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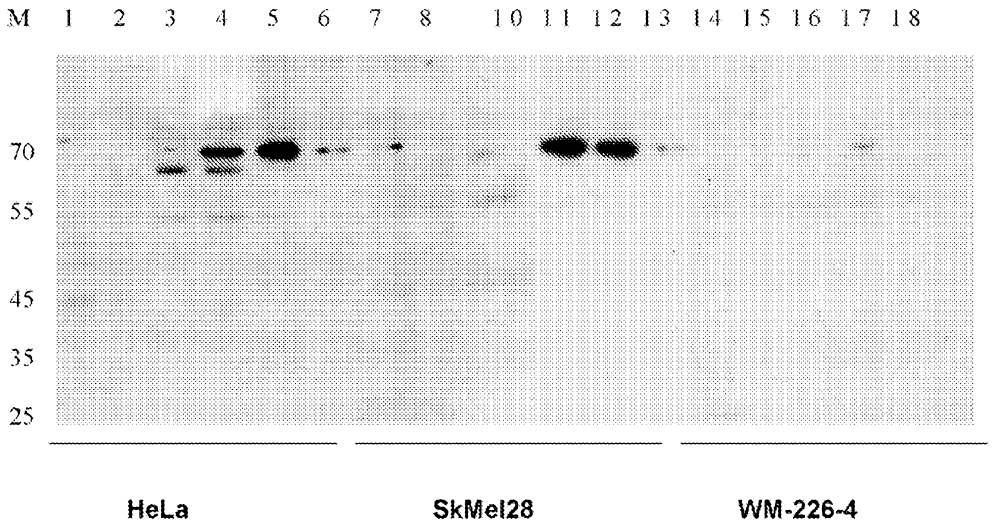

Figure 2

(57) Abstract: The invention is related to isoforms of components of transcription factor complexes that are specifically expressed in cancer cells. These isoforms can be used as biomarkers for detection, diagnosis, prognosis and monitoring of treatments of cancer, and as drug targets of pharmaceutical compositions for the treatment of various cancers expressing the targeted isoforms. Methods, molecules, materials and kits for these uses are disclosed.

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CANCER RELATED ISOFORMS OF COMPONENTS OF TRANSCRIPTION FACTOR COMPLEXES AS BIOMARKERS AND DRUG TARGETS

The instant application contains a lengthy Sequence Listing which has been submitted via text file (.txt) in lieu of a printed paper (or .pdf) copy, and is hereby incorporated by reference in its entirety. The instant application also contains a lengthy Table (Table 1) describing the sequences disclosed herein that has been submitted via text file (.txt) in lieu of a printed paper (or .pdf) copy, and is hereby incorporated by reference in its entirety.

This application claims the benefit of United States provisional patent applications, serial number 60/941,678, filed June 3, 2007, and number 60/941,747, filed June 4, 2007, the entire contents of each of which are incorporated herein by reference.

TECHNICAL FIELD OF THE INVENTION

The present invention relates to detection and therapy of cancer. The invention is more specifically related to isoforms of components of transcription factor complexes that are specifically expressed in cancer cells. These isoforms can be used as biomarkers for detection, diagnosis, prognosis and monitoring of treatments of cancer, and as drug targets of pharmaceutical compositions for the treatment of various cancers expressing the targeted isoforms.

BACKGROUND OF THE INVENTION

Cancer remains a significant health problem throughout the world. Current therapies, which are generally based on a combination of chemotherapy or surgery and radiation, continue to prove inadequate in many patients.

The molecular and cell biology of cancer is enormously complex. To date, thousands of genes representing virtually every sub-group of genes have been implicated in the pathophysiology of cancer, including mechanisms regulating uncontrolled growth of tumor cells and metastasis. Currently, it is well established that many cancers, if not all, develop from proliferating stem or progenitor cells with either mutated genes or rearranged chromosomes. As a result of these genetic alterations, tumor cells possess an altered gene and protein expression compared with normal cells (Perou et al., 2000, Hedenfalk et al., 2001, West et al., 2001, Zajchowski et al., 2001). Furthermore, differences in gene expression exist between different types of the same cancer or between histologically similar tumors. For example, data on whole-genome analyses have demonstrated that regulatory networks that determine the expression of specific genes are also different in malignant and non-malignant cells.

Regulation of gene expression at the transcriptional level is a key biological process in determining cell-type and signal-specific gene expression patterns. The above objectives are mainly focused on proteins forming the regulatory networks that control fundamental biological processes in normal and cancer cell contexts. Successful execution of cell-specific gene regulation, which combines interdisciplinary efforts, promises new breakthroughs in the field of transcription regulation and cancer, since they address novel aspects in the process, including:

- the specific functions of individual basal RNA polymerase II transcription complexes and how they participate in regulation of gene expression in normal and cancer cells;
- how gene specific transcription is achieved during cell differentiation in normal and cancer cells; and
- how the normal and cancer cell transcription process is spatially organized in the nucleus.

