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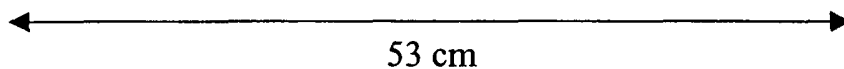
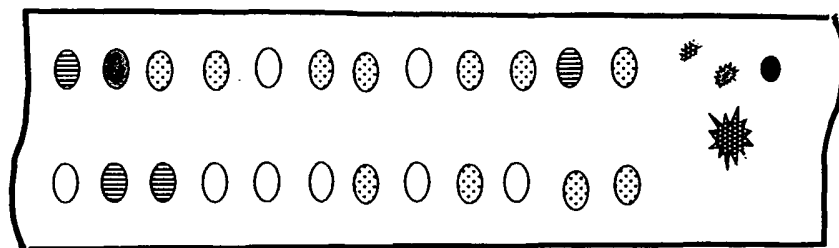
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(54) Title: BIOMARKER PANEL FOR COLORECTAL CANCER

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(57) Abstract: A panel of biomarkers has been identified for analysis of colorectal cancer. The panel, originally identified using a mouse colon cancer model, has been used to assess changes in human tissue from surgical and biopsy samples against a normal human control panel of biomarkers. The panel may be used for providing a cost effective, rapid, noninvasive procedure for risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, detecting relapse, and for the discovery of therapeutic intervention of colorectal cancer.

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BIOMARKER PANEL FOR COLORECTAL CANCER

Reference to Related Applications

5 This application claims priority to U.S. Provisional Patent Application 60/488,660 entitled Molecular Marker Panel for Determination of Colorectal Cancer, by Nancy M. Lee et al., filed July 18, 2003 (Attorney Docket CPMC-01000US0); and U.S. Patent Application 10/690,880 entitled Biomarker
10 Panel for Colorectal Cancer, by Nancy M. Lee et al., filed October 22, 2003 (Attorney Docket CPMC-01000US1), both of which are incorporated herein by reference.

Background

 The field of art of this disclosure concerns biomarkers for colorectal cancer (CRC). These biomarkers are useful for risk assessment, early
15 detection, establishing prognosis, evaluation of intervention, recurrence of CRC, and discovery of therapeutic intervention, and methods of use thereof.

 In the field of medicine, clinical procedures providing for the risk assessment and early detection of CRC have been long sought. Currently, CRC is the second leading cause of cancer-related deaths in the Western
20 world. One picture that has clearly emerged through decades of research into CRC is that early detection is critical to enhanced survival rates.

 The currently accepted methods for CRC screening include the fecal occult blood test (FOBT), x-ray using double contrast between barium enema and air (DCBE), sigmoidoscopy, and colonoscopy. Sigmoidoscopy is
25 an invasive procedure that visually examines the lower third of the colon using a lighted, flexible endoscope, while a related method, colonoscopy, is a procedure that examines the entire colon. In both cases, biopsy samples can be taken during the procedure.

 Concerning the accepted methods for screening, none clearly
30 possess what is desired in a screening examination for CRC. While FOBT is

rapid, it is a very general, and therefore a very non-specific screening method for CRC. Though DCBE has proven useful in specifically imaging abnormalities in the colon, the drawbacks of the DCBE method include: 1.) Patient discomfort in preparation of and during the examination, creating
5 reluctance for compliance of DCBE as a screening method. 2.) Exposure of a patient to x-ray radiation, limiting DCBE in terms of frequency of use as a screening method. 3.) Research indicating that DCBE is more effective in detecting larger growths, which contraindicates its use for early detection. 4.) Biopsy samples cannot be taken during the procedure. 5.) Due to the cost
10 involved, not all insurance providers pay for DCBE screening exams.

Though sigmoidoscopy has gained favor from many physicians, the drawbacks of this method include: 1.) Patient discomfort in preparation of and during the examination, creating reluctance for compliance of sigmoidoscopy as a screening method. 2.) Due to the cost involved, not all
15 insurance providers pay for sigmoidoscopy screening exams. 3.) Since only the lower third of the colon is inspected, there is a suggestion by studies that many significant lesions are in the proximal end of the colon, rendering sigmoidoscopy inadequate. Though colonoscopy addresses the issue of complete inspection of the colon, the drawbacks of colonoscopy as a
20 screening method include: 1.) Creating even more patient discomfort than sigmoidoscopy, therefore generally requiring sedation, and thereby exacerbating the issue with patient compliance. 2.) Due to the cost involved, not all insurance providers pay for colonoscopy screening exams. 3.) There are risks of colonoscopy that include bleeding, and puncture of the lining of
25 the colon.

Emerging spectroscopic technologies, such as magnetic resonance imaging and tomographic imaging each have drawbacks that are drawn from the list of drawbacks for the currently accepted screening methodologies.

Accordingly, there is a need in the art for approaches that have value
30 in early detection and treatment of CRC that are cost effective, rapid, and

minimally or noninvasive. Additional utility would be realized from an approach that would also serve as the basis for establishing prognosis, monitoring patient treatment, and detecting relapse, as well as the discovery of therapeutic intervention of CRC.

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Brief Description of Figures

FIG 1 is a summary of the sequence listings.

FIGS 2A-2C show data that illustrate a panel of biomarkers for samples taken from adenomous polyps, and suspect tissues vs. normal controls. FIGS 2A-2B are tables that compare the results of model studies done in mouse (2A) for a selection of members of the set of 22 biomarkers listed in the sequence listings with the comparable selection in of biomarkers for human subjects (2B). FIG 2C shows the multivariate analysis for 9 markers for 78 biopsies taken from 12 normal patients and 63 biopsies taken from 6 patients with CRC.

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FIGS 3B-3C show expression levels for representative biomarkers, IL-8 (3A), CXCR-2 (3B), and COX-2 (3C) for a series of samples taken from a human subject comparing a histologically identified cancerous lesion, a polyp, and an adjacent non-cancerous tissue vs. a normal control.

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FIGS 4A-4C show the results of multiple analysis across a 53 cm distance of a colon for a patient with CRC: 4A shows expression levels for IL-8; 4B shows expression levels for COX-2; and 4C shows expression levels for CXCR-2.

Detailed Description

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Still another sought after approach apart from currently accepted methods for screening for CRC, has been the search for biomarkers that have value in detection and treatment of CRC. For more than four decades, since the discovery of alpha-fetoprotein (AFP) and carcinogenic embryonic antigen (CEA), the search for biomarkers for cancer detection and treatment in general has been in a state of evolution. Biomarkers for cancer have five potential uses in the management of patient care. Ideally, they would be

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used for risk assessment, for early diagnosis, for establishing prognosis, for monitoring treatment, and for detecting relapse. Additionally, such markers could play a valuable role in developing therapeutic interventions.

5 It is further advantageous for the sampling methods used in conjunction with biomarker analysis to be minimally invasive or non-invasive. Examples of such sampling methods include serum, stool, swabs, and the like. Non-invasive and minimally invasive methods increase patient compliance, and generally reduce cost.

10 Clinically, the two criteria that are important for assessing the effectiveness of biomarkers are selectivity and sensitivity. Selectivity of a biomarker defined clinically refers to percentage of patients correctly diagnosed. Sensitivity of a biomarker in a clinical context is defined as the probability that the disease is detected at a curable stage. Ideally, biomarkers would have 100% clinical selectivity and 100% clinical sensitivity.
15 To date, no single biomarker has been identified that has an acceptably high degree of selectivity and sensitivity required to be effective in for the broad range of needs in patient care management. However, from the clinical perspective, single serum biomarkers, such as AFP and CEA have proven to provide value in some aspects of patient care management.

20 For example, elevated serum levels of CEA were first discovered in 1965 in patients with adenocarcinoma of the colon. Elevated levels can be found in a variety of benign and malignant conditions other than colon cancer. Additionally, the production of CEA by early localized tumors of the colon is in the normal range. Therefore CEA lacks both the sensitivity and
25 selectivity required to be of value for risk assessment or early diagnosis. Further, elevated levels of CEA correlate poorly with colon tumor differentiation and stage, rendering CEA as a biomarker for prognosis of colon cancer of limited value. The two areas for which CEA has proven helpful clinically in managing patient care are in evaluating the effectiveness
30 of treatment, and for detecting relapse. Illustrative of this, numerous studies

have found that there is high correlation between elevated serum levels of CEA preceding clinical detection of recurrence of colon cancer. This has proven to be of value in managing the care of high-risk patients with second-look surgical procedures based on rising levels of CEA.

5 Currently, investigations across numerous areas of oncology research, including CRC, ovarian, breast, and head and neck, are finding increased sensitivity and selectivity in panels of markers. It is now generally held that many mutations must take place before normal cell processes are altered, resulting in a disease, such as cancer. Still, given the complexity of
10 biological systems, discovery of panels useful in providing value in patient care management for CRC is in the nascent stage.

 To date, a greater understanding of the biology of CRC has been gained through the research on adenomatous polyposis coli (APC), p53, and Ki-ras genes, as well as the corresponding proteins, and related pathways
15 involved in the regulation thereof. However, there is a distinct difference between research on a specific a gene, its expression, protein product, and regulation, and understanding what genes are critical to include in a panel used to for the analysis of CRC that is useful in the management of patient care for the disease. To date, panels that have been suggested for CRC are
20 comprised of specific point mutations of APC, p53, and Ki-ras, as well as BAT-26, which is a gene that is a microsatellite instability marker.

 What is disclosed herein is based on studies conducted in mouse multiple intestinal neoplasia (MIN) model, in which expressions levels of genes were screened in adenomatous polyps. In the mouse MIN subjects, a
25 chemically induced mutation of the APC gene is effected. The normal control is defined by littermates for which there was no aberration of the APC gene, and are therefore designated wildtype. From studies based on the mouse MIN model, candidate genes were selected for studying human subjects. From these human subject studies, a panel of biomarkers is disclosed
30 herein. Further, what is disclosed are methods for measuring gene and

protein expression levels based on the panel. Additionally, another aspect of what is disclosed are kits which provide the reagents and instructions for measuring gene and protein expression levels based on the panel. The panel, methods and kits are useful in the management of patient care for CRC. Additionally, the panel, methods, and kits are believed useful as the basis for discovery of therapeutic interventions for CRC.

FIG 1 is a table that gives an overview of the sequence listing for the disclosed biomarkers. The combination of biomarkers disclosed forms the basis for monitoring CRC with enhanced selectivity and sensitivity, and therefore providing enhanced management of patient care for CRC. It is to be understood that fragments and variants of the biomarkers described in the sequence listings are also useful biomarkers in a panel used for the analysis of CRC. What is meant by fragment is any incomplete or isolated portion of a polynucleotide or polypeptide in the sequence listing. It is recognized that almost daily, new discoveries are announced for gene variants, particularly for those genes under intense study, such as genes implicated in diseases like cancer. Therefore, the sequence listings given are exemplary of what is now reported for a gene, but it recognized that for the purpose of an analytical methodology, variants of the gene, and their fragments are also included.

One embodiment of what is disclosed is a panel of biomarkers with the selectivity and sensitivity required for managing patient care for CRC. In Table 1, entries 1-22 are the polynucleotide coding sequences for a panel of biomarkers, and include the name and abbreviation of the gene. Entries 23-44 in Table 1 are the protein, or polypeptide, amino acid sequences that correspond to the coding sequences for entries 1-22. A biomarker, as defined by the National Institutes of Health (NIH) is a molecular indicator of a specific biological property; a biochemical feature or facet that can be used to measure the progress of disease or the effects of treatment. A panel of biomarkers is a selection of biomarkers. Biomarkers may be from a variety of

classes of molecules. As previously mentioned, there is still a need for biomarkers for CRC having the selectivity and sensitivity required to be effective for all aspects of patient care management. Therefore, the selection of an effective set of biomarkers is differentiating in providing the basis for effective determination of CRC.

In another embodiment of this disclosure, expression levels of polynucleotides for the biomarkers indicated in SEQ ID NOs 1-22, are used in the determination of CRC. Such analysis of polynucleotide expression levels is frequently referred to in the art as gene expression profiling. In gene expression profiling, levels of mRNA in a sample are measured as a leading indicator of a biological state, in this case, as an indicator of CRC. One of the most common methods for analyzing gene expression profiling is to create multiple copies from mRNA in a biological sample using a process known as reverse transcription. In the process of reverse transcription, the mRNA from the sample is used to create copies of the corresponding DNA sequence from which the mRNA was originally transcribed. In the reverse transcription amplification process, copies of DNA are created without the regulatory regions in the gene known as introns. These multiple copies made from mRNA are therefore referred to as copy DNA, or cDNA. Entries 45-88 are the sets of primers used in the reverse transcription process for each gene listed in entries 1-22.

Since the reverse transcription procedure amplifies copies of cDNA proportional to the original level of mRNA in a sample, it has become a standard method that allows the analysis of even low levels of mRNA present in a biological sample. Genes may either be up regulated or down regulated in any particular biological state, and hence mRNA levels shift accordingly.

In still another embodiment of this disclosure, expression levels of proteins listed in SEQ ID NOs 23-44, which correspond to the genes indicated in SEQ ID NOs 1-22, are disclosed. The term "polypeptide" or

“polypeptides” is used interchangeably with the term “protein” or “proteins” herein. As discussed previously, proteins have been long investigated for their potential as biomarkers, with limited success. There is value in protein biomarkers as complementary to polynucleotide biomarkers. Reasons for having the information provided by both types of biomarkers include the current observations that mRNA expression levels are not good predictors of protein expression levels, and that mRNA expression levels tell nothing of the post-translational modifications of proteins that are key to their biological activity. Therefore, in order to understand the expression levels of proteins, and their complete structure, the direct analysis of proteins is required.

FIGS 2A-2B show an exemplary panel of biomarkers from the list of 22 biomarkers for which gene expression levels are compared in the mouse MIN model, and in human subjects. The selection for the panel is taken from across the list of the 22 biomarkers and is taken for the purpose of easy visual assimilation of data in order to demonstrate the utility of a panel. Typically, for complex data sets represented in the 22 member panel of biomarkers, multivariate analysis (MANOVA) is applied, such as that demonstrated in **FIG 2c**.

In **FIG 2A**, the data reported for the mouse MIN studies represent statistical averaging of a number of animal subjects, and the standard error is reported. The p value on the right indicates the degree of confidence that the values are significantly different. As an example, the first gene listed, SDF-1, is related to the human IL-8 gene, and is in the same super family. For SDF-1, the p value of 0.003 indicates that the probability that the differences in the values of the wildtype control and that of the adenomous polyps of the MIN mice occurred by chance alone is only 3 in 1000. Screening the expression levels in adenomous polyps in the subject mice was specifically targeted, since it has been established that adenomous polyps are useful in risk assessment for CRC. What is demonstrated in **FIG**

2A is that the panel of 6 clearly differentiate the results of the MIN mice over that of the wildtype control.

FIGS 2B-2C address the issue of selectivity for biomarker panels.

Regarding biomarkers that have an acceptable level of selectivity for CRC, the incidence of CRC for individuals in families with a history of CRC is 3-4 times that of the general population. However, It is now estimated that 6% of all Americans will develop CRC, and of those 70-80% will occur in people of average risk. There is clearly a need for biomarkers that have the necessary selectivity required for confidence in the determination of CRC.

In **FIG 2B**, the same panel of 6 biomarkers established in the mouse MIN model in **FIG 2A** are the basis for determination of CRC in human subjects. In **FIG 2B**, the results of biopsy tissue determined to be normal by histological evaluation taken from patients known to have CRC are compared to biopsy tissue from individuals validated as normal controls. It should be noted that histological methodologies are the accepted standard for the identification of a cancerous colonic lesion. There are two aspects of **FIG 2B** to further discuss. First, values for gene expression profiling for patient vs. normal control may vary either up, as in the case of IL 8, or down, as in the case of PPAR- δ . It is the determination of the collective shift for the patient vs. normal control that is significant when using a panel of biomarkers. Second, in glancing through the patient data, sample-to-sample variation can be noted, which is anticipated, given all the patient-to-patient variables. It is clear at a glance that the expression levels for the panel taken as a group distinguish the patient samples overall from the normal control group, even though a value for any one specific biomarker may not in itself distinguish the patient sample from the normal control. For example, the patient designated as H008 has an expression level for PPAR- δ that is not distinct from the normal control. However, at a glance it is clear that the results of the panel for H008 distinguish it from the normal control set. This demonstrates in principle why a validated panel of markers, given the

complexity and variability of biology, enhance the selectivity of a determination vs. a single marker alone.

Fig 2c further serves to emphasize the value of a panel of biomarkers in enhancing the selectivity of a determination between patient vs. normal samples. An example of demonstrating the use of MANOVA for a panel of 9 biomarkers selected from the group of 22 is demonstrated in **Fig 2c**. In this study, 78 sigmoidal-rectal biopsies from 12 normal patients, and 63 sigmoidal-rectal biopsies from non-cancerous sections of 6 patients with sigmoidal-rectal carcinoma were compared. The Wilks' Lambda criterion was used to assess the difference between the patient samples and normal control samples using the 9 biomarkers listed. The lambda value close to 1.0 signifies a significant difference between the patient and normal samples is indicated, with the probability of about 9 chances in 1000 that the difference is by chance alone.

FIGS 3A-3C and **FIGS 4A-4C** address the issue of sensitivity for biomarker panels. As previously mentioned, since survival rates are greatly enhanced with the earliest indication of CRC, biomarkers for risk assessment and early detection of CRC have been long sought. The difference between risk assessment and early detection is the degree of certainty regarding acquiring CRC. Biomarkers that are used for risk assessment confer less than 100% certainty of CRC within a time interval, whereas biomarkers used for early detection confer an almost 100% certainty of the onset of the disease within a specified time interval. Risk factors may be used as surrogate end points for individuals not diagnosed with cancer, providing they there is an established relationship between the surrogate end point and a definitive outcome. An example of an established surrogate end point for CRC is the example of adenomous polyps. What has been established is that the occurrence of adenomous polyps are a necessary, but not sufficient condition for an individual to later develop CRC. This is demonstrated by the fact that 90% percent of all preinvasive

cancerous lesions are adenomous polyps or precursors, but not all individuals with adenomous polyps go on to later develop CRC.

FIGS 3A-3C show graphs of gene expression levels taken for multiple biopsy samples taken from the colon of one exemplary patient diagnosed with CRC. The determination of cancerous lesions, polyps, and adjacent tissues was made by conventional histological methods. The expression levels for three of the panel of biomarkers are shown for the biopsy samples categorized in that fashion. Again, as was demonstrated with the examples given in **FIGS 2A-2C**, it is evident that the three markers taken together for the cancerous lesions sampled are significantly different than the normal controls, even though one by itself (CXCR2) would not have been differentiating for this patient. What is additionally indicated in this representation is the distinction between the results of the polyp vs. the normal control. Given that polyps are already accepted as surrogate endpoints for CRC, then a determination of the presence of polyps by a validated analytical methodology using a minimally invasive method, such as a swab, or a non-invasive sampling method, such as a stool sample, would also serve as surrogate end point for risk assessment.

FIGS 4A-4C show the results of gene expression levels for three of the biomarkers in biopsy samples taken over a 53 cm region of the colon of a patient with CRC. The irregularly shaped objects represent biopsy samples that were confirmed to be cancerous lesions by histological methodology, while the oval shapes represent samples that were determined to be non-cancerous by histological methodology. Gene expression profiling was done for each of the biopsy samples, as well. The results of the expression profiling, where the legend indicates relative levels in the patient biopsy samples as compared to normal controls, are depicted in **FIGS 4A-4C**.

The representation of **FIGS 4A-4C** indicates the distance over which the biomarkers are able to distinguish differences in the colon tissue for the patient, where these biopsy samples were rendered normal by conventional

histological analysis. These results demonstrate that it is possible to sample cells through a minimally invasive swabbing collection method from an area distant from a cancerous lesion, but capable of indicating a non-normal colon condition. Moreover, collection of a stool sample is an already validated sampling method for collecting sloughed cells or cell debris from which these determinations may be made. In that regard, samples taken either minimally invasively or non-invasively would render samples that could be analyzed using the disclosed panel of biomarkers. Such non-invasive procedures not only reduce the cost of determination of CRC, but reduce the discomfort and risk associated with current methodology. All these factors together increase the attractiveness of regular testing, and hence patient compliance. Increased patient compliance, coupled with an effective determination for CRC, enhance the prospects for early detection, and enhanced survival rates.

Methods and kits for the polynucleotide and polypeptide expression profiling for the panel of molecular markers are also contemplated as part of the present disclosure.

In one embodiment, a method for gene expression profiling comprises measuring cDNA levels for biomarkers selected in the claimed panel. Such a method requires the use of primers, enzymes, and other reagents for the preparation, detection, and quantitation of cDNAs. The method of creating cDNA from mRNA in a sample is referred to as the reverse transcriptase polymer chain reaction (RT-PCR). The primers listed in SEQ ID NOs 45-88 are particularly suited for use in gene expression profiling using RT-PCR based on the claimed panel. A series of primers were designed using Primer Express Software (Applied Biosystems, Foster City, CA). Specific candidates were chosen, and then tested to verify that only cDNA was amplified, and not contaminated by genomic DNA. The primers listed in SEQ ID NOs 45-88 were specifically designed, selected, and tested accordingly. In addition to the primers, reagents such as one including a dinucleotide triphosphate

mixture having all four dinucleotide triphosphates (e.g. dATP, dGTP, dCTP, and dTTP), one having the reverse transcriptase enzyme, and one having a thermostable DNA polymerase are required for RT-PCR. Additionally buffers, inhibitors and activators are also required for the RT-PCR process.

5 Once the cDNA has been sufficiently amplified to a specified end point, the cDNA sample must be prepared for detection and quantitation. Though a number of detection schemes are contemplated, as will be discussed in more detail below, one method contemplated for detection of polynucleotides is fluorescence spectroscopy, and therefore chromophores
10 that are suited to fluorescence spectroscopy are desirable for labeling polynucleotides. One example of such a fluorescent label is SYBR Green, though numerous related chromophores exist, and are known in the art.

In another embodiment, a method for protein expression profiling comprises using an antibody panel based on the claimed panel of
15 biomarkers for measuring targeted polypeptide levels from a biological sample. In one embodiment contemplated for the method, the antibodies for the panel are bound to a solid support. The method for protein expression profiling may use a second antibody having specificity to some portion of the bound polypeptide. Such a second antibody may be labeled with molecules
20 useful for detection and quantitation of the bound polypeptides, and therefore in binding to the polypeptide label it for detection and quantitation. Additionally, other reagents are contemplated for labeling the bound polypeptides for detection and quantitation. Such reagents may either directly label the bound polypeptide or, analogous to a second antibody, may
25 be a moiety with specificity for the bound polypeptide having labels. Examples of such moieties include but are not limited to small molecules such as cofactors, substrates, complexing agents, and the like, or large molecules, such as lectins, peptides, oligonucleotides, and the like. Such moieties may be either naturally occurring or synthetic.

