaatggtgt gcgagctgtt acgtcgaaa gaagatcctt ctccagaaaa 3360
 cagaaccctg tgggagaacc tctcatgat ccgaagggtc ctacgtctc ctacgccaga 3420
 acgtgatgcc atttatgaac aggagagcaa cgcggtgcat cccatggcg acaggccgcc 3480
 ccacattatc catgttcag cagagcagat tcagcaacag cagcagcaac agcaacagca 3540
 gcagcagcag cagcaggcac cgccgctcc acagccacag cagcagccac agacaggccc 3600
 tcggctcccc ccacggcaac ccacggtggc ctctccagca gagtcagatg aggaaaaccg 3660
 acagaagacc cggccacgaa caaaaatttc agtgaagcc ttgggaatcc tccagagttt 3720

Sequence_Listing.txt

catacaagac gtgggcctgt accctgacga agaggccatc cagactctgt ctgccagct 3780
cgacctccc aagtacacca tcatcaagtt cttcagaac cagcggctact atctcaagca 3840
ccacggcaaa ctgaaggaca attccggttt agaggctgat gtggcagaat ataaagaaga 3900
ggagctgctg aaggatttgg aagagagtgt ccaagataaa aatactaaca ccctttttc 3960
agtgaacta gaagaagagc tgtcagtga aggaaacaca gacattaata ctgattgaa 4020
agactgagat aaaagtattt gtttcttca acagtgccac tggattttac taacaaaatg 4080
aaaagtcac ctgtcttct ctcaaaaac cttgttgtt cattgtttg ccaatgaatc 4140
ttcaaaaact tgcacaaaca gaaaagtgg aaaaggataa tacagactgc actaaatgtt 4200
ttcctctgt ttacaaactg ctggcagcc ccagggaag catcaaggat tgtttggtat 4260
taaaattgt gttcacggga tgcacaaag tgtgtacccc gtaagcatga aaccagtgtt 4320
tttgtttt ttttagtgc ttattccgga gcctcaaaca agcattatac cttctgtgat 4380
tatgattcc tctctataa ttattctgt agcactccac actgatctt ggaaacttgc 4440
ccctattta aaaaaaaaaa agaaaaaaaa gagtttgta ctctattgta tgttacaaaa 4500
gaactataga ctgtggaatg cagtttaaag atgacatatg ccaacaaatg cctgtatta 4560
tatggcactg ccgtaattca aattgtttt tttttggaa ataaaagtc actgtacttt 4620
ttttcattc tcattgttac atgattttt aaaaaaagga aaagaaaatg tgaacacaa 4680
tttagtctc attatttatt ttagatcct gcagcatcat gttgtaatta atttttgga 4740
agttccgtt aaatgtaata ttgcttctt tgtaccata ctgattctt tctattata 4800
aatgtattt gatgggcagt aaaacaaagt gtctaaaag ttttaaatag agaaaatgtg 4860
cttacacag ttgcctataa aaagtgtct atgttatcca agcaattcat actataagct 4920
tcactctat tgtgtatgc aatttttact atcatgcaaa taagcttagg taaataaac 4980

Sequence_Listing.txt

taatagatca ccttagaaaa ttatgcaatt aatgtgaaaa taattgatgt ttgcaatgtg 5040
 tcttccttgg gtttacaatc aattttaag ctacatctgt ataaaatttc tgtataaagg 5100
 tgtatttctt tttatgagt ttatggctat gaaaacagct atttgttac agctggctgt 5160
 tttataagt gtaacacaat tttcttatg cagaaatgtt ctgactagga gtggttattg 5220
 actgtaacta cacaattaaa attgtttgta tcgtatgaca tggtaggggtt tgtctgctta 5280
 tgtgaagtaa ctaaaggagt caaaggatgg ccctctcatt taggtgcatg ttaataactt 5340
 gttatttcac tgattttaaa aagagcaatt gacaagttac ttgaaacact gtaaatttaa 5400
 atcacaacaa catgctcatt tttaaataagg tatgaaattt cacaatgaaa ataacctgtt 5460
 tggtaacat ttgcttaat aagtagagat aggatggatc aaagactctc cgacaaaaac 5520
 aaatccagtc tctagcagtt atgttgtagg aatgga 5556

<210> 64
 <211> 763
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Asp His Leu Asn Glu Ala Thr Gln Gly Lys Glu His Ser Glu Met
 1 5 10 15

Ser Asn Asn Val Ser Asp Pro Lys Gly Pro Pro Ala Lys Ile Ala Arg
 20 25 30

Leu Glu Gln Asn Gly Ser Pro Leu Gly Arg Gly Arg Leu Gly Ser Thr
 35 40 45

Gly Ala Lys Met Gln Gly Val Pro Leu Lys His Ser Gly His Leu Met
 50 55 60

Sequence_Listing.txt

Lys Thr Asn Leu Arg Lys Gly Thr Met Leu Pro Val Phe Cys Val Val
65 70 75 80

Glu His Tyr Glu Asn Ala Ile Glu Tyr Asp Cys Lys Glu Glu His Ala
 85 90 95

Glu Phe Val Leu Val Arg Lys Asp Met Leu Phe Asn Gln Leu Ile Glu
 100 105 110

Met Ala Leu Leu Ser Leu Gly Tyr Ser His Ser Ser Ala Ala Gln Ala
 115 120 125

Lys Gly Leu Ile Gln Val Gly Lys Trp Asn Pro Val Pro Leu Ser Tyr
 130 135 140

Val Thr Asp Ala Pro Asp Ala Thr Val Ala Asp Met Leu Gln Asp Val
145 150 155 160

Tyr His Val Val Thr Leu Lys Ile Gln Leu His Ser Cys Pro Lys Leu
 165 170 175

Glu Asp Leu Pro Pro Glu Gln Trp Ser His Thr Thr Val Arg Asn Ala
 180 185 190

Leu Lys Asp Leu Leu Lys Asp Met Asn Gln Ser Ser Leu Ala Lys Glu
 195 200 205

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

Sequence_Listing.txt

Tyr Ala Asn Val Ser Ala Ala Lys Cys Gln Glu Phe Gly Arg Trp Tyr
225 230 235 240

Lys His Phe Lys Lys Thr Lys Asp Met Met Val Glu Met Asp Ser Leu
245 250 255

Ser Glu Leu Ser Gln Gln Gly Ala Asn His Val Asn Phe Gly Gln Gln
260 265 270

Pro Val Pro Gly Asn Thr Ala Glu Gln Pro Pro Ser Pro Ala Gln Leu
275 280 285

Ser His Gly Ser Gln Pro Ser Val Arg Thr Pro Leu Pro Asn Leu His
290 295 300

Pro Gly Leu Val Ser Thr Pro Ile Ser Pro Gln Leu Val Asn Gln Gln
305 310 315 320

Leu Val Met Ala Gln Leu Leu Asn Gln Gln Tyr Ala Val Asn Arg Leu
325 330 335

Leu Ala Gln Gln Ser Leu Asn Gln Gln Tyr Leu Asn His Pro Pro Pro
340 345 350

Val Ser Arg Ser Met Asn Lys Pro Leu Glu Gln Gln Val Ser Thr Asn
355 360 365

Thr Glu Val Ser Ser Glu Ile Tyr Gln Trp Val Arg Asp Glu Leu Lys
370 375 380

Arg Ala Gly Ile Ser Gln Ala Val Phe Ala Arg Val Ala Phe Asn Arg
385 390 395 400

Sequence_Listing.txt

Thr Gln Gly Leu Leu Ser Glu Ile Leu Arg Lys Glu Glu Asp Pro Lys
405 410 415

Thr Ala Ser Gln Ser Leu Leu Val Asn Leu Arg Ala Met Gln Asn Phe
420 425 430

Leu Gln Leu Pro Glu Ala Glu Arg Asp Arg Ile Tyr Gln Asp Glu Arg
435 440 445

Glu Arg Ser Leu Asn Ala Ala Ser Ala Met Gly Pro Ala Pro Leu Ile
450 455 460

Ser Thr Pro Pro Ser Arg Pro Pro Gln Val Lys Thr Ala Thr Ile Ala
465 470 475 480

Thr Glu Arg Asn Gly Lys Pro Glu Asn Asn Thr Met Asn Ile Asn Ala
485 490 495

Ser Ile Tyr Asp Glu Ile Gln Gln Glu Met Lys Arg Ala Lys Val Ser
500 505 510

Gln Ala Leu Phe Ala Lys Val Ala Ala Thr Lys Ser Gln Gly Trp Leu
515 520 525

Cys Glu Leu Leu Arg Trp Lys Glu Asp Pro Ser Pro Glu Asn Arg Thr
530 535 540

Leu Trp Glu Asn Leu Ser Met Ile Arg Arg Phe Leu Ser Leu Pro Gln
545 550 555 560

Sequence_Listing.txt

Pro Glu Arg Asp Ala Ile Tyr Glu Gln Glu Ser Asn Ala Val His His
565 570 575

His Gly Asp Arg Pro Pro His Ile Ile His Val Pro Ala Glu Gln Ile
580 585 590

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala
595 600 605

Pro Pro Pro Pro Gln Pro Gln Gln Gln Pro Gln Thr Gly Pro Arg Leu
610 615 620

Pro Pro Arg Gln Pro Thr Val Ala Ser Pro Ala Glu Ser Asp Glu Glu
625 630 635 640

Asn Arg Gln Lys Thr Arg Pro Arg Thr Lys Ile Ser Val Glu Ala Leu
645 650 655

Gly Ile Leu Gln Ser Phe Ile Gln Asp Val Gly Leu Tyr Pro Asp Glu
660 665 670

Glu Ala Ile Gln Thr Leu Ser Ala Gln Leu Asp Leu Pro Lys Tyr Thr
675 680 685

Ile Ile Lys Phe Phe Gln Asn Gln Arg Tyr Tyr Leu Lys His His Gly
690 695 700

Lys Leu Lys Asp Asn Ser Gly Leu Glu Val Asp Val Ala Glu Tyr Lys
705 710 715 720

Glu Glu Glu Leu Leu Lys Asp Leu Glu Glu Ser Val Gln Asp Lys Asn
725 730 735

Sequence_Listing.txt

Thr Asn Thr Leu Phe Ser Val Lys Leu Glu Glu Glu Leu Ser Val Glu
740 745 750

Gly Asn Thr Asp Ile Asn Thr Asp Leu Lys Asp
755 760

<210> 65
<211> 2315
<212> DNA
<213> Homo sapiens

<400> 65
ccggcgctcc aagtgagtgg agggggggtc cgcactccag tccggggcct tggccagcgg 60
agccgcgcta ttcggaagcg ggaatccac tcagagcccg ggctgtagg ggcggggcgt 120
cccgggcacc cgggattggg gcgtctccg tcgtgcaccg gggcaccggc gactcaccg 180
gaaggagaag ccgtgatctg gctatatggt ggggcgcggg cgggtgtcgt gtggggagct 240
ggtgtgttc tcagatgtt ccttcaatg ggcttttgt gtaggatgtc ggagaaccaa 300
gaacaggagg aggtgattac agtgcgtgt caggacccc gagtcagaa tgagggtcc 360
tggaactct atgtggatta taagatatt cccatacca acagcaaagc cttactgcc 420
aagacttct gtgtgcggcg ccgctaccgt gagttcgtt ggctgagaaa gcagctacag 480
agaaatgctg gtttgggtcc tgttctgaa ctctctggga agtcaacctt cttcggcacc 540
tcagatgagt tcattgagaa gcgacgacaa ggtctgcagc acttcttga aaaggctctg 600
cagagtgtgg ttctctgtc agacagccag ttgcacatat tctgcaaag ccagctctg 660
gtgcctgaga tagaagcctg tgtccagggc cgaagtacca tgactgtgtc tgatgccatt 720
cttcgatatg ctatgtcaaa ctgtggctgg gccaggaag agaggcagag ctctctcac 780