We postulate that a virtually infinite number of transcriptional complexes can recruit the basal transcription machinery in a gene-specific manner to regulate precisely the expression of genes during differentiation, growth and development in response to external signals (drugs, chemicals, stress etc). The materials and methods disclosed herein serve to decipher how these transcription complexes are deregulated in cancer cells.

Precise temporal and spatial regulation of the transcription of protein-encoding genes by RNA polymerase II (Pol II) is vital to the execution of cellular programs, such as growth, responses to complex developmental and homeostatic signals etc. The molecular circuitry that enables coordinated gene expression is based on DNA-binding transcription factors (TFs) and several transcription co-regulator complexes (TCCs) that modulate chromatin structure and bridge TFs to PolII including, SWI/SNF, MED, GTF and TAF-containing complexes. Numerous data show that different cell types including cancer cells express specific patterns of components of TFs and TCCs. Cell type specific expression of components of TCCs (and their isoforms) is the basis of assembly of transcription complexes with different functions. Different transcription complexes target different sets of DNA binding factors leading to inactivation of different target gene sets and ultimately to realization of different cellular programs.

One of the well-known characteristics of cancer cells is the expression of mRNA splice variants encoding specific isoforms of proteins that are not present in normal

cells. A large number of studies report identification of cancer specific or enriched mRNA alternative splice variants. For example, a genome-wide computational screening of 11,014 genes using 3,471,822 human expressed sequence tag (EST) sequences identified 26,258 alternatively spliced transcripts/mRNAs of which 845 were significantly associated with cancer (Wang et al., 2003). Several of the gene-specific splice variants have been shown to have a prognostic value. High level of expression of low molecular weight isoforms of cyclin E has a very strong correlation with survival of both node-negative and node-positive breast cancer patients (Porter and Keyomarsi, 2000, Keyomarsi et al., 2002). Patients with a high expression of the alternative splice variant of helix-loop-helix transcription factor ARNT have a worse relapse-free and overall survival than patients with a low expression (Qin et al., 2001).

Computational analysis of human EST databases identified a large number of mRNA splice variants of regulatory factors (TCCs) that are expressed in a variety of cancer cells. The present invention is based on in silico analysis using a variety of gene expression and EST databases, which has revealed a large number of alternative splice variants of (TCCs) that have cell type and disease specific expression. Splice variants encoding protein isoforms are expressed in cancer cells as relatively abundant isoforms. These isoforms modify transcriptional machinery that results in altered gene expression and may contribute to the development of cancer.

The central role of the transcriptional complexes in the cellular regulatory mechanisms makes them attractive drug targets. Interference at the function or formation of cancer-specific transcription machinery could enable researchers and clinicians to control or correct expression of a large number of genes. TCCs contain at least 100 subunits, whereas their composition in different cell types and on different promoters varies and contains different members of TCC complexes. This cell specific variability of TCC complexes assures specificity of potential treatments that target TCCs. We have isolated a large number of isoforms of components of TCCs with a potentially altered activity from a variety of cancer cells. TAF-containing complexes have been shown to control several aspects of cancer cell proliferation and metastasis (Guipaud et al., 2006). In addition, several isoforms of TAF4 function as dominant negative forms to regulate nuclear hormone receptor targets (Brunkhorst et al., 2004).

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Any discussion of the prior art throughout the specification should in no way be considered as an admission that such prior art is widely known or forms part of common general knowledge in the field.

SUMMARY OF THE INVENTION

According to a first aspect, the present invention provides an isolated isoform of a transcriptional co-regulator, wherein the isoform is an isoform of MED as set forth in SEQ ID NOs: 4-5, 87-93, 95-99, 105-107 or 109-164 or a sequence fully complementary thereto.

According to a second aspect, the present invention provides a fusion protein comprising an isoform of the first aspect fused with a heterologous peptide.

According to a third aspect, the present invention provides an isolated antibody that specifically binds an isoform of the first aspect.

According to a fourth aspect, the present invention provides an isolated polynucleotide that encodes an isoform of the first aspect or a complementary sequence thereof.

According to a fifth aspect, the present invention provides a composition comprising an isoform of the first aspect, a protein of the second aspect, or an antibody of the third aspect, and a pharmaceutically acceptable carrier.

According to a sixth aspect, the present invention provides a method for detecting cancer in a tissue specimen comprising detecting the presence of an isoform of the first aspect in the tissue specimen, wherein presence of the isoform is indicative of cancer.

According to a seventh aspect, the present invention provides a method for monitoring cancer in a subject, the method comprising:

(a) assaying a tissue specimen obtained from the subject to measure the amount of an isoform of the first aspect present in the specimen; and

(b) comparing the amount of the isoform present in the specimen to the amount of isoform determined under a previous condition, wherein a change in the amount of the isoform is indicative of a change in the progression of the cancer.

According to an eighth aspect, the present invention provides a method of killing cancer cells, the method comprising contacting the cancer cells with the peptide of the first aspect or the fusion protein of the second aspect.