30 Examples of detection modes contemplated for the disclosed

methods include, but are not limited to spectroscopic techniques, such as fluorescence and UV-Vis spectroscopy, scintillation counting, and mass spectroscopy. Complementary to these modes of detection, examples of labels for the purpose of detection and quantitation used in these methods include, but are not limited to chromophoric labels, scintillation labels, and mass labels. The expression levels of polynucleotides and polypeptides measured using these methods may be normalized to a control established for the purpose of the targeted determination. These methods are believed useful in providing determinations as the basis of effective management of patient care for CRC. These methods may also be used in the discovery of therapeutic interventions for CRC. Additionally, not only biopsy samples from sigmoidoscopy, colonoscopy, or surgery may be analyzed by these methods, but biological samples from non-invasive or minimally evasive collection methods are indicated for these methods, as well.

It is further contemplated in what is disclosed to provide kits having the reagents and procedures that facilitate the ready implementation of the methods, and provide consistency and quality control thereby.

In one embodiment, a kit for gene expression profiling comprises the reagents and instructions necessary for the gene expression profiling of the claimed panel. Thus, for example, the reagents may include primers, enzymes, and other reagents for the preparation, detection, and quantitation of cDNAs for the claimed panel of biomarkers. As discussed above, the method of creating cDNA from mRNA in a sample is referred to as the reverse transcriptase polymer chain reaction (RT-PCR). The primers listed in SEQ ID NOs 45-88 are particularly suited for use in gene expression profiling using RT-PCR based on the claimed panel. The primers listed in SEQ ID NOs 45-88 were specifically designed, selected, and tested accordingly. In addition to the primers, reagents such as one including a dinucleotide triphosphate mixture having all four dinucleotide triphosphates (e.g. dATP, dGTP, dCTP, and dTTP), one having the reverse transcriptase

enzyme, and one having a thermostable DNA polymerase are required for RT-PCR. Additionally buffers, inhibitors and activators used for the RT-PCR process are suitable reagents for inclusion in the kit embodiment. Once the cDNA has been sufficiently amplified to a specified end point, the cDNA
5 sample must be prepared for detection and quantitation. One method contemplated for detection of polynucleotides is fluorescence spectroscopy, and therefore chromophores that are suited to fluorescence spectroscopy are desirable for labeling polynucleotides and may also be included in reagents of the kit embodiment. Instructions included with the kit
10 embodiment for gene expression profiling preferably teach the user the following steps: to obtain a biological sample; to isolate cellular RNA from the sample; to amplify copies of cDNA from the sample for each biomarker in the panel, and the panel for which the reagents are provided; and to quantify levels of cDNA amplified from the sample. Though tissue samples from a
15 variety of procedures may be used, the instructions for obtaining a biological sample are preferably whereby the user obtains a sample of colorectal cells in a minimally invasive manner, such as by use of a swab or collection of a stool sample. The instructions may also preferably include the step of comparing the cDNA levels quantified to a control.

20 In another embodiment, a kit for protein expression profiling comprises the reagents and instructions necessary for protein expression profiling of the claimed panel. Thus, in this embodiment, the kit for protein expression profiling includes supplying an antibody panel based on the claimed panel of biomarkers for measuring targeted polypeptide levels from
25 a biological sample. One embodiment contemplated for such a panel includes the antibody panel bound to a solid support. Additionally, the reagents included with the kit for protein expression profiling may use a second antibody having specificity to some portion of the bound polypeptide. Such a second antibody may be labeled with molecules useful for detection
30 and quantitation of the bound polypeptides, and therefore in binding to the

polypeptide label it for detection and quantitation. Additionally, other reagents are contemplated for labeling the bound polypeptides for detection and quantitation. Such reagents may either directly label the bound polypeptide or, analogous to a second antibody, may be a moiety with specificity for the bound polypeptide having labels. Examples of such moieties include but are not limited to small molecules such as cofactors, substrates, complexing agents, and the like, or large molecules, such as lectins, peptides, oligonucleotides, and the like. Such moieties may be either naturally occurring or synthetic. Instructions for the protein expression profiling kit preferably teach the user: to obtain a biological sample; to use the antibody panel supplied with the kit for each biomarker in the panel to bind the polypeptides from the sample; and to quantify levels of polypeptides bound from the sample to the antibody panel. Preferably, the kit instructions also include a step of comparing the polypeptide levels to a control. Preferably the biological sample is obtained by a minimally invasive procedure such as use of a swab to through a stool sample.

Additionally, consumable labware required for sample collection, preparation, and analysis may be provided with the kits.

What has been disclosed herein has been provided for the purposes of illustration and description. It is not intended to be exhaustive or to limit what is disclosed to the precise forms described. Many modifications and variations will be apparent to the practitioner skilled in the art. What is disclosed was chosen and described in order to best explain the principles and practical application of the disclosed embodiments of the art described, thereby enabling others skilled in the art to understand the various embodiments and various modifications that are suited to the particular use contemplated. It is intended that the scope of what is disclosed be defined by the following claims and their equivalence.

What Is Claimed:

1. A panel of biomarkers for colorectal cancer and colorectal polyps comprising at least two polynucleotides selected from SEQ ID NOs 1-5.
2. The panel of claim 1, where the panel is selected for analysis of polynucleotide expression levels for colorectal cancer and colorectal polyps.
3. The panel of claim 2, where the polynucleotide expression levels are mRNAs.
4. The panel of claim 2, where the polynucleotide expression levels are cDNAs.
5. The panel of claim 1, where at least one of the polynucleotides is a fragment.
6. The panel of claim 1, where at least one of the polynucleotides is a variant.
7. The panel of claim 1, where the panel is used for the management of patient care in colorectal cancer and colorectal polyps.
8. The panel of claim 7, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.
9. The panel of claim 1, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.

10. A panel of biomarkers for colorectal cancer and colorectal polyps comprising:
 - at least two polynucleotides selected from SEQ ID NOs 1-5; and
 - at least one polynucleotide selected from SEQ ID NOs 6-14
11. The panel of claim 10, where the panel is selected for analysis of polynucleotide expression levels for colorectal cancer and colorectal polyps.
12. The panel of claim 11, where the polynucleotide expression levels are mRNAs.
13. The panel of claim 11, where the polynucleotide expression levels are cDNAs.
14. The panel of claim 10, where at least one of the polynucleotides is a fragment.
15. The panel of claim 10, where at least one of the polynucleotides is a variant.
16. The panel of claim 10, where the panel is used in the management of patient care for colorectal cancer and colorectal polyps.
17. The panel of claim 16, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.
18. The panel of claim 10, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.

19. A panel of biomarkers for colorectal cancer and colorectal polyps comprising:
- at least two polynucleotides selected from SEQ ID NOs 1-5;
 - at least one polynucleotide selected from SEQ ID NOs 6-14; and
 - at least one polynucleotide selected from SEQ ID NOs 15-22.
20. The panel of claim 19, where the panel is selected for analysis of polynucleotide expression levels for colorectal cancer and colorectal polyps.
21. The panel of claim 20, where the polynucleotide expression levels are mRNAs.
22. The panel of claim 20, where the polynucleotide expression levels are cDNAs.
23. The panel of claim 19, where at least one of the polynucleotides is a fragment.
24. The panel of claim 19, where at least one of the polynucleotides is a variant.
25. The panel of claim 25, where the panel is the basis for management of patient care in colorectal cancer and colorectal polyps.
26. The panel of claim 19, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.

27. The panel of claim 25, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.
28. A panel of biomarkers for colorectal cancer and colorectal polyps comprising at least two polypeptides selected from SEQ ID NOs 23-27.
29. The panel of claim 28, where the panel is selected for analysis of polypeptide expression levels for colorectal cancer and colorectal polyps.
30. The panel of claim 28, where at least one of the polypeptides is a fragment.
31. The panel of claim 28, where at least one of the polypeptides is a variant.
32. The panel of claim 28, where the panel is used in the management of patient care in colorectal cancer and colorectal polyps.
33. The panel of claim 32, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.
34. The panel of claim 28, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.
35. A panel of biomarkers for colorectal cancer and colorectal polyps comprising:
at least two polypeptides selected from SEQ ID NOs 23-27; and
at least one polypeptide selected from SEQ ID NOs 28-36.

36. The panel of claim 35, where the panel is selected for analysis of polypeptide expression levels for colorectal cancer and colorectal polyps.
37. The panel of claim 35, where at least one of the polypeptides is a fragment.
38. The panel of claim 35, where at least one of the polypeptides is a variant.
39. The panel of claim 35, where the panel is used in the management of patient care in colorectal cancer and colorectal polyps.
40. The panel of claim 39, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.
41. The panel of claim 35, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.
42. A panel of biomarkers for colorectal cancer and colorectal polyps comprising:
at least two polypeptides selected from SEQ ID NOs 23-27;
at least one polypeptide selected from SEQ ID NOs 28-36; and
at least one polypeptide selected from SEQ ID NOs 37-44.
43. The panel of claim 42, where the panel is selected for analysis of polypeptide expression levels for colorectal cancer and colorectal polyps.

44. The panel of claim 42, where at least one of the polypeptides is a fragment.
45. The panel of claim 42, where at least one of the polypeptides is a variant.
46. The panel of claim 42, where the panel is used in the management of patient care in colorectal cancer and colorectal polyps.
47. The panel of claim 46, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.
48. The panel of claim 42, where the panel is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.
49. A method for measuring expression levels of polynucleotides from biomarkers for colorectal cancer and colorectal polyps, comprising:
selecting a panel of biomarkers comprising at least two polynucleotides from SEQ ID NOs 1-5;
obtaining a biological sample;
isolating cellular RNA from the sample;
amplifying copies of cDNA from the sample for each biomarker in the panel; and
quantifying levels of cDNA amplified from the sample.
50. The method of claim 49, where the step of selecting a panel of biomarkers further comprises at least one polynucleotide from SEQ ID NOs 6-14.

51. The method of claim 49, where the step of selecting a panel of biomarkers further comprises:
at least one polynucleotide from SEQ ID NOs 6-14; and
at least one polynucleotide from SEQ ID NOs 15-22.
52. The method of claim 49, where the step of amplifying copies of cDNA further comprises at least two sets of primers chosen from SEQ. ID NOs 45-50.
53. The method of claim 52, where the step of amplifying copies of cDNA further comprises using enzymes and reagents for the preparation of cDNAs.
54. The method of claim 49, where the step of quantifying the levels of cDNA further comprises labeling cDNA.
55. The method of claim 54, where labeling cDNA includes at least one chromophore.
56. The method of claim 49, where the cDNA levels for the sample are compared to a control.
57. The method of claim 56, where the comparison is used in the management of patient care in colorectal cancer and colorectal polyps.
58. The method of claim 57, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.

59. The method of claim 56, where the comparison is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.

60. The method of claim 49, where the step of obtaining a biological sample is by obtaining a sample of colorectal cells.

61. The method of claim 60, where the step of obtaining a sample of colorectal cells is minimally invasive.

62. The method of claim 61, where the minimally invasive step is by use of a swab.

63. The method of claim 60, where the step of obtaining a sample of colorectal cells is non-invasive.

64. The method of claim 63, where the non-invasive step is by collection of a stool sample.

65. A method for measuring expression levels of polypeptides from biomarkers for colorectal cancer and colorectal cancer, comprising:
selecting a panel of biomarkers comprising at least two polypeptides from SEQ ID NOs 23-27;
obtaining a biological sample;
creating an antibody panel for each biomarker in the panel;
using the antibody panel to bind the polypeptides from the sample;
and
quantifying levels of polypeptides bound from the sample to the antibody panel.

66. The method of claim 65, where the step of selecting a panel of biomarkers further comprises at least one polypeptide from SEQ ID NOs 28-36.
67. The method of claim 65, where the step of selecting a panel of biomarkers further comprises:
at least one polypeptide from SEQ ID NOs 28-36; and
at least one polypeptide from SEQ ID NOs 37-44.
68. The method of claim 65, where the polypeptide levels for the sample are compared to a control.
69. The method of claim 68, where the comparison is used in the management of patient care in colorectal cancer and colorectal polyps.
70. The method of claim 69, where the management of patient care includes one or more of risk assessment, early diagnosis, establishing prognosis, monitoring patient treatment, and detecting relapse.
71. The method of claim 68, where the comparison is used in discovery of therapeutic intervention of colorectal cancer and colorectal polyps.
72. The method of claim 65, where the step of obtaining a biological sample is by obtaining a sample of colorectal cells.
73. The method of claim 72, where the step of obtaining a sample of colorectal cells is minimally invasive.

74. The method of claim 73, where the minimally invasive step is by use of a swab.

75. The method of claim 72, where the step of obtaining a sample of colorectal cells is non-invasive.

76. The method of claim 75, where the non-invasive step is by collection of a stool sample.

77. The method of claim 65, where the step of quantifying the bound polypeptides further comprises labeling the polypeptides.

78. The method of claim 77, where labeling the polypeptides comprises using a second antibody.

79. A kit for the determination of colorectal cancer and colorectal polyps comprising:

at least one reagent that is used in analysis of polynucleotide expression levels for a panel of biomarkers for colorectal cancer and colorectal polyps, where the panel comprises at least two polynucleotides listed in SEQ ID NOs 1-5; and

instructions for using the kit for analyzing the expression levels.

80. The kit of claim 79, where the panel of biomarkers further comprises at least one polynucleotides listed in SEQ ID NOs 6-14.

81. The kit of claim 79, where the panel of biomarkers further comprises:
at least one polynucleotide selected from SEQ ID NOs 6-14; and
at least one polynucleotide selected from SEQ ID NOs 15-22.

82. The kit of claim 79, where the polynucleotide expression levels are mRNAs.
83. The kit of claim 79, where the polynucleotide expression levels are cDNAs.
84. The kit of claim 83, where the reagent comprises at least two sets of primers chosen from SEQ. ID NOs 45-50.
85. The kit of claim 84, further comprising reagents for the preparation of cDNA.
86. The kit of claim 79, comprising a reagent that is used for detection and quantitation of polynucleotides.
87. The kit of claim 86, where the reagent includes at least one chromophore.
88. The kit of claim 79, further comprising consumable labware for at least one of sample collection, sample preparation, and sample analysis.
89. A kit for the determination of colorectal cancer and colorectal polyps comprising:
at least one reagent used in that analysis of polypeptide expression levels for a panel of biomarkers for colorectal cancer and colorectal polyps, where the panel comprises at least two polypeptides listed in SEQ. ID NOs 23-27; and
instructions for using the kit for analyzing the expression levels.

90. The kit of claim 89, where the panel of biomarkers further comprises at least one polynucleotides listed in SEQ ID NOs 28-36.
91. The kit of claim 89, where the panel of biomarkers further comprises:
at least one polynucleotide selected from SEQ ID NOs 28-36; and
at least one polynucleotide selected from SEQ ID NOs 37-44.
92. The kit of claim 89, where the reagent is an antibody reagent that binds a polypeptide selected in the panel.
93. The kit of claim 89, further comprising a reagent that is used for detection and quantitation of a bound polypeptide.
94. The kit of claim 93, where the reagent includes a second antibody.
95. The kit of claim 89, further comprising consumable labware for at least one of sample collection, sample preparation, and sample analysis.

Sequence ID No. / ID	NCBI Entrez Database	Name	Abbreviation
1. Coding sequence	XM_031289	Interleukin 8	IL8
2. Coding sequence	XM_051900	Prostaglandin-endoperoxide synthase 2	PTGS2
3. Coding sequence	M94582	Interleukin 8 receptor B	ILR8RB
4. Coding sequence	NM_005555	Lipocalin 2	LCN2
5. Coding sequence	NM_000331	Serum amyloid A1	SAA1
6. Coding sequence	NM_000757	Macrophage colony stimulating factor 1	CSF1 (MCSF1)
7. Coding sequence	X54489	Melanoma growth stimulatory activity	MGSA
8. Coding sequence	NM_002090	Chemokine (C-X-C motif) ligand 3	CXCL3
9. Coding sequence	XM_032429	Secreted phosphoprotein 1	SPP1 (OPN)
10. Coding sequence	M64349	Cyclin D	CCND1
11. Coding sequence	AX057136	c-Myc	c-Myc
12. Coding sequence	L25610	Cyclin-dependent kinase inhibitor	HUMCDK1
13. Coding sequence	BC021998	Cyclin-dependent kinase inhibitor 2A	CDKN2A
14. Coding sequence	NM_058195	Alternative reading frame p14	CDKN2A
15. Coding sequence	NM_005036	Peroxisome proliferative activated receptor, alpha	PPARA
16. Coding sequence	XM_003059	Peroxisome proliferative activated receptor, gamma	PPARG
17. Coding sequence	NM_006238	Peroxisome proliferative activated receptor, delta	PPARD
18. Coding sequence	XM_030326	CD44 antigen	CD44
19. Coding sequence	XM_044882	Prostaglandin-endoperoxide synthase 1	PTGS1
20. Coding sequence	NM_002131	High-mobility group AT-hook1 isoform B	HMGAI
21. Coding sequence	X54942	CKSHS2	CKSHS2
22. Coding sequence	U22055	100 kDa coactivator	p100 coactivator
23. Protein	XP_031289	Interleukin 8	IL8
24. Protein	XP_051900	Prostaglandin-endoperoxide synthase 2	COX2
25. Protein	AAA36108	Interleukin 8 receptor B	CXCR2
26. Protein	NP_005555	Lipocalin 2	LCN2
27. Protein	NP_000331	Serum amyloid A1	SAA1
28. Protein	NP_000757	Macrophage colony stimulating factor 1	MCSF1
29. Protein	CAA38361	Melanoma growth stimulatory activity	Groα
30. Protein	NM-002090	Chemokine (C-X-C motif) ligand 3	Groγ

Figure 1

Sequence ID No. / ID	NCBI Entrez Database	Name	Abbreviation
31. Protein	XP_032429	Osteopontin	OPN
32. Protein	AAA52136	Cyclin D	cyclin D1
33. Protein	CAC22425	c-Myc	c-Myc
34. Protein	AAA16109	Cyclin-dependent kinase inhibitor	p21
35. Protein	AAH21998	Cyclin-dependent kinase inhibitor 2A	p16
36. Protein	NP_047862	Alternative reading frame p14	p14ARF
37. Protein	NP_005027	Peroxisome proliferative activated receptor, alpha	PPAR α
38. Protein	XP_003059	Peroxisome proliferative activated receptor, gamma	PPAR γ
39. Protein	NP_006229	Peroxisome proliferative activated receptor, delta	PPAR δ
40. Protein	XP_030326	CD44 antigen	CD44
41. Protein	XP_044882	Prostaglandin-endoperoxide synthase 1	COX1
42. Protein	NP_002122	High-mobility group AT-hook1 isoform B	HYGYI
43. Protein	CAA38703	CKS1 protein homolog	CKS1
44. Protein	AAA80488	100 kDa coactivator	p100 coactivator
45. Forward primer		Interleukin 8	IL8
46. Reverse primer			
47. Forward primer		Prostaglandin-endoperoxide synthase 2	PTGS2
48. Reverse primer			
49. Forward primer		Interleukin 8 receptor B	ILR8RB
50. Reverse primer			
51. Forward primer		Lipocalin 2	LCN2
52. Reverse primer			
53. Forward primer		Serum amyloid A1	SAA1
54. Reverse primer			
55. Forward primer		Macrophage colony stimulating factor 1	CSF1 (MCSF1)
56. Reverse primer			
57. Forward primer		Melanoma growth stimulatory activity	MGSA
58. Reverse primer			
59. Forward primer		Chemokine (C-X-C motif) ligand 3	MGSA
60. Reverse primer			

Figure 1 – cont'd

Sequence ID No. / ID	NCBI Entrez Database	Name	Abbreviation
61. Forward primer		Secreted phosphoprotein 1	SPP1 (OPN)
62. Reverse primer			
63. Forward primer		Cyclin D	CCND1
64. Reverse primer			
65. Forward primer		c-Myc	c-Myc
66. Reverse primer			
67. Forward primer		Cyclin-dependent kinase inhibitor	HUMCDK1
68. Reverse primer			
69. Forward primer		Cyclin-dependent kinase inhibitor 2A	CDKN2A
70. Reverse primer			
71. Forward primer		Alternative reading frame p14	CDKN2A
72. Reverse primer			
73. Forward primer		Peroxisome proliferative activated receptor, alpha	PPAR α
74. Reverse primer			
75. Forward primer		Peroxisome proliferative activated receptor, gamma	PPAR γ
76. Reverse primer			
77. Forward primer		Peroxisome proliferative activated receptor, delta	PPAR δ
78. Reverse primer			
79. Forward primer		CD44 antigen	CD44
80. Reverse primer			
81. Forward primer		Prostaglandin-endoperoxide synthase 1	COX1
82. Reverse primer			
83. Forward primer		High-mobility group AT-hook1 isoform B	HMGY1
84. Reverse primer			
85. Forward primer		CKS1 protein homolog	CKS1
86. Reverse primer			
87. Forward primer		100 kDa coactivator	p100 coactivator
88. Reverse primer			

Figure 1 – cont'd

Relative Gene Expression Levels in Colon Polyps (Average $\pm$ SE)

No.	Genes	Wild-Type Littermate	Individual Poly	P Value
1	SDF-1	1.23 $\pm$ 0.34	11.02 $\pm$ 2.45	0.003
2	COX2	1.41 $\pm$ 0.25	87.48 $\pm$ 16.50	<0.001
3	CXCR2	1.41 $\pm$ 0.35	11221 $\pm$ 23.76	<0.001
4	OPN	1.62 $\pm$ 0.60	463.37 $\pm$ 130.49	0.004
5	MCSFI	1.05 $\pm$ 0.15	4.26 $\pm$ 1.60	0.08
6	PPAR δ	1.16 $\pm$ 0.27	0.44 $\pm$ 0.05	0.04

FIG. 2A

Relative Gene Expressions in Normal-Appearing Mucosa from Colon Cancer										
	Sigmoid and Rectum						Ascending Colon			
	NB	H002	H004	H006	H008	H011	NB	H003	H009	H010
IL-8	1.80 $\pm$ 0.26	28.91	7.14	6.88	18.35	24.67	1.72 $\pm$ 0.35	16.03	4.90	28.26
COX2	1.85 $\pm$ 0.29	13.54	10.34	18.23	14.63	1.87	1.74 $\pm$ 0.45	25.48	11.98	33.06
CXCR2	1.31 $\pm$ 0.14	11.35	6.82	6.85	7.18	100.20	1.26 $\pm$ 0.17	10.23	22.62	11.20
OPN	2.11 $\pm$ 0.52	10.85	9.84	11.88	21.29	3.41	1.43 $\pm$ 0.20	26.83	23.97	64.13
MCSF1	1.69 $\pm$ 0.19	4.49	11.88	12.84	7.24	7.98	1.57 $\pm$ 0.22	12.40	17.89	14.97
PPAR- δ	1.14 $\pm$ 0.07	0.10	0.09	0.12	1.28	0.96	1.16 $\pm$ 0.11	0.09	1.10	0.30