Sequence_Listing.txt

ctggctaaag gagaccagcc taagagtgc tgctttctc caagatcggg taggaggagc 840

tctccctcac cgctccag tgaagaaaag gaccatttag aagtgtggc tccagttgt 900

gactctgagg ttcttcctt ggaaagtccc actctccac ccctctctc accattatgc 960

tgtgatttg gaagaccaa agaggggaacc tccactctc agtctgtgag gagggctgtg 1020

ggaggagatc atgctgtgcc ttggaccct ggtcagttag aaacagttt ggaaaagtga 1080

gctctgggtt ctgctcag atgtcagag aagatcggg ccaggagact tactcaggtg 1140

ggactgggca cagggcaggt atgtggagg ctgggctgt tagtgtctc tagtcacctc 1200

tgctgggt gattgacaga ggtcagtcac tacagcccct tatgcctctt ccatgggaac 1260

aaatactgtg cagatgttg taagttaaac ataagacaca ggggctgtt ctttgaaca 1320

gaaccctata ttactctct gggatctgag ttctgcagg tcatttgtat gtaggaccag 1380

gagtatctc tcaggtagc agtttggg acccgtatgt ggcaaattct aagctgcat 1440

attgaacatc atccactgg gagtggttat gtgtatccc catctggct ggcttcagtt 1500

tttctgtag ccctagagca cttgtttgt gggaggctgg cctctgcct acctcctgc 1560

atggacaggg ggaatgaat ttacttccc acctcctgc ttttcttc actgatacca 1620

ctgaatggaa ctggtcgtg gactcctgt gctggggatt tatgtccga gacctagcc 1680

tggctgagtg gagcctgaga cctgcacaac agctcatgt catgcatgag agagaagtgg 1740

ctggccacag ccagaggga cagtaacagc ccaggggcct ttatttggg aaaggctgtc 1800

ccgggctgtt actgtctct ctggtataa agcagacatg tggccatct ttccgcaggg 1860

ttagagtggg ctcttctt ttggaatcc tttctctc ctttggtagc agctccctgc 1920

ctccagggt tccgccacca gcgtctctc tgttgtcgc agtcagtg ggtgcaagg 1980

ctttgttct gcctgcctga aagagagggc tctgggatg gagatgagaa acaacacgt 2040

Sequence_Listing.txt

ctccttcaga caatgaggca ttctgtctc ctgtgccat tctcatctc cactgagagc 2100
cagagctggg aggagccgag tgccacaggc attctgcatt gctctactct taggtttgtg 2160
tgtgtgatcc ttccctccc tgcgcccac tctccctcc tctggctatc ctaccctgtc 2220
tgtgggtctt ttactacca gcctatgctg tgggactgtc atggcattta gttcagagtg 2280
gaggggcttt ggctgaaat aaaatgcaag tattt 2315

<210> 66

<211> 270

<212> PRT

<213> Homo sapiens

<400> 66

Met Gly Phe Trp Cys Arg Met Ser Glu Asn Gln Glu Gln Glu Glu Val
1 5 10 15

Ile Thr Val Arg Val Gln Asp Pro Arg Val Gln Asn Glu Gly Ser Trp
20 25 30

Asn Ser Tyr Val Asp Tyr Lys Ile Phe Leu His Thr Asn Ser Lys Ala
35 40 45

Phe Thr Ala Lys Thr Ser Cys Val Arg Arg Arg Tyr Arg Glu Phe Val
50 55 60

Trp Leu Arg Lys Gln Leu Gln Arg Asn Ala Gly Leu Val Pro Val Pro
65 70 75 80

Glu Leu Pro Gly Lys Ser Thr Phe Phe Gly Thr Ser Asp Glu Phe Ile
85 90 95

Glu Lys Arg Arg Gln Gly Leu Gln His Phe Leu Glu Lys Val Leu Gln

Sequence_Listing.txt

100 105 110

Ser Val Val Leu Leu Ser Asp Ser Gln Leu His Leu Phe Leu Gln Ser
115 120 125

Gln Leu Ser Val Pro Glu Ile Glu Ala Cys Val Gln Gly Arg Ser Thr
130 135 140

Met Thr Val Ser Asp Ala Ile Leu Arg Tyr Ala Met Ser Asn Cys Gly
145 150 155 160

Trp Ala Gln Glu Glu Arg Gln Ser Ser Ser His Leu Ala Lys Gly Asp
165 170 175

Gln Pro Lys Ser Cys Cys Phe Leu Pro Arg Ser Gly Arg Arg Ser Ser
180 185 190

Pro Ser Pro Pro Pro Ser Glu Glu Lys Asp His Leu Glu Val Trp Ala
195 200 205

Pro Val Val Asp Ser Glu Val Pro Ser Leu Glu Ser Pro Thr Leu Pro
210 215 220

Pro Leu Ser Ser Pro Leu Cys Cys Asp Phe Gly Arg Pro Lys Glu Gly
225 230 235 240

Thr Ser Thr Leu Gln Ser Val Arg Arg Ala Val Gly Gly Asp His Ala
245 250 255

Val Pro Leu Asp Pro Gly Gln Leu Glu Thr Val Leu Glu Lys
260 265 270

Sequence_Listing.txt

<210> 67

<211> 8017

<212> DNA

<213> Homo sapiens

<400> 67

tatgtcttct aaagataatg tcgatttgt atggctgatg ggattctagg accaagcaag 60

aggtttttt tttcccca cataactaac gttctatat ttctattga attcgactgg 120

acagtccat ttgaattatt tctctctc tctctctg acacattta tcttgccagg 180

ttctaaacct ttaggaaaaa tggagcaatt tcaaaggaa accgttgtgg agagcagtgg 240

gccaaagggt ttgaaacag cagaagagat ccaggagagg cgtcaggaag tgtgactcg 300

gtatcaaagt ttcaaggagc gggctgctga gaggggtcag aagcttgagg attcctatca 360

cttacaagtt ttcaagcgag atgcagatga tctggggaag tggatcatgg agaaagtcaa 420

tatcttaacc gataagagct atgaagaccc aactaatata caggggaaat atcagaagca 480

tcaatccctt gaagcagagg tgcaacaaa atcaagactc atgtctgaac tggaaaaaac 540

aaggaagaa cgattacca tgggtcattc tgcccacgaa gaaacgaagg cccatataga 600

ggagctacgc cacctgtggg acctgtgtt agagctgacc ctggagaagg gtgaccagtt 660

gctgcgggcc ctgaagtcc agcagtatgt acaggagtgt gctgacatct tagagtggat 720

tggagacaag gaggtatag cgacatcagt ggagctaggt gaagactggg agcgcaccga 780

agttctcat aagaaattg aagactcca agtggagctg gtagctaaag aaggagagat 840

tgtgaagtg aaccaatatg ccaatgagtg tgccgaggaa aaccatcctg acctaccctt 900

aattcagict aagcaaatg aggtgaatgc tgctgggag cgcctctgtg gtttggtctt 960

ccagagacag aaagctctgt ccaatgctgc aaacttaca cgattcaaaa gggatgtgac 1020

tgaagccatc cagtggatca aggagaagga acctgtactc acctctgagg actatggcaa 1080

Sequence_Listing.txt

agacctgtgt gcctctgaag gactgtttca cagtcacaag ggacttgaga gaaatcttgc 1140

tgctatgagt gacaagggtga aggagttatg tgctaaagca gagaagctga cactttccca 1200

tccttcagat gcacctcaga tccaggagat gaaagaagat ctggctcca gctgggagca 1260

tattcgtgcc ctggccacca gcagatatga aaaactgcag gctactatt ggtaccatcg 1320

atfttcatct gactttgatg aactctcagg ctggatgaac gagaagactg ctgcatcaa 1380

tgctgatgag ctgccaacag atgtggctgg tggagaagtt ctgctggaca ggcatcagca 1440

gcataagcat gagattgact cttacgatga ccgatttcaa tctgctgatg agactggtca 1500

agacctcgtg aatgccaatc atgaagcctc tgatgaagtt cgggaaaaga tggaaatact 1560

tgacaacaac tggactgccc tgctggaact gtgggacgag cgtcatcgtc agtatgagca 1620

gtgcttgac ttcatctct tctacagaga cagttagcaa gtggacagtt ggatgagtag 1680

acaagaggcc ttcttgaaa acgaggatct gggaaactca ctgggcagtg cagaagccct 1740

tcttcagaag catgaagact ttgaggaagc cttactgcc caggaagaga agatcataac 1800

tgtagacaag actgcaacca aattgattgg tgatgacat tatgattcag agaacatcaa 1860

ggctatccgt gacgggctgt tagcccgcg ggatgcccta cgtgaaaagg ctgccactag 1920

acgtagattg ctgaaggagt cattgcttct gcaaaaactg tatgaggact cagatgacct 1980

aaagaactgg atcaacaaga agaaaaagtt ggcagatgat gaagattaca aggacataca 2040

gaacttgaag agcagggttc aaaagcagca agtctttgaa aaggagtgg cagttaataa 2100

gacctcagctg gaaaacatac agaaaactgg ccaagagatg attgagggtg gtcactatgc 2160

ctctgacaat gtgaccactc gtctgagtga agttgccagc ctctgggagg agttgctgga 2220

ggctacaaaa cagaaaggga ccagttgca tgaggccaac cagcagctgc aatttgaaaa 2280

taatgcagaa gatttcagc gctggctgga ggatgttgag tggcaagtca cctctgagga 2340

Sequence_Listing.txt

ttatgggaaa ggctggccg aggtacagaa tcgactcagg aaacacggcc tctggagtc 2400
 ggctgtggct gctcgtcagg atcaggtgga tatccttaca gacctggctg catatttga 2460
 agaaataggc catcctgatt ctaaggatat aagggcaagg caagagtcct tggatgccg 2520
 attgaagct ctgaaagagc cactggccac ccgaaagaag aagctcttag accttctcca 2580
 tctgcagctg attgtagag acacagagga tgaggaggcc tggatccaag agactgaacc 2640
 ctgagctact tccacctacc ttgaaagga cctgattgct tcaaaaagc ttctgaatag 2700
 gcatagagtc atcctggaga acattgccag ccatgaacca cgcattcaag agataacaga 2760
 aaggggaaac aaaatggtag aggaaggaca ctttctgca gaagatgtgg cctctagggt 2820
 caagagttg aaccagaata tggagtcct cctgtctga gctgctaggc gacaaaatga 2880
 tctgaagcc aatgtccagt tccagcagta cctggctgac ctgcatgaag cagaaacatg 2940
 gatcagagag aaggaaccta tttagataa tactaactat ggtgctgatg aagaagcagc 3000
 tggggctctt ctaaagaagc atgaggcctt tctattagat ctcaattcat ttggagacag 3060
 tatgaaagct ctgcggaatc aggcaaacgc ctgccagcaa caacaggctg caccagtga 3120
 gggagttgct ggagaacaaa gggatcaggc ttatatgac ttccaggccc gcagccccg 3180
 agaagtcacc atgaagaaag gtgatgtctt aacgtgctc agttccatca ataaggactg 3240
 gtggaagggt gaagctgctg atcatcaggc cattgtcca gctgtctatg tcagaagact 3300
 ggcccacgat gagttccga tgctcccaca gggcgacga gaagagccag gaaacatcac 3360
 ccagcgccag gagcagattg agaaccaata ccgtccctc ttgatcggg cagaagaacg 3420
 cagacgtcgt ctattgcaac gttataatga attttattg gcctatgagg caggagacat 3480
 gctggaatgg attcaagaga aaaaggcaga aaactctgga gtggaactag atgatgttg 3540
 ggagctgcag aaaaagttg atgagttcca aaaggattg aataccaatg agcctcggct 3600