According to a ninth aspect, the present invention provides a method of treating cancer in a subject, the method comprising administering to the subject an effective amount of an isoform of the first aspect; a protein of the second aspect; an antibody of the third aspect; or a composition of the fifth aspect.

According to a tenth aspect, the present invention provides use of an isoform of the first aspect; a protein of the second aspect; or an antibody of the third aspect; or a composition of the fifth aspect, in the manufacture of a medicament for the treatment of cancer.

According to an eleventh aspect, the present invention provides a kit for detecting cancer in a tissue specimen comprising an antibody of the third aspect.

Unless the context clearly requires otherwise, throughout the description and the claims, the words "comprise", "comprising", and the like are to be construed in an inclusive sense as opposed to an exclusive or exhaustive sense; that is to say, in the sense of "including, but not limited to".

The invention provides an isoform of a transcriptional co-regulator selected from the isoforms shown in SEQ ID NO: 4-207. In one embodiment, the isoform is an isoform of GTF (SEQ ID NO: 6-56). In another embodiment, the isoform is an isoform of TAF (SEQ ID NO: 57-86). In another embodiment, the isoform is an isoform of SWI/SNF (SEQ ID NO: 165-201). In a further embodiment, the isoform is an isoform of MED (SEQ ID NO: 4, 5, 87-164). In yet another embodiment, the isoform is an isoform of a co-activator or co-repressor (SEQ ID NO: 202-207). Also provided is a peptide of at least 6 amino acids in length that specifically binds to an isoform of the invention. The peptide can comprise a fusion protein comprising an isoform of or a peptide of the invention that is fused with a heterologous peptide. In some embodiments, the heterologous peptide is a CPP or NLS, such as one of SEQ ID NO: 1-3. In some optional embodiments, the peptide is fused to a toxic agent.

The invention further provides an antibody that specifically binds an isoform of the invention. In one embodiment, the antibody is labeled with a detectable marker. In

another embodiment, the antibody is conjugated to a toxic agent. The isoforms, peptides and antibodies of the invention can be useful in therapeutic and/or diagnostic compositions. Accordingly, the invention also provides a composition comprising one of these molecules and a pharmaceutically acceptable carrier. In addition to a method of treating cancer, the invention also provides a method of killing cancer cells. The method comprising contacting the cancer cells with a peptide of the invention, optionally one conjugated to a toxic agent. Toxic agents are not required, however, as molecules such as peptides, that bind to the isoform is sufficient to interfere with normal functioning of cancer cells by disrupting transcription complexes and therefore altering expression of genes necessary to cancer cell survival.

The invention additionally provides a method for detecting cancer in a tissue specimen. The method comprises detecting the presence of an isoform of claim 1 in the tissue specimen. The presence of the isoform is indicative of cancer. In one embodiment, the detecting comprises contacting a tissue specimen with a detectable molecule that specifically binds an isoform of the invention and detecting binding of the detectable molecule. For example, the detecting may comprise detecting cancer-specific mRNAs or protein isoforms of TCCs. Presence or binding of the detectable molecule is indicative of cancer.

In another embodiment, the invention provides a method for monitoring cancer in a subject. The method comprises assaying a tissue specimen obtained from the subject to measure the amount of an isoform of the invention present in the specimen and comparing the amount of isoform present in the specimen to the amount determined under a previous condition, wherein a change in the amount of the isoform is indicative of a change in the progression of the cancer. For example, an increase in the level indicates the cancer is progressing, while a decrease indicates the cancer is regressing. The previous condition may have been prior to or at an earlier stage in the course of treatment of a cancerous condition, and a decrease in the amount of isoform present can be indicative of treatment efficacy. In one embodiment, the method comprises contacting a tissue specimen obtained from the subject with a detectable molecule that specifically binds an isoform of the invention. The method further comprises determining a level of binding of the detectable molecule with the isoform. Alternatively, the method can comprise detecting the level of isoform present in the specimen. The level of binding of the detectable molecule with the isoform, or the level of isoform present, is then compared to the level of binding determined, or the level of isoform present, under a previous condition. A change in the levels of expression of the TCC isoforms, or of binding of the detectable molecule is indicative of a change in the progression of the cancer.

Representative cancers to be detected, monitored or treated by the methods of the invention include, but are not limited to, melanoma, colorectal cancer, lung cancer, hepatoma, pancreatic cancer, prostate cancer, brain tumors (astrocytoma, glioblastoma, neuroblastoma), sarcoma, chondrosarcoma, breast cancer, ovarian cancer, or teratocarcinoma. In a typical embodiment, the molecule that specifically binds the isoform is a peptide. The peptide is optionally labeled with a detectable marker, e.g., for in vivo imaging.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. Analysis of BAF complexes from HeLa and human melanoma SK-Mel 28 and WM266-4 cells. Aliquots of HeLa, SKMel28 and WM 266-4 cell nuclear extracts were chromatographed on ion-exchange PE11 column containing. After washing the column extensively with buffer containing 0.1M KCl, bound proteins were eluted with buffer containing 0.2 (lanes 2, 8 and 14), 0.3M KCl (lanes 3, 9 and 15), 0.5M KCl (lanes 4, 10 and 16), 0.75MKCl (lanes 5, and 11) and 1.0M KCl (lanes 6, and 12). Initial "flow through" is depicted on lanes 1, 7 and 13.