FIG. 2B

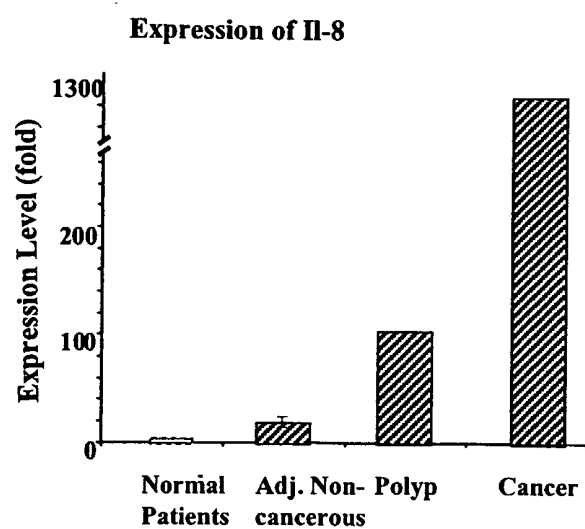
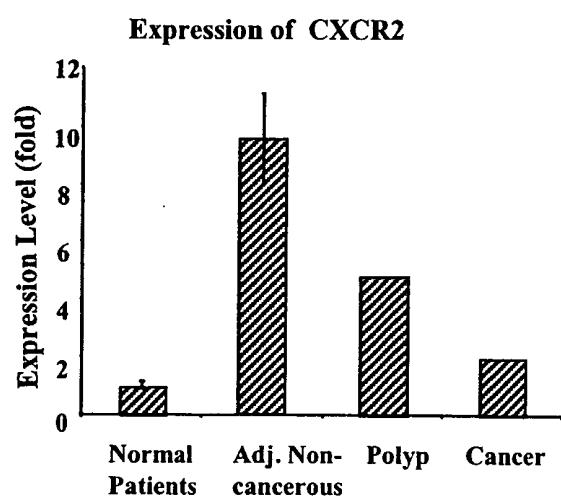
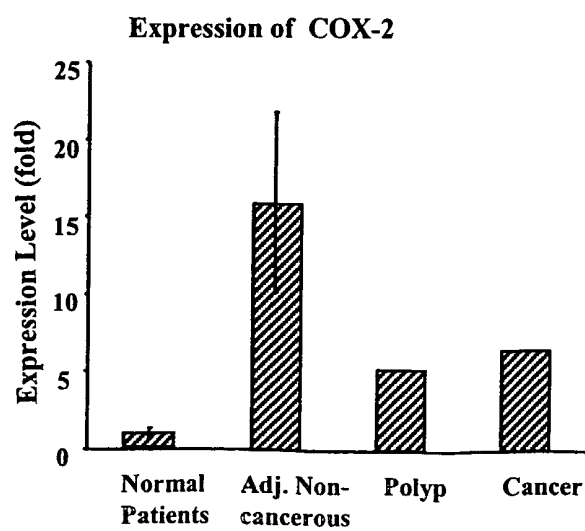
Dependent Variable: IL-8, M-CSF-1, COX-2, OPN, p21, PPAR- γ , CXCR2, CD44, PPAR- δ

Results for Multivariate Analysis: Wilks Lambda Criterion

Source	Lambda	probability
Cancer	0.989	0.0086

FIG. 2C

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**Fig. 3A****Fig. 3B****Fig. 3C**

IL-8

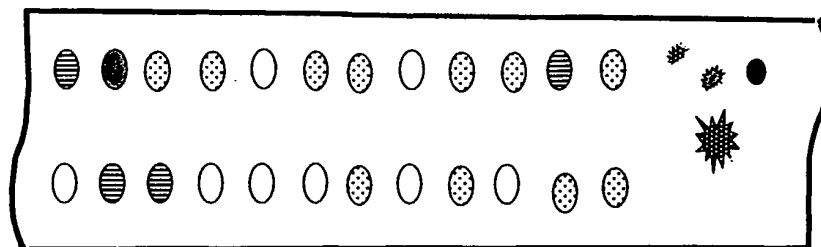
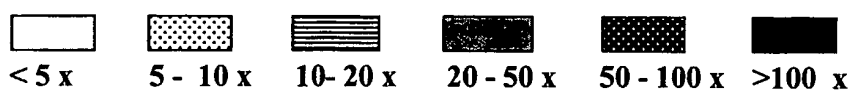


Fig. 4A



← 53 cm →

COX2

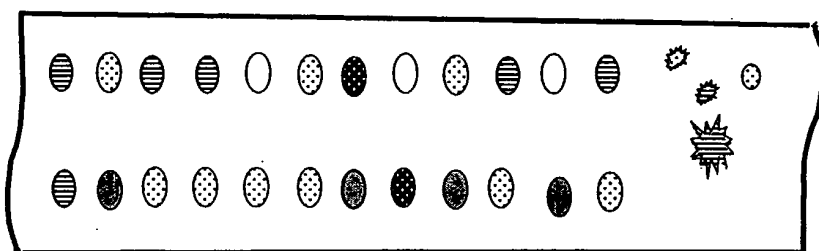
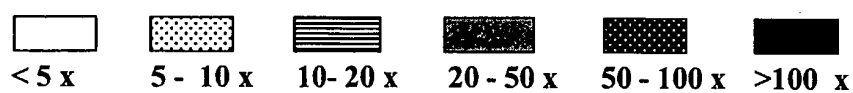


Fig. 4B



← 53 cm →

CXCR2

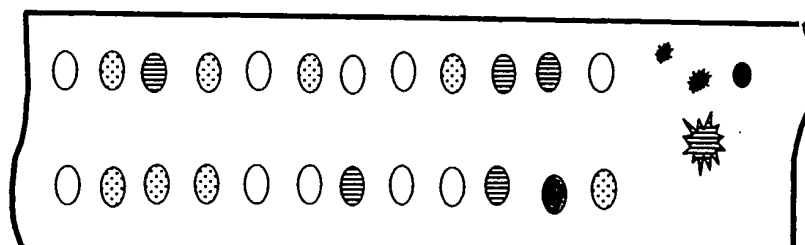
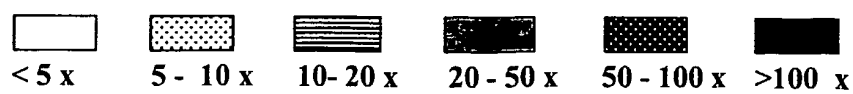


Fig. 4C



← 53 cm →

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2/88

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Asp His Lys Arg Gly Pro Ala Phe Thr Asn Gly Leu Gly His Gly Val			
	200	205	210
gac tta aat cat att tac ggt gaa act ctg gct aga cag cgt aaa ctg			787
Asp Leu Asn His Ile Tyr Gly Glu Thr Leu Ala Arg Gln Arg Lys Leu			
	215	220	225
			230

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cgc ctt ttc aag gat gga aaa atg aaa tat cag ata att gat gga gag	835
Arg Leu Phe Lys Asp Gly Lys Met Lys Tyr Gln Ile Ile Asp Gly Glu	
235 240 245	
atg tat cct ccc aca gtc aaa gat act cag gca gag atg atc tac cct	883
Met Tyr Pro Pro Thr Val Lys Asp Thr Gln Ala Glu Met Ile Tyr Pro	
250 255 260	
cct caa gtc cct gag cat cta cgg ttt gct gtg ggg cag gag gtc ttt	931
Pro Gln Val Pro Glu His Leu Arg Phe Ala Val Gly Gln Glu Val Phe	
265 270 275	
ggg ctg gtg cct ggt ctg atg atg tat gcc aca atc tgg ctg cgg gaa	979
Gly Leu Val Pro Gly Leu Met Met Tyr Ala Thr Ile Trp Leu Arg Glu	
280 285 290	
cac aac aga gta tgc gat gtg ctt aaa cag gag cat cct gaa tgg ggt	1027
His Asn Arg Val Cys Asp Val Leu Lys Gln Glu His Pro Glu Trp Gly	
295 300 305 310	
gat gag cag ttg ttc cag aca agc agg cta ata ctg ata gga gag act	1075
Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu Ile Leu Ile Gly Glu Thr	
315 320 325	
att aag att gtg att gaa gat tat gtg caa cac ttg agt ggc tat cac	1123
Ile Lys Ile Val Ile Glu Asp Tyr Val Gln His Leu Ser Gly Tyr His	
330 335 340	
ttc aaa ctg aaa ttt gac cca gaa cta ctt ttc aac aaa caa ttc cag	1171
Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu Phe Asn Lys Gln Phe Gln	
345 350 355	
tac caa aat cgt att gct gct gaa ttt aac acc ctc tat cac tgg cat	1219
Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn Thr Leu Tyr His Trp His	
360 365 370	
ccc ctt ctg cct gac acc ttt caa att cat gac cag aaa tac aac tat	1267
Pro Leu Leu Pro Asp Thr Phe Gln Ile His Asp Gln Lys Tyr Asn Tyr	
375 380 385 390	
caa cag ttt atc tac aac aac tct ata ttg ctg gaa cat gga att acc	1315
Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu Leu Glu His Gly Ile Thr	
395 400 405	
cag ttt gtt gaa tca ttc acc agg caa att gct ggc agg gtt gct ggt	1363
Gln Phe Val Glu Ser Phe Thr Arg Gln Ile Ala Gly Arg Val Ala Gly	
410 415 420	
ggg agg aat gtt cca ccc gca gta cag aaa gta tca cag gct tcc att	1411
Gly Arg Asn Val Pro Pro Ala Val Gln Lys Val Ser Gln Ala Ser Ile	
425 430 435	
gac cag agc agg cag atg aaa tac cag tct ttt aat gag tac cgc aaa	1459
Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser Phe Asn Glu Tyr Arg Lys	
440 445 450	

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cgc ttt atg ctg aag ccc tat gaa tca ttt gaa gaa ctt aca gga gaa 1507
 Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe Glu Glu Leu Thr Gly Glu
 455 460 465 470

aag gaa atg tct gca gag ttg gaa gca ctc tat ggt gac atc gat gct 1555
 Lys Glu Met Ser Ala Glu Leu Glu Ala Leu Tyr Gly Asp Ile Asp Ala
 475 480 485

gtg gag ctg tat cct gcc ctt ctg gta gaa aag cct cgg cca gat gcc 1603
 Val Glu Leu Tyr Pro Ala Leu Leu Val Glu Lys Pro Arg Pro Asp Ala
 490 495 500

atc ttt ggt gaa acc atg gta gaa gtt gga gca cca ttc tcc ttg aaa 1651
 Ile Phe Gly Glu Thr Met Val Glu Val Gly Ala Pro Phe Ser Leu Lys
 505 510 515

gga ctt atg ggt aat gtt ata tgt tct cct gcc tac tgg aag cca agc 1699
 Gly Leu Met Gly Asn Val Ile Cys Ser Pro Ala Tyr Trp Lys Pro Ser
 520 525 530

act ttt ggt gga gaa gtg ggt ttt caa atc atc aac act gcc tca att 1747
 Thr Phe Gly Gly Glu Val Gly Phe Gln Ile Ile Asn Thr Ala Ser Ile
 535 540 545 550

cag tct ctc atc tgc aat aac gtg aag ggc tgt ccc ttt act tca ttc 1795
 Gln Ser Leu Ile Cys Asn Asn Val Lys Gly Cys Pro Phe Thr Ser Phe
 555 560 565

agt gtt cca gat cca gag ctc att aaa aca gtc acc atc aat gca agt 1843
 Ser Val Pro Asp Pro Glu Leu Ile Lys Thr Val Thr Ile Asn Ala Ser
 570 575 580

tct tcc cgc tcc gga cta gat gat atc aat ccc aca gta cta cta aaa 1891
 Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn Pro Thr Val Leu Leu Lys
 585 590 595

gaa cgt tcg act gaa ctg tagaagtcta atgatcatat ttattttattt 1939
 Glu Arg Ser Thr Glu Leu
 600

atatgaacca tgtctattaa tttaattatt taataatatt tatattaaac tccttatgtt 1999
 acttaacatc ttctgtaaca gaagtcagta ctctgttgc ggagaaagga gtcatacttg 2059
 tgaagacttt tatgtcacta ctctaaagat ttgtgtgttg ctgttaagtt tggaaaacag 2119
 tttttattct gttttataaa ccagagagaa atgagttttg acgtcttttt acttgaattt 2179
 caacttatat tataagaacg aaagtaaaga tgtttgaata cttaaact gtcacaagat 2239
 ggcaaaatgc tgaaagtgtt tacactgtcg atgtttccaa tgcactctcc atgatgcatt 2299
 agaagtaact aatgtttgaa attttaaagt acttttggtt atttttctgt catcaaacaa 2359
 aaacaggtat cagtgcatta ttaaatgaat atttaaatta gacattacca gtaatttcat 2419
 gtctactttt taaaatcagc aatgaaacaa taatttgaaa tttctaaatt catagggtag 2479

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aatcacctgt aaaagcttgt ttgatttctt aaagttatta aacttgtaga tataacaaaa 2539
agaagctgtc ttggatttaa atctgtaaaa tcagtagaaa ttttactaca attgcttggt 2599
aaaatatttt ataagtgatg ttcctttttc accaagagta taaacctttt tagtgtagact 2659
gttaaaactt cctttttaa caaaatgcc aatttattaa ggtgggtggag ccactgcagt 2719
gttatcttaa aataagaata ttttggtgag atattccaga atttggttat atggctggta 2779
acatgtaaaa tctatatcag caaaagggtc tacctttaaa ataagcaata acaaagaaga 2839
aaaccaaatt attgttcaaa tttaggttta aacttttgaa gcaaactttt ttttatcctt 2899
gtgcactgca ggcctggtac tcagattttg ctatgagggt aatgaagtag caagctgtgc 2959
ttgaataatg atatgttttc tcagattttc tgttgtagag ttttaatttag cagtccatat 3019
cacattgcaa aagtagcaat gacctcataa aatacctctt caaaatgctt aaattcattt 3079
cacacattaa ttttatctca gtcttgaagc caattcagta ggtgcattgg aatcaagcct 3139
ggctacctgc atgctgttcc ttttcttttc ttcttttagc ctttttgcta agagacacag 3199
tcttctcatc acttcgtttc tcctattttg ttttactagt ttttaagatca gagttcactt 3259
tctttggact ctgcctatat tttcttacct gaacttttgc aagttttcag gtaaacctca 3319
gctcaggact gctatttagc tcctcttaag aagatta 3356

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<210> 3
<211> 1750
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (53)..(1132)

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<400> 3
cctacaggtg aaaagcccag cgacccagtc aggatttaag tttacctcaa aa atg gaa 58
                                         Met Glu
                                         1

gat ttt aac atg gag agt gac agc ttt gaa gat ttc tgg aaa ggt gaa 106
Asp Phe Asn Met Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys Gly Glu
      5              10              15

gat ctt agt aat tac agt tac agc tct acc ctg ccc cct ttt cta cta 154
Asp Leu Ser Asn Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu
      20              25              30

gat gcc gcc cca tgt gaa cca gaa tcc ctg gaa atc aac aag tat ttt 202
Asp Ala Ala Pro Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe
      35              40              45              50

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gtg gtc att atc tat gcc ctg gta ttc ctg ctg agc ctg ctg gga aac	250
Val Val Ile Ile Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn	
55 60 65	
tcc ctc gtg atg ctg gtc atc tta tac agc agg gtc ggc cgc tcc gtc	298
Ser Leu Val Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val	
70 75 80	
act gat gtc tac ctg ctg aac cta gcc ttg gcc gac cta ctc ttt gcc	346
Thr Asp Val Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala	
85 90 95	
ctg acc ttg ccc atc tgg gcc gcc tcc aag gtg aat ggc tgg att ttt	394
Leu Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe	
100 105 110	
ggc aca ttc ctg tgc aag gtg gtc tca ctc ctg aag gaa gtc aac ttc	442
Gly Thr Phe Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe	
115 120 125 130	
tat agt ggc atc ctg cta ctg gcc tgc atc agt gtg gac cgt tac ctg	490
Tyr Ser Gly Ile Leu Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu	
135 140 145	
gcc att gtc cat gcc aca cgc aca ctg acc cag aag cgc tac ttg gtc	538
Ala Ile Val His Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val	
150 155 160	
aaa ttc ata tgt ctc agc atc tgg ggt ctg tcc ttg ctc ctg gcc ctg	586
Lys Phe Ile Cys Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu Ala Leu	
165 170 175	
cct gtc tta ctt ttc cga agg acc gtc tac tca tcc aat gtt agc cca	634
Pro Val Leu Leu Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro	
180 185 190	
gcc tgc tat gag gac atg ggc aac aat aca gca aac tgg cgg atg ctg	682
Ala Cys Tyr Glu Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu	
195 200 205 210	
tta cgg atc ctg ccc cag tcc ttt ggc ttc atc gtg cca ctg ctg atc	730
Leu Arg Ile Leu Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile	
215 220 225	
atg ctg ttc tgc tac gga ttc acc ctg cgt acg ctg ttt aag gcc cac	778
Met Leu Phe Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His	
230 235 240	
atg ggg cag aag cac cgg gcc atg cgg gtc atc ttt gct gtc gtc ctc	826
Met Gly Gln Lys His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu	
245 250 255	
atc ttc ctg ctt tgc tgg ctg ccc tac aac ctg gtc ctg ctg gca gac	874
Ile Phe Leu Leu Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp	
260 265 270	

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acc ctc atg agg acc cag gtg atc cag gag acc tgt gag cgc cgc aat 922
Thr Leu Met Arg Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn
275                280                285                290

cac atc gac cgg gct ctg gat gcc acc gag att ctg ggc atc ctt cac 970
His Ile Asp Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His
                295                300                305

agc tgc ctc aac ccc ctc atc tac gcc ttc att ggc cag aag ttt cgc 1018
Ser Cys Leu Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg
                310                315                320

cat gga ctc ctc aag att cta gct ata cat ggc ttg atc agc aag gac 1066
His Gly Leu Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp
                325                330                335

tcc ctg ccc aaa gac agc agg cct tcc ttt gtt ggc tct tct tca ggg 1114
Ser Leu Pro Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly
                340                345                350

cac act tcc act act ctc taagacctcc tgcctaagtg cagccccgtg 1162
His Thr Ser Thr Thr Leu
355                360

gggttcctcc cttctcttca cagtcacatt ccaagcctca tgtccactgg ttcttcttgg 1222

tctcagtgtc aatgcagccc ccattgtggt cacaggaagc agaggaggcc acgttcttac 1282

tagtttccct tgcattggtt agaaagcttg ccctgggtgcc tcaccccttg ccataattac 1342

tatgtcattt gctggagctc tgcccatcct gccctgagc ccatggcact ctatgttcta 1402

agaagtgaaa atctacactc cagtgaagaca gctctgcata ctcattagga tggctagtat 1462

caaaagaaaag aaaatcaggc tggccaacgg gatgaaaccc tgtctctact aaaaatacaa 1522

aaaaaaaaa aaaaattagc cgggcgtggt ggtgagtgcc tgtaatcaca gctacttggg 1582

aggctgagat gggagaatca cttgaacccg ggaggcagag gttgcagtga gccgagattg 1642

tgcccctgca ctccagcctg agcgacagtg agactctgtc tcagtccatg aagatgtaga 1702

ggagaaaactg gaactctcga gcgttgctgg gggggattgt aaaatggt 1750

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<210> 4

<211> 597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(597)

<400> 4

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atg ccc cta ggt ctc ctg tgg ctg ggc cta gcc ctg ttg ggg gct ctg 48
Met Pro Leu Gly Leu Leu Trp Leu Gly Leu Ala Leu Leu Gly Ala Leu
1                5                10                15

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cat gcc cag gcc cag gac tcc acc tca gac ctg atc cca gcc cca cct 96
His Ala Gln Ala Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro
          20          25          30

ctg agc aag gtc cct ctg cag cag aac ttc cag gac aac caa ttc cag 144
Leu Ser Lys Val Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe Gln
          35          40          45

ggg aag tgg tat gtg gta ggc ctg gca ggg aat gca att ctc aga gaa 192
Gly Lys Trp Tyr Val Val Gly Leu Ala Gly Asn Ala Ile Leu Arg Glu
          50          55          60

gac aaa gac ccg caa aag atg tat gcc acc atc tat gag ctg aaa gaa 240
Asp Lys Asp Pro Gln Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu
          65          70          75          80

gac aag agc tac aat gtc acc tcc gtc ctg ttt agg aaa aag aag tgt 288
Asp Lys Ser Tyr Asn Val Thr Ser Val Leu Phe Arg Lys Lys Lys Cys
          85          90          95

gac tac tgg atc agg act ttt gtt cca ggt tgc cag ccc ggc gag ttc 336
Asp Tyr Trp Ile Arg Thr Phe Val Pro Gly Cys Gln Pro Gly Glu Phe
          100          105          110

acg ctg ggc aac att aag agt tac cct gga tta acg agt tac ctc gtc 384
Thr Leu Gly Asn Ile Lys Ser Tyr Pro Gly Leu Thr Ser Tyr Leu Val
          115          120          125

cga gtg gtg agc acc aac tac aac cag cat gct atg gtg ttc ttc aag 432
Arg Val Val Ser Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys
          130          135          140

aaa gtt tct caa aac agg gag tac ttc aag atc acc ctc tac ggg aga 480
Lys Val Ser Gln Asn Arg Glu Tyr Phe Lys Ile Thr Leu Tyr Gly Arg
          145          150          155          160

acc aag gag ctg act tcg gaa cta aag gag aac ttc atc cgc ttc tcc 528
Thr Lys Glu Leu Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser
          165          170          175

aaa tat ctg ggc ctc cct gaa aac cac atc gtc ttc cct gtc cca atc 576
Lys Tyr Leu Gly Leu Pro Glu Asn His Ile Val Phe Pro Val Pro Ile
          180          185          190

gac cag tgt atc gac ggc tga 597
Asp Gln Cys Ile Asp Gly
          195

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<210> 5

<211> 369

<212> DNA

<213> Homo sapiens

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<220>

<221> CDS

<222> (1)..(369)

<400> 5

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atg aag ctt ctc acg ggc ctg gtt ttc tgc tcc ttg gtc ctg ggt gtc 48
Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
  1             5             10             15

agc agc cga agc ttc ttt tcg ttc ctt ggc gag gct ttt gat ggg gct 96
Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
          20             25             30

cgg gac atg tgg aga gcc tac tct gac atg aga gaa gcc aat tac atc 144
Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
          35             40             45

ggc tca gac aaa tac ttc cat gct cgg ggg aac tat gat gct gcc aaa 192
Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
          50             55             60

agg gga cct ggg ggt gtc tgg gct gca gaa gcg atc agc gat gcc aga 240
Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
          65             70             75             80

gag aat atc cag aga ttc ttt ggc cat ggt gcg gag gac tcg ctg gct 288
Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
          85             90             95

gat cag gct gcc aat gaa tgg ggc agg agt ggc aaa gac ccc aat cac 336
Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
          100             105             110

ttc cga cct gct ggc ctg cct gag aaa tac tga 369
Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
          115             120

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<210> 6

<211> 3939

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (106)..(1767)

<400> 6

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gccgggggcgc ccactccgca gcagccagcg agccagctgc cccgt atg acc gcg ccg 117
Met Thr Ala Pro
          1

ggc gcc gcc ggg cgc tgc cct ccc acg aca tgg ctg ggc tcc ctg ctg 165
Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu Gly Ser Leu Leu
  5             10             15             20