Sequence_Listing.txt

aaggatatac aacaaggtag ctgatgatct actatttgaa ggacttctaa caccagaagg 3660
agctcaaatac cggcaggaat tgaattcccg ctgggggttct ttgcagaggc ttgcagatga 3720
acagcggcag ctgctgggca gtgccatgc tgtgaagtgt ttacacagag aagcagatga 3780
cacgaaggag cagattgaga agaaatgccg gccctcagt gctgcagacc ctggctcaga 3840
tctgttcagt gttcaggctc ttacgcgacg gcatgagggc ttgaaaggg acctcgtacc 3900
cctgggagat aaggtagacca tactggggga gacagcagag cggctcagt agtcccatcc 3960
agatgccact gaggacctgc agagacagaa aatggagctg aatgaggcct gggaagacct 4020
gcaggggcgt acaaaggatc gtaaggagag cctaaatgag gccagaaat tctacctgtt 4080
cctcagcaag gccagggatc tgcagaactg gatcagtagc attggtggca tggatcatc 4140
acaggagctg gccgaagact taactggcat agagatcttg ctggagagac atcaggagca 4200
ccgtgctgac atggaggcag aggtccccc cttccaggcc ttagaggact tcagtgcaga 4260
acttatcgac agtgggcacc atgctagccc tgaaattgaa aaaaagcttc aagctgtcaa 4320
gctagagaga gatgatttgg agaaggcttg ggaaaaacgc aagaagatcc tagaccagt 4380
cctggagttg cagatgttcc aggggaactg tgatcaagtt gagagctgga tggtagcacg 4440
tgagaattcc ctgaggtcag atgacaaaag ttcttagac agtctggagg ctttgatgaa 4500
gaaacgggac gatttgaca aagcaatcac tgcccaggaa gggaagatca ctgacctaga 4560
acattttgct gagagcctca ttgctgatga acactatgcc aaagaagaga ttgctacgag 4620
gctccaacgt gtactagaca ggtggaaggc tctcaaagca caactgattg atgagcggac 4680
aaagcttggg gactatgcc acctaaaaca attctaccga gacctgagg agctggaaga 4740
atggatcagt gagatgctgc ccacagcctg tgatgaatcc taaaagacg ccactaacat 4800
tcagaggaaa tacctgaaac accagacctt tgacatgaa gtcgatggcc gatctgagca 4860

Sequence_Listing.txt

ggatcatggc gtcataacc tggggaactc cctgattgag ttagcgctt gtgatggcaa 4920
tgaagaggcc atgaaggagc aactggaaca gctgaaggaa cattgggatc atctgctga 4980
gagaacaaat gacaaagga agaagctcaa tgaggccagt cgtcaacaga ggtcaacac 5040
aagcatccgg gactttgagt tctggctctc agaggcagag acattgctgg ccatgaaaga 5100
tcaggccagg gacttggctt cagcaggaaa cctactcaag aagcatcagc tattggagag 5160
agagatgttg gctcgagagg atgcactcaa ggacctgaat acattggctg aagatttgc 5220
ctccagcggg acttcaacg ttgatcagat tgtgaagaaa aaagataatg tcaacaagcg 5280
tttctgaat gtccaagaat tggcagctgc acaccacgaa aaattgaaag aggcctatgc 5340
cttgtccag ttctccagg atctagatga tgaggaatcc tggatagagg agaagttgat 5400
acgagtgagc tcccaggact atgggagaga tcttcagggg gttcagaact tgctgaagaa 5460
gcacaaacgc cttagagggg agctggtggc ccatgagcct gccatccaga atgtgctgga 5520
tatggcagag aagctgaaag acaaggctgc tgtggggcaa gaggagatcc agttgcggct 5580
ggctcagttt gttgaacact gggagaagct caaagagttg gccaaggccc gaggactaa 5640
gttgaagaa tccctagaat acttgaatt catgcagaat gctgaggaag aggaagcttg 5700
gatcaatgaa aagaatgctt tggtgtccg aggagattgt ggagatacat tagctgctac 5760
tcagagcttg ctaatgaagc atgaagcttt ggaaaatgac ttgtgttc atgagacccg 5820
agtacaaaat gtgtgtgcac aaggagaaga catcctaaat aagggtgtgc aggaggaaag 5880
tcagaacaaa gagatttctt ccaagataga ggctctgaat gaaaagaccc ctctctggc 5940
taaggcaata gctgcttga agttgcaatt ggaagacgat tatgccttc aggaattcaa 6000
ctggaaggct gatgtgtag aggcttggat agctgataag gaaacaagcc taaagaccaa 6060
tggcaatggt gcagaccttg gtgacttct cactctctg gcaaacagg acactctga 6120

Sequence_Listing.txt

tgccagctctg cagagtttcc agcaagagag acttcccag atcactgacc tgaaggacaa 6180
actgatttct gctcaacaca accagtctaa agccattgaa gagcgttatg ccgctctgct 6240
gaagcgcctgg gaacagttgc tggaaagcctc ggcagtccac agacagaaat tgctggagaa 6300
acagctgcct ctacagaagg ctgaggacct gttcgtggaa ttgcacata aggcttcagc 6360
tttgaacaac tgggtgtaaa agatggaaga aaactgtca gagcctgtgc actgtgtctc 6420
cctgaatgaa attcggcagc tgcagaaaga ccatgaggac ttcttggcct ccctggctag 6480
ggctcaagca gactttaaat gtttctgga gctagaccag cagattaagg ccttagtgt 6540
gccttcagc ccttatacct ggtaacagt ggagggtctg gaaaggacct ggaagcacct 6600
atctgacatc attgaggaac gggagcagga gctgcaaaag gaagaggcaa gacaggtaa 6660
gaactttgag atgtgtcagg agttgaaca gaatgccagt accttcctc aatggatcct 6720
ggaaaccagg gcttacttc tggatggatc attgtcaaa gaaacaggaa ctctggaatc 6780
tcagctggaa gcaaataaaa gaaaacagaa ggagatccag gcgatgaagc gtcaactaac 6840
caagattgtg gacctggggg acaacttga agacgctctg atccttgata tcaaatacag 6900
caccattgga ttggctcagc agtgggacca gctctaccag cttgggttgc ggatgcaaca 6960
caacctggag caacagatcc aggccaagga catcaaaggt gtgagtgaag agactctaaa 7020
ggaatttagc acaatctata aacacttga tgagaattg acagggcgcc tgactcaca 7080
agagttccgg tctgcctga gaggactcaa ttactactg cccatggtg aggaggatga 7140
acatgagccc aagtttgaga agttcctgga tgctgtggat ccaggaggga agggctatgt 7200
ctcactggag gactatactg ctttctgat tgacaaggag tcagaaaaca tcaagtccag 7260
tgatgaaata gagaatgcct tccaagccct ggcagagggc aagtcataa ttaccaaaga 7320
agacatgaag caggccctta cccagagca agtgcattc tgtccacac atatgcagca 7380

Sequence_Listing.txt

atatatggac ccacgggggc gaagccatct cctggctat gactacgttg gcttcaccaa 7440
 ttctacttt ggcaactaat aagcagctcc tcgtggatcg tagaaaatct tagtgtctg 7500
 ggaaatttac tggggggcaa agagtacagg caaatgtgga agataaagat ggcctcgtgt 7560
 gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gcttgtgttt gtgtgcatat tacatttatt 7620
 gtaggatctt aaaaaatctc aagggtggga gatagaaagg ttaatagagt tggaggagt 7680
 gaagctattt tgtatgcaac tagtcactgc tgaggggtgt caaagtttct atttttattt 7740
 gttctgtttt gcacgtcttt atcattttgc ttattccga ttatagaata aagtaattct 7800
 ttttaaaaat atttttggg gcaaagftaa gtaaaatgtt gagcttctat atttctggga 7860
 actgtactca tataagagtg ggcagctaatt ttactgtaa agaagggcca tggatataga 7920
 gataaataaa atccaaggca atttcaaac aatttttta aactttggaa tgtgtttaa 7980
 tttaaatttg aaaataaaga tatttgattt tctgggg 8017

<210> 68
 <211> 2419
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Glu Gln Phe Pro Lys Glu Thr Val Val Glu Ser Ser Gly Pro Lys
 1 5 10 15