Figure 2. Analysis of fractionation of GTF complex by detecting p62 (TFIIH subunit) using Western blot detection from HeLa cells and human melanoma SK-Mel 28 and WM266-4 cells. Aliquots of HeLa, SKMel28 and WM 266-4 cell nuclear extracts were chromatographed on ion-exchange PE11 column.. After washing the column extensively with buffer containing 0.1M KCl, bound proteins were eluted with buffer containing 0.2 (lanes 2, 8 and 14), 0.3M KCl (lanes 3, 9 and 15), 0.5M KCl (lanes 4, 10 and 16), 0.75MKCl (lanes 5, 11 and 17) and 1.0M KCl (lanes 6, 12 and 18). Initial "flow through" is depicted on lanes 1, 7 and 13.

Figure 3. Mediator complex purification conditions were assessed by detecting MED-16 in NER fractions from HeLa cells as compared to melanoma SK-Mel 28 cells. Aliquots of HeLa and SKMel28 cell nuclear extracts were chromatographed on ion-exchange PE11 column. After washing the column extensively with buffer containing 0.1M KCl, bound proteins were eluted with buffer containing 0.2 (lanes 2 and 8), 0.3M KCl (lanes 3 and 9), 0.5M KCl (lanes 4 and 10), 0.75MKCl (lanes 5 and 11) and 1.0M KCl (lanes 6and 12). Initial "flow through" is depicted on lanes 1 and 7.

Figure 4. Binding of peptide BAF57p12 to GST-BAF57 and GST-BAF57iso purified proteins in solution. Binding is represented as fluorescence intensity of released peptide in arbitrary units.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is based on the discovery of cancer-specific isoforms of components of transcription factor complexes, or transcription co-regulatory complexes (TCCs), that are specific to human cancers. These isoforms provide novel targets for treatment and detection of cancer.

Isoforms of components of TCCs as novel promising drug targets

Transcriptional regulators determine regulatory networks that control gene-specific transcription. The misregulation of these networks is correlated with a growing number of human diseases that are characterized by altered gene expression patterns. Discovery of cancer specific alterations in composition and function of TCCs suggests that targeting these modified components of TCCs with specific chemical compounds will result in modification of patterns of gene expression that will suppress proliferation and induce apoptosis of specific cancer cells. Since expression of isoforms of transcriptional co-regulators is cancer specific then treatments that target these molecules is likely also cancer specific without significant side effects. For a long time TCCs have been considered to be difficult targets for effective drug development. Recently numerous reports show that small molecules

can be developed that interact with specific TFs and TCCs to control activity of specific TCCs.

Cancer and transcriptional control

Cancer is a disease of enormous complexity. To date, thousands of genes representing virtually every sub-group of genes have been implicated in cancer. Currently, cancer is thought to develop from proliferating stem or progenitor cells with either mutated genes or rearranged chromosomes. As a result of these genetic alterations, tumor cells also possess an altered gene and protein expression compared with non-malignant cells. Whole-genome analysis of gene expression clearly shows specific differences between normal and cancerous cells as well as between cancer types. This suggests that regulatory networks determining the expression of specific genes are different in malignant and non-malignant cells.

Cancer patients have a highly variable clinical course and outcome. Intrinsic genetic heterogeneity of the primary tumor has been suggested to play a role in this variability and may explain it in part (Chang, et al., 2003). Pathological and clinical factors are insufficient to capture the complex cascade of events that drive the clinical behavior of tumors. Extensive analyses of gene expression patterns of a variety of tumors have resulted in an understanding that histologically similar tumors have different gene expression patterns. Oligonucleotide and cDNA microarray techniques have identified molecular subgroups of specific types of cancer (Perou et al., 2000, Hedenfalk et al., 2001, West et al., 2001, Zajchowski et al., 2001). Molecular profiling of tumors has also been used to predict survival of patients and to select patients for adjuvant therapy (van't Veer et al., 2002, van de Vijever et al., 2002).