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ttg ttg gtc tgt ctc ctg gcg agc agg agt atc acc gag gag gtg tcg	213
Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr Glu Glu Val Ser	
25 30 35	
gag tac tgt agc cac atg att ggg agt gga cac ctg cag tct ctg cag	261
Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu Gln Ser Leu Gln	
40 45 50	
cgg ctg att gac agt cag atg gag acc tcg tgc caa att aca ttt gag	309
Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln Ile Thr Phe Glu	
55 60 65	
ttt gta gac cag gaa cag ttg aaa gat cca gtg tgc tac ctt aag aag	357
Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys Tyr Leu Lys Lys	
70 75 80	
gca ttt ctc ctg gta caa gac ata atg gag gac acc atg cgc ttc aga	405
Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr Met Arg Phe Arg	
85 90 95 100	
gat aac acc gcc aat ccc atc gcc att gtg cag ctg cag gaa ctc tct	453
Asp Asn Thr Ala Asn Pro Ile Ala Ile Val Gln Leu Gln Glu Leu Ser	
105 110 115	
ttg agg ctg aag agc tgc ttc acc aag gat tat gaa gag cat gac aag	501
Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu Glu His Asp Lys	
120 125 130	
gcc tgc gtc cga act ttc tat gag aca cct ctc cag ttg ctg gag aag	549
Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln Leu Leu Glu Lys	
135 140 145	
gtc aag aat gtc ttt aat gaa aca aag aat ctc ctt gac aag gac tgg	597
Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu Asp Lys Asp Trp	
150 155 160	
aat att ttc agc aag aac tgc aac aac agc ttt gct gaa tgc tcc agc	645
Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala Glu Cys Ser Ser	
165 170 175 180	
caa gat gtg gtg acc aag cct gat tgc aac tgc ctg tac ccc aaa gcc	693
Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu Tyr Pro Lys Ala	
185 190 195	
atc cct agc agt gac ccg gcc tct gtc tcc cct cat cag ccc ctc gcc	741
Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His Gln Pro Leu Ala	
200 205 210	
ccc tcc atg gcc cct gtg gct ggc ttg acc tgg gag gac tct gag gga	789
Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu Asp Ser Glu Gly	
215 220 225	
act gag ggc agc tcc ctc ttg cct ggt gag cag ccc ctg cac aca gtg	837
Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro Leu His Thr Val	
230 235 240	

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gat cca ggc agt gcc aag cag cgg cca ccc agg agc acc tgc cag agc	885
Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser Thr Cys Gln Ser	
245 250 255 260	
ttt gag ccg cca gag acc cca gtt gtc aag gac agc acc atc ggt ggc	933
Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser Thr Ile Gly Gly	
265 270 275	
tca cca cag cct cgc ccc tct gtc ggg gcc ttc aac ccc ggg atg gag	981
Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn Pro Gly Met Glu	
280 285 290	
gat att ctt gac tct gca atg ggc act aat tgg gtc cca gaa gaa gcc	1029
Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val Pro Glu Glu Ala	
295 300 305	
tct gga gag gcc agt gag att ccc gta ccc caa ggg aca gag ctt tcc	1077
Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly Thr Glu Leu Ser	
310 315 320	
ccc tcc agg cca gga ggg ggc agc atg cag aca gag ccc gcc aga ccc	1125
Pro Ser Arg Pro Gly Gly Gly Ser Met Gln Thr Glu Pro Ala Arg Pro	
325 330 335 340	
agc aac ttc ctc tca gca tct tct cca ctc cct gca tca gca aag ggc	1173
Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala Ser Ala Lys Gly	
345 350 355	
caa cag ccg gca gat gta act gct aca gcc ttg ccc agg gtg ggc ccc	1221
Gln Gln Pro Ala Asp Val Thr Ala Thr Ala Leu Pro Arg Val Gly Pro	
360 365 370	
gtg atg ccc act ggc cag gac tgg aat cac acc ccc cag aag aca gac	1269
Val Met Pro Thr Gly Gln Asp Trp Asn His Thr Pro Gln Lys Thr Asp	
375 380 385	
cat cca tct gcc ctg ctc aga gac ccc ccg gag cca ggc tct ccc agg	1317
His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro Gly Ser Pro Arg	
390 395 400	
atc tca tca ctg cgc ccc cag gcc ctc agc aac ccc tcc acc ctc tct	1365
Ile Ser Ser Leu Arg Pro Gln Ala Leu Ser Asn Pro Ser Thr Leu Ser	
405 410 415 420	
gct cag cca cag ctt tcc aga agc cac tcc tcg ggc agc gtg ctg ccc	1413
Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly Ser Val Leu Pro	
425 430 435	
ctt ggg gag ctg gag ggc agg agg agc acc agg gat cgg acg agc ccc	1461
Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp Arg Thr Ser Pro	
440 445 450	
gca gag cca gaa gca gca cca gca agt gaa ggg gca gcc agg ccc ctg	1509
Ala Glu Pro Glu Ala Ala Pro Ala Ser Glu Gly Ala Ala Arg Pro Leu	
455 460 465	

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ccc cgt ttt aac tcc gtt cct ttg act gac aca ggc cat gag agg cag 1557
Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly His Glu Arg Gln
    470                475                480

tcc gag gga tcc tcc agc ccg cag ctc cag gag tct gtc ttc cac ctg 1605
Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser Val Phe His Leu
485                490                495                500

ctg gtg ccc agt gtc atc ctg gtc ttg ctg gct gtc gga ggc ctc ttg 1653
Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val Gly Gly Leu Leu
                    505                510                515

ttc tac agg tgg agg cgg cgg agc cat caa gag cct cag aga gcg gat 1701
Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro Gln Arg Ala Asp
                    520                525                530

tct ccc ttg gag caa cca gag ggc agc ccc ctg act cag gat gac aga 1749
Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr Gln Asp Asp Arg
    535                540                545

cag gtg gaa ctg cca gtg tagaggggaat tctaagctgg acgcacagaa 1797
Gln Val Glu Leu Pro Val
    550

cagtctcttc gtgggaggag acattatggg gcgtccacca ccacctctcc ctggccatcc 1857

tcttggaatg tggctctgccc tccaccagag ctctgcctg ccaggactgg accagagcag 1917

ccaggctggg gccctctgt ctcaaccgc agaccttga ctgaatgaga gaggccagag 1977

gatgctcccc atgctgccac tatttattgt gagcctgga ggctcccatg tgcttgagga 2037

aggctgggtga gcccggtca ggacctctt cctcagggg ctgcagcctc ctctcactcc 2097

cttccatgcc ggaaccagag ccagggaccc accggcctgt ggtttgtggg aaagcagggg 2157

gcacgctgag gagtgaaca accctgcacc cagagggcct gcctggtgcc aaggtatccc 2217

agcctggaca ggcattgacc tgtctccaga cagaggagcc tgaagtctgt ggggcgggac 2277

agcctcggcc tgatttccc taaagggtgt cagcctgaga gacgggaaga ggaggcctct 2337

gcacctgctg gtctgcactg acagcctgaa gggctctacac cctcggctca cctaagtccc 2397

tgtgctggtt gccaggccca gaggggaggc cagccctgcc ctccaggacct gcctgacctg 2457

ccagtgatgc caagaggggg atcaagcact ggcctctgcc cctcctcctt ccagcacctg 2517

ccagagcttc tccagcaggc caagcagagg cccccctcat gaaggagcc attgactgt 2577

gaacactgta cctgcctgct gaacagcctc ccccgctcca tccatgagcc agcatccgtc 2637

cgtcctccac tctccagcct ctcccagcc tctgcactg agctggcctc accagtgcac 2697

tgagggagcc cctcagccct gaccttctcc tgacctggcc tttagctccc cggagtggag 2757

tgggggtggga gaacctctg ggccgccagc cagagccgct ctttaggctg tgttcttcgc 2817

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ccagggtttct gcatcttcca ctttgacatt cccaagaggg aagggactag tgggagagag 2877
caagggaggg gagggcacag acagagagcc tacagggcga gctctgactg aagatgggcc 2937
tttgaaatat aggtatgcac ctgaggttgg gggaggggtct gcactcccaa accccagcgc 2997
agtgtccttt ccctgctgcc gacaggaacc tggggctgag cagggttatcc ctgtcaggag 3057
ccctggactg ggctgcatct cagccccacc tgcattggtat ccagctccca tccacttctc 3117
acccttcttt cctcctgacc ttggtcagca gtgatgacct ccaactctca cccacccctc 3177
ctaccatcac ctctaaccag gcaagccagg gtgggagagc aatcaggaga gccaggcctc 3237
agcttccaat gcctggaggg cctccacttt gtggccagcc tgtggtgctg gctctgaggc 3297
ctaggcaacg agcgacaggg ctgccagttg cccctgggtt cctttgtgct gctgtgtgcc 3357
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tgatgccgac agcttaggga agggcactga acttgcatat ggggcttagc cttctagtca 3537
cagcctctat atttgatgct agaaaacaca tattttttaa tggaagaaaa ataaaaaggc 3597
attccccctt catcccccta ccttaaacad ataatatatt aaaggtcaaa aaagcaatcc 3657
aaccactgca agaagctctt tttgagcact tgggtggcatc agagcaggag gagccccaga 3717
gccacctctg gtgtcccca ggctacctgc tcaggaaccc cttctgttct ctgagaactc 3777
aacagaggac attggctcac gcactgtgag attttgtttt tatacttgca actggtgaat 3837
tattttttat aaagtcattt aaatatctat ttaaaagata ggaagctgct tatatattta 3897
ataataaaaag aagtgcacaa gctgccgttg acgtagctcg ag 3939

```

```

<210> 7
<211> 1024
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)..(321)

```

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<400> 7
atg gcc cgc gct gct ctc tcc gcc gcc ccc agc aat ccc cgg ctc ctg 48
Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
  1             5             10             15

cga gtg gca ctg ctg ctc ctg ctc ctg gta gcc gct ggc cgg cgc gca 96
Arg Val Ala Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala
      20             25             30

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15/88

```

gca gga gcg tcc gtg gcc act gaa ctg cgc tgc cag tgc ttg cag acc 144
Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
      35              40              45

ctg cag gga att cac ccc aag aac atc caa agt gtg aac gtg aag tcc 192
Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
      50              55              60

ccc gga ccc cac tgc gcc caa acc gaa gtc ata gcc aca ctc aag aat 240
Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
      65              70              75              80

ggg cgg aaa gct tgc ctc aat cct gca tcc ccc ata gtt aag aaa atc 288
Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
      85              90              95

atc gaa aag atg ctg aac agt gac aaa tcc aac tgaccagaag ggaggaggaa 341
Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
      100              105

gctcactggt ggctgttcct gaaggaggcc ctgcccttat aggaacagaa gaggaaagag 401

agacacagct gcagaggcca cctggattgt gcctaattgtg tttgagcatc gcttaggaga 461

agtcttctat ttatttatatt attcattagt tttgaagatt ctatgttaat attttagggtg 521

taaaataatt aagggtatga ttaactctac ctgcacactg tcctattata ttcattcttt 581

ttgaaatgtc aaccccaagt tagttcaatc tggattcata tttaatttga aggtagaatg 641

ttttcaaatg ttctccagtc attatgttaa tttttctgag gagcctgcaa catgccagcc 701

actgtgatag aggctggcgg atccaagcaa atggccaatg agatcattgt gaaggcaggg 761

gaatgtatgt gcacatctgt tttgtaactg tttagatgaa tgtcagttgt tatttattga 821

aatgatttca cagtgtgtgg tcaacatttc tcatgttgaa actttaagaa ctaaaatggt 881

ctaaatatcc cttggacatt ttatgtcttt cttgtaaggc atactgcctt gtttaatggt 941

agttttacag tgtttctggc ttagaacaaa ggggcttaat tattgatggt ttcatagaga 1001

atataaaaat aaagcactta tag 1024

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<210> 8

<211> 1064

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78)..(395)

<220>

<221> modified_base

16/88

<222> (27)

<223> a, c, t, g, other or unknown

<220>

<221> modified_base

<222> (766)

<223> a, c, t, g, other or unknown

<400> 8

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cacagccggg tcgcaggcac ctccccngcc agctctcccg cattctgcac agcttcccga 60
cgcgctctgct gagcccc atg gcc cac gcc acg ctc tcc gcc gcc ccc agc    110
                Met Ala His Ala Thr Leu Ser Ala Ala Pro Ser
                  1                5                10

aat ccc cgg ctc ctg cgg gtg gcg ctg ctg ctc ctg ctc ctg gtg ggc    158
Asn Pro Arg Leu Leu Arg Val Ala Leu Leu Leu Leu Leu Val Gly
                15                20                25

agc cgg cgc gca gca gga gcg tcc gtg gtc act gaa ctg cgc tgc cag    206
Ser Arg Arg Ala Ala Gly Ala Ser Val Val Thr Glu Leu Arg Cys Gln
                30                35                40

tgc ttg cag aca ctg cag gga att cac ctc aag aac atc caa agt gtg    254
Cys Leu Gln Thr Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val
                45                50                55

aat gta agg tcc ccc gga ccc cac tgc gcc caa acc gaa gtc ata gcc    302
Asn Val Arg Ser Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala
                60                65                70                75

aca ctc aag aat ggg aag aaa gct tgt ctc aac ccc gca tcc ccc atg    350
Thr Leu Lys Asn Gly Lys Lys Ala Cys Leu Asn Pro Ala Ser Pro Met
                80                85                90

gtt cag aaa atc atc gaa aag ata ctg aac aag ggg agc acc aac    395
Val Gln Lys Ile Ile Glu Lys Ile Leu Asn Lys Gly Ser Thr Asn
                95                100                105

tgacaggaga gaagtaagaa gcttatcagc gtatcattga cacttcctgc aggggtggtcc 455
ctgcccttac cagagctgaa aatgaaaaag agaacagcag ctttctaggg acagctggaa 515
agggacttaa tgtgtttgac ttttcttac gagggttcta cttatttatg tttttatttt 575
tgaaagcttg ttttttaata ttttacatgc tgttatttaa agatgtgagt gtgtttcatc 635
aaacatagct cagtctgat ttttaattg gaatatgatg gggttttaaat gtgtcattaa 695
actaatatct agtgggagac cataatgtgt cagccacctt gataaatgac aggggtgggga 755
actggagggt ngggggattg aaatgcaagc aattagtgga tcactgttag ggtaagggaa 815
tgtatgtaca catctatctt ttatactttt ttttttaaaa aagaatgtca gttgttattt 875
attcaaatta tctcacatta tgtgttcaac atttttatgc tgaagtttcc cttagacatt 935
ttatgtcttg cttgtagggc ataatgcctt gtttaatgtc cattctgcag cgtttctctt 995

```

[illegible]

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```

gtt tat gga ctg agg tca aaa tct aag aag ttt cgc aga cct gac atc 596
Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg Pro Asp Ile
150                      155                      160                      165

cag tac cct gat gct aca gac gag gac atc acc tca cac atg gaa agc 644
Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His Met Glu Ser
170                      175                      180

gag gag ttg aat ggt gca tac aag gcc atc ccc gtt gcc cag gac ctg 692
Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala Gln Asp Leu
185                      190                      195

aac gcg cct tct gat tgg gac agc cgt ggg aag gac agt tat gaa acg 740
Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser Tyr Glu Thr
200                      205                      210

agt cag ctg gat gac cag agt gct gaa acc cac agc cac aag cag tcc 788
Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His Ser His Lys Gln Ser
215                      220                      225

aga tta tat aag cgg aaa gcc aat gat gag agc aat gag cat tcc gat 836
Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu His Ser Asp
230                      235                      240                      245

gtg att gat agt cag gaa ctt tcc aaa gtc agc cgt gaa ttc cac agc 884
Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu Phe His Ser
250                      255                      260

cat gaa ttt cac agc cat gaa gat atg ctg gtt gta gac ccc aaa agt 932
His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp Pro Lys Ser
265                      270                      275

aag gaa gaa gat aaa cac ctg aaa ttt cgt att tct cat gaa tta gat 980
Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His Glu Leu Asp
280                      285                      290

agt gca tct tct gag gtc aat taaaaggaga aaaaatacaa tttctcactt 1031
Ser Ala Ser Ser Glu Val Asn
295                      300

tgcatttagt caaaagaaaa aatgctttat agcaaatga aagagaacat gaaatgcttc 1091

tttctcagtt tattggttga atgtgtatct atttgagtct ggaaataact aatgtgtttg 1151

ataattagtt tagtttgttg cttcatggaa actccctgta aactaaaagc ttcagggtta 1211

tgtctatgtt cattctatag aagaaatgca aactatcact gtattttaat atttgttatt 1271

ctctcatgaa tagaaattta tgtagaagca aacaaaatac ttttaccac ttaaaaagag 1331

aatataacat tttatgtcac tataatcttt tgttttttaa gttagtgtat attttgttgt 1391

gattatcttt ttgtggtgtg aataaatctt ttatcttgaa tgtaataaga aaaaaaaaaa 1451

aaaaacaaaa aaaaaaaaaa 1469

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<220>  
<221> CDS  
<222> (145) .. (1029)
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<400>	10																	
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gcgcgggggca	gcagaagcga	gagccgagcg	cggacccagc	caggacccac	agccctcccc	120												
agctgcccag	gaagagcccc	agcc	atg	gaa	cac	cag	ctc	ctg	tgc	tgc	gaa	171						
			Met	Glu	His	Gln	Leu	Leu	Cys	Cys	Glu							
			1				5											
gtg	gaa	acc	atc	cgc	cgc	gcg	tac	ccc	gat	gcc	aac	ctc	ctc	aac	gac	219		
Val	Glu	Thr	Ile	Arg	Arg	Ala	Tyr	Pro	Asp	Ala	Asn	Leu	Leu	Asn	Asp			
10					15					20					25			
cgg	gtg	ctg	cgg	gcc	atg	ctg	aag	gcg	gag	gag	acc	tgc	gcg	ccc	tcg	267		
Arg	Val	Leu	Arg	Ala	Met	Leu	Lys	Ala	Glu	Glu	Thr	Cys	Ala	Pro	Ser			
				30					35					40				
gtg	tcc	tac	ttc	aaa	tgt	gtg	cag	aag	gag	gtc	ctg	ccg	tcc	atg	cgg	315		
Val	Ser	Tyr	Phe	Lys	Cys	Val	Gln	Lys	Glu	Val	Leu	Pro	Ser	Met	Arg			
			45					50					55					
aag	atc	gtc	gcc	acc	tgg	atg	ctg	gag	gtc	tgc	gag	gaa	cag	aag	tgc	363		
Lys	Ile	Val	Ala	Thr	Trp	Met	Leu	Glu	Val	Cys	Glu	Glu	Gln	Lys	Cys			
		60					65					70						
gag	gag	gag	gtc	ttc	ccg	ctg	gcc	atg	aac	tac	ctg	gac	cgc	ttc	ctg	411		
Glu	Glu	Glu	Val	Phe	Pro	Leu	Ala	Met	Asn	Tyr	Leu	Asp	Arg	Phe	Leu			
		75					80					85						
tcg	ctg	gag	ccc	gtg	aaa	aag	agc	cgc	ctg	cag	ctg	ctg	ggg	gcc	act	459		
Ser	Leu	Glu	Pro	Val	Lys	Lys	Ser	Arg	Leu	Gln	Leu	Leu	Gly	Ala	Thr			
90					95					100					105			
tgc	atg	ttc	gtg	gcc	tct	aag	atg	aag	gag	acc	atc	ccc	ctg	acg	gcc	507		
Cys	Met	Phe	Val	Ala	Ser	Lys	Met	Lys	Glu	Thr	Ile	Pro	Leu	Thr	Ala			
				110					115					120				
gag	aag	ctg	tgc	atc	tac	acc	gac	ggc	tcc	atc	cgg	ccc	gag	gag	ctg	555		
Glu	Lys	Leu	Cys	Ile	Tyr	Thr	Asp	Gly	Ser	Ile	Arg	Pro	Glu	Glu	Leu			
			125					130					135					
ctg	caa	atg	gag	ctg	ctc	ctg	gtg	aac	aag	ctc	aag	tgg	aac	ctg	gcc	603		
Leu	Gln	Met	Glu	Leu	Leu	Leu	Val	Asn	Lys	Leu	Lys	Trp	Asn	Leu	Ala			
		140					145					150						
gca	atg	acc	ccg	cac	gat	ttc	att	gaa	cac	ttc	ctc	tcc	aaa	atg	cca	651		
Ala	Met	Thr	Pro	His	Asp	Phe	Ile	Glu	His	Phe	Leu	Ser	Lys	Met	Pro			
	155					160					165							

20/88

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gag gcg gag gag aac aaa cag atc atc cgc aaa cac gcg cag acc ttc 699
Glu Ala Glu Glu Asn Lys Gln Ile Ile Arg Lys His Ala Gln Thr Phe
170 175 180 185

gtt gcc tct tgt gcc aca gat gtg aag ttc att tcc aat ccg ccc tcc 747
Val Ala Ser Cys Ala Thr Asp Val Lys Phe Ile Ser Asn Pro Pro Ser
190 195 200

atg gtg gca gcg ggg agc gtg gtg gcc gca gtg caa ggc ctg aac ctg 795
Met Val Ala Ala Gly Ser Val Val Ala Ala Val Gln Gly Leu Asn Leu
205 210 215

agg agc ccc aac aac ttc ctg tcc tac tac cgc ctc aca cgc ttc ctc 843
Arg Ser Pro Asn Asn Phe Leu Ser Tyr Tyr Arg Leu Thr Arg Phe Leu
220 225 230

tcc aga gtg atc aag tgt gac cca gac tgc ctc cgg gcc tgc cag gag 891
Ser Arg Val Ile Lys Cys Asp Pro Asp Cys Leu Arg Ala Cys Gln Glu
235 240 245

cag atc gaa gcc ctg ctg gag tca agc ctg cgc cag gcc cag cag aac 939
Gln Ile Glu Ala Leu Leu Glu Ser Ser Leu Arg Gln Ala Gln Gln Asn
250 255 260 265

atg gac ccc aag gcc gcc gag gag gag gaa gag gag gag gag gag gtg 987
Met Asp Pro Lys Ala Ala Glu Glu Glu Glu Glu Glu Glu Glu Glu Val
270 275 280

gac ctg gct tgc aca ccc acc gac gtg cgg gac gtg gac atc 1029
Asp Leu Ala Cys Thr Pro Thr Asp Val Arg Asp Val Asp Ile
285 290 295

tgagggggccc aggcaggcgg gcgccaccgc caccgcagc gagggcggag ccggccccag 1089

gtgtccacaca tgacagtccc tcctctccgg agcattttga taccagaagg gaaagcttca 1149

ttctccttgt tgttggttgt ttttctctt gctctttccc ccttccatct ctgacttaag 1209

caaaagaaaa agattacca aaaactgtct ttaaagaga gagagag 1256

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<210> 11

<211> 2121

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (559) .. (1875)

<400> 11

ctgctcgagg ccgccaccgc cgggccccgg ccgtccctgg ctcccctcct gcctcgagaa 60

gggcagggct tctcagaggc ttggcgggaa aaaagaacgg agggagggat cgcgctgagt 120

ataaaagccg gttttcgggg ctttatctaa ctgcgtgtag taattccagc gagaggcaga 180

21/88