Val Leu Glu Thr Ala Glu Glu Ile Gln Glu Arg Arg Gln Glu Val Leu
 20 25 30

Thr Arg Tyr Gln Ser Phe Lys Glu Arg Val Ala Glu Arg Gly Gln Lys
 35 40 45

Sequence_Listing.txt

Leu Glu Asp Ser Tyr His Leu Gln Val Phe Lys Arg Asp Ala Asp Asp
50 55 60

Leu Gly Lys Trp Ile Met Glu Lys Val Asn Ile Leu Thr Asp Lys Ser
65 70 75 80

Tyr Glu Asp Pro Thr Asn Ile Gln Gly Lys Tyr Gln Lys His Gln Ser
85 90 95

Leu Glu Ala Glu Val Gln Thr Lys Ser Arg Leu Met Ser Glu Leu Glu
100 105 110

Lys Thr Arg Glu Glu Arg Phe Thr Met Gly His Ser Ala His Glu Glu
115 120 125

Thr Lys Ala His Ile Glu Glu Leu Arg His Leu Trp Asp Leu Leu Leu
130 135 140

Glu Leu Thr Leu Glu Lys Gly Asp Gln Leu Leu Arg Ala Leu Lys Phe
145 150 155 160

Gln Gln Tyr Val Gln Glu Cys Ala Asp Ile Leu Glu Trp Ile Gly Asp
165 170 175

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

Thr Glu Val Leu His Lys Lys Phe Glu Asp Phe Gln Val Glu Leu Val
195 200 205

Ala Lys Glu Gly Arg Val Val Glu Val Asn Gln Tyr Ala Asn Glu Cys
210 215 220

Sequence_Listing.txt

Ala Glu Glu Asn His Pro Asp Leu Pro Leu Ile Gln Ser Lys Gln Asn
225 230 235 240

Glu Val Asn Ala Ala Trp Glu Arg Leu Arg Gly Leu Ala Leu Gln Arg
 245 250 255

Gln Lys Ala Leu Ser Asn Ala Ala Asn Leu Gln Arg Phe Lys Arg Asp
 260 265 270

Val Thr Glu Ala Ile Gln Trp Ile Lys Glu Lys Glu Pro Val Leu Thr
 275 280 285

Ser Glu Asp Tyr Gly Lys Asp Leu Val Ala Ser Glu Gly Leu Phe His
 290 295 300

Ser His Lys Gly Leu Glu Arg Asn Leu Ala Val Met Ser Asp Lys Val
305 310 315 320

Lys Glu Leu Cys Ala Lys Ala Glu Lys Leu Thr Leu Ser His Pro Ser
 325 330 335

Asp Ala Pro Gln Ile Gln Glu Met Lys Glu Asp Leu Val Ser Ser Trp
 340 345 350

Glu His Ile Arg Ala Leu Ala Thr Ser Arg Tyr Glu Lys Leu Gln Ala
 355 360 365

Thr Tyr Trp Tyr His Arg Phe Ser Ser Asp Phe Asp Glu Leu Ser Gly
 370 375 380

Sequence_Listing.txt

Trp Met Asn Glu Lys Thr Ala Ala Ile Asn Ala Asp Glu Leu Pro Thr
385 390 395 400

Asp Val Ala Gly Gly Glu Val Leu Leu Asp Arg His Gln Gln His Lys
405 410 415

His Glu Ile Asp Ser Tyr Asp Asp Arg Phe Gln Ser Ala Asp Glu Thr
420 425 430

Gly Gln Asp Leu Val Asn Ala Asn His Glu Ala Ser Asp Glu Val Arg
435 440 445

Glu Lys Met Glu Ile Leu Asp Asn Asn Trp Thr Ala Leu Leu Glu Leu
450 455 460

Trp Asp Glu Arg His Arg Gln Tyr Glu Gln Cys Leu Asp Phe His Leu
465 470 475 480

Phe Tyr Arg Asp Ser Glu Gln Val Asp Ser Trp Met Ser Arg Gln Glu
485 490 495

Ala Phe Leu Glu Asn Glu Asp Leu Gly Asn Ser Leu Gly Ser Ala Glu
500 505 510

Ala Leu Leu Gln Lys His Glu Asp Phe Glu Glu Ala Phe Thr Ala Gln
515 520 525

Glu Glu Lys Ile Ile Thr Val Asp Lys Thr Ala Thr Lys Leu Ile Gly
530 535 540

Asp Asp His Tyr Asp Ser Glu Asn Ile Lys Ala Ile Arg Asp Gly Leu
545 550 555 560

Sequence_Listing.txt

Leu Ala Arg Arg Asp Ala Leu Arg Glu Lys Ala Ala Thr Arg Arg Arg
565 570 575

Leu Leu Lys Glu Ser Leu Leu Leu Gln Lys Leu Tyr Glu Asp Ser Asp
580 585 590

Asp Leu Lys Asn Trp Ile Asn Lys Lys Lys Lys Leu Ala Asp Asp Glu
595 600 605

Asp Tyr Lys Asp Ile Gln Asn Leu Lys Ser Arg Val Gln Lys Gln Gln
610 615 620

Val Phe Glu Lys Glu Leu Ala Val Asn Lys Thr Gln Leu Glu Asn Ile
625 630 635 640

Gln Lys Thr Gly Gln Glu Met Ile Glu Gly Gly His Tyr Ala Ser Asp
645 650 655

Asn Val Thr Thr Arg Leu Ser Glu Val Ala Ser Leu Trp Glu Glu Leu
660 665 670

Leu Glu Ala Thr Lys Gln Lys Gly Thr Gln Leu His Glu Ala Asn Gln
675 680 685

Gln Leu Gln Phe Glu Asn Asn Ala Glu Asp Leu Gln Arg Trp Leu Glu
690 695 700

Asp Val Glu Trp Gln Val Thr Ser Glu Asp Tyr Gly Lys Gly Leu Ala
705 710 715 720

Sequence_Listing.txt

Glu Val Gln Asn Arg Leu Arg Lys His Gly Leu Leu Glu Ser Ala Val
725 730 735

Ala Ala Arg Gln Asp Gln Val Asp Ile Leu Thr Asp Leu Ala Ala Tyr
740 745 750

Phe Glu Glu Ile Gly His Pro Asp Ser Lys Asp Ile Arg Ala Arg Gln
755 760 765

Glu Ser Leu Val Cys Arg Phe Glu Ala Leu Lys Glu Pro Leu Ala Thr
770 775 780

Arg Lys Lys Lys Leu Leu Asp Leu Leu His Leu Gln Leu Ile Cys Arg
785 790 795 800

Asp Thr Glu Asp Glu Glu Ala Trp Ile Gln Glu Thr Glu Pro Ser Ala
805 810 815

Thr Ser Thr Tyr Leu Gly Lys Asp Leu Ile Ala Ser Lys Lys Leu Leu
820 825 830

Asn Arg His Arg Val Ile Leu Glu Asn Ile Ala Ser His Glu Pro Arg
835 840 845

Ile Gln Glu Ile Thr Glu Arg Gly Asn Lys Met Val Glu Glu Gly His
850 855 860

Phe Ala Ala Glu Asp Val Ala Ser Arg Val Lys Ser Leu Asn Gln Asn
865 870 875 880

Met Glu Ser Leu Arg Ala Arg Ala Ala Arg Arg Gln Asn Asp Leu Glu
885 890 895

Sequence_Listing.txt

Ala Asn Val Gln Phe Gln Gln Tyr Leu Ala Asp Leu His Glu Ala Glu
900 905 910

Thr Trp Ile Arg Glu Lys Glu Pro Ile Val Asp Asn Thr Asn Tyr Gly
915 920 925

Ala Asp Glu Glu Ala Ala Gly Ala Leu Leu Lys Lys His Glu Ala Phe
930 935 940

Leu Leu Asp Leu Asn Ser Phe Gly Asp Ser Met Lys Ala Leu Arg Asn
945 950 955 960

Gln Ala Asn Ala Cys Gln Gln Gln Gln Ala Ala Pro Val Glu Gly Val
965 970 975

Ala Gly Glu Gln Arg Val Met Ala Leu Tyr Asp Phe Gln Ala Arg Ser
980 985 990

Pro Arg Glu Val Thr Met Lys Lys Gly Asp Val Leu Thr Leu Leu Ser
995 1000 1005

Ser Ile Asn Lys Asp Trp Trp Lys Val Glu Ala Ala Asp His Gln
1010 1015 1020

Gly Ile Val Pro Ala Val Tyr Val Arg Arg Leu Ala His Asp Glu
1025 1030 1035

Phe Pro Met Leu Pro Gln Arg Arg Arg Glu Glu Pro Gly Asn Ile
1040 1045 1050

Sequence_Listing.txt

Thr Gln Arg Gln Glu Gln Ile Glu Asn Gln Tyr Arg Ser Leu Leu
1055 1060 1065

Asp Arg Ala Glu Glu Arg Arg Arg Arg Leu Leu Gln Arg Tyr Asn
1070 1075 1080

Glu Phe Leu Leu Ala Tyr Glu Ala Gly Asp Met Leu Glu Trp Ile
1085 1090 1095

Gln Glu Lys Lys Ala Glu Asn Thr Gly Val Glu Leu Asp Asp Val
1100 1105 1110

Trp Glu Leu Gln Lys Lys Phe Asp Glu Phe Gln Lys Asp Leu Asn
1115 1120 1125

Thr Asn Glu Pro Arg Leu Arg Asp Ile Asn Lys Val Ala Asp Asp
1130 1135 1140

Leu Leu Phe Glu Gly Leu Leu Thr Pro Glu Gly Ala Gln Ile Arg
1145 1150 1155

Gln Glu Leu Asn Ser Arg Trp Gly Ser Leu Gln Arg Leu Ala Asp
1160 1165 1170

Glu Gln Arg Gln Leu Leu Gly Ser Ala His Ala Val Glu Val Phe
1175 1180 1185

His Arg Glu Ala Asp Asp Thr Lys Glu Gln Ile Glu Lys Lys Cys
1190 1195 1200

Gln Ala Leu Ser Ala Ala Asp Pro Gly Ser Asp Leu Phe Ser Val
1205 1210 1215

Sequence_Listing.txt

Gln Ala Leu Gln Arg Arg His Glu Gly Phe Glu Arg Asp Leu Val
1220 1225 1230

Pro Leu Gly Asp Lys Val Thr Ile Leu Gly Glu Thr Ala Glu Arg
1235 1240 1245

Leu Ser Glu Ser His Pro Asp Ala Thr Glu Asp Leu Gln Arg Gln
1250 1255 1260

Lys Met Glu Leu Asn Glu Ala Trp Glu Asp Leu Gln Gly Arg Thr
1265 1270 1275

Lys Asp Arg Lys Glu Ser Leu Asn Glu Ala Gln Lys Phe Tyr Leu
1280 1285 1290

Phe Leu Ser Lys Ala Arg Asp Leu Gln Asn Trp Ile Ser Ser Ile
1295 1300 1305

Gly Gly Met Val Ser Ser Gln Glu Leu Ala Glu Asp Leu Thr Gly
1310 1315 1320

Ile Glu Ile Leu Leu Glu Arg His Gln Glu His Arg Ala Asp Met
1325 1330 1335

Glu Ala Glu Ala Pro Thr Phe Gln Ala Leu Glu Asp Phe Ser Ala
1340 1345 1350

Glu Leu Ile Asp Ser Gly His His Ala Ser Pro Glu Ile Glu Lys
1355 1360 1365

Sequence_Listing.txt

Lys Leu Gln Ala Val Lys Leu Glu Arg Asp Asp Leu Glu Lys Ala
1370 1375 1380

Trp Glu Lys Arg Lys Lys Ile Leu Asp Gln Cys Leu Glu Leu Gln
1385 1390 1395

Met Phe Gln Gly Asn Cys Asp Gln Val Glu Ser Trp Met Val Ala
1400 1405 1410

Arg Glu Asn Ser Leu Arg Ser Asp Asp Lys Ser Ser Leu Asp Ser
1415 1420 1425

Leu Glu Ala Leu Met Lys Lys Arg Asp Asp Leu Asp Lys Ala Ile
1430 1435 1440

Thr Ala Gln Glu Gly Lys Ile Thr Asp Leu Glu His Phe Ala Glu
1445 1450 1455

Ser Leu Ile Ala Asp Glu His Tyr Ala Lys Glu Glu Ile Ala Thr
1460 1465 1470

Arg Leu Gln Arg Val Leu Asp Arg Trp Lys Ala Leu Lys Ala Gln
1475 1480 1485

Leu Ile Asp Glu Arg Thr Lys Leu Gly Asp Tyr Ala Asn Leu Lys
1490 1495 1500

Gln Phe Tyr Arg Asp Leu Glu Glu Leu Glu Glu Trp Ile Ser Glu
1505 1510 1515

Met Leu Pro Thr Ala Cys Asp Glu Ser Tyr Lys Asp Ala Thr Asn
1520 1525 1530

Sequence_Listing.txt

Ile Gln Arg Lys Tyr Leu Lys His Gln Thr Phe Ala His Glu Val
1535 1540 1545

Asp Gly Arg Ser Glu Gln Val His Gly Val Ile Asn Leu Gly Asn
1550 1555 1560

Ser Leu Ile Glu Cys Ser Ala Cys Asp Gly Asn Glu Glu Ala Met
1565 1570 1575

Lys Glu Gln Leu Glu Gln Leu Lys Glu His Trp Asp His Leu Leu
1580 1585 1590

Glu Arg Thr Asn Asp Lys Gly Lys Lys Leu Asn Glu Ala Ser Arg
1595 1600 1605

Gln Gln Arg Phe Asn Thr Ser Ile Arg Asp Phe Glu Phe Trp Leu
1610 1615 1620

Ser Glu Ala Glu Thr Leu Leu Ala Met Lys Asp Gln Ala Arg Asp
1625 1630 1635

Leu Ala Ser Ala Gly Asn Leu Leu Lys Lys His Gln Leu Leu Glu
1640 1645 1650

Arg Glu Met Leu Ala Arg Glu Asp Ala Leu Lys Asp Leu Asn Thr
1655 1660 1665

Leu Ala Glu Asp Leu Leu Ser Ser Gly Thr Phe Asn Val Asp Gln
1670 1675 1680

Sequence_Listing.txt

Ile Val Lys Lys Lys Asp Asn Val Asn Lys Arg Phe Leu Asn Val