Cancer specific isoforms of TCCs – novel drug targets with high specificity

Well-known characteristics of cancer cells are mutations in a variety of regulatory molecules including transcription factors, misexpression of transcription factors, expression of mRNA splice variants encoding specific isoforms of proteins and presence of posttranslational modifications that are not present in normal cells. Mutations and expression of fusion proteins are described in almost every single type of cancer (Leroy H, Roumier C, Huyghe P, Biggio V, Fenaux P, Preudhomme C., CEBPA point mutations in hematological malignancies. Leukemia. 2005 Mar; 19(3):329-34; Xia and Barr, Chromosome translocations in sarcomas and the emergence of oncogenic transcription factors. Eur J Cancer. 2005 Nov; 41(16):2513-27). A large number of papers report identification of cancer specific or enriched

mRNA alternative splice variants. For example, a genome-wide computational screening of 11014 genes using 3,471,822 human expressed sequence tag (EST) sequences identified 26,258 alternatively spliced transcripts/mRNAs of which 845 were significantly associated with cancer (Wang et al., 2003). Several of the gene-specific splice variants have been shown to have a prognostic value. Patients with a high expression of the alternative splice variant of helix-loop-helix transcription factor ARNT have a worse relapse-free and overall survival than patients with a low expression (Qin et al., 2001). As a rule the expression of cancer-specific or enriched alternatively spliced mRNAs is not related to the mutations in splice donor or acceptor sites but due to the changes in the expression of splicing factors.

We have identified 204 cancer specific or enriched isoforms of GTF (51), TAF (30), SWI/SNF (37), and MED (80) complexes and co-activators and co-repressors (6). Also we have demonstrated that some of the isoforms become integral components of TCCs. These changed TCCs may contribute to the development of cancer. Incorporation of isoforms into functional TCCs confirms that these isoforms are suitable drug targets and drugs that modify function of these isoforms or TCC containing these isoforms can be used to treat cancer.

Definitions

All scientific and technical terms used in this application have meanings commonly used in the art unless otherwise specified. As used in this application, the following words or phrases have the meanings specified.

As used herein, "peptide" or "polypeptide" includes fragments of proteins, and peptides, whether isolated from natural sources, produced by recombinant techniques or chemically synthesized. Polypeptides (and peptides) of the invention typically comprise at least about 6 amino acids. In some embodiments, the polypeptides are at least about 12 amino acids in length.

As used herein, "CSTC-targeting molecule" (wherein CSTC refers to cancer-specific transcription complex) includes CSTC-targeting peptides, polynucleotides encoding CSTC-targeting peptides, polynucleotides complementary to those encoding CSTC-targeting peptides, peptides that specifically recognize and bind CSTCs, and other small molecules exhibiting the same targeting activity.

A "small molecule" means a molecule having a molecular weight of less than 2000 Daltons, in some embodiments less than 1000 Daltons, and in still other embodiments less than 500 Daltons or less. Such molecules include, for example,

heterocyclic compounds, carboxylic compounds, sterols, amino acids, lipids, and nucleic acids.

As used herein, "CSTC-targeting" refers to the specific binding of a CSTC-targeting molecule to a cancer-specific transcription complex, wherein the specificity is such that the CSTC-targeting molecule essentially does not bind normal or native transcription complex.

As used herein, "vector" means a construct, which is capable of delivering, and preferably expressing, one or more gene(s) or sequence(s) of interest in a host cell. Examples of vectors include, but are not limited to, viral vectors, naked DNA or RNA expression vectors, plasmid, cosmid or phage vectors, DNA or RNA expression vectors associated with cationic condensing agents, DNA or RNA expression vectors encapsulated in liposomes, and certain eukaryotic cells, such as producer cells.

As used herein, "expression control sequence" means a nucleic acid sequence that directs transcription of a nucleic acid. An expression control sequence can be a promoter, such as a constitutive or an inducible promoter, or an enhancer. The expression control sequence is operably linked to the nucleic acid sequence to be transcribed.

The term "nucleic acid" or "polynucleotide" refers to a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, and unless otherwise limited, encompasses known analogs of natural nucleotides that hybridize to nucleic acids in a manner similar to naturally-occurring nucleotides.

As used herein, "tumor protein" is a protein that is expressed by tumor cells. A tumor protein is tumor specific if it is not expressed in non-tumor cells.

As used herein, "pharmaceutically acceptable carrier" includes any material which, when combined with an active ingredient, allows the ingredient to retain biological activity and is non-reactive with the subject's immune system. Examples include, but are not limited to, any of the standard pharmaceutical carriers such as a phosphate buffered saline solution, water, emulsions such as oil/water emulsion, and various types of wetting agents. Preferred diluents for aerosol or parenteral administration are phosphate buffered saline or normal (0.9%) saline.

Compositions comprising such carriers are formulated by well known conventional methods (see, for example, *Remington's Pharmaceutical Sciences*, 18th edition, A. Gennaro, ed., Mack Publishing Co., Easton, PA, 1990).

As used herein, "a" or "an" means at least one, unless clearly indicated otherwise.