```

gggagcgagc gggcgggccgg ctagggtgga agagccgggc gagcagagct gcgctgcggg 240
cgtcctggga agggagatcc ggagcgaata gggggcttcg cctctggccc agccctcccg 300
cttgatcccc caggccagcg gtccgcaacc cttgccgcat ccacgaaact ttgcccatag 360
cagcggggcgg gcactttgca ctggaactta caacacccga gcaaggacgc gactctcccg 420
acgcgggggag gctattctgc ccatttgggg acacttcccc gccgctgcca ggacccgctt 480
ctctgaaagg ctctccttgc agctgcttag acgctggatt ttttctgggt agtggaatac 540

cagcagcctc ccgcgacg atg ccc ctc aac gtt agc ttc acc aac agg aac 591
                Met Pro Leu Asn Val Ser Phe Thr Asn Arg Asn
                  1             5             10

tat gac ctc gac tac gac tcg gtg cag ccg tat ttc tac tgc gac gag 639
Tyr Asp Leu Asp Tyr Asp Ser Val Gln Pro Tyr Phe Tyr Cys Asp Glu
                15             20             25

gag gag aac ttc tac cag cag cag cag cag agc gag ctg cag ccc ccg 687
Glu Glu Asn Phe Tyr Gln Gln Gln Gln Gln Ser Glu Leu Gln Pro Pro
                30             35             40

gcg ccc agc gag gat atc tgg aag aaa ttc gag ctg ctg ccc acc ccg 735
Ala Pro Ser Glu Asp Ile Trp Lys Lys Phe Glu Leu Leu Pro Thr Pro
                45             50             55

ccc ctg tcc cct agc cgc cgc tcc ggg ctc tgc tcg ccc tcc tac gtt 783
Pro Leu Ser Pro Ser Arg Arg Ser Gly Leu Cys Ser Pro Ser Tyr Val
                60             65             70             75

gcg gtc aca ccc ttc tcc ctt cgg gga gac aac gac ggc ggt ggc ggg 831
Ala Val Thr Pro Phe Ser Leu Arg Gly Asp Asn Asp Gly Gly Gly Gly
                80             85             90

agc ttc tcc acg gcc gac cag ctg gag atg gtg acc gag ctg ctg gga 879
Ser Phe Ser Thr Ala Asp Gln Leu Glu Met Val Thr Glu Leu Leu Gly
                95             100             105

gga gac atg gtg aac cag agt ttc atc tgc gac ccg gac gac gag acc 927
Gly Asp Met Val Asn Gln Ser Phe Ile Cys Asp Pro Asp Asp Glu Thr
                110             115             120

ttc atc aaa aac atc atc atc cag gac tgt atg tgg agc ggc ttc tcg 975
Phe Ile Lys Asn Ile Ile Ile Gln Asp Cys Met Trp Ser Gly Phe Ser
                125             130             135

gcc gcc gcc aag ctc gtc tca gag aag ctg gcc tcc tac cag gct gcg 1023
Ala Ala Ala Lys Leu Val Ser Glu Lys Leu Ala Ser Tyr Gln Ala Ala
                140             145             150             155

cgc aaa gac agc ggc agc ccg aac ccc gcc cgc ggc cac agc gtc tgc 1071
Arg Lys Asp Ser Gly Ser Pro Asn Pro Ala Arg Gly His Ser Val Cys
                160             165             170

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tcc acc tcc agc ttg tac ctg cag gat ctg agc gcc gcc gcc tca gag	1119
Ser Thr Ser Ser Leu Tyr Leu Gln Asp Leu Ser Ala Ala Ala Ser Glu	
175 180 185	
tgc atc gac ccc tcg gtg gtc ttc ccc tac cct ctc aac gac agc agc	1167
Cys Ile Asp Pro Ser Val Val Phe Pro Tyr Pro Leu Asn Asp Ser Ser	
190 195 200	
tcg ccc aag tcc tgc gcc tcg caa gac tcc agc gcc ttc tct ccg tcc	1215
Ser Pro Lys Ser Cys Ala Ser Gln Asp Ser Ser Ala Phe Ser Pro Ser	
205 210 215	
tcg gat tct ctg ctc tcc tcg acg gag tcc tcc ccg cag ggc agc ccc	1263
Ser Asp Ser Leu Leu Ser Ser Thr Glu Ser Ser Pro Gln Gly Ser Pro	
220 225 230 235	
gag ccc ctg gtg ctc cat gag gag aca ccg ccc acc acc agc agc gac	1311
Glu Pro Leu Val Leu His Glu Glu Thr Pro Pro Thr Thr Ser Ser Asp	
240 245 250	
tct gag gag gaa caa gaa gat gag gaa gaa atc gat gtt gtt tct gtg	1359
Ser Glu Glu Glu Gln Glu Asp Glu Glu Glu Ile Asp Val Val Ser Val	
255 260 265	
gaa aag agg cag gct cct ggc aaa agg tca gag tct gga tca cct tct	1407
Glu Lys Arg Gln Ala Pro Gly Lys Arg Ser Glu Ser Gly Ser Pro Ser	
270 275 280	
gct gga ggc cac agc aaa cct cct cac agc cca ctg gtc ctc aag agg	1455
Ala Gly Gly His Ser Lys Pro Pro His Ser Pro Leu Val Leu Lys Arg	
285 290 295	
tgc cac gtc tcc aca cat cag cac aac tac gca gcg cct ccc tcc act	1503
Cys His Val Ser Thr His Gln His Asn Tyr Ala Ala Pro Pro Ser Thr	
300 305 310 315	
cgg aag gac tat cct gct gcc aag agg gtc aag ttg gac agt gtc aga	1551
Arg Lys Asp Tyr Pro Ala Ala Lys Arg Val Lys Leu Asp Ser Val Arg	
320 325 330	
gtc ctg aga cag atc agc aac aac cga aaa tgc acc agc ccc agg tcc	1599
Val Leu Arg Gln Ile Ser Asn Asn Arg Lys Cys Thr Ser Pro Arg Ser	
335 340 345	
tcg gac acc gag gag aat gtc aag agg cga aca cac aac gtc ttg gag	1647
Ser Asp Thr Glu Glu Asn Val Lys Arg Arg Thr His Asn Val Leu Glu	
350 355 360	
cgc cag agg agg aac gag cta aaa cgg agc ttt ttt gcc ctg cgt gac	1695
Arg Gln Arg Arg Asn Glu Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp	
365 370 375	
cag atc ccg gag ttg gaa aac aat gaa aag gcc ccc aag gta gtt atc	1743
Gln Ile Pro Glu Leu Glu Asn Asn Glu Lys Ala Pro Lys Val Val Ile	
380 385 390 395	

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ctt aaa aaa gcc aca gca tac atc ctg tcc gtc caa gca gag gag caa 1791
 Leu Lys Lys Ala Thr Ala Tyr Ile Leu Ser Val Gln Ala Glu Glu Gln
 400 405 410

aag ctc att tct gaa gag gac ttg ttg cgg aaa cga cga gaa cag ttg 1839
 Lys Leu Ile Ser Glu Glu Asp Leu Leu Arg Lys Arg Arg Glu Gln Leu
 415 420 425

aaa cac aaa ctt gaa cag cta cgg aac tct tgt gcg taaggaaaag 1885
 Lys His Lys Leu Glu Gln Leu Arg Asn Ser Cys Ala
 430 435

taaggaaaac gattccttct aacagaaatg tcctgagcaa tcacctatga acttgtttca 1945

aatgcatgat caaatgcaac ctcaaacct tggctgagtc ttgagactga aagatttagc 2005

cataatgtaa actgcctcaa attggacttt gggcataaaa gaactttttt atgcttacca 2065

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<210> 12

<211> 2098

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (79) .. (570)

<400> 12

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gcactcagag gaggcgcc atg tca gaa ccg gct ggg gat gtc cgt cag aac 111
 Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn
 1 5 10

cca tgc ggc agc aag gcc tgc cgc cgc ctc ttc ggc cca gtg gac agc 159
 Pro Cys Gly Ser Lys Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser
 15 20 25

gag cag ctg agc cgc gac tgt gat gcg cta atg gcg ggc tgc atc cag 207
 Glu Gln Leu Ser Arg Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln
 30 35 40

gag gcc cgt gag cga tgg aac ttc gac ttt gtc acc gag aca cca ctg 255
 Glu Ala Arg Glu Arg Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu
 45 50 55

gag ggt gac ttc gcc tgg gag cgt gtg cgg ggc ctt ggc ctg ccc aag 303
 Glu Gly Asp Phe Ala Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys
 60 65 70 75

ctc tac ctt ccc acg ggg ccc cgg cga ggc cgg gat gag ttg gga gga 351
 Leu Tyr Leu Pro Thr Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly
 80 85 90

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ggc agg cgg cct ggc acc tca cct gct ctg ctg cag ggg aca gca gag 399
 Gly Arg Arg Pro Gly Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu
 95 100 105

gaa gac cat gtg gac ctg tca ctg tct tgt acc ctt gtg cct cgc tca 447
 Glu Asp His Val Asp Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser
 110 115 120

ggg gag cag gct gaa ggg tcc cca ggt gga cct gga gac tct cag ggt 495
 Gly Glu Gln Ala Glu Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly
 125 130 135

cga aaa cgg cgg cag acc agc atg aca gat ttc tac cac tcc aaa cgc 543
 Arg Lys Arg Arg Gln Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg
 140 145 150 155

cgg ctg atc ttc tcc aag agg aag ccc taatccgccc acaggaagcc 590
 Arg Leu Ile Phe Ser Lys Arg Lys Pro
 160

tgcagtctctg gaagcgcgag ggccctcaaag gcccgctcta catcttctgc cttagtctca 650
 gtttgtgtgt cttaattatt atttgtgttt taatttaaac acctcctcat gtacataccc 710
 tggccgcccc ctgcccccca gcctctggca ttagaattat ttaaacaaaa actaggcggg 770
 tgaatgagag gttcctaaga gtgctgggca tttttatttt atgaaatact atttaaagcc 830
 tcctcatccc gtgttctcct tttcctctct cccggagggt ggggtggccg gcttcatgcc 890
 agctacttcc tcctccccac ttgtccgctg ggtggtaccc tctggagggg tgtggctcct 950
 tcccatcgct gtcacaggcg gttatgaaat tcacccctt tcctggacac tcagacctga 1010
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 catcatcaaa aactttggag tcccctcacc tcctctaagg ttgggcaggg tgacctgaa 1130
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 ggctctgagg tgctgtccc acccccaccc ccagctcaat ggactggaag ggggaaggac 1490
 acacaagaag aagggcaccc tagttctacc tcaggcagct caagcagcga ccgccccctc 1550
 ctctagctgt gggggtgagg gtcccatgtg gtggcacagg ccccttgag tggggttata 1610
 tctgtgttag gggatatga tgggggagta gatctttcta ggaggagac actggcccct 1670
 caaatcgtec agcgacctc ctcateccacc ccatccctcc ccagttcatt gcactttgat 1730

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tagcagcggg	acaaggagtc	agacatttta	agatggtggc	agtagaggct	atggacaggg	1790
catgccacgt	gggctcatat	ggggctggga	gtagttgtct	ttcctggcac	taacgttgag	1850
cccctggagg	cactgaagtg	cttagtgtac	ttggagtatt	ggggtctgac	cccaaacacc	1910
ttccagctcc	tgtaacatac	tggcctggac	tgttttctct	eggctcccca	tgtgtcctgg	1970
ttcccgtttc	tccacctaga	ctgtaaacct	ctcgagggca	gggaccacac	cctgtactgt	2030
tctgtgtctt	tcacagctcc	tcccacaatg	ctgatataca	gcaggtgctc	aataaacgat	2090
tcttagtg						2098

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<210> 13
<211> 827
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (256) .. (570)
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tggtgcgcag	gttcttggtg	accctccgga	ttcggcgcgc	gtgcggcccc	ccgcgagtga	120												
gggttttcgt	ggttcacatc	tcgtggttca	cgggggagtg	ggcagcgcca	ggggcgcccc	180												
ccgctgtggc	cctcgtgctg	atgctactga	ggagccagcg	tctagggcag	cagccgcttc	240												
ctagaagacc	aggtc	atg	atg	atg	ggc	agc	gcc	cga	gtg	gcg	gag	ctg	ctg	291				
	Met	Met	Met	Gly	Ser	Ala	Arg	Val	Ala	Glu	Leu	Leu						
	1				5						10							
ctg	ctc	cac	ggc	gcg	gag	ccc	aac	tgc	gcc	gac	ccc	gcc	act	ctc	acc	339		
Leu	Leu	His	Gly	Ala	Glu	Pro	Asn	Cys	Ala	Asp	Pro	Ala	Thr	Leu	Thr			
		15					20					25						
cga	ccc	gtg	cac	gac	gct	gcc	cgg	gag	ggc	ttc	ctg	gac	acg	ctg	gtg	387		
Arg	Pro	Val	His	Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val			
		30				35					40							
gtg	ctg	cac	cgg	gcc	ggg	gcg	cgg	ctg	gac	gtg	cgc	gat	gcc	tgg	ggc	435		
Val	Leu	His	Arg	Ala	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly			
45					50					55					60			
cgt	ctg	ccc	gtg	gac	ctg	gct	gag	gag	ctg	ggc	cat	cgc	gat	gtc	gca	483		
Arg	Leu	Pro	Val	Asp	Leu	Ala	Glu	Glu	Leu	Gly	His	Arg	Asp	Val	Ala			
				65					70					75				
cgg	tac	ctg	cgc	gcg	gct	gcg	ggg	ggc	acc	aga	ggc	agt	aac	cat	gcc	531		
Arg	Tyr	Leu	Arg	Ala	Ala	Ala	Gly	Gly	Thr	Arg	Gly	Ser	Asn	His	Ala			
			80					85					90					

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cgc ata gat gcc gcg gaa ggt ccc tca gac atc ccc gat tgaaagaacc 580
Arg Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
      95              100              105

agagaggctc tgagaaacct ccggaacctt agatcatcag tcaccgaagg tcctacaggg 640

ccacaactgc ccccgccaca acccaccctc ctttcgtagt tttcatttag aaaatagagc 700

ttttaaaaat gtccctgcctt ttaacgtaga tatatgcctt cccccactac cgtaaatgtc 760

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aaaaaaaaa 827

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<210> 14
 <211> 1275
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (163) .. (681)

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gatcttggag gtccgggtgg gagtgggggt ggggtggggg tgggggtgaa ggtggggggc 120

gggcgcgctc agggaaggcg ggtgcgcgcc tgcggggcgg ag atg ggc agg ggg 174
                               Met Gly Arg Gly
                               1

cgg tgc gtg ggt ccc agt ctg cag tta agg ggg cag gag tgg cgc tgc 222
Arg Cys Val Gly Pro Ser Leu Gln Leu Arg Gly Gln Glu Trp Arg Cys
      5              10              15              20

tca cct ctg gtg cca aag ggc ggc gca gcg gct gcc gag ctg ggc cct 270
Ser Pro Leu Val Pro Lys Gly Gly Ala Ala Ala Glu Leu Gly Pro
      25              30              35

gga ggc ggc gag aac atg gtg cgc agg ttc ttg gtg acc ctg cgg att 318
Gly Gly Gly Glu Asn Met Val Arg Arg Phe Leu Val Thr Leu Arg Ile
      40              45              50

cgg cgc gcg tgc ggc ccg ccg cga gtg agg gtt ttc gtg gtt cac atc 366
Arg Arg Ala Cys Gly Pro Pro Arg Val Arg Val Phe Val Val His Ile
      55              60              65

ccg cgg ctg acg ggg gag tgg gca gcg cca ggg gcg ccc gcc gct gtg 414
Pro Arg Leu Thr Gly Glu Trp Ala Ala Pro Gly Ala Pro Ala Ala Val
      70              75              80

gcc ctg gtg ctg atg cta ctg agg agc cag cgt cta ggg cag cag ccg 462
Ala Leu Val Leu Met Leu Leu Arg Ser Gln Arg Leu Gly Gln Gln Pro
      85              90              95              100

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ctt cct aga aga cca ggt cat gat gat ggg cag cgc ccg agt ggc gga 510
Leu Pro Arg Arg Pro Gly His Asp Asp Gly Gln Arg Pro Ser Gly Gly
      105                      110                      115

gct gct gct gct cca cgg cgc gga gcc caa ctg cgc cga ccc cgc cac 558
Ala Ala Ala Ala Pro Arg Arg Gly Ala Gln Leu Arg Arg Pro Arg His
      120                      125                      130

tct cac ccg acc cgt gca cga cgc tgc ccg gga ggg ctt cct gga cac 606
Ser His Pro Thr Arg Ala Arg Arg Cys Pro Gly Gly Leu Pro Gly His
      135                      140                      145

gct ggt ggt gct gca ccg ggc cgg ggc gcg gct gga cgt gcg cga tgc 654
Ala Gly Gly Ala Ala Pro Gly Arg Gly Ala Ala Gly Arg Ala Arg Cys
      150                      155                      160

ctg ggg ccg tct gcc cgt gga cct ggc tgaggagctg ggccatcgcg 701
Leu Gly Pro Ser Ala Arg Gly Pro Gly
165                      170

atgtcgcacg gtacctgcgc gcggctgcgg ggggcaccag aggcagtaac catgcccgcga 761

tagatgccgc ggaagggtccc tcagacatcc ccgattgaaa gaaccagaga ggctctgaga 821

aacctcggga aacttagatc atcagtcacc gaaggctccta cagggccaca actgcccccg 881

ccacaacca ccccgctttc gtagttttca tttagaaaat agagctttta aaaatgtcct 941

gcctttttaac gtagatatat gccttcccc actaccgtaa atgtccattht atatcatttt 1001

ttatatattc ttataaaaat gtaaaaaaga aaaacaccgc ttctgccttt tcactgtgtt 1061

ggagttttct ggagtgcgca ctacgcctt aagcgcacat tcatgtgggc atttcttgcg 1121

agcctcgcag cctccggaag ctgtcgactt catgacaagc attttgtgaa ctagggaagc 1181

tcaggggggt tactggcttc tcttgagtca cactgctagc aaatggcaga accaaagctc 1241

aaataaaaat aaaataattt tcattcattc actc 1275

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<210> 15

<211> 1850

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (213)..(1616)

<400> 15

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aagctcagaa ctgagaagct gtcaccacag ttctggaggc tgggaagttc aagatcaaag 120

tgccagcaga ttcagtgtca tgtgaggacg tgcttcctgc ttcataagata agagcttgga 180

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gctcggcgca caaccagcac catctggtcg cg atg gtg gac acg gaa agc cca	233
Met Val Asp Thr Glu Ser Pro	
1 5	
ctc tgc ccc ctc tcc cca ctc gag gcc ggc gat cta gag agc ccg tta	281
Leu Cys Pro Leu Ser Pro Leu Glu Ala Gly Asp Leu Glu Ser Pro Leu	
10 15 20	
tct gaa gag ttc ctg caa gaa atg gga aac atc caa gag att tcg caa	329
Ser Glu Glu Phe Leu Gln Glu Met Gly Asn Ile Gln Glu Ile Ser Gln	
25 30 35	
tcc atc ggc gag gat agt tct gga agc ttt ggc ttt acg gaa tac cag	377
Ser Ile Gly Glu Asp Ser Ser Gly Ser Phe Gly Phe Thr Glu Tyr Gln	
40 45 50 55	
tat tta gga agc tgt cct ggc tca gat ggc tcg gtc atc acg gac acg	425
Tyr Leu Gly Ser Cys Pro Gly Ser Asp Gly Ser Val Ile Thr Asp Thr	
60 65 70	
ctt tca cca gct tcg agc ccc tcc tcg gtg act tat cct gtg gtc ccc	473
Leu Ser Pro Ala Ser Ser Pro Ser Ser Val Thr Tyr Pro Val Val Pro	
75 80 85	
ggc agc gtg gac gag tct ccc agt gga gca ttg aac atc gaa tgt aga	521
Gly Ser Val Asp Glu Ser Pro Ser Gly Ala Leu Asn Ile Glu Cys Arg	
90 95 100	
atc tgc ggc gac aag gcc tca ggc tat cat tac gga gtc cac gcg tgt	569
Ile Cys Gly Asp Lys Ala Ser Gly Tyr His Tyr Gly Val His Ala Cys	
105 110 115	
gaa ggc tgc aag ggc ttc ttt cgg cga acg att cga ctc aag ctg gtg	617
Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Val	
120 125 130 135	
tat gac aag tgc gac cgc agc tgc aag atc cag aaa aag aac aga aac	665
Tyr Asp Lys Cys Asp Arg Ser Cys Lys Ile Gln Lys Lys Asn Arg Asn	
140 145 150	
aaa tgc cag tat tgt cga ttt cac aag tgc ctt tct gtc ggg atg tca	713
Lys Cys Gln Tyr Cys Arg Phe His Lys Cys Leu Ser Val Gly Met Ser	
155 160 165	
cac aac gcg att cgt ttt gga cga atg cca aga tct gag aaa gca aaa	761
His Asn Ala Ile Arg Phe Gly Arg Met Pro Arg Ser Glu Lys Ala Lys	
170 175 180	
ctg aaa gca gaa att ctt acc tgt gaa cat gac ata gaa gat tct gaa	809
Leu Lys Ala Glu Ile Leu Thr Cys Glu His Asp Ile Glu Asp Ser Glu	
185 190 195	
act gca gat ctc aaa tct ctg gcc aag aga atc tac gag gcc tac ttg	857
Thr Ala Asp Leu Lys Ser Leu Ala Lys Arg Ile Tyr Glu Ala Tyr Leu	
200 205 210 215	