1685 1690 1695

Gln Glu Leu Ala Ala Ala His His Glu Lys Leu Lys Glu Ala Tyr
1700 1705 1710

Ala Leu Phe Gln Phe Phe Gln Asp Leu Asp Asp Glu Glu Ser Trp
1715 1720 1725

Ile Glu Glu Lys Leu Ile Arg Val Ser Ser Gln Asp Tyr Gly Arg
1730 1735 1740

Asp Leu Gln Gly Val Gln Asn Leu Leu Lys Lys His Lys Arg Leu
1745 1750 1755

Glu Gly Glu Leu Val Ala His Glu Pro Ala Ile Gln Asn Val Leu
1760 1765 1770

Asp Met Ala Glu Lys Leu Lys Asp Lys Ala Ala Val Gly Gln Glu
1775 1780 1785

Glu Ile Gln Leu Arg Leu Ala Gln Phe Val Glu His Trp Glu Lys
1790 1795 1800

Leu Lys Glu Leu Ala Lys Ala Arg Gly Leu Lys Leu Glu Glu Ser
1805 1810 1815

Leu Glu Tyr Leu Gln Phe Met Gln Asn Ala Glu Glu Glu Glu Ala
1820 1825 1830

Trp Ile Asn Glu Lys Asn Ala Leu Ala Val Arg Gly Asp Cys Gly
1835 1840 1845

Sequence_Listing.txt

Asp Thr Leu Ala Ala Thr Gln Ser Leu Leu Met Lys His Glu Ala
1850 1855 1860

Leu Glu Asn Asp Phe Ala Val His Glu Thr Arg Val Gln Asn Val
1865 1870 1875

Cys Ala Gln Gly Glu Asp Ile Leu Asn Lys Val Leu Gln Glu Glu
1880 1885 1890

Ser Gln Asn Lys Glu Ile Ser Ser Lys Ile Glu Ala Leu Asn Glu
1895 1900 1905

Lys Thr Pro Ser Leu Ala Lys Ala Ile Ala Ala Trp Lys Leu Gln
1910 1915 1920

Leu Glu Asp Asp Tyr Ala Phe Gln Glu Phe Asn Trp Lys Ala Asp
1925 1930 1935

Val Val Glu Ala Trp Ile Ala Asp Lys Glu Thr Ser Leu Lys Thr
1940 1945 1950

Asn Gly Asn Gly Ala Asp Leu Gly Asp Phe Leu Thr Leu Leu Ala
1955 1960 1965

Lys Gln Asp Thr Leu Asp Ala Ser Leu Gln Ser Phe Gln Gln Glu
1970 1975 1980

Arg Leu Pro Glu Ile Thr Asp Leu Lys Asp Lys Leu Ile Ser Ala
1985 1990 1995

Sequence_Listing.txt

Gln His Asn Gln Ser Lys Ala Ile Glu Glu Arg Tyr Ala Ala Leu
2000 2005 2010

Leu Lys Arg Trp Glu Gln Leu Leu Glu Ala Ser Ala Val His Arg
2015 2020 2025

Gln Lys Leu Leu Glu Lys Gln Leu Pro Leu Gln Lys Ala Glu Asp
2030 2035 2040

Leu Phe Val Glu Phe Ala His Lys Ala Ser Ala Leu Asn Asn Trp
2045 2050 2055

Cys Glu Lys Met Glu Glu Asn Leu Ser Glu Pro Val His Cys Val
2060 2065 2070

Ser Leu Asn Glu Ile Arg Gln Leu Gln Lys Asp His Glu Asp Phe
2075 2080 2085

Leu Ala Ser Leu Ala Arg Ala Gln Ala Asp Phe Lys Cys Leu Leu
2090 2095 2100

Glu Leu Asp Gln Gln Ile Lys Ala Leu Gly Val Pro Ser Ser Pro
2105 2110 2115

Tyr Thr Trp Leu Thr Val Glu Val Leu Glu Arg Thr Trp Lys His
2120 2125 2130

Leu Ser Asp Ile Ile Glu Glu Arg Glu Gln Glu Leu Gln Lys Glu
2135 2140 2145

Glu Ala Arg Gln Val Lys Asn Phe Glu Met Cys Gln Glu Phe Glu
2150 2155 2160

Sequence_Listing.txt

Gln Asn Ala Ser Thr Phe Leu Gln Trp Ile Leu Glu Thr Arg Ala
2165 2170 2175

Tyr Phe Leu Asp Gly Ser Leu Leu Lys Glu Thr Gly Thr Leu Glu
2180 2185 2190

Ser Gln Leu Glu Ala Asn Lys Arg Lys Gln Lys Glu Ile Gln Ala
2195 2200 2205

Met Lys Arg Gln Leu Thr Lys Ile Val Asp Leu Gly Asp Asn Leu
2210 2215 2220

Glu Asp Ala Leu Ile Leu Asp Ile Lys Tyr Ser Thr Ile Gly Leu
2225 2230 2235

Ala Gln Gln Trp Asp Gln Leu Tyr Gln Leu Gly Leu Arg Met Gln
2240 2245 2250

His Asn Leu Glu Gln Gln Ile Gln Ala Lys Asp Ile Lys Gly Val
2255 2260 2265

Ser Glu Glu Thr Leu Lys Glu Phe Ser Thr Ile Tyr Lys His Phe
2270 2275 2280

Asp Glu Asn Leu Thr Gly Arg Leu Thr His Lys Glu Phe Arg Ser
2285 2290 2295

Cys Leu Arg Gly Leu Asn Tyr Tyr Leu Pro Met Val Glu Glu Asp
2300 2305 2310

Sequence_Listing.txt

Glu His Glu Pro Lys Phe Glu Lys Phe Leu Asp Ala Val Asp Pro
2315 2320 2325

Gly Arg Lys Gly Tyr Val Ser Leu Glu Asp Tyr Thr Ala Phe Leu
2330 2335 2340

Ile Asp Lys Glu Ser Glu Asn Ile Lys Ser Ser Asp Glu Ile Glu
2345 2350 2355

Asn Ala Phe Gln Ala Leu Ala Glu Gly Lys Ser Tyr Ile Thr Lys
2360 2365 2370

Glu Asp Met Lys Gln Ala Leu Thr Pro Glu Gln Val Ser Phe Cys
2375 2380 2385

Ala Thr His Met Gln Gln Tyr Met Asp Pro Arg Gly Arg Ser His
2390 2395 2400

Leu Ser Gly Tyr Asp Tyr Val Gly Phe Thr Asn Ser Tyr Phe Gly
2405 2410 2415

Asn

<210> 69

<211> 2215

<212> DNA

<213> Homo sapiens

<400> 69

agggtttgag acacaggtaa agggaggag acagagagaa atactgcag agccagcagg 60

tagctgggca gtccttccc ggacggacgg atggacagac gctggggacc ctccactcca 120

Sequence_Listing.txt

tatggaaaga tgacatgacc ttgtggtaga tcccagaact gaggccccag gatgacagaa	180
caggagaccc tggccctact ggaagtgaag aggtctgatt cccagagaa gagctaccc	240
caggccttgg ttccaatgg ccggcagcca gaaggggaag gtggggccga atccccgga	300
gctgagtccc tcagagtggg gtcttcagct ggaatccca cagccataga gggggctgag	360
gatggtctag acagcacagt aagtgaggct gccacctgc cctgggggac tggccctcag	420
cccagtgtc cgtcccga tccccctgc tggcgggaca ttgaaccaga gccccctgag	480
tcagaaccac ttaccaagct agaggagctg cccgaagacg atgccaacct gctgcctgag	540
aaagcgccc gtgccttctg gcctattgac ctacagtga ttgagcggca gcccgaaga	600
gacctatcg tgcgtgtga ggcaggcgag ggcgagtgc gaacctcat gccccccgg	660
gtcaccacc ccgaccacac tgagcgcaag tgggctgagg cagtgtgag gccgcctggc	720
tgttctgtg ggggctgcgg gagctgtga gacctgagt ggctaaggc tgtgcctcc	780
gtgggagccg cactcattct ctccctgc ctactatac gggcatatgc ctctcgccg	840
tttgatgcc caggctgcc caccatgagt tccgcctga tctacacact gcgctcggg	900
gtctttgcca ccttcccat tgtctgggg atcctggtgt acgggctgag cctgttatgc	960
ttttctgcc ttcgccctt tggggagcca cggcgggagg tggagatcca ccggcgatat	1020
gtggcccagt cggtcacgt ctttatttc tacttctca acctggccgt gcttccact	1080
tacctcccc aggataccct caaactgtc cctctgtca ctggtctct tgcgctctc	1140
cggctgatct actggctgac cttgcccgt ggccgctct tccgaggct cggctacggc	1200
ctgacgttc tgccactgct gtcgatgtg atgtggaacc tctactacat gttcgtgtg	1260
gagccggagc gcatgtcac tgccaccgag agccgcctgg actaccgga ccacgccgc	1320
tcggcctccg actacagggc ccgccctgg ggtgagcct ctccgccct gccctcgag	1380

Sequence_Listing.txt

taggggtag cggcttgggt ctgacacatc ttgaacctt gtggccaggc ctggacttcg 1440
 cccccaggcc taggaccgcg gtgggtggaa cctgtctact gcccacacag ggactccaat 1500
 caatcggagt tctccccctg ccggagctgc ccttcacctt tggggcccga gacagtcata 1560
 agggatggac ttagttttct tgcagggaaa aagggtggaca gccgtgttc ttaaggatgc 1620
 tgagggcatg gggccaggac caggggagag gcacagctcc ttctgagca gcctctcacc 1680
 actgccacaa ggctccctaa tgctgtctc tgctccactc cccggcttc cgtgaggcag 1740
 gaggcagagc cacagccaag gccctgacca ctctgtgcc agttgtctaa gcagagcgcc 1800
 tcagggacgc tggaaatgcc ttaaggatag aggctgggca tcacatcaaa tgggactgtg 1860
 gtgttgggtg aaaaccttc tgaggatctg gattcaggac cctccatgac tggcctattt 1920
 actgtttaca gctggccagt gcagagctgc tgctcttta ccttttagg cccctgtaac 1980
 ttccacctt taaactgcc agaaggcatg cctctccac aggaagaggg gagcagacag 2040
 ggaaatctgc ctaccaagag ggggtgtgtg gtctttgtc ccacacgtgg tggctgggga 2100
 gtgcctggat ggtgcggtgg ttgatgttaa cctagtgtgt gtgtgtgtgt gtgtgtgtgt 2160
 gtgtgtgtgt gtgtgtgtgt aacaataaat tactaccagt caaaaaaaaa aaaaa 2215

<210> 70

<211> 394

<212> PRT

<213> Homo sapiens

<400> 70

Met Thr Glu Gln Glu Thr Leu Ala Leu Leu Glu Val Lys Arg Ser Asp

1 5 10 15

Ser Pro Glu Lys Ser Ser Pro Gln Ala Leu Val Pro Asn Gly Arg Gln

20 25 30

Sequence_Listing.txt

Pro Glu Gly Glu Gly Gly Ala Glu Ser Pro Gly Ala Glu Ser Leu Arg
35 40 45

Val Gly Ser Ser Ala Gly Ser Pro Thr Ala Ile Glu Gly Ala Glu Asp
50 55 60

Gly Leu Asp Ser Thr Val Ser Glu Ala Ala Thr Leu Pro Trp Gly Thr
65 70 75 80

Gly Pro Gln Pro Ser Ala Pro Phe Pro Asp Pro Pro Gly Trp Arg Asp
85 90 95

Ile Glu Pro Glu Pro Pro Glu Ser Glu Pro Leu Thr Lys Leu Glu Glu
100 105 110

Leu Pro Glu Asp Asp Ala Asn Leu Leu Pro Glu Lys Ala Ala Arg Ala
115 120 125

Phe Val Pro Ile Asp Leu Gln Cys Ile Glu Arg Gln Pro Gln Glu Asp
130 135 140

Leu Ile Val Arg Cys Glu Ala Gly Glu Gly Glu Cys Arg Thr Phe Met
145 150 155 160

Pro Pro Arg Val Thr His Pro Asp Pro Thr Glu Arg Lys Trp Ala Glu
165 170 175

Ala Val Val Arg Pro Pro Gly Cys Ser Cys Gly Gly Cys Gly Ser Cys
180 185 190

Gly Asp Arg Glu Trp Leu Arg Ala Val Ala Ser Val Gly Ala Ala Leu

Sequence_Listing.txt

```

195          200          205
Ile Leu Phe Pro Cys Leu Leu Tyr Gly Ala Tyr Ala Phe Leu Pro Phe
210          215          220

Asp Val Pro Arg Leu Pro Thr Met Ser Ser Arg Leu Ile Tyr Thr Leu
225          230          235          240

Arg Cys Gly Val Phe Ala Thr Phe Pro Ile Val Leu Gly Ile Leu Val
245          250          255

Tyr Gly Leu Ser Leu Leu Cys Phe Ser Ala Leu Arg Pro Phe Gly Glu
260          265          270

Pro Arg Arg Glu Val Glu Ile His Arg Arg Tyr Val Ala Gln Ser Val
275          280          285

Gln Leu Phe Ile Leu Tyr Phe Phe Asn Leu Ala Val Leu Ser Thr Tyr
290          295          300

Leu Pro Gln Asp Thr Leu Lys Leu Leu Pro Leu Leu Thr Gly Leu Phe
305          310          315          320

Ala Val Ser Arg Leu Ile Tyr Trp Leu Thr Phe Ala Val Gly Arg Ser
325          330          335

Phe Arg Gly Phe Gly Tyr Gly Leu Thr Phe Leu Pro Leu Leu Ser Met
340          345          350

Leu Met Trp Asn Leu Tyr Tyr Met Phe Val Val Glu Pro Glu Arg Met
355          360          365