CSTC-Targeting Peptides

CSTC-targeting peptides and polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences retain the ability to modulate transcription complex. In a typical embodiment, the peptide further comprises additional sequence selected to facilitate delivery into cells and into nuclei. For example, a cell penetrating peptide (CPP) can be added, such as the following amino acid sequence: RRRRRRR (SEQ ID NO: 1). Those skilled in the art are aware of other CPPs that can be suitable for use with the invention, such as those described in Ulo Langel, ed., *Cell-Penetrating Peptides: Processes and Applications*, Culinary & Hospitality Industry Publications Services (CHIPS), Weimar, Texas, 2002. An example of a peptide that facilitates nuclear delivery is a nuclear localizing signal (NLS). Typically, this signal consists of a few short sequences of positively charged lysines or arginines, such as PPKKRKV (SEQ ID NO: 2). In one embodiment, the NLS has the amino acid sequence PKKRKV (SEQ ID NO: 3).

In some embodiments, the peptide comprises D-amino acids and/or has been structurally modified to enhance its utility for a given purpose. In some embodiments, the peptide comprises chemically modified amino acids. Aptamers are also encompassed within the invention.

Those skilled in the art will appreciate that certain variants thereof will be useful in the treatment and detection of cancer. A peptide "variant," as used herein, is a peptide that differs from a native CSTC-targeting peptide in one or more substitutions, deletions, additions and/or insertions, such that the transcription complex targeting activity of the peptide is not substantially diminished. In other words, the ability of a variant to bind the transcription complex may be enhanced or unchanged, relative to the native peptide, or may be diminished by less than 50%, and preferably less than 20%, relative to the native peptide. Such variants may generally be identified by modifying one of the above peptide sequences and evaluating the binding of the modified peptide with the targeted transcription complex as described herein. Peptide variants preferably exhibit at least about 85%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified peptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would

expect the secondary structure and hydropathic nature of the peptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant peptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer.

Recombinant peptides encoded by DNA sequences as described herein may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant peptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast, insect cells or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems that secrete recombinant protein or peptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant peptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In some embodiments, polypeptides of 10-50 amino acids in length are preferred, with lengths of 15-30 amino acids particularly suited to some uses. Such peptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, J. Am. Chem. Soc. 85:2149-2146, 1963. Equipment for automated synthesis of peptides is commercially available from

suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Peptides can be synthesized on a Perkin Elmer/Applied Biosystems Division 430A peptide synthesizer using FMOC chemistry with HPTU (O-BenzotriazoleN,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

In general, peptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" peptide or polynucleotide is one that is removed from its original environment. For example, a naturally occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such peptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

Antibodies

The term "antibody" is used in the broadest sense and specifically covers single anti-isoform monoclonal antibodies and anti-isoform antibody compositions with polyepitopic specificity. The term "monoclonal antibody" (mAb) as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e. the antibodies comprising the individual population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

The invention provides antibodies that bind to isoforms. The most preferred antibodies will specifically bind to an isoform and will not bind (or will bind weakly) to non-isoform counterparts or non-cancerous specimens. Antibodies that are particularly contemplated include monoclonal and polyclonal antibodies as well as

fragments containing the antigen binding domain and/or one or more complementarity determining regions of these antibodies. As used herein, an antibody fragment is defined as at least a portion of the variable region of the immunoglobulin molecule that binds to its target, i.e., the antigen binding region.

Antibodies of the invention may be particularly useful in cancer diagnostic and prognostic assays, and imaging methodologies. Intracellularly expressed antibodies (e.g., single chain antibodies) may be therapeutically useful in treating cancers in which the expression of isoform is involved.

The invention also provides various immunological assays useful for the detection and quantification of isoforms. Such assays generally comprise one or more antibodies capable of recognizing and binding an isoform of the invention, and may be performed within various immunological assay formats well known in the art, including but not limited to various types of radioimmunoassays, enzyme-linked immunosorbent assays (ELISA), enzyme-linked immunofluorescent assays (ELIFA), and the like. In addition, immunological imaging methods capable of detecting cancers expressing isoforms are also provided by the invention, including but not limited to radioscintigraphic imaging methods using labeled antibodies. Such assays may be clinically useful in the detection, monitoring, and prognosis of isoform-expressing cancers.

Various methods for the preparation of antibodies are well known in the art. For example, antibodies may be prepared by immunizing a suitable mammalian host using an isoform or fragment thereof, in isolated or immunoconjugated form (Antibodies: A Laboratory Manual, CSH Press, Eds., Harlow, and Lane (1988); Harlow, Antibodies, Cold Spring Harbor Press, NY (1989)). In addition, fusion proteins of isoforms may also be used, such as a GST-fusion protein. In another embodiment, an isoform may be synthesized and used as an immunogen.

The antibodies or fragments may also be produced, using current technology, by recombinant means. Regions that bind specifically to the desired regions of the isoform can also be produced in the context of chimeric or CDR grafted antibodies of multiple species origin. Humanized or human antibodies may also be produced and are preferred for use in therapeutic contexts. Methods for humanizing murine and other non-human antibodies by substituting one or more of the non-human antibody CDRs for corresponding human antibody sequences are well known (see for example, Jones et al., 1986, Nature 321: 522 525; Riechmann et al., 1988, Nature 332: 323 327; Verhoeyen et al., 1988, Science 239: 1534 1536). See also, Carter et

al., 1993, Proc. Natl. Acad. Sci. USA 89: 4285 and Sims et al., 1993, J. Immunol. 151: 2296. Methods for producing fully human monoclonal antibodies include phage display and transgenic methods (for review, see Vaughan et al., 1998, Nature Biotechnology 16: 535 539).