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aag aac ttc aac atg aac aag gtc aaa gcc cgg gtc atc ctc tca gga	905
Lys Asn Phe Asn Met Asn Lys Val Lys Ala Arg Val Ile Leu Ser Gly	
220 225 230	
aag gcc agt aac aat cca cct ttt gtc ata cat gat atg gag aca ctg	953
Lys Ala Ser Asn Asn Pro Pro Phe Val Ile His Asp Met Glu Thr Leu	
235 240 245	
tgt atg gct gag aag acg ctg gtg gcc aag ctg gtg gcc aat ggc atc	1001
Cys Met Ala Glu Lys Thr Leu Val Ala Lys Leu Val Ala Asn Gly Ile	
250 255 260	
cag aac aag gag gcg gag gtc cgc atc ttt cac tgc tgc cag tgc acg	1049
Gln Asn Lys Glu Ala Glu Val Arg Ile Phe His Cys Cys Gln Cys Thr	
265 270 275	
tca gtg gag acc gtc acg gag ctc acg gaa ttc gcc aag gcc atc cca	1097
Ser Val Glu Thr Val Thr Glu Leu Thr Glu Phe Ala Lys Ala Ile Pro	
280 285 290 295	
ggc ttc gca aac ttg gac ctg aac gat caa gtg aca ttg cta aaa tac	1145
Gly Phe Ala Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr	
300 305 310	
gga gtt tat gag gcc ata ttc gcc atg ctg tct tct gtg atg aac aaa	1193
Gly Val Tyr Glu Ala Ile Phe Ala Met Leu Ser Ser Val Met Asn Lys	
315 320 325	
gac ggg atg ctg gta gcg tat gga aat ggg ttt ata act cgt gaa ttc	1241
Asp Gly Met Leu Val Ala Tyr Gly Asn Gly Phe Ile Thr Arg Glu Phe	
330 335 340	
cta aaa agc cta agg aaa ccg ttc tgt gat atc atg gaa ccc aag ttt	1289
Leu Lys Ser Leu Arg Lys Pro Phe Cys Asp Ile Met Glu Pro Lys Phe	
345 350 355	
gat ttt gcc atg aag ttc aat gca ctg gaa ctg gat gac agt gat atc	1337
Asp Phe Ala Met Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Ile	
360 365 370 375	
tcc ctt ttt gtg gct gct atc att tgc tgt gga gat cgt cct ggc ctt	1385
Ser Leu Phe Val Ala Ala Ile Ile Cys Cys Gly Asp Arg Pro Gly Leu	
380 385 390	
cta aac gta gga cac att gaa aaa atg cag gag ggt att gta cat gtg	1433
Leu Asn Val Gly His Ile Glu Lys Met Gln Glu Gly Ile Val His Val	
395 400 405	
ctc aga ctc cac ctg cag agc aac cac ccg gac gat atc ttt ctc ttc	1481
Leu Arg Leu His Leu Gln Ser Asn His Pro Asp Asp Ile Phe Leu Phe	
410 415 420	
cca aaa ctt ctt caa aaa atg gca gac ctc cgg cag ctg gtg acg gag	1529
Pro Lys Leu Leu Gln Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu	
425 430 435	

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cat gcg cag ctg gtg cag atc atc aag aag acg gag tcg gat gct gcg 1577
 His Ala Gln Leu Val Gln Ile Ile Lys Lys Thr Glu Ser Asp Ala Ala
 440 445 450 455

ctg cac ccg cta ctg cag gag atc tac agg gac atg tac tgagttcctt 1626
 Leu His Pro Leu Leu Gln Glu Ile Tyr Arg Asp Met Tyr
 460 465

cagatcagcc acaccttttc caggagttct gaagctgaca gcactacaaa ggagacgggg 1686

gagcagcacg attttgcaca aatatccacc actttaacct tagagcttgg acagtctgag 1746

ctgtaggtaa ccggcatatt attccatatac tttgttttaa ccagtacttc taagagcata 1806

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<210> 16

<211> 1609

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (92)..(1606)

<400> 16

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gaattacagc aaacccttat tccatgctgt t atg ggt gaa act ctg gga gat 112
 Met Gly Glu Thr Leu Gly Asp
 1 5

tct cct att gac cca gaa agc gat tcc ttc act gat aca ctg tct gca 160
 Ser Pro Ile Asp Pro Glu Ser Asp Ser Phe Thr Asp Thr Leu Ser Ala
 10 15 20

aac ata tca caa gaa atg acc atg gtt gac aca gag atg cca ttc tgg 208
 Asn Ile Ser Gln Glu Met Thr Met Val Asp Thr Glu Met Pro Phe Trp
 25 30 35

ccc acc aac ttt ggg atc agc tcc gtg gat ctc tcc gta atg gaa gac 256
 Pro Thr Asn Phe Gly Ile Ser Ser Val Asp Leu Ser Val Met Glu Asp
 40 45 50 55

cac tcc cac tcc ttt gat atc aag ccc ttc act act gtt gac ttc tcc 304
 His Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr Val Asp Phe Ser
 60 65 70

agc att tct act cca cat tac gaa gac att cca ttc aca aga aca gat 352
 Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe Thr Arg Thr Asp
 75 80 85

cca gtg gtt gca gat tac aag tat gac ctg aaa ctt caa gag tac caa 400
 Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu Gln Glu Tyr Gln
 90 95 100

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agt gca atc aaa gtg gag cct gca tct cca cct tat tat tct gag aag	448
Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr Tyr Ser Glu Lys	
105 110 115	
act cag ctc tac aat aag cct cat gaa gag cct tcc aac tcc ctc atg	496
Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser Asn Ser Leu Met	
120 125 130 135	
gca att gaa tgt cgt gtc tgt gga gat aaa gct tct gga ttt cac tat	544
Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr	
140 145 150	
gga gtt cat gct tgt gaa gga tgc aag ggt ttc ttc cgg aga aca atc	592
Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile	
155 160 165	
aga ttg aag ctt atc tat gac aga tgt gat ctt aac tgt cgg atc cac	640
Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp Leu Asn Cys Arg Ile His	
170 175 180	
aaa aaa agt aga aat aaa tgt cag tac tgt cgg ttt cag aaa tgc ctt	688
Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu	
185 190 195	
gca gtg ggg atg tct cat aat gcc atc agg ttt ggg cgg atg cca cag	736
Ala Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Gln	
200 205 210 215	
gcc gag aag gag aag ctg ttg gcg gag atc tcc agt gat atc gac cag	784
Ala Glu Lys Glu Lys Leu Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln	
220 225 230	
ctg aat cca gag tcc gct gac ctc cgg gcc ctg gca aaa cat ttg tat	832
Leu Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr	
235 240 245	
gac tca tac ata aag tcc ttc ccg ctg acc aaa gca aag gcg agg gcg	880
Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala	
250 255 260	
atc ttg aca gga aag aca aca gac aaa tca cca ttc gtt atc tat gac	928
Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp	
265 270 275	
atg aat tcc tta atg atg gga gaa gat aaa atc aag ttc aaa cac atc	976
Met Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile	
280 285 290 295	
acc ccc ctg cag gag cag agc aaa gag gtg gcc atc cgc atc ttt cag	1024
Thr Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln	
300 305 310	
ggc tgc cag ttt cgc tcc gtg gag gct gtg cag gag atc aca gag tat	1072
Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr	
315 320 325	

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gcc aaa agc att cct ggt ttt gta aat ctt gac ttg aac gac caa gta 1120
Ala Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val
      330                      335                      340

act ctc ctc aaa tat gga gtc cac gag atc att tac aca atg ctg gcc 1168
Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala
      345                      350                      355

tcc ttg atg aat aaa gat ggg gtt ctc ata tcc gag ggc caa ggc ttc 1216
Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe
      360                      365                      370                      375

atg aca agg gag ttt cta aag agc ctg cga aag cct ttt ggt gac ttt 1264
Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe
      380                      385                      390

atg gag ccc aag ttt gag ttt gct gtg aag ttc aat gca ctg gaa tta 1312
Met Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu
      395                      400                      405

gat gac agc gac ttg gca ata ttt att gct gtc att att ctc agt gga 1360
Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly
      410                      415                      420

gac cgc cca ggt ttg ctg aat gtg aag ccc att gaa gac att caa gac 1408
Asp Arg Pro Gly Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp
      425                      430                      435

aac ctg cta caa gcc ctg gag ctc cag ctg aag ctg aac cac cct gag 1456
Asn Leu Leu Gln Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu
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tcc tca cag ctg ttt gcc aag ctg ctc cag aaa atg aca gac ctc aga 1504
Ser Ser Gln Leu Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg
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cag att gtc acg gaa cac gtg cag cta ctg cag gtg atc aag aag acg 1552
Gln Ile Val Thr Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr
      475                      480                      485

gag aca gac atg agt ctt cac ccg ctc ctg cag gag atc tac aag gac 1600
Glu Thr Asp Met Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp
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Leu Tyr
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33/88

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gaa gcc cct gag gtc cgg gaa gag gag gag aaa gag gaa gtg gca gag 403
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ctg gac caa ctg cag atg ggc tgt gac ggg gcc tca tgc ggc agc ctc 547
Leu Asp Gln Leu Gln Met Gly Cys Asp Gly Ala Ser Cys Gly Ser Leu
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aac atg gag tgc cgg gtg tgc ggg gac aag gca tgc ggc ttc cac tac 595
Asn Met Glu Cys Arg Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr
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ggc gtt cat gca tgt gag ggg tgc aag ggc ttc ttc cgt cgt acg atc 643
Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile
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cgc atg aag ctg gag tac gag aag tgt gag cgc agc tgc aag att cag 691
Arg Met Lys Leu Glu Tyr Glu Lys Cys Glu Arg Ser Cys Lys Ile Gln
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aag aag aac cgc aac aag tgc cag tac tgc cgc ttc cag aag tgc ctg 739
Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu
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gca ctg ggc atg tca cac aac gct atc cgt ttt ggt cgg atg ccg gag 787
Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Glu
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Gln Tyr Asn Pro Gln Val Ala Asp Leu Lys Ala Phe Ser Lys His Ile	
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Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met Thr Lys Lys Lys Ala Arg	
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agc atc ctc acc ggc aaa gcc agc cac acg gcg ccc ttt gtg atc cac	979
Ser Ile Leu Thr Gly Lys Ala Ser His Thr Ala Pro Phe Val Ile His	
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Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys Gly Leu Val Trp Lys Gln	
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Leu Val Asn Gly Leu Pro Pro Tyr Lys Glu Ile Ser Val His Val Phe	
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tac cgc tgc cag tgc acc aca gtg gag acc gtg cgg gag ctc act gag	1123
Tyr Arg Cys Gln Cys Thr Thr Val Glu Thr Val Arg Glu Leu Thr Glu	
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Phe Ala Lys Ser Ile Pro Ser Phe Ser Ser Leu Phe Leu Asn Asp Gln	
265 270 275	
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Val Thr Leu Leu Lys Tyr Gly Val His Glu Ala Ile Phe Ala Met Leu	
280 285 290	
gcc tct atc gtc aac aag gac ggg ctg ctg gta gcc aac ggc agt ggc	1267
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Phe Val Thr Arg Glu Phe Leu Arg Ser Leu Arg Lys Pro Phe Ser Asp	
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atc att gag cct aag ttt gaa ttt gct gtc aag ttc aac gcc ctg gaa	1363
Ile Ile Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu	
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ctt gat gac agt gac ctg gcc cta ttc att gcg gcc atc att ctg tgt	1411
Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile Ala Ala Ile Ile Leu Cys	
345 350 355	
gga gac cgg cca ggc ctc atg aac gtt cca cgg gtg gag gct atc cag	1459
Gly Asp Arg Pro Gly Leu Met Asn Val Pro Arg Val Glu Ala Ile Gln	
360 365 370	

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gac acc atc ctg cgt gcc ctc gaa ttc cac ctg cag gcc aac cac cct 1507
 Asp Thr Ile Leu Arg Ala Leu Glu Phe His Leu Gln Ala Asn His Pro
 375 380 385 390

gat gcc cag tac ctc ttc ccc aag ctg ctg cag aag atg gct gac ctg 1555
 Asp Ala Gln Tyr Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp Leu
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cgg caa ctg gtc acc gag cac gcc cag atg atg cag cgg atc aag aag 1603
 Arg Gln Leu Val Thr Glu His Ala Gln Met Met Gln Arg Ile Lys Lys
 410 415 420

acc gaa acc gag acc tcg ctg cac cct ctg ctc cag gag atc tac aag 1651
 Thr Glu Thr Glu Thr Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys
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 Asp Met Tyr
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Met Asp Lys Phe Trp																
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Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu Ser Leu Ala Gln																
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Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val Phe His Val Glu																
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Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala Ala Asp Leu Cys																
40 45 50																
aag gct ttc aat agc acc ttg ccc aca atg gcc cag atg gag aaa gct																368
Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln Met Glu Lys Ala																
55 60 65																
ctg agc atc gga ttt gag acc tgc agg tat ggg ttc ata gaa ggg cac																416
Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe Ile Glu Gly His																
70 75 80 85																

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Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys Ala Ala Asn Asn	
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aca ggg gtg tac atc ctc aca tcc aac acc tcc cag tat gac aca tat	512
Thr Gly Val Tyr Ile Leu Thr Ser Asn Thr Ser Gln Tyr Asp Thr Tyr	
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Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys Thr Ser Val Thr	
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Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile Thr Ile Val Asn	
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150 155 160 165	
gaa gac atc tac ccc agc aac cct act gat gat gac gtg agc agc ggc	704
Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp Val Ser Ser Gly	
170 175 180	
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Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr Ile Phe Tyr Thr	
185 190 195	
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Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser Pro Trp Ile Thr	
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Ser Trp Leu Phe Leu Pro Ser Glu Ser Lys Asn His Leu His Thr Thr	
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265 270 275	
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Pro Asn Glu Glu Asn Glu Asp Glu Arg Asp Arg His Leu Ser Phe Ser	
280 285 290	
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Gly Ser Gly Ile Asp Asp Asp Glu Asp Phe Ile Ser Ser Thr Ile Ser	
295 300 305	

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Phe Asn Pro Ile Ser His Pro Met Gly Arg Gly His Gln Ala Gly Arg	
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agg atg gat atg gac tcc agt cat agt ata acg ctt cag cct act gca	1616
Arg Met Asp Met Asp Ser Ser His Ser Ile Thr Leu Gln Pro Thr Ala	
470 475 480 485	
aat cca aac aca ggt ttg gtg gaa gat ttg gac agg aca gga cct ctt	1664
Asn Pro Asn Thr Gly Leu Val Glu Asp Leu Asp Arg Thr Gly Pro Leu	
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tca atg aca acg cag cag agt aat tct cag agc ttc tct aca tca cat	1712
Ser Met Thr Thr Gln Gln Ser Asn Ser Gln Ser Phe Ser Thr Ser His	
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gaa ggc ttg gaa gaa gat aaa gac cat cca aca act tct act ctg aca	1760
Glu Gly Leu Glu Glu Asp Lys Asp His Pro Thr Thr Ser Thr Leu Thr	
520 525 530	

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Ser Ser Asn Arg Asn Asp Val Thr Gly Gly Arg Arg Asp Pro Asn His	
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tct gaa ggc tca act act tta ctg gaa ggt tat acc tct cat tac cca	1856
Ser Glu Gly Ser Thr Thr Leu Leu Glu Gly Tyr Thr Ser His Tyr Pro	
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His Thr Lys Glu Ser Arg Thr Phe Ile Pro Val Thr Ser Ala Lys Thr	
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Gly Ser Phe Gly Val Thr Ala Val Thr Val Gly Asp Ser Asn Ser Asn	
585 590 595	
gtc aat cgt tcc tta tca gga gac caa gac aca ttc cac ccc agt ggg	2000
Val Asn Arg Ser Leu Ser Gly Asp Gln Asp Thr Phe His Pro Ser Gly	
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Ser Gln Glu Gly Gly Ala Asn Thr Thr Ser Gly Pro Ile Arg Thr Pro	
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Gln Ile Pro Glu Trp Leu Ile Ile Leu Ala Ser Leu Leu Ala Leu Ala	
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Leu Ile Leu Ala Val Cys Ile Ala Val Asn Ser Arg Arg Arg Cys Gly	
665 670 675	
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Gln Lys Lys Lys Leu Val Ile Asn Ser Gly Asn Gly Ala Val Glu Asp	
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Arg Lys Pro Ser Gly Leu Asn Gly Glu Ala Ser Lys Ser Gln Glu Met	
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Val His Leu Val Asn Lys Glu Ser Ser Glu Thr Pro Asp Gln Phe Met	
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Thr Ala Asp Glu Thr Arg Asn Leu Gln Asn Val Asp Met Lys Ile Gly	
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Val	
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<221> CDS

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 Asn Leu Ile Pro Ser Pro Pro Thr Tyr Asn Ser Ala His Asp Tyr Ile
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 Ser Trp Glu Ser Phe Ser Asn Val Ser Tyr Tyr Thr Arg Ile Leu Pro
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 Ser Val Pro Lys Asp Cys Pro Thr Pro Met Gly Thr Lys Gly Lys Lys
 45 50 55

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Lys Phe Ile Pro Asp Pro Gln Gly Thr Asn Leu Met Phe Ala Phe Phe	
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Pro Gly Phe Thr Lys Ala Leu Gly His Gly Val Asp Leu Gly His Ile	
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Gly Lys Leu Lys Tyr Gln Val Leu Asp Gly Glu Met Tyr Pro Pro Ser	
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gag gag tac gtg cag cag ctg agt ggc tat ttc ctg cag ctg aaa ttt	1073
Glu Glu Tyr Val Gln Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe	
240 245 250	
gac cca gag ctg ctg ttc ggt gtc cag ttc caa tac cgc aac cgc att	1121
Asp Pro Glu Leu Leu Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile	
255 260 265	
gcc atg gag ttc aac cat ctc tac cac tgg cac ccc ctc atg cct gac	1169
Ala Met Glu Phe Asn His Leu Tyr His Trp His Pro Leu Met Pro Asp	
270 275 280	

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tcc ttc aag gtg ggc tcc cag gag tac agc tac gag cag ttc ttg ttc	1217
Ser Phe Lys Val Gly Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe	
285 290 295	
aac acc tcc atg ttg gtg gac tat ggg gtt gag gcc ctg gtg gat gcc	1265
Asn Thr Ser Met Leu Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala	
300 305 310 315	
ttc tct cgc cag att gct ggc cgg atc ggt ggg ggc agg aac atg gac	1313
Phe Ser Arg Gln Ile Ala Gly Arg Ile Gly Gly Gly Arg Asn Met Asp	
320 325 330	
cac cac atc ctg cat gtg gct gtg gat gtc atc agg gag tct cgg gag	1361
His His Ile Leu His Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu	
335 340 345	
atg cgg ctg cag ccc ttc aat gag tac cgc aag agg ttt ggc atg aaa	1409
Met Arg Leu Gln Pro Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys	
350 355 360	
ccc tac acc tcc ttc cag gag ctc gta gga gag aag gag atg gca gca	1457
Pro Tyr Thr Ser Phe Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala	
365 370 375	
gag ttg gag gaa ttg tat gga gac att gat gcg ttg gag ttc tac cct	1505
Glu Leu Glu Glu Leu Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro	
380 385 390 395	
gga ctg ctt ctt gaa aag tgc cat cca aac tct atc ttt ggg gag agt	1553
Gly Leu Leu Leu Glu Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser	
400 405 410	
atg ata gag att ggg gct ccc ttt tcc ctc aag ggt ctc cta ggg aat	1601
Met Ile Glu Ile Gly Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn	
415 420 425	
ccc atc tgt tct ccg gag tac tgg aag ccg agc aca ttt ggc ggc gag	1649
Pro Ile Cys Ser Pro Glu Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu	
430 435 440	
gtg ggc ttt aac att gtc aag acg gcc aca ctg aag aag ctg gtc tgc	1697
Val Gly Phe Asn Ile Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys	
445 450 455	
ctc aac acc aag acc tgt ccc tac gtt tcc ttc cgt gtg ccg gat gcc	1745
Leu Asn Thr Lys Thr Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala	
460 465 470 475	
agt cag gat gat ggg cct gct gtg gag cga cca tcc aca gag	1787
Ser Gln Asp Asp Gly Pro Ala Val Glu Arg Pro Ser Thr Glu	
480 485	
ctctgagggg caggaaagca gcattctgga ggggagagct ttgtgcttgt cattccagag	1847
tgctgaggcc agggctgatg gtcttaaagt ctcattttct gggttgccat ggtgagtgtt	1907
ggggttgaca tttagaactt taagtctcac ccattatctg gaatattgtg attctgttta	1967

ttcttccaga	atgctgaact	ccttggttagc	ccttcagatt	gttaggagtg	gttctcattt	2027
ggctctgccag	aatactgggt	tcttagttga	caacctagaa	tgtcagattt	ctgggttgatt	2087
tgtaacacag	tcattctagg	atgtggagct	actgatgaaa	tctgctagaa	agttaggggg	2147
ttctttatttt	gcattccaga	atcttgactt	tctgattggg	gattcaaagt	gttgtgttcc	2207
tggctgatga	tccagaacag	tggctcgtat	cccaaactcg	tcagcatctg	gctgtctaga	2267
atgtggattt	gattcatttt	cctgttcagt	gagatatcat	agagacggag	atcctaaggt	2327
ccaacaagaa	tgcattccct	gaatctgtgc	ctgcactgag	agggcaagga	agtgggggtg	2387
tcttcttggg	acccccacta	agaccctggg	ctgaggatgt	agagagaaca	gggtgggctgt	2447
attcacgcca	ttggttgga	gctaccagag	ctctatcccc	atccaggtct	tgactcatgg	2507
cagctgtttc	tcatgaagct	aataaaattc	gc			2539