```

Sequence_Listing.txt

Leu Thr Ala Thr Glu Ser Arg Leu Asp Tyr Pro Asp His Ala Arg Ser
370 375 380

Ala Ser Asp Tyr Arg Pro Arg Pro Trp Gly
385 390

<210> 71
<211> 1282
<212> DNA
<213> Homo sapiens

<400> 71
ggaagctgt caactgggag ggggagaggg gggatgagg ccaggaatgg ggtccccggg 60
catggtgctg ggctcctgg tgcagatctg ggccctgcaa gaagcctcaa gcctgagcgt 120
gcagcagggg cccaacttgc tgcaggtgag gcagggcagt caggcgacct tggctgcca 180
ggcggaccag gccacagcct gggaacggct ccgtgttaag tggacaaagg atggggccat 240
cctgtgtcaa ccgtacatca ccaacggcag cctcagcctg ggggtctgcg ggccccaggg 300
acggctctcc tggcaggcac ccagccatct caccctgcag ctggaccctg tgagcctcaa 360
ccacagcggg gcgtacgtgt gctgggcggc cgtagagatt cctgagttgg aggaggctga 420
gggcaacata acaaggctct ttgtggacct agatgacccc acacagaaca gaaaccggat 480
cgcaagcttc ccaggattcc tctcgtgct gctgggggtg ggaagcatgg gtgtggctgc 540
gatcgtgtgg ggtgcctggt tctggggccg ccgcagctgc cagcaaaggg actcaggtaa 600
cagcccagga aatgattctt acagcaacgt cctataccgg ccccgggggg ccccaaagaa 660
gagtgaggac tgctctggag aggggaagga ccagaggggc cagagcattt attcaacctc 720
cttcccga cgggcccccc gccagccgca cctggcgtca agaccctgcc ccagcccag 780
accctgccc agcccaggc ccggccacct cgtctctatg gtcagggtct ctctagacc 840

Sequence_Listing.txt

```

aagccccacc cagcagccga ggccaaaagg gttcccaaaa gtgggagagg agtgagagat   900
cccaggagac ctcaacagga cccaccccat aggtacacac aaaaaagggg ggatcgaggc   960
cagacacggt ggctcacgcc tgtaatccca gcagtttggg aagccgaggc ggttggaaca  1020
cttgaggcca ggggtttgag accagcctgg ctgaacctg ggaggcggag gttgcagtga  1080
gccgagattg cgccactgca ctccagcctg ggcgacagag tgagactccg tctcaaaaaa  1140
aacaaaaagc aggaggattg ggagcctgtc agcccatcc tgagaccccg tctcatttc  1200
tgtaatgatg gatctgctc ccactttccc ccaagaacct aataaaggct tgtgaagaaa  1260
aagcaaaaaa aaaaaaaaaa aa                                     1282

```

<210> 72
 <211> 282
 <212> PRT
 <213> Homo sapiens

```

<400> 72
Met Gly Ser Pro Gly Met Val Leu Gly Leu Leu Val Gln Ile Trp Ala
1      5      10      15

Leu Gln Glu Ala Ser Ser Leu Ser Val Gln Gln Gly Pro Asn Leu Leu
      20      25      30

Gln Val Arg Gln Gly Ser Gln Ala Thr Leu Val Cys Gln Val Asp Gln
      35      40      45

Ala Thr Ala Trp Glu Arg Leu Arg Val Lys Trp Thr Lys Asp Gly Ala
      50      55      60

Ile Leu Cys Gln Pro Tyr Ile Thr Asn Gly Ser Leu Ser Leu Gly Val
      65      70      75      80

```

Sequence_Listing.txt

Cys Gly Pro Gln Gly Arg Leu Ser Trp Gln Ala Pro Ser His Leu Thr
85 90 95

Leu Gln Leu Asp Pro Val Ser Leu Asn His Ser Gly Ala Tyr Val Cys
100 105 110

Trp Ala Ala Val Glu Ile Pro Glu Leu Glu Glu Ala Glu Gly Asn Ile
115 120 125

Thr Arg Leu Phe Val Asp Pro Asp Asp Pro Thr Gln Asn Arg Asn Arg
130 135 140

Ile Ala Ser Phe Pro Gly Phe Leu Phe Val Leu Leu Gly Val Gly Ser
145 150 155 160

Met Gly Val Ala Ala Ile Val Trp Gly Ala Trp Phe Trp Gly Arg Arg
165 170 175

Ser Cys Gln Gln Arg Asp Ser Gly Asn Ser Pro Gly Asn Ala Phe Tyr
180 185 190

Ser Asn Val Leu Tyr Arg Pro Arg Gly Ala Pro Lys Lys Ser Glu Asp
195 200 205

Cys Ser Gly Glu Gly Lys Asp Gln Arg Gly Gln Ser Ile Tyr Ser Thr
210 215 220

Ser Phe Pro Gln Pro Ala Pro Arg Gln Pro His Leu Ala Ser Arg Pro
225 230 235 240

Sequence_Listing.txt

Cys Pro Ser Pro Arg Pro Cys Pro Ser Pro Arg Pro Gly His Pro Val
 245 250 255

Ser Met Val Arg Val Ser Pro Arg Pro Ser Pro Thr Gln Gln Pro Arg
 260 265 270

Pro Lys Gly Phe Pro Lys Val Gly Glu Glu
 275 280

<210> 73

<211> 1843

<212> DNA

<213> Homo sapiens

<400> 73

gggcacgagg gcagagccag ttctagcgc agagccgcgc ccgcatgag ggagatcgtg 60
 cacatccagg cgggccagtg cggaaccag atcggcacca agttttgga agtgatcagc 120
 gatgagcacg gcatcgaccc ggccggaggc tacgtgggag actcggcgct gcagctggag 180
 agaatcaacg tctactacaa tgagtcatcg tctcagaaat atgtgccag ggccgccctg 240
 gtggacttag agccaggcac catggacagc gtgcggtctg ggccttttg gcagcttttc 300
 cggcctgaca acttcatctt tggccagacg ggtgcaggga acaactgggc gaaagggcac 360
 tacacggagg gcgcggagct ggtggacgca gtgctggacg tggcgcgaa ggagtgcgag 420
 cactgcgact gcctgcaggg ctccagctc acgcactcgc tggcgggcgg cacgggctca 480
 ggcattggga cgctgctcat cagcaagatc cgtgaggagt tccggaccg catcatgaac 540
 accttcagcg tcatgccctc gccaagggtg tcggacacgg tggtagagcc ctacaatgcc 600
 acactgtcgg tgcaccagct ggtggagaat acagacgaga cctactgcat cgacaacgag 660
 gcgctctatg acatctgctt ccgcactctg aagctgacaa cgccaccta cggggacctc 720

Sequence_Listing.txt

aaccacctgg tgcgccac catgagtggg gtcaccacct cgtgcgctt cccgggccag 780
 ctcaatgctg acctgcgcaa gctggcgggtg aacatggtgc cctcccgcg cctgcacttc 840
 ttcatgctg gcttcgcgcc gtcaccagc cgcggcagcc agcagtaccg ggcctgacc 900
 gtgcccagc tcaccagca gatgttcgac gccaggaaca tgatggccgc ctgcgatccg 960
 cgccatggcc gctacctgac cgtggccacc gtgtccgcg ggcccatgtc catgaaggag 1020
 gtggacgagc agatgctggc catccagagt aagaacagca gctacttcgt ggagtggatt 1080
 cccaacaacg tgaagggtgc cgtgtgcgac atccgcccc gcggcctgaa gatggcctcc 1140
 accttcacg gcaacagcac ggccatccag gagctgttca agcgcatctc cgagcagttc 1200
 tcagccatgt tccggcgcaa ggccttctg cactggttca cgggtgaggg catggatgaa 1260
 atggagtcca ccgaggcgga gagcaacatg aacgacctgg tatccgagta ccagcagtac 1320
 caggatgcca ccgccaatga cggggaggaa gctttgagg atgaggaaga ggagatcgat 1380
 ggatagtcgg aatagagccg cccaactca gatctacaa cacgcaagtt ccttctgaa 1440
 cctggtgcc tcctacccta tggccctgaa tggtcactg gtttaattgt gttggtgctg 1500
 gccctcaca aatgcagcca agtcatgtaa ttagtcatct ggaacaaaga ctaaaaacag 1560
 cagagaattg cgggttctac ccagtcagaa gatcacacca tggagacttt ctactagagg 1620
 actgaaaga gaactgaggg gccacaaaat aaacttcacc ttccattaag tgtcaagca 1680
 tgctgcaaa ttaggaggga gtagaaaca gtcttttca tcctttgtga tgaagcctga 1740
 aattgtgccg tgtgcctta tatgaatatg cagtatggga ctttgaaata atgattcata 1800
 ataaaatact aaacgtgtgt cttcaaaaaa aaaaaaaaaa aaa 1843

<210> 74
 <211> 446
 <212> PRT

Sequence_Listing.txt

<213> Homo sapiens

<400> 74

Met Arg Glu Ile Val His Ile Gln Ala Gly Gln Cys Gly Asn Gln Ile
1 5 10 15

Gly Thr Lys Phe Trp Glu Val Ile Ser Asp Glu His Gly Ile Asp Pro
20 25 30

Ala Gly Gly Tyr Val Gly Asp Ser Ala Leu Gln Leu Glu Arg Ile Asn
35 40 45

Val Tyr Tyr Asn Glu Ser Ser Ser Gln Lys Tyr Val Pro Arg Ala Ala
50 55 60

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

Phe Gly Gln Leu Phe Arg Pro Asp Asn Phe Ile Phe Gly Gln Thr Gly
85 90 95

Ala Gly Asn Asn Trp Ala Lys Gly His Tyr Thr Glu Gly Ala Glu Leu
100 105 110

Val Asp Ala Val Leu Asp Val Val Arg Lys Glu Cys Glu His Cys Asp
115 120 125

Cys Leu Gln Gly Phe Gln Leu Thr His Ser Leu Gly Gly Gly Thr Gly
130 135 140

Ser Gly Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Phe Pro
145 150 155 160

Sequence_Listing.txt

Asp Arg Ile Met Asn Thr Phe Ser Val Met Pro Ser Pro Lys Val Ser
165 170 175

Asp Thr Val Val Glu Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu
180 185 190

Val Glu Asn Thr Asp Glu Thr Tyr Cys Ile Asp Asn Glu Ala Leu Tyr
195 200 205

Asp Ile Cys Phe Arg Thr Leu Lys Leu Thr Thr Pro Thr Tyr Gly Asp
210 215 220

Leu Asn His Leu Val Ser Ala Thr Met Ser Gly Val Thr Thr Ser Leu
225 230 235 240

Arg Phe Pro Gly Gln Leu Asn Ala Asp Leu Arg Lys Leu Ala Val Asn
245 250 255

Met Val Pro Phe Pro Arg Leu His Phe Phe Met Pro Gly Phe Ala Pro
260 265 270

Leu Thr Ser Arg Gly Ser Gln Gln Tyr Arg Ala Leu Thr Val Pro Glu
275 280 285

Leu Thr Gln Gln Met Phe Asp Ala Arg Asn Met Met Ala Ala Cys Asp
290 295 300

Pro Arg His Gly Arg Tyr Leu Thr Val Ala Thr Val Phe Arg Gly Pro
305 310 315 320

Met Ser Met Lys Glu Val Asp Glu Gln Met Leu Ala Ile Gln Ser Lys

Sequence_Listing.txt

325

330

335

Asn Ser Ser Tyr Phe Val Glu Trp Ile Pro Asn Asn Val Lys Val Ala
340 345 350

Val Cys Asp Ile Pro Pro Arg Gly Leu Lys Met Ala Ser Thr Phe Ile
355 360 365

Gly Asn Ser Thr Ala Ile Gln Glu Leu Phe Lys Arg Ile Ser Glu Gln
370 375 380

Phe Ser Ala Met Phe Arg Arg Lys Ala Phe Leu His Trp Phe Thr Gly
385 390 395 400

Glu Gly Met Asp Glu Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn
405 410 415

Asp Leu Val Ser Glu Tyr Gln Gln Tyr Gln Asp Ala Thr Ala Asn Asp
420 425 430

Gly Glu Glu Ala Phe Glu Asp Glu Glu Glu Glu Ile Asp Gly
435 440 445

<210> 75

<211> 605

<212> DNA

<213> Homo sapiens

<400> 75

agacttcctc cttcacttgc ctggacgctg cgccacatcc caccggccct tacactgtgg 60

tgtccagcag catccggctt catgggggga cttgaaccct gcagcaggct cctgtctctg 120

cctctctctg ttgctgtaag tggctccgt cctgtccagg cccaggccca gagcgattgc 180

Sequence_Listing.txt

```

agttgctcta cggtagagccc gggcgtgctg gcagggatcg tgatgggaga cctggtgctg    240
acagtgtcta ttgccctggc cgtgtacttc ctgggccggc tggccctcg ggggcgaggg    300
gctgcggagg cgacccggaa acagcgtatc actgagaccg agtcgcctta tcaggagctc    360
cagggtcaga ggtcggatgt ctacagcgac ctcaacacac agaggccgta ttacaaatga    420
gcccgaaatc tgacagttag caacatgata cctggatcca gccattctg aagcccaccc    480
tgcacctcat tccaactcct accgcgatac agaccacag agtgccatcc ctgagagacc    540
agaccgtccc ccaatactct ctaaaataa acatgaagca caaaaacaaa aaaaaaaaaa    600
aaaaa                                         605