Fully human monoclonal antibodies may be generated using cloning technologies employing large human Ig gene combinatorial libraries (i.e., phage display) (Griffiths and Hoogenboom, Building an in vitro immune system: human antibodies from phage display libraries. In: Protein Engineering of Antibody Molecules for Prophylactic and Therapeutic Applications in Man. Clark, M. (Ed.), Nottingham Academic, pp 45 64 (1993); Burton and Barbas, Human Antibodies from combinatorial libraries. Id., pp 65 82). Fully human monoclonal antibodies may also be produced using transgenic mice engineered to contain human immunoglobulin gene loci as described in PCT Patent Application WO98/24893, Kucherlapati and Jakobovits et al., published Dec. 3, 1997 (see also, Jakobovits, 1998, Exp. Opin. Invest. Drugs 7(4): 607 614). This method avoids the in vitro manipulation required with phage display technology and efficiently produces high affinity authentic human antibodies.

Reactivity of antibodies with an isoform of the invention may be established by a number of well known means, including western blot, immunoprecipitation, ELISA, and FACS analyses using, as appropriate, isoforms, isoform-expressing cells or extracts thereof

An antibody or fragment thereof of the invention may be labeled with a detectable marker or conjugated to a second molecule. Suitable detectable markers include, but are not limited to, a radioisotope, a fluorescent compound, a bioluminescent compound, chemiluminescent compound, a metal chelator or an enzyme. A second molecule for conjugation to the antibody can be selected in accordance with the intended use. Further, bi-specific antibodies specific for two or more isoform epitopes may be generated using methods generally known in the art. Homodimeric antibodies may also be generated by cross-linking techniques known in the art (e.g., Wolff et al., Cancer Res. 53: 2560 2565).

Polynucleotides of the Invention

The invention provides polynucleotides that encode one or more CSTC-targeting peptides, or an isoform of a component of a TCC, as described above. The encoding sequence for a particular isoform can be obtained from GenBank by searching the corresponding isoform name (see Table 1). Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and

more preferably 35 consecutive nucleotides, that encode a CSTC-targeting peptide or an isoform of a TCC, such as those listed in the Table below (see Example 1). Polynucleotides that are fully complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials. Portions of such CSTC-targeting polynucleotides can be useful as primers and probes for the amplification and detection of CSTC-targeting molecules.

Polynucleotides may comprise a native sequence (i.e., a sequence that encodes a CSTC-targeting peptide or isoform of a TCC as described above or a portion thereof) or may comprise a variant of such a sequence, or an aptamer. Polynucleotide variants contain one or more substitutions, additions, deletions and/or insertions such that activity (including specific binding) of the encoded peptide is not diminished, relative to a native peptide. Variants preferably exhibit at least about 60% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native CSTC-targeting peptide or a portion thereof.

Two polynucleotide or peptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins - Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenes pp. 626-645 Methods in Enzymology

vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) CABIOS 5:151-153; Myers, E.W. and Muller W. (1988) CABIOS 4:11-17; Robinson, E.D. (1971) Comb. Theor. 11:105; Santou, N., Nes, M. (1987) Mol. Biol. Evol. 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) Numerical Taxonomy the Principles and Practice of Numerical Taxonomy, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) Proc. Natl. Acad. Sci. USA 80:726-730.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or peptide sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native protein (or a complementary sequence).

Suitable "moderately stringent conditions" include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0. 1 % SDS.

As used herein, "highly stringent conditions" or "high stringency conditions" are those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC

(sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a peptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques known in the art, including, for example, oligonucleotide synthesis. Libraries can be screened with probes designed to identify the gene of interest or the peptide encoded by it. Screening the cDNA or other library with the selected probe may be conducted using standard procedures, such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* (New York: Cold Spring Harbor Laboratory Press, 1989).

The oligonucleotide sequences selected as probes should be sufficiently long and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels, such as ^{32}P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., *supra*.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (see Adelman et al., DNA 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a

CSTC-targeting peptide, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded peptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded peptide is generated *in vivo* (e.g., by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a CSTC-targeting peptide, and administering the transfected cells to the patient).

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine. Aptamers, oligonucleotides that recognize and bind to specific protein surfaces and therefore can interfere with the protein activity of co-regulator isoforms, are typically modified for therapeutic use. Where rapid clearance is desired, however, non-modified aptamers can be used in methods of the invention.