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<220>  
<221> CDS  
<222> (232) .. (519)
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<400> 20  
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ggctccaaga aggcattccgc atttgctacc agcggcgggc gcggcgaggc caggccggtc 120  
  
ctcagcgccc agcacccgcg ctccccggcaa cccggagcgc gcaccgcagc cggcgggccga 180  
  
gctcgcgcat cccagccatc actcttccac ctgctcetta gagaagggaa g atg agt 237  
Met Ser  
1  
  
gag tcg agc tCG aag tCC agC caG CCC ttG gcc tCC aag caG gaA aAG 285  
Glu Ser Ser Ser Lys Ser Ser Gln Pro Leu Ala Ser Lys Gln Glu Lys  
5 10 15  
  
gac ggc act gag aag cgG ggC cgG ggC agg CCg CGC aag caG CCT CCg 333  
Asp Gly Thr Glu Lys Arg Gly Arg Gly Arg Pro Arg Lys Gln Pro Pro  
20 25 30  
  
aag gag CCC agC gaA gtG cCA aCa CCT aaG aga CCT CGG ggC CgA cCA 381  
Lys Glu Pro Ser Glu Val Pro Thr Pro Lys Arg Pro Arg Gly Arg Pro  
35 40 45 50  
  
aag gGa agC aaa aAc aaG gGT gCT GCC aaG acc CGG aaa acc acc aCa 429  
Lys Gly Ser Lys Asn Lys Gly Ala Ala Lys Thr Arg Lys Thr Thr Thr  
55 60 65
```

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act cca gga agg aaa cca agg ggc aga ccc aaa aaa ctg gag aag gag 477
 Thr Pro Gly Arg Lys Pro Arg Gly Arg Pro Lys Lys Leu Glu Lys Glu
 70 75 80

gaa gag gag ggc atc tcg cag gag tcc tcg gag gag gag cag 519
 Glu Glu Glu Gly Ile Ser Gln Glu Ser Ser Glu Glu Glu Gln
 85 90 95

tgacccatgc gtgccgctg ctctcactg gaggagcagc ttccttctgg gactggacag 579
 ctttgtctcg ctcccaccgc cccgcacct tcccaggcc caccatcacc accgcctctg 639
 gccgccaccc ccattctcca cctgtgccct caccaccaca ctacacagca caccagccgc 699
 tgcagggtc ccatgggctg agtggggagc agttttcccc tggcctcagt tcccagctcc 759
 ccccgccac ccacgcatac acacatgcc tcctggacaa ggctaacatc ccacttagcc 819
 gcacctgca cctgctgctg cccactccc ttggtggtgg ggacattgct ctctgggctt 879
 ttggtttggg ggcgccctct ctgcctcctt cactgttccc tctggcttcc catagtgggg 939
 cctgggaggg ttccccctgg ccttaaaagg ggcccaagcc catctcatcc tggcacgccc 999
 tactccactg ccctggcagc agcaggtgtg gccaatggag gggggtgctg gccccagga 1059
 ttccccagc caaactgtct ttgtcaccac gtggggctca cttttcatcc ttcccact 1119
 tccctagtc ccgtactagg ttggacagcc cccttcggct acaggaaggc aggaggggtg 1179
 agtccctac tcctcttca ctgtggccac agcccccttg ccctccgctt gggatctgag 1239
 tacatatgt ggtgatggag atgcagtcac ttattgtcca ggtgaggccc aagagccctg 1299
 tggccgccac ctgaggtggg ctggggctgc tcccctaacc ctactttgt tccgccactc 1359
 agccatttcc ccctcctcag atggggcacc aataacaagg agtcaccctt gcccgtccc 1419
 aacccccctc ctgctcctcc ctgcccccca aggttctggt tccatttttc ctctgttcac 1479
 aaactacctc tggacagttg tgttgttttt tgttcaatgt tccattcttc gacatccgtc 1539
 attgctgctg ctaccagcgc caaatgttca tcctcattgc ctctgttct gccacgac 1599
 ccctccccca agatactctt tgtggggaag aggggctggg gcatggcagg ctgggtgacc 1659
 gactacccca gtcccaggga aggtgccctg cccctaggat gctgcagcag agtgagcaag 1719
 gggggccgaa tcgaccataa aggggtgtagg ggccacctcc tccccctgtt ctgttgggga 1779
 ggggtagcca tgatttgtcc cagcctgggg ctccctctct ggtttcctat ttacagttac 1839
 ttgaataaaa aaaatatacct tttctgga aa

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<210> 21
<211> 626
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (96) .. (332)
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<400> 21
agttctccggc gagttgttgc ctgggctgga cgtgggtttg tctgctgcgc ccgctcttcg 60
cgctctcggt tcattttctg cagcgcgccg cgagg atg gcc cac aag cag atc 113
Met Ala His Lys Gln Ile
1 5
tac tac tcg gac aag tac ttc gac gaa cac tac gag tac cgg cat gtt 161
Tyr Tyr Ser Asp Lys Tyr Phe Asp Glu His Tyr Glu Tyr Arg His Val
10 15 20
atg tta ccc aga gaa ctt tcc aaa caa gta cct aaa act cat ctg atg 209
Met Leu Pro Arg Glu Leu Ser Lys Gln Val Pro Lys Thr His Leu Met
25 30 35
tct gaa gag gag tgg agg aga ctt ggt gtc caa cag agt cta ggc tgg 257
Ser Glu Glu Glu Trp Arg Arg Leu Gly Val Gln Gln Ser Leu Gly Trp
40 45 50
gtt cat tac atg att cat gag cca gaa cca cat att ctt ctc ttt aga 305
Val His Tyr Met Ile His Glu Pro Glu Pro His Ile Leu Leu Phe Arg
55 60 65 70
cga cct ctt cca aaa gat caa caa aaa tgaagtttat ctgggggatcg 352
Arg Pro Leu Pro Lys Asp Gln Gln Lys
75
tcaaattcttt ttcaaattta atgtatatgt gtatataagg tagtattcag tgaatacttg 412
agaaatgtac aaatctttca tccatacctg tgcatagagct gtattcttca cagcaacaga 472
gctcagttaa atgcaactgc aagtaggtta ctgtaagatg ttttaagataa aagttcttcc 532
agtcagtttt tctcttaagt gcctgtttga gtttactgaa acagtttact tttgttcaat 592
aaagtttgta tgttgcattt aaaaaaaaaa aaaa 626

```

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<210> 22
<211> 3480
<212> DNA
<213> Homo sapiens
```

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<220>  
<221> CDS  
<222> (268) .. (2922)
```

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<400> 22

ggcggagatc gcgctctcttt cgctccgtgt ccgctgctgc tcctgtgagc gcccggcgag 60

tccgtcccgt ccaccgtccg cagctggttag ccagcctgcc cctcgccctcg actccctttc 120

accaacaccg acaccacat tgacacctcc agtccggcca gccgctccac tcgttgccctt 180

tgcattctcca cacatggcgt cctcgcgag agcggcggt cctccggggg acccgcggtc 240

cccaccgtgc agcggggcat catcaag atg gtc ctc tca ggg tgc gcc atc att 294

Met Val Leu Ser Gly Cys Ala Ile Ile
1 5

gtc cga ggt cag cct cgt ggt ggg cct cct cct gag cgg cag atc aac 342

Val Arg Gly Gln Pro Arg Gly Gly Pro Pro Pro Glu Arg Gln Ile Asn
10 15 20 25

ctc agc aac att cgt gct gga aat ctt gct cgc cgg gca gcc gcc aca 390

Leu Ser Asn Ile Arg Ala Gly Asn Leu Ala Arg Arg Ala Ala Ala Thr
30 35 40

caa cct gat gca aag gat acc cct gat gag ccc tgg gca ttt cca gct 438

Gln Pro Asp Ala Lys Asp Thr Pro Asp Glu Pro Trp Ala Phe Pro Ala
45 50 55

cga gag ttc ctt cga aag aag ctg att ggg aag gaa gtc tgt ttc acg 486

Arg Glu Phe Leu Arg Lys Lys Leu Ile Gly Lys Glu Val Cys Phe Thr
60 65 70

ata gaa aac aag act ccc cag ggg cga gag tat ggc atg atc tac ctt 534

Ile Glu Asn Lys Thr Pro Gln Gly Arg Glu Tyr Gly Met Ile Tyr Leu
75 80 85

gga aaa gat acc aat ggg gaa aac att gca gaa tca ctg gtt gca gag 582

Gly Lys Asp Thr Asn Gly Glu Asn Ile Ala Glu Ser Leu Val Ala Glu
90 95 100 105

ggc tta gcc acc cgg aga gaa ggc atg aga gct aat aat cct gag cag 630

Gly Leu Ala Thr Arg Arg Glu Gly Met Arg Ala Asn Asn Pro Glu Gln
110 115 120

aac cgg ctt tca gaa tgt gaa gaa caa gca aag gca gcc aag aaa ggg 678

Asn Arg Leu Ser Glu Cys Glu Glu Gln Ala Lys Ala Ala Lys Lys Gly
125 130 135

atg tgg agt gag ggg aac ggt tca cat act atc cgg gat ctc aag tat 726

Met Trp Ser Glu Gly Asn Gly Ser His Thr Ile Arg Asp Leu Lys Tyr
140 145 150

acc att gaa aac cca agg cac ttt gtg gac tca cac cac cag aag cct 774

Thr Ile Glu Asn Pro Arg His Phe Val Asp Ser His His Gln Lys Pro
155 160 165

gtt aat gct atc atc gag cat gtg cgg gac ggc agt gtg gtc agg gcc 822

Val Asn Ala Ile Ile Glu His Val Arg Asp Gly Ser Val Val Arg Ala
170 175 180 185

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ctg ctc ctc cca gat tac tac ctg gtt aca gtc atg ctg tca ggc atc	870
Leu Leu Leu Pro Asp Tyr Tyr Leu Val Thr Val Met Leu Ser Gly Ile	
190 195 200	
aag tgc cca act ttt cga cgg gaa gca gat ggc agt gaa act cca gag	918
Lys Cys Pro Thr Phe Arg Arg Glu Ala Asp Gly Ser Glu Thr Pro Glu	
205 210 215	
cct ttt gct gca gaa gcc aaa ttt ttc act gag tcg cga ctg ctt cag	966
Pro Phe Ala Ala Glu Ala Lys Phe Phe Thr Glu Ser Arg Leu Leu Gln	
220 225 230	
aga gat gtt cag atc att ctg gag agc tgc cac aac cag aac att gtg	1014
Arg Asp Val Gln Ile Ile Leu Glu Ser Cys His Asn Gln Asn Ile Val	
235 240 245	
ggg acc atc ctt cat cca aat ggc aac atc aca gag ctc ctc ctg aag	1062
Gly Thr Ile Leu His Pro Asn Gly Asn Ile Thr Glu Leu Leu Leu Lys	
250 255 260 265	
gaa ggt ttc gca cgc tgt gtg gac tgg tcg att gca gtt tac acc cgg	1110
Glu Gly Phe Ala Arg Cys Val Asp Trp Ser Ile Ala Val Tyr Thr Arg	
270 275 280	
ggc gca gaa aag ctg agg gcg gca gag agg ttt gcc aaa gag cgc agg	1158
Gly Ala Glu Lys Leu Arg Ala Ala Glu Arg Phe Ala Lys Glu Arg Arg	
285 290 295	
ctg aga ata tgg aga gac tat gtg gct ccc aca gct aat ttg gac caa	1206
Leu Arg Ile Trp Arg Asp Tyr Val Ala Pro Thr Ala Asn Leu Asp Gln	
300 305 310	
aag gac aag cag ttt gtt gcc aag gtg atg cag gtt ctg aat gct gat	1254
Lys Asp Lys Gln Phe Val Ala Lys Val Met Gln Val Leu Asn Ala Asp	
315 320 325	
gcc att gtt gtg aag ctg aac tca ggc gat tac aag acg att cac ctg	1302
Ala Ile Val Val Lys Leu Asn Ser Gly Asp Tyr Lys Thr Ile His Leu	
330 335 340 345	
tcc agc atc cga cca ccg agg ctg gag ggg gag aac acc cag gat aag	1350
Ser Ser Ile Arg Pro Pro Arg Leu Glu Gly Glu Asn Thr Gln Asp Lys	
350 355 360	
aac aag aaa ctg cgt ccc ctg tat gac att cct tac atg ttt gag gcc	1398
Asn Lys Lys Leu Arg Pro Leu Tyr Asp Ile Pro Tyr Met Phe Glu Ala	
365 370 375	
cgg gaa ttt ctt cga aaa aag ctt att ggg aag aag gtc aat gtg acg	1446
Arg Glu Phe Leu Arg Lys Lys Leu Ile Gly Lys Lys Val Asn Val Thr	
380 385 390	
gtg gac tac att aga cca gcc agc cca gcc aca gag aca gtg cct gcc	1494
Val Asp Tyr Ile Arg Pro Ala Ser Pro Ala Thr Glu Thr Val Pro Ala	
395 400 405	

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ttt tca gag cgt acc tgt gcc act gtc acc att gga gga ata aac att	1542
Phe Ser Glu Arg Thr Cys Ala Thr Val Thr Ile Gly Gly Ile Asn Ile	
410 415 420 425	
gct gag gct ctt gtc agc aaa ggt cta gcc aca gtg atc aga tac cgg	1590
Ala Glu Ala Leu Val Ser Lys Gly Leu Ala Thr Val Ile Arg Tyr Arg	
430 435 440	
cag gat gat gac cag aga tca tca cac tac gat gaa ctg ctt gct gca	1638
Gln Asp Asp Asp Gln Arg Ser Ser His Tyr Asp Glu Leu Leu Ala Ala	
445 450 455	
gag gcc aga gct att aag aat ggc aaa gga ttg cat agc aag aag gaa	1686
Glu Ala Arg Ala Ile Lys Asn Gly Lys Gly Leu His Ser Lys Lys Glu	
460 465 470	
gtg cct atc cac cgt gtt gca gat ata tct ggg gat acc caa aaa gca	1734
Val Pro Ile His Arg Val Ala Asp Ile Ser Gly Asp Thr Gln Lys Ala	
475 480 485	
aag cag ttc ctg cct ttt ctt cag cgg gca ggt cgt tct gaa gct gtg	1782
Lys Gln Phe Leu Pro Phe Leu Gln Arg Ala Gly Arg Ser Glu Ala Val	
490 495 500 505	
gtg gaa tac gtc ttc agt ggt tct cgt ctc aaa ctc tat ttg cca aag	1830
Val Glu Tyr Val Phe Ser Gly Ser Arg Leu Lys Leu Tyr Leu Pro Lys	
510 515 520	
gaa act tgc ctt atc acc ttc ttg ctt gca ggc att gaa tgc ccc aga	1878
Glu Thr Cys Leu Ile Thr Phe Leu Leu Ala Gly Ile Glu Cys Pro Arg	
525 530 535	
gga gcc cga aac ctc cca ggc ttg gtg cag gaa gga gag ccc ttc agc	1926
Gly Ala Arg Asn Leu Pro Gly Leu Val Gln Glu Gly Glu Pro Phe Ser	
540 545 550	
gag gaa gct aca ctt ttc acc aag gaa ctg gtg ctg cag cga gag gtg	1974
Glu Glu Ala Thr Leu Phe Thr Lys Glu Leu Val Leu Gln Arg Glu Val	
555 560 565	
gag gtg gag gtg gag agc atg gac aag gcc ggc aac ttt atc ggc tgg	2022
Glu Val Glu Val Glu Ser Met Asp Lys Ala Gly Asn Phe Ile Gly Trp	
570 575 580 585	
ctg cac atc gac ggt gcc aac ctg tcc gtc ctg ctg gtg gag cac gcg	2070
Leu His Ile Asp Gly Ala Asn Leu Ser Val Leu Leu Val Glu His Ala	
590 595 600	
ctc tcc aag gtc cac ttc acc gcc gaa cgc agc tcc tac tac aag tcc	2118
Leu Ser Lys Val His Phe Thr Ala Glu Arg Ser Ser Tyr Tyr Lys Ser	
605 610 615	
ctg ctg tct gcc gag gag gcc gca aag cag aag aaa gag aag gtc tgg	2166
Leu Leu Ser Ala Glu Glu Ala Ala Lys Gln Lys Lys Glu Lys Val Trp	
620 625 630	

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gcc cac tat gag gag cag ccc gtg gag gag gtg atg cca gtg ctg gag	2214
Ala His Tyr Glu Glu Gln Pro Val Glu Glu Val Met Pro Val Leu Glu	
635 640 645	
 gag aag gag cga tct gct agc tac aag ccc gtg ttt gtg acc gag atc	2262
Glu Lys Glu Arg Ser Ala Ser Tyr Lys Pro Val Phe Val Thr Glu Ile	
650 655 660 665	
 act gat gac ctg cac ttc tac gtg cag gat gtg gag acc ggc acc cag	2310
Thr Asp Asp Leu His Phe Tyr Val Gln Asp Val Glu Thr Gly Thr Gln	
670 675 680	
 ttc cag aag ctg atg gag aac atg cgc aat gac att gcc agt cac ccc	2358
Phe Gln Lys Leu Met Glu Asn Met Arg Asn Asp Ile Ala Ser His Pro	
685 690 695	
 cct gta gag ggc tcc tat gcc ccc cgc agg gga gag ttc tgc att gcc	2406
Pro Val Glu Gly Ser Tyr Ala Pro Arg Arg Gly Glu Phe Cys Ile Ala	
700 705 710	
 aaa ttt gta gat gga gaa tgg tac cgt gcc cga gta gag aaa gtc gag	2454
Lys Phe Val Asp Gly Glu Trp Tyr Arg Ala Arg Val Glu Lys Val Glu	
715 720 725	
 tct cct gcc aaa ata cat gtc ttc tac att gac tac ggc aac aga gag	2502
Ser Pro Ala Lys Ile His Val Phe Tyr Ile Asp Tyr Gly Asn Arg Glu	
730 735 740 745	
 gtc ctg cca tcc acc cgc ctg ggt acc cta tca cct gcc ttc agc act	2550
Val Leu Pro Ser Thr Arg Leu Gly Thr Leu Ser Pro Ala Phe Ser Thr	
750 755 760	
 cgg gtg ctg cca gct caa gcc acg gag tat gcc ttc gcc ttc atc cag	2598
Arg Val Leu Pro Ala Gln Ala Thr Glu Tyr Ala Phe Ala Phe Ile Gln	
765 770 775	
 gtg ccc caa gat gat gat gcc cgc acg gac gcc gtg gac agc gta gtt	2646
Val Pro Gln Asp Asp Asp Ala Arg Thr Asp Ala Val Asp Ser Val Val	
780 785 790	
 cgg gat atc cag aac act cag tgc ctg ctc aac gtg gaa cac ctg agt	2694
Arg Asp Ile Gln Asn Thr Gln Cys Leu Leu Asn Val Glu His Leu Ser	
795 800 805	
 gcc ggc tgc ccc cat gtc acc ctg cag ttt gca gat tcc aag ggc gat	2742
Ala Gly Cys Pro His Val Thr Leu Gln Phe Ala Asp Ser Lys Gly Asp	
810 815 820 825	
 gtg ggg ctg ggc ttg gtg aag gaa ggg ctg gtc atg gtg gag gtg cgc	2790
Val Gly Leu Gly Leu Val Lys Glu Gly Leu Val Met Val Glu Val Arg	
830 835 840	
 aag gag aaa cag ttc cag aaa gtg atc aca gaa tac ctg aat gcc caa	2838
Lys Glu Lys Gln Phe Gln Lys Val Ile Thr Glu Tyr Leu Asn Ala Gln	
845 850 855	

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gag tca gcc aag agc gcc agg ctg aac ctg tgg cgc tat gga gac ttt 2886
 Glu Ser Ala Lys Ser Ala Arg Leu Asn Leu Trp Arg Tyr Gly Asp Phe
 860 865 870

cga gct gat gat gca gac gaa ttt ggc tac agc cgc taaggagggg 2932
 Arg Ala Asp Asp Ala Asp Glu Phe Gly Tyr Ser Arg
 875 880 885

atcggggttg gccccagcc cccgtcacgc cagtcctctt tcctctgccg ggagggtgtt 2992
 ttcaactcca aaccccagag aggggttgta cattgggtcc agctttgctt cagtgtgtgg 3052
 aaatgtctcg tggggtggca tcggggctgc ggggtgggga cccaaggct ttctggggca 3112
 gacccttgtc ctctgggatg atgggcactg ctatccacag tctctgccag ttggttttat 3172
 ttggagggtt gtgggctttt ttaaaaaaaaa aaaagtcctc aaatcaggaa gaaacatcaa 3232
 agactatgtc ctagtggagg gagtaatcct aacacccagg ctggccgcca gctggcacct 3292
 gcctctatcc cagactgccc tcgtcccagc tctctgtcca actgttgatt atgtgatttt 3352
 tctgatacgt ccattctcaa atgccagtgt gttcacatct tcgctctggc cagcccatto 3412
 tgtattttaa gctttttgag gccaataaaa atagtacgtg ctgctgcagc ccttattgat 3472
 caaaaaaa 3480

<210> 23
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 23
 Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
 1 5 10 15
 Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
 20 25 30
 Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
 35 40 45
 Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
 50 55 60
 Glu Ile Met
 65

<210> 24
 <211> 604
 <212> PRT
 <213> Homo sapiens

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<400> 24

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Met  Leu  Ala  Arg  Ala  Leu  Leu  Leu  Cys  Ala  Val  Leu  Ala  Leu  Ser  His
 1          5          10          15

Thr  Ala  Asn  Pro  Cys  Cys  Ser  His  Pro  Cys  Gln  Asn  Arg  Gly  Val  Cys
          20          25          30

Met  Ser  Val  Gly  Phe  Asp  Gln  Tyr  Lys  Cys  Asp  Cys  Thr  Arg  Thr  Gly
          35          40          45

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

Leu  Phe  Leu  Lys  Pro  Thr  Pro  Asn  Thr  Val  His  Tyr  Ile  Leu  Thr  His
          65          70          75          80

Phe  Lys  Gly  Phe  Trp  Asn  Val  Val  Asn  Asn  Ile  Pro  Phe  Leu  Arg  Asn
          85          90          95

Ala  Ile  Met  Ser  Tyr  Val  Leu  Thr  Ser  Arg  Ser  His  Leu  Ile  Asp  Ser
          100          105          110

Pro  Pro  Thr  Tyr  Asn  Ala  Asp  Tyr  Gly  Tyr  Lys  Ser  Trp  Glu  Ala  Phe
          115          120          125

Ser  Asn  Leu  Ser  Tyr  Tyr  Thr  Arg  Ala  Leu  Pro  Pro  Val  Pro  Asp  Asp
          130          135          140

Cys  Pro  Thr  Pro  Leu  Gly  Val  Lys  Gly  Lys  Lys  Gln  Leu  Pro  Asp  Ser
          145          150          155          160

Asn  Glu  Ile  Val  Glu  Lys  Leu  Leu  Leu  Arg  Arg  Lys  Phe  Ile  Pro  Asp
          165          170          175

Pro  Gln  Gly  Ser  Asn  Met  Met  Phe  Ala  Phe  Phe  Ala  Gln  His  Phe  Thr
          180          185          190

His  Gln  Phe  Phe  Lys  Thr  Asp  His  Lys  Arg  Gly  Pro  Ala  Phe  Thr  Asn
          195          200          205

Gly  Leu  Gly  His  Gly  Val  Asp  Leu  Asn  His  Ile  Tyr  Gly  Glu  Thr  Leu
          210          215          220

Ala  Arg  Gln  Arg  Lys  Leu  Arg  Leu  Phe  Lys  Asp  Gly  Lys  Met  Lys  Tyr
          225          230          235          240

Gln  Ile  Ile  Asp  Gly  Glu  Met  Tyr  Pro  Pro  Thr  Val  Lys  Asp  Thr  Gln
          245          250          255

Ala  Glu  Met  Ile  Tyr  Pro  Pro  Gln  Val  Pro  Glu  His  Leu  Arg  Phe  Ala
          260          265          270

Val  Gly  Gln  Glu  Val  Phe  Gly  Leu  Val  Pro  Gly  Leu  Met  Met  Tyr  Ala
          275          280          285

Thr  Ile  Trp  Leu  Arg  Glu  His  Asn  Arg  Val  Cys  Asp  Val  Leu  Lys  Gln
          290          295          300

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52/88

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

53/88

<210> 25

<211> 360

<212> PRT

<213> Homo sapiens

<400> 25

Met	Glu	Asp	Phe	Asn	Met	Glu	Ser	Asp	Ser	Phe	Glu	Asp	Phe	Trp	Lys
1				5					10					15	

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

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

Tyr	Phe	Val	Val	Ile	Ile	Tyr	Ala	Leu	Val	Phe	Leu	Leu	Ser	Leu	Leu
50						55					60				

Gly	Asn	Ser	Leu	Val	Met	Leu	Val	Ile	Leu	Tyr	Ser	Arg	Val	Gly	Arg
65					70					75					80

Ser	Val	Thr	Asp	Val	Tyr	Leu	Leu	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu
				85					90					95	

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

Ile	Phe	Gly	Thr	Phe	Leu	Cys	Lys	Val	Val	Ser	Leu	Leu	Lys	Glu	Val
		115					120					125			

Asn	Phe	Tyr	Ser	Gly	Ile	Leu	Leu	Leu	Ala	Cys	Ile	Ser	Val	Asp	Arg
130						135					140				

Tyr	Leu	Ala	Ile	Val	His	Ala	Thr	Arg	Thr	Leu	Thr	Gln	Lys	Arg	Tyr
145					150					155					160