```

```

<210> 76
<211> 112
<212> PRT
<213> Homo sapiens

```

```

<400> 76
Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
1      5      10      15

```

```

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp
      20      25      30

```

```

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
      35      40      45

```

```

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
      50      55      60

```

```

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Thr Arg Lys
      65      70      75      80

```

Sequence_Listing.txt

Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln
85 90 95

Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr Lys
100 105 110

<210> 77
<211> 3277
<212> DNA
<213> Homo sapiens

<400> 77
gcgtgcacgc tgacgccgcg cagtctcgtc cctgcccgc gccgtgccg ctgctgtcgc 60
cgccgccgcc gccattggag tcgacgcctc ctcagtgcgt ccgcgtcccg ggctcaccgc 120
cgctgccgcc tcgccagggg cccgcgcgcc cagcagccgc cgccgccgcc cggccggcgc 180
ccggggaatt ggcgggggg cccggggccg cgcgagctag ggtgacaggc ccggcctcta 240
ggggaggccc gagccggcgg gcgccccggc cccgcgtcta gttgttcattg aagcatgtcg 300
gccaccagcg tggacacca gagaacaaaa ggacaagata ataaagtaca aaatggttcg 360
ttacatcaga aggatacagt tcattgacaat gactttgagc cctaccttac tggacagtca 420
aatcagagta acagttacc ctcaatgagc gaccctacc tgtccagcta ttaccgccg 480
tcattggat ttcttactc cctcaatgag gctccgtggt ctactgcagg ggaccctccg 540
attccatacc tcaccaccta cggacagctc agtaacggag accatcattt tatgcacgat 600
gctgtttttg ggcagcctgg gggcctgggg aacaacatct atcagcacag gttcaatttt 660
ttccctgaaa accctgcgtt ctacgcatgg gggacaagtg ggtctcaagg tcagcagacc 720
cagagctccg cgtatgggag cagctacacc tacccccga gctccctggg tggcacggtg 780

Sequence_Listing.txt

gttgatgggc agccaggctt tcacagcgac accctcagca agggccccgg gatgaacagc 840

ctggagcagg gcatggttgg cctgaagatt ggggacgtca gctcctccgc cgtaagacg 900

gtgggctctg tcgtcagcag cgtggcactg actggtgtcc ttctggcaa cgggtgggaca 960

aatgtgaaca tgccagtttc aaagccgacc tcgtgggctg ccattgccag caagcctgca 1020

aaaccacagc ctaaaatgaa aacaagagc gggcctgtca tggggggtgg gctgccccct 1080

ccaccataa agcataacat ggacattggc acctgggata acaaggggcc tgtgccgaag 1140

gccccagtcc cccagcaggc accctctcca caggctgccc cacagcccca gcagggtggct 1200

cagcctctcc cagcacagcc cccagctttg gctcaaccgc agtatcagag ccctcagcag 1260

ccaccccaga cccgctgggt tgccccacgc aacagaaacg cggcgtttgg gcagagcgga 1320

ggggctggca gcatagcaa ctctctgga aacgtccagc ctaattctgc cccagcgtc 1380

gaatcccacc ccgtcttga aaaactgaag gctgtcaca gctacaacc gaaagagttt 1440

gagtggaaac tgaaaagcgg gcgtgtgttc atcatcaaga gctactctga ggacgacatc 1500

caccgctcca ttaagtactc catctggtgt agcacagagc acggcaacaa gcgcctggac 1560

agcgcttcc gctgcatgag cagcaagggg cccgtctacc tgctcttcag cgtcaatggg 1620

agtgggcatt ttgtgggggt ggccgagatg aagtcctccg tggactacgg caccagtgcc 1680

ggggtctggt ctcaggacaa gtggaagggg aagtttgatg tccagtggat tttgttaag 1740

gatgtacca ataaccagct ccggcacatc aggttgaga ataacgacaa caaaccggtc 1800

acaaactccc gggacacca ggaggtgccc ttagaaaaag ccaagcaagt gctgaaaatt 1860

atcagttcct acaagcacac aacctccatc ttgacgact ttgtcacta cgagaagcgc 1920

caggaggagg aggaggtggt gcgcaaggaa cggcagagtc gaaacaaaca atgagggcga 1980

accagtttct tacatgttct aacgtttgac ttgaaaaca gtttaaaca cgtgtgcttg 2040

Sequence_Listing.txt

gtcagctcca gtgtgtcgtc ccgtgcgggg gttgagtgtt gcacatttgc ctttctgtc 2100
gttgattttt gccagatgg atctgcattt attgtactt ttctatgta ttataatcct 2160
gtagaagtca ctaataaagg agtattttt ttgtcagctt atcaatcaga ctgatctaata 2220
gtgaaatgta agtatcccta aaaacaaagc atctattttg gcagaaattg tgttcttaaa 2280
ttcagtcatt tgatattctg tgagacttca tatttctcat ccctttattg ctttttagca 2340
aacataagaa accatgagtc atttgtcat tttagattt ctgataaaat ctctgaaaa 2400
tactgaaatc aaaagggtta tgatttttg ttcattctga ttgtcattt tattatctgt 2460
tatcggctca aagtgtcta ttaccattt gattttctg ctagacagat aacttttaata 2520
tttcaaatt tggcagacac tttttttt ttttgaaaa tcttccctc cagatctgtt 2580
gccactgaa cagccacccg tccctcactg tctgtgtgtc cgattgggct ggatgggtgt 2640
ggggcatgat gtgtggagga actggaagg gctttaggtc tgggtcaggg tcgggcattc 2700
ttgtgttt gcacatctt ttaaatttta cacctttct taagaattct aatgccgtct 2760
taagtttta taccaataat gctgagctt aagtgtagga tctggtagta cagacagtgt 2820
gatggatgat gctgctggtt gttaaattca tctgtgtgt ctaattttt ttctgttga 2880
atgggtaaaa acaaaacaaa actttttta gaagatgaat ttgtgtcat gtttgtgga 2940
atgagggacc gttgagctca ctaccacctg gagtttgagt tgaagcatga aaatgggtgcc 3000
catgcctgac gctccagcgc ctggatctgc acgtgccctt gtagaggatc cttaccgtcc 3060
tagagagcag acgctttctg aaaactactt gctccaaaag accctctgag ttaacgtttc 3120
agctgtatca ttgacttgt atttagagcg tgcacttcc tctgaactgt tactgcctga 3180
atggagtctt ggacgacatt gggttttcc ttaggagaa tacaagcctt aataaacaat 3240
actatttagc aaaaaaaaaa aaaaaaaaaa aaaaaaa 3277

Sequence_Listing.txt

<210> 78

<211> 559

<212> PRT

<213> Homo sapiens

<400> 78

Met Ser Ala Thr Ser Val Asp Thr Gln Arg Thr Lys Gly Gln Asp Asn

1 5 10 15

Lys Val Gln Asn Gly Ser Leu His Gln Lys Asp Thr Val His Asp Asn

20 25 30

Asp Phe Glu Pro Tyr Leu Thr Gly Gln Ser Asn Gln Ser Asn Ser Tyr

35 40 45

Pro Ser Met Ser Asp Pro Tyr Leu Ser Ser Tyr Tyr Pro Pro Ser Ile

50 55 60

Gly Phe Pro Tyr Ser Leu Asn Glu Ala Pro Trp Ser Thr Ala Gly Asp

65 70 75 80

Pro Pro Ile Pro Tyr Leu Thr Thr Tyr Gly Gln Leu Ser Asn Gly Asp

85 90 95

His His Phe Met His Asp Ala Val Phe Gly Gln Pro Gly Gly Leu Gly

100 105 110

Asn Asn Ile Tyr Gln His Arg Phe Asn Phe Phe Pro Glu Asn Pro Ala

115 120 125

Phe Ser Ala Trp Gly Thr Ser Gly Ser Gln Gly Gln Gln Thr Gln Ser

130 135 140

Sequence_Listing.txt

Ser Ala Tyr Gly Ser Ser Tyr Thr Tyr Pro Pro Ser Ser Leu Gly Gly
145 150 155 160

Thr Val Val Asp Gly Gln Pro Gly Phe His Ser Asp Thr Leu Ser Lys
 165 170 175

Ala Pro Gly Met Asn Ser Leu Glu Gln Gly Met Val Gly Leu Lys Ile
 180 185 190

Gly Asp Val Ser Ser Ser Ala Val Lys Thr Val Gly Ser Val Val Ser
 195 200 205

Ser Val Ala Leu Thr Gly Val Leu Ser Gly Asn Gly Gly Thr Asn Val
 210 215 220

Asn Met Pro Val Ser Lys Pro Thr Ser Trp Ala Ala Ile Ala Ser Lys
225 230 235 240

Pro Ala Lys Pro Gln Pro Lys Met Lys Thr Lys Ser Gly Pro Val Met
 245 250 255

Gly Gly Gly Leu Pro Pro Pro Pro Ile Lys His Asn Met Asp Ile Gly
 260 265 270

Thr Trp Asp Asn Lys Gly Pro Val Pro Lys Ala Pro Val Pro Gln Gln
 275 280 285

Ala Pro Ser Pro Gln Ala Ala Pro Gln Pro Gln Gln Val Ala Gln Pro
 290 295 300

Leu Pro Ala Gln Pro Pro Ala Leu Ala Gln Pro Gln Tyr Gln Ser Pro

Sequence_Listing.txt

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

Sequence_Listing.txt

Val Lys Asp Val Pro Asn Asn Gln Leu Arg His Ile Arg Leu Glu Asn
485 490 495

Asn Asp Asn Lys Pro Val Thr Asn Ser Arg Asp Thr Gln Glu Val Pro
500 505 510

Leu Glu Lys Ala Lys Gln Val Leu Lys Ile Ile Ser Ser Tyr Lys His
515 520 525

Thr Thr Ser Ile Phe Asp Asp Phe Ala His Tyr Glu Lys Arg Gln Glu
530 535 540

Glu Glu Glu Val Val Arg Lys Glu Arg Gln Ser Arg Asn Lys Gln
545 550 555

<210> 79

<211> 4607

<212> DNA

<213> Homo sapiens

<400> 79

gcggccgcaa gcacgggggc gaatccccgc tgggtcgagg gcctgaacgg gagccaatcg 60

agcagccgag gctactgcca atcacgcggc tccctccaat cccaccgtg ccatttcaa 120

aatctcggtc ccactgtgca gctcaaatgt ggtgttact ctgccaatcg ctggaggata 180

gagtgggaac aggaataagc agagttaaga ggccaggaca aaagaagta aagagcgccc 240

aatacatata tgttttgaa ggcgggcaga gggaataaag tccccccagt gaggttctat 300

gggcctgatt gtgtagttct gatggagccc ccttgagca agaggaaccc gccagcgctg 360

agattagcgg atttggaac ggctcaggtc cagccgcttc agaatatgac aggcttcccg 420

gcgctggccg gcccggccgc ccactcccaa ctccgggccg ccgtcgcgca cctccgcctg 480

Sequence_Listing.txt

cgggacctgg gcgctgacct cggcgtggcc accactccgc tcggacctga gcacatggcc 540
 caggcgagca cgctgggcct cagccctccc tcccaggcgt tccggcaca cccggaggct 600
 ccggcagccg ccgcccgtgc tgcagccttg gtcgcgcacc ccggcgcggg cagctacccc 660
 tgcggcgggg gcagcagtgg cgcgcagccc tccgcgcccc cgccccagc cctcctctt 720
 cctccacccc cttaccccc tccccctccc cgcctctc ctcctcctgc cctctcgggc 780
 tacaccacca ccaacagtgg cggcggcgcc agcagcggca aaggccacag cagggaactc 840
 gtctccgga gggaccttc cgccacggcc cccgcggcgg ccatgcacgg ggccccgctc 900
 ggaggggagc agcggctcgg caccggctcc cccagcacc cgccccgcc tccccactcg 960
 gccggcatgt tcctcctgc cagcggcacc tacgcgggcc cggacggcag cggcgggccc 1020
 gcgctcttc ccgcgtgca cgacacggcg ggggccccag gcggccaccc gcaccgctc 1080
 aacggccaga tgcgcctggg gctggcgggc gcagcggcag ccgcggcggc tgagctgtac 1140
 ggccgcgccg aaccgccctt cgcgcgcgc tctggggacg cgcactacgg ggcggttgcg 1200
 gccgcagcgg cggccgccct gcacggctac ggagccgtga acttaacct gaacctggcg 1260
 gctgcggcgg ccgcagcagc ggccggggccc gggccccacc tgcagcacca cgcgccgccc 1320
 ccggcgccgc cgccgccgc ggccggcgcg cagcaccgc accagcacca cccccactc 1380
 ccagggcgcg ctggggcctt cctgcgtac atgcggcagc caatcaagca ggagctcatc 1440
 tgcaagtga tcgacctga cgagctggcc gggctgccgc cgccgccgc gccgcgccg 1500
 ccgccgccgc caccgcccc ggccggcggc gccaagccct gctccaaaac ttcggcacc 1560
 atgcacgagc tggatgaatc cgtcacggtg gagcacgtgg gaggccccga gcagagcagc 1620
 cacgtctgct tctgggagga ctgtccgcgc gagggcaagc cctcaaggc caatacaag 1680
 ctcatcaacc acatccgct gcacaccggc gagaagccct ttcctgccc ttccccggc 1740