Nucleotide sequences can be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and to permit expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or

selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art. Some embodiments of the peptides of the invention have been described herein with a cell penetrating peptide (CPP) incorporated into the peptide for facilitation of entry into a cell.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (i.e., an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

Antisense and inhibitory nucleic acid molecules

The antisense molecules of the present invention comprise a sequence substantially complementary, or preferably fully complementary, to all or a fragment of a nucleic acid molecule that encodes a CSTC-targeting peptide and/or a cancer-specific isoform of a transcription modulator as described herein. Included are fragments of oligonucleotides within a coding sequence, and inhibitory nucleotides that inhibit the expression of CSTCs and/or cancer-specific isoforms of transcription modulators. Antisense oligonucleotides of DNA or RNA complementary to sequences at the boundary between introns and exons can be employed to prevent the maturation of newly-generated nuclear RNA transcripts of specific genes into mRNA for transcription. Antisense RNA, including siRNA, complementary to specific genes can hybridize with the mRNA for that gene and prevent its translation. The antisense molecule can be DNA, RNA, or a derivative or hybrid thereof, such as a chimeric gapmer. Examples of such derivative molecules include, but are not limited to, peptide nucleic acid (PNA) and phosphorothioate-based molecules such as deoxyribonucleic guanidine (DNG) or ribonucleic guanidine (RNG).

The antisense molecules of the invention are complementary to nucleic acid sequences that encode an isoform of the invention. The degree of homology necessary will depend on the particular polynucleotide of the invention. A homology of at least about 60% is sufficient for siRNAs, while larger antisense molecules and PCR primers require a homology of about 70% or greater.

Antisense RNA can be provided to the cell as "ready-to-use" RNA synthesized in vitro or as an antisense gene stably transfected into cells which will yield antisense

RNA upon transcription. Hybridization with mRNA results in degradation of the hybridized molecule by RNAse H and/or inhibition of the formation of translation complexes. Both result in a failure to produce the product of the original gene.

Both antisense RNA and DNA molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of RNA molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro or in vivo transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly can be introduced into cell lines, cells or tissues.

The design of siRNA molecules is known in the art and can be provided by vendors (e.g., Applied Biosystems/Ambion, Austin, Texas). Beginning with the AUG start codon of the transcript, one can begin by scanning for AA dinucleotide sequences. Each AA and the 3' adjacent 19 nucleotides can be identified as potential siRNA target sites. This strategy for choosing siRNA target sites is based on the observation by Elbashir et al. (2001, EMBO J 20: 6877-6888) that siRNAs with 3' overhanging UU dinucleotides are the most effective. This is also compatible with using RNA pol III to transcribe hairpin siRNAs because RNA pol III terminates transcription at 4-6 nucleotide poly(T) tracts creating RNA molecules with a short poly(U) tail. In some embodiments, the selection of the siRNA target sequence is purely empirically determined, as long as the target sequence starts with GG and does not share significant sequence homology with other genes as analyzed by BLAST search. Alternatively, any accessible site in endogenous mRNA can be targeted for degradation by the synthetic oligodeoxyribonucleotide/RNase H method (Lee, N.S., et al. (2002) Nature Biotechnology 20 : 500-505). Any accessible site identified in this fashion is then used as insert sequence in the U6 promoter-driven siRNA constructs. Typically, the siRNA expression cassette has a stem length of 19 nucleotides. siRNA stems ranging from 21 nucleotides-long to 25-29 nucleotides-long can also be useful in gene silencing.

DNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences of the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. Other modifications include the use of chimeric antisense compounds.

Chimeric antisense compounds of the invention may be formed as composite structures of two or more oligonucleotides, modified oligonucleotides, oligonucleosides and/or oligonucleotide mimetics. Such compounds have also been referred to in the art as hybrids or gapmers. Representative United States patents that teach the preparation of such hybrid structures include, but are not limited to, U.S. Pat. Nos.: 5,700,922 and 6,277,603.

The antisense compounds used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is sold by several vendors including, for example, Applied Biosystems (Foster City, Calif.). Any other means for such synthesis known in the art may additionally or alternatively be employed. It is well known to use similar techniques to prepare oligonucleotides such as the phosphorothioates and alkylated derivatives.

Antisense compositions of the invention include oligonucleotides formed of homopyrimidines that can recognize local stretches of homopurines in the DNA double helix and bind to them in the major groove to form a triple helix. See: Helen, C and Toulme, J J. Specific regulation of gene expression by antisense, sense, and antigene nucleic acids. Biochem. Biophys Acta, 1049:99-125, 1990. Formation of the triple helix would interrupt the ability of the specific gene to undergo transcription by RNA polymerase. Triple helix formation using myc-specific oligonucleotides has been observed. See: Cooney, M, et al. Science 241:456-459.

Antisense sequences of DNA or RNA can be delivered to cells. Several chemical modifications have been developed to prolong the stability and improve the function of these molecules without interfering with their ability to recognize specific sequences. These include increasing their resistance to degradation by DNases, including phosphotriesters, methylphosphonates, phosphorothioates, alpha-anomers, increasing their affinity for binding partners by covalent linkage to various intercalating agents such as psoralens, and increasing uptake by cells by conjugation