Leu	Val	Lys	Phe	Ile	Cys	Leu	Ser	Ile	Trp	Gly	Leu	Ser	Leu	Leu	Leu
			165						170					175	

Ala	Leu	Pro	Val	Leu	Leu	Phe	Arg	Arg	Thr	Val	Tyr	Ser	Ser	Asn	Val
			180					185						190	

Ser	Pro	Ala	Cys	Tyr	Glu	Asp	Met	Gly	Asn	Asn	Thr	Ala	Asn	Trp	Arg
		195					200					205			

Met	Leu	Leu	Arg	Ile	Leu	Pro	Gln	Ser	Phe	Gly	Phe	Ile	Val	Pro	Leu
210						215					220				

Leu	Ile	Met	Leu	Phe	Cys	Tyr	Gly	Phe	Thr	Leu	Arg	Thr	Leu	Phe	Lys
225					230					235					240

Ala	His	Met	Gly	Gln	Lys	His	Arg	Ala	Met	Arg	Val	Ile	Phe	Ala	Val
			245						250					255	

Val	Leu	Ile	Phe	Leu	Leu	Cys	Trp	Leu	Pro	Tyr	Asn	Leu	Val	Leu	Leu
			260					265					270		

54/88

Ala Asp Thr Leu Met Arg Thr Gln Val Ile Gln Glu Thr Cys Glu Arg
 275 280 285

Arg Asn His Ile Asp Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile
 290 295 300

Leu His Ser Cys Leu Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys
 305 310 315 320

Phe Arg His Gly Leu Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser
 325 330 335

Lys Asp Ser Leu Pro Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser
 340 345 350

Ser Gly His Thr Ser Thr Thr Leu
 355 360

<210> 26

<211> 198

<212> PRT

<213> Homo sapiens

<400> 26

Met Pro Leu Gly Leu Leu Trp Leu Gly Leu Ala Leu Leu Gly Ala Leu
 1 5 10 15

His Ala Gln Ala Gln Asp Ser Thr Ser Asp Leu Ile Pro Ala Pro Pro
 20 25 30

Leu Ser Lys Val Pro Leu Gln Gln Asn Phe Gln Asp Asn Gln Phe Gln
 35 40 45

Gly Lys Trp Tyr Val Val Gly Leu Ala Gly Asn Ala Ile Leu Arg Glu
 50 55 60

Asp Lys Asp Pro Gln Lys Met Tyr Ala Thr Ile Tyr Glu Leu Lys Glu
 65 70 75 80

Asp Lys Ser Tyr Asn Val Thr Ser Val Leu Phe Arg Lys Lys Lys Cys
 85 90 95

Asp Tyr Trp Ile Arg Thr Phe Val Pro Gly Cys Gln Pro Gly Glu Phe
 100 105 110

Thr Leu Gly Asn Ile Lys Ser Tyr Pro Gly Leu Thr Ser Tyr Leu Val
 115 120 125

Arg Val Val Ser Thr Asn Tyr Asn Gln His Ala Met Val Phe Phe Lys
 130 135 140

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

Thr Lys Glu Leu Thr Ser Glu Leu Lys Glu Asn Phe Ile Arg Phe Ser
 165 170 175

55/88

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

Asp Gln Cys Ile Asp Gly
 195

<210> 27
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 27
 Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
 1 5 10 15

Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
 20 25 30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
 35 40 45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
 50 55 60

Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
 65 70 75 80

Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
 85 90 95

Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
 100 105 110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
 115 120

<210> 28
 <211> 554
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
 1 5 10 15

Gly Ser Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
 20 25 30

Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
 35 40 45

Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
 50 55 60

56/88

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

57/88

Arg Val Gly Pro Val Met Pro Thr Gly Gln Asp Trp Asn His Thr Pro
 370 375 380
 Gln Lys Thr Asp His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro
 385 390 395 400
 Gly Ser Pro Arg Ile Ser Ser Leu Arg Pro Gln Ala Leu Ser Asn Pro
 405 410 415
 Ser Thr Leu Ser Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly
 420 425 430
 Ser Val Leu Pro Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp
 435 440 445
 Arg Thr Ser Pro Ala Glu Pro Glu Ala Ala Pro Ala Ser Glu Gly Ala
 450 455 460
 Ala Arg Pro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly
 465 470 475 480
 His Glu Arg Gln Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser
 485 490 495
 Val Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val
 500 505 510
 Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro
 515 520 525
 Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr
 530 535 540
 Gln Asp Asp Arg Gln Val Glu Leu Pro Val
 545 550

<210> 29

<211> 107

<212> PRT

<213> Homo sapiens

<400> 29

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

58/88

Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
 85 90 95

Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
 100 105

<210> 30

<211> 106

<212> PRT

<213> Homo sapiens

<400> 30

Met Ala His Ala Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
 1 5 10 15

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

Gly Ala Ser Val Val Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu
 35 40 45

Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Asn Val Arg Ser Pro
 50 55 60

Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly
 65 70 75 80

Lys Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln Lys Ile Ile
 85 90 95

Glu Lys Ile Leu Asn Lys Gly Ser Thr Asn
 100 105

<210> 31

<211> 300

<212> PRT

<213> Homo sapiens

<400> 31

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

Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
 20 25 30

Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
 35 40 45

Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser
 50 55 60

Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp
 65 70 75 80

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

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<400> 32
Met Glu His Gln Leu Leu Cys Cys Glu Val Glu Thr Ile Arg Arg Ala
  1                      5                      10                      15
Tyr Pro Asp Ala Asn Leu Leu Asn Asp Arg Val Leu Arg Ala Met Leu
          20                      25                      30

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60/88

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

<210> 33

<211> 439

<212> PRT

<213> Homo sapiens

61/88

<400> 33

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Met  Pro  Leu  Asn  Val  Ser  Phe  Thr  Asn  Arg  Asn  Tyr  Asp  Leu  Asp  Tyr
 1              5              10              15

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

Gln  Gln  Gln  Gln  Gln  Ser  Glu  Leu  Gln  Pro  Pro  Ala  Pro  Ser  Glu  Asp
          35              40              45

Ile  Trp  Lys  Lys  Phe  Glu  Leu  Leu  Pro  Thr  Pro  Pro  Leu  Ser  Pro  Ser
 50              55              60

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

Ser  Leu  Arg  Gly  Asp  Asn  Asp  Gly  Gly  Gly  Gly  Ser  Phe  Ser  Thr  Ala
              85              90              95

Asp  Gln  Leu  Glu  Met  Val  Thr  Glu  Leu  Leu  Gly  Gly  Asp  Met  Val  Asn
              100              105              110

Gln  Ser  Phe  Ile  Cys  Asp  Pro  Asp  Asp  Glu  Thr  Phe  Ile  Lys  Asn  Ile
          115              120              125

Ile  Ile  Gln  Asp  Cys  Met  Trp  Ser  Gly  Phe  Ser  Ala  Ala  Ala  Lys  Leu
 130              135              140

Val  Ser  Glu  Lys  Leu  Ala  Ser  Tyr  Gln  Ala  Ala  Arg  Lys  Asp  Ser  Gly
 145              150              155              160

Ser  Pro  Asn  Pro  Ala  Arg  Gly  His  Ser  Val  Cys  Ser  Thr  Ser  Ser  Leu
              165              170              175

Tyr  Leu  Gln  Asp  Leu  Ser  Ala  Ala  Ala  Ser  Glu  Cys  Ile  Asp  Pro  Ser
          180              185              190

Val  Val  Phe  Pro  Tyr  Pro  Leu  Asn  Asp  Ser  Ser  Ser  Pro  Lys  Ser  Cys
          195              200              205

Ala  Ser  Gln  Asp  Ser  Ser  Ala  Phe  Ser  Pro  Ser  Ser  Asp  Ser  Leu  Leu
 210              215              220

Ser  Ser  Thr  Glu  Ser  Ser  Pro  Gln  Gly  Ser  Pro  Glu  Pro  Leu  Val  Leu
 225              230              235              240

His  Glu  Glu  Thr  Pro  Pro  Thr  Thr  Ser  Ser  Asp  Ser  Glu  Glu  Glu  Gln
          245              250              255

Glu  Asp  Glu  Glu  Glu  Ile  Asp  Val  Val  Ser  Val  Glu  Lys  Arg  Gln  Ala
          260              265              270

Pro  Gly  Lys  Arg  Ser  Glu  Ser  Gly  Ser  Pro  Ser  Ala  Gly  Gly  His  Ser
          275              280              285

Lys  Pro  Pro  His  Ser  Pro  Leu  Val  Leu  Lys  Arg  Cys  His  Val  Ser  Thr
 290              295              300

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62/88

His Gln His Asn Tyr Ala Ala Pro Pro Ser Thr Arg Lys Asp Tyr Pro
 305 310 315 320
 Ala Ala Lys Arg Val Lys Leu Asp Ser Val Arg Val Leu Arg Gln Ile
 325 330 335
 Ser Asn Asn Arg Lys Cys Thr Ser Pro Arg Ser Ser Asp Thr Glu Glu
 340 345 350
 Asn Val Lys Arg Arg Thr His Asn Val Leu Glu Arg Gln Arg Arg Asn
 355 360 365
 Glu Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp Gln Ile Pro Glu Leu
 370 375 380
 Glu Asn Asn Glu Lys Ala Pro Lys Val Val Ile Leu Lys Lys Ala Thr
 385 390 395 400
 Ala Tyr Ile Leu Ser Val Gln Ala Glu Glu Gln Lys Leu Ile Ser Glu
 405 410 415
 Glu Asp Leu Leu Arg Lys Arg Arg Glu Gln Leu Lys His Lys Leu Glu
 420 425 430
 Gln Leu Arg Asn Ser Cys Ala
 435

<210> 34

<211> 164

<212> PRT

<213> Homo sapiens

<400> 34

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

63/88

Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln
 130 135 140

Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser
 145 150 155 160

Lys Arg Lys Pro

<210> 35

<211> 105

<212> PRT

<213> Homo sapiens

<400> 35

Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly
 1 5 10 15

Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His
 20 25 30

Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
 35 40 45

Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val
 50 55 60

Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg
 65 70 75 80

Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala
 85 90 95

Ala Glu Gly Pro Ser Asp Ile Pro Asp
 100 105

<210> 36

<211> 173

<212> PRT

<213> Homo sapiens

<400> 36

Met Gly Arg Gly Arg Cys Val Gly Pro Ser Leu Gln Leu Arg Gly Gln
 1 5 10 15

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

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

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

64/88

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

<210> 37

<211> 468

<212> PRT

<213> Homo sapiens

<400> 37

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

65/88

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

66/88

Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr
 450 455 460

Arg Asp Met Tyr
 465

<210> 38
 <211> 505
 <212> PRT
 <213> Homo sapiens

<400> 38
 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
 1 5 10 15

Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
 20 25 30

Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
 35 40 45

Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
 50 55 60

Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
 65 70 75 80

Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp
 85 90 95

Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
 100 105 110

Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu
 115 120 125

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

Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
 145 150 155 160

Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
 165 170 175

Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr
 180 185 190

Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile
 195 200 205

Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu
 210 215 220

Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg
 225 230 235 240

67/88

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

<210> 39

<211> 441

<212> PRT

<213> Homo sapiens

68/88

<400> 39

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Met Glu Gln Pro Gln Glu Glu Ala Pro Glu Val Arg Glu Glu Glu Glu
 1           5           10           15

Lys Glu Glu Val Ala Glu Ala Glu Gly Ala Pro Glu Leu Asn Gly Gly
      20           25           30

Pro Gln His Ala Leu Pro Ser Ser Ser Tyr Thr Asp Leu Ser Arg Ser
      35           40           45

Ser Ser Pro Pro Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly
      50           55           60

Ala Ser Cys Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys
      65           70           75           80

Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly
      85           90           95

Phe Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Glu
      100          105          110

Arg Ser Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys
      115          120          125

Arg Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg
      130          135          140

Phe Gly Arg Met Pro Glu Ala Glu Lys Arg Lys Leu Val Ala Gly Leu
      145          150          155          160

Thr Ala Asn Glu Gly Ser Gln Tyr Asn Pro Gln Val Ala Asp Leu Lys
      165          170          175

Ala Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met
      180          185          190

Thr Lys Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ala Ser His Thr
      195          200          205

Ala Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys
      210          215          220

Gly Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Lys Glu
      225          230          235          240

Ile Ser Val His Val Phe Tyr Arg Cys Gln Cys Thr Thr Val Glu Thr
      245          250          255

Val Arg Glu Leu Thr Glu Phe Ala Lys Ser Ile Pro Ser Phe Ser Ser
      260          265          270

Leu Phe Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu
      275          280          285

Ala Ile Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu
      290          295          300

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69/88

Val Ala Asn Gly Ser Gly Phe Val Thr Arg Glu Phe Leu Arg Ser Leu
305 310 315 320

Arg Lys Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val
325 330 335

Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile
340 345 350

Ala Ala Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro
355 360 365

Arg Val Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His
370 375 380

Leu Gln Ala Asn His Pro Asp Ala Gln Tyr Leu Phe Pro Lys Leu Leu
385 390 395 400

Gln Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu His Ala Gln Met
405 410 415

Met Gln Arg Ile Lys Lys Thr Glu Thr Glu Thr Ser Leu His Pro Leu
420 425 430

Leu Gln Glu Ile Tyr Lys Asp Met Tyr
435 440

<210> 40

<211> 742

<212> PRT

<213> Homo sapiens

<400> 40

Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
1 5 10 15

Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
20 25 30

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
35 40 45

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
50 55 60

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
65 70 75 80

Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
85 90 95

Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Ser Asn Thr Ser
100 105 110

70/88

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

71/88

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

72/88

Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu Gln Asn Val
 725 730 735

Asp Met Lys Ile Gly Val
 740

<210> 41

<211> 489

<212> PRT

<213> Homo sapiens

<400> 41

Met Leu Met Arg Leu Val Leu Thr Val Arg Ser Asn Leu Ile Pro Ser
 1 5 10 15

Pro Pro Thr Tyr Asn Ser Ala His Asp Tyr Ile Ser Trp Glu Ser Phe
 20 25 30

Ser Asn Val Ser Tyr Tyr Thr Arg Ile Leu Pro Ser Val Pro Lys Asp
 35 40 45

Cys Pro Thr Pro Met Gly Thr Lys Gly Lys Lys Gln Leu Pro Asp Ala
 50 55 60

Gln Leu Leu Ala Arg Arg Phe Leu Leu Arg Arg Lys Phe Ile Pro Asp
 65 70 75 80

Pro Gln Gly Thr Asn Leu Met Phe Ala Phe Phe Ala Gln His Phe Thr
 85 90 95

His Gln Phe Phe Lys Thr Ser Gly Lys Met Gly Pro Gly Phe Thr Lys
 100 105 110

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

Glu Arg Gln Tyr Gln Leu Arg Leu Phe Lys Asp Gly Lys Leu Lys Tyr
 130 135 140

Gln Val Leu Asp Gly Glu Met Tyr Pro Pro Ser Val Glu Glu Ala Pro
 145 150 155 160

Val Leu Met His Tyr Pro Arg Gly Ile Pro Pro Gln Ser Gln Met Ala
 165 170 175

Val Gly Gln Glu Val Phe Gly Leu Leu Pro Gly Leu Met Leu Tyr Ala
 180 185 190

Thr Leu Trp Leu Arg Glu His Asn Arg Val Cys Asp Leu Leu Lys Ala
 195 200 205

Glu His Pro Thr Trp Gly Asp Glu Gln Leu Phe Gln Thr Thr Arg Leu
 210 215 220

Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Glu Tyr Val Gln
 225 230 235 240

73/88

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

<210> 42

<211> 96

<212> PRT

<213> Homo sapiens

<400> 42

Met Ser Glu Ser Ser Ser Lys Ser Ser Gln Pro Leu Ala Ser Lys Gln
 1 5 10 15

74/88

Glu Lys Asp Gly Thr Glu Lys Arg Gly Arg Gly Arg Pro Arg Lys Gln
 20 25 30
 Pro Pro Lys Glu Pro Ser Glu Val Pro Thr Pro Lys Arg Pro Arg Gly
 35 40 45
 Arg Pro Lys Gly Ser Lys Asn Lys Gly Ala Ala Lys Thr Arg Lys Thr
 50 55 60
 Thr Thr Thr Pro Gly Arg Lys Pro Arg Gly Arg Pro Lys Lys Leu Glu
 65 70 75 80
 Lys Glu Glu Glu Glu Gly Ile Ser Gln Glu Ser Ser Glu Glu Glu Gln
 85 90 95

<210> 43
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Ala His Lys Gln Ile Tyr Tyr Ser Asp Lys Tyr Phe Asp Glu His
 1 5 10 15
 Tyr Glu Tyr Arg His Val Met Leu Pro Arg Glu Leu Ser Lys Gln Val
 20 25 30
 Pro Lys Thr His Leu Met Ser Glu Glu Glu Trp Arg Arg Leu Gly Val
 35 40 45
 Gln Gln Ser Leu Gly Trp Val His Tyr Met Ile His Glu Pro Glu Pro
 50 55 60
 His Ile Leu Leu Phe Arg Arg Pro Leu Pro Lys Asp Gln Gln Lys
 65 70 75

<210> 44
 <211> 885
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Val Leu Ser Gly Cys Ala Ile Ile Val Arg Gly Gln Pro Arg Gly
 1 5 10 15
 Gly Pro Pro Pro Glu Arg Gln Ile Asn Leu Ser Asn Ile Arg Ala Gly
 20 25 30
 Asn Leu Ala Arg Arg Ala Ala Ala Thr Gln Pro Asp Ala Lys Asp Thr
 35 40 45
 Pro Asp Glu Pro Trp Ala Phe Pro Ala Arg Glu Phe Leu Arg Lys Lys
 50 55 60

75/88

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

76/88

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

77/88

Val Gln Asp Val Glu Thr Gly Thr Gln Phe Gln Lys Leu Met Glu Asn
 675 680 685
 Met Arg Asn Asp Ile Ala Ser His Pro Pro Val Glu Gly Ser Tyr Ala
 690 695 700
 Pro Arg Arg Gly Glu Phe Cys Ile Ala Lys Phe Val Asp Gly Glu Trp
 705 710 715 720
 Tyr Arg Ala Arg Val Glu Lys Val Glu Ser Pro Ala Lys Ile His Val
 725 730 735
 Phe Tyr Ile Asp Tyr Gly Asn Arg Glu Val Leu Pro Ser Thr Arg Leu
 740 745 750
 Gly Thr Leu Ser Pro Ala Phe Ser Thr Arg Val Leu Pro Ala Gln Ala
 755 760 765
 Thr Glu Tyr Ala Phe Ala Phe Ile Gln Val Pro Gln Asp Asp Asp Ala
 770 775 780
 Arg Thr Asp Ala Val Asp Ser Val Val Arg Asp Ile Gln Asn Thr Gln
 785 790 795 800
 Cys Leu Leu Asn Val Glu His Leu Ser Ala Gly Cys Pro His Val Thr
 805 810 815
 Leu Gln Phe Ala Asp Ser Lys Gly Asp Val Gly Leu Gly Leu Val Lys
 820 825 830
 Glu Gly Leu Val Met Val Glu Val Arg Lys Glu Lys Gln Phe Gln Lys
 835 840 845
 Val Ile Thr Glu Tyr Leu Asn Ala Gln Glu Ser Ala Lys Ser Ala Arg
 850 855 860
 Leu Asn Leu Trp Arg Tyr Gly Asp Phe Arg Ala Asp Asp Ala Asp Glu
 865 870 875 880
 Phe Gly Tyr Ser Arg
 885

<210> 45

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 45

agatattgca cgggagaata tacaaa

78/88

<210> 46
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 46
tcaattcctg aaattaaagt tcggata

27

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 47
tctgcagagt tggaagcact cta

23

<210> 48
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 48
gccgaggctt ttctaccaga a

21

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 49
catggcttga tcagcaagga

20

79/88

<210> 50
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 50
tggaagtgtg ccctgaagaa g 21

<210> 51
<211> 23
<212> DNA
<213> Homo sapiens

<400> 51
caaggagctg acttcggaac taa 23

<210> 52
<211> 22
<212> DNA
<213> Homo sapiens

<400> 52
agggaagacg atgtggtttt ca 22

<210> 53
<211> 22
<212> DNA
<213> Homo sapiens

<400> 53
gggacatgtg gagagcctac tc 22

<210> 54
<211> 21
<212> DNA
<213> Homo sapiens

<400> 54
catcatagtt ccccgagca t 21

<210> 55
<211> 21
<212> DNA
<213> Artificial Sequence

80/88

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 55

aagcagcacc agcaagtgaa g

21

<210> 56

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 56

tcatggcctg tgtcagtcaa a

21

<210> 57

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 57

acatgccagc cactgtgata ga

22

<210> 58

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 58

ccctgccttc acaatgatct c

21

<210> 59

<211> 23

<212> DNA

<213> Artificial Sequence

81/88

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 59

ggaattcacc tcaagaacat cca

23

<210> 60

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 60

agtgtggcta tgacttcggt ttg

23

<210> 61

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 61

cagccacaag cagtccagat ta

22

<210> 62

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 62

cctgactatc aatcacatcg gaat

24

<210> 63

<211> 21

<212> DNA

<213> Artificial Sequence

82/88

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 63

ccaggtgctc cacatgacag t

21

<210> 64

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 64

aaacaaccaa caacaaggag aatg

24

<210> 65

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 65

cgtctccaca catcagcaca a

21

<210> 66

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 66

tcttggcagc aggatagtcc tt

22

<210> 67

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

83/88

<400> 67
gcagaccagc atgacagatt tc 22

<210> 68
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 68
gcggattagg gcttcctctt 20

<210> 69
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 69
ggcaccagag gcagtaacca t 21

<210> 70
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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primer

<400> 70
agcctctctg gttctttcaa tcg 23

<210> 71
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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primer

84/88

<400> 71
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<210> 72
<211> 20
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primer

<400> 72
tggctcctca gtagcatcag 20

<210> 73
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primer

<400> 73
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<210> 74
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primer

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<210> 75
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primer

<400> 75
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85/88

<210> 76
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primer

<400> 76
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19

<210> 77
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<223> Description of Artificial Sequence: Synthetic
primer

<400> 77
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21

<210> 78
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<223> Description of Artificial Sequence: Synthetic
primer

<400> 78
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23

<210> 79
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<223> Description of Artificial Sequence: Synthetic
primer

<400> 79
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23

86/88

<210> 80
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primer

<400> 80
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18

<210> 81
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primer

<400> 81
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22

<210> 82
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primer

<400> 82
tgccagtggg agagatgggt ga

22

<210> 83
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primer

<400> 83
acaactccag gaaggaaacc aa

22

<210> 84
<211> 19
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87/88

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 84

cgaggactcc tgcgagatg

19

<210> 85

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 85

tgaagaggag tggaggagac ttg

23

<210> 86

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 86

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24

<210> 87

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 87

gagaaggagc gatctgctag ct

22

<210> 88

<211> 23

<212> DNA

<213> Artificial Sequence

88/88

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 88

cacgtagaag tgcaggatcat cag

23