Sequence_Listing.txt

tgcggaagg tcttcgctg ctcgagaac ctcaagatcc acaagcgtac tcatacagg 1800
gaaaagcctt tcaaatgtga attgatggc tgtgacagga agtttgcaa tagcagtga 1860
cggaagaaac attcccatgt ccacaccagt gacaagccct actactgcaa gattcgaggc 1920
tgtgacaaat cctacactca cccaagctcc ctgaggaagc acatgaagat tcactgcaag 1980
tccccgccac cttctccagg accccttggg tactcatcag tggggactcc agtgggctcc 2040
ccctgtccc ctgtgtgga ccagccagg agtcactcca gcactctgtc ccctcagggtg 2100
accaacctca atgagtggta cgtttgccag gccagtgggg ccccgagcca cctccacacc 2160
cctccagca acggaaccac ctctgagact gaagatgagg aaatttacgg gaaccctgaa 2220
gttgtcgga cgatacatta gaattatta ttaataataa taagtgaat aataagtgg 2280
agtccttga ccacatccta acctgagaca atgccgagcc tgagacaaac ccgtgactca 2340
gacttgccac cgggtctaatt tagccctatt tattcagtat gaaaccctat ggtgtttgta 2400
catttaatta atttaattaa gatatttggg cttttttt ttttttctt aaaaaacaaa 2460
caaaaaacaa ccaagctgga ctgtacatt gcaggaggat ggggctgggg gcaaattgta 2520
ccaaggaaaa tgaatggaga gattagttaa tggcgataca cactgccgat gcaatatata 2580
tatatatata tatatacata tatatatata ttattttt taaaaggggg agaaaaagag 2640
cattaagtca gaacttaaca cagcaccaag gccctctgca ttcccagag tgccttcaa 2700
atgccttga caccatacca tgggctgctt ttgagcctcc ttgtggacc ctaattctgc 2760
caaggcctct tgattgtaaa ccacacacct gctgcattgc caacagatcc tgtccgtac 2820
ctgtgtccaa aaacatttgt aaaaaccctt tgagttaaat attgtaatt ttaatttc 2880
actctttat tactgatctt agcttaatac aatatttta tacaggatta ttcttcagt 2940
atcctactgt gtgattttaa aaaaagatgc agcaacctta atatatctcc atatctgtg 3000

Sequence_Listing.txt

ctactgtgat tgttaagca aaagtggaga gaagaaaagc tgctgcaaaa gacaactgtg 3060
aaactgtgat atttataaa atagaagaaa ttcaagtgtc ttcttttcc tatatgttt 3120
ttttttta tctgaattct cagatactgc ctctaactg tgcctaaact tcttgttaa 3180
taaagagatt ctgtttcga tctaagttc ttgggatgc caacattcac agtcaagtct 3240
tgaggagggtg tgatgatggc atcatgccta ttttttga aagctgtgt tttaaaaca 3300
ggccaacacc tctttatac tgttgtatca gccttttaa aagtctatt ttcaatgcct 3360
gaaactgcat ttaatgcat ttcttcac ctgagcactg agcacaccaa actggaatcc 3420
attgaaaat gacagtgtg gaagtgtatg atttacatta aaagagggga gggagttgcc 3480
atacatatta aaaatttta aaaggttat agttaccacc aaactgat gaatgtgtga 3540
ccttgccag agctgtcaag ctaggataaa aaaggtaag gacctaggac aataactctt 3600
agtcgattta tttcggttg gtacaacaca tctcctgtc aaaatgtagt ccatcagaaa 3660
catcctacag atacactaaa gagcactaat ttatccttag agaccccgaa gacacccct 3720
cccagggtt ttagaaaatt tgtttgtg gctgtgagtg gttgatgtg tctgtcatt 3780
gttaataact tgatgtgaa cactattatt gtacagttg aattaattta tttcagaca 3840
tcatccttt ttttttct tctggaaga gtcaaagca caccaaagaa ttatattata 3900
catttggtg aaagattgtc atttatgac catggttat ttaaaaaaaaaa aaggaaagaa 3960
aatggaaaaa tatatttta agcttactg aatgaacaac gtaatgtgaa aaccaagact 4020
ctcctgcat gctttttg cattgtgtg ataagattat atatagtta tagatatatt 4080
atattactag tacagtgcac ggtgctgtca cttggaaagc cttcaatgt tgcctcaga 4140
ttgtgtgat gaatatgaaa catgcagacc ctctttata aagaaaaaga ccttaaaact 4200
tgaatatgag ataattttac atttaaaag ttatttgat ttcatatta ttcacttca 4260

Sequence_Listing.txt

aagcccttc aaatagaaaa ggtatgaact ttgggggga taatttatgt atcgtaaact 4320

tattagaaca aaatattcct gatgtataat gagttgtttt atttatacaa cttttcaat 4380

ggtagttgc actattcttt attatgctac aggtttattt attatgaaac aaaggaatat 4440

gtatttatg tattttacca tgcatagggt aactctttgc cacagattta ttggtcttg 4500

atacacctaa aataaaaaaa aatgtgtacc tccaatagag agcaagcaag aatgattatg 4560

aagtaacaaa ttaataaag gtattcttgt tattattaaa aaaaaaa 4607

<210> 80

<211> 663

<212> PRT

<213> Homo sapiens

<400> 80

Met Phe Leu Lys Ala Gly Arg Gly Asn Lys Val Pro Pro Val Arg Val

1 5 10 15

Tyr Gly Pro Asp Cys Val Val Leu Met Glu Pro Pro Leu Ser Lys Arg

20 25 30

Asn Pro Pro Ala Leu Arg Leu Ala Asp Leu Ala Thr Ala Gln Val Gln

35 40 45

Pro Leu Gln Asn Met Thr Gly Phe Pro Ala Leu Ala Gly Pro Pro Ala

50 55 60

His Ser Gln Leu Arg Ala Ala Val Ala His Leu Arg Leu Arg Asp Leu

65 70 75 80

Gly Ala Asp Pro Gly Val Ala Thr Thr Pro Leu Gly Pro Glu His Met

85 90 95

Sequence_Listing.txt

Ala Gln Ala Ser Thr Leu Gly Leu Ser Pro Pro Ser Gln Ala Phe Pro
100 105 110

Ala His Pro Glu Ala Pro Ala Ala Ala Arg Ala Ala Ala Leu Val
115 120 125

Ala His Pro Gly Ala Gly Ser Tyr Pro Cys Gly Gly Gly Ser Ser Gly
130 135 140

Ala Gln Pro Ser Ala Pro Pro Pro Pro Ala Pro Pro Leu Pro Pro Thr
145 150 155 160

Pro Ser Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Ala Leu Ser
165 170 175

Gly Tyr Thr Thr Thr Asn Ser Gly Gly Gly Gly Ser Ser Gly Lys Gly
180 185 190

His Ser Arg Asp Phe Val Leu Arg Arg Asp Leu Ser Ala Thr Ala Pro
195 200 205

Ala Ala Ala Met His Gly Ala Pro Leu Gly Gly Glu Gln Arg Ser Gly
210 215 220

Thr Gly Ser Pro Gln His Pro Ala Pro Pro Pro His Ser Ala Gly Met
225 230 235 240

Phe Ile Ser Ala Ser Gly Thr Tyr Ala Gly Pro Asp Gly Ser Gly Gly
245 250 255

Sequence_Listing.txt

Pro Ala Leu Phe Pro Ala Leu His Asp Thr Pro Gly Ala Pro Gly Gly
260 265 270

His Pro His Pro Leu Asn Gly Gln Met Arg Leu Gly Leu Ala Ala Ala
275 280 285

Ala Ala Ala Ala Ala Ala Glu Leu Tyr Gly Arg Ala Glu Pro Pro Phe
290 295 300

Ala Pro Arg Ser Gly Asp Ala His Tyr Gly Ala Val Ala Ala Ala Ala
305 310 315 320

Ala Ala Ala Leu His Gly Tyr Gly Ala Val Asn Leu Asn Leu Asn Leu
325 330 335

Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Pro Gly Pro His Leu Gln
340 345 350

His His Ala Pro Pro Pro Ala Pro Pro Pro Pro Ala Pro Ala Gln
355 360 365

His Pro His Gln His His Pro His Leu Pro Gly Ala Ala Gly Ala Phe
370 375 380

Leu Arg Tyr Met Arg Gln Pro Ile Lys Gln Glu Leu Ile Cys Lys Trp
385 390 395 400

Ile Asp Pro Asp Glu Leu Ala Gly Leu Pro Pro Pro Pro Pro Pro
405 410 415

Pro Pro Pro Pro Pro Pro Pro Ala Gly Gly Ala Lys Pro Cys Ser
420 425 430

Sequence_Listing.txt

Lys Thr Phe Gly Thr Met His Glu Leu Val Asn His Val Thr Val Glu
435 440 445

His Val Gly Gly Pro Glu Gln Ser Ser His Val Cys Phe Trp Glu Asp
450 455 460

Cys Pro Arg Glu Gly Lys Pro Phe Lys Ala Lys Tyr Lys Leu Ile Asn
465 470 475 480

His Ile Arg Val His Thr Gly Glu Lys Pro Phe Pro Cys Pro Phe Pro
485 490 495

Gly Cys Gly Lys Val Phe Ala Arg Ser Glu Asn Leu Lys Ile His Lys
500 505 510

Arg Thr His Thr Gly Glu Lys Pro Phe Lys Cys Glu Phe Asp Gly Cys
515 520 525

Asp Arg Lys Phe Ala Asn Ser Ser Asp Arg Lys Lys His Ser His Val
530 535 540

His Thr Ser Asp Lys Pro Tyr Tyr Cys Lys Ile Arg Gly Cys Asp Lys
545 550 555 560

Ser Tyr Thr His Pro Ser Ser Leu Arg Lys His Met Lys Ile His Cys
565 570 575

Lys Ser Pro Pro Pro Ser Pro Gly Pro Leu Gly Tyr Ser Ser Val Gly
580 585 590

Sequence_Listing.txt

Thr Pro Val Gly Ala Pro Leu Ser Pro Val Leu Asp Pro Ala Arg Ser
595 600 605

His Ser Ser Thr Leu Ser Pro Gln Val Thr Asn Leu Asn Glu Trp Tyr
610 615 620

Val Cys Gln Ala Ser Gly Ala Pro Ser His Leu His Thr Pro Ser Ser
625 630 635 640

Asn Gly Thr Thr Ser Glu Thr Glu Asp Glu Glu Ile Tyr Gly Asn Pro
645 650 655

Glu Val Val Arg Thr Ile His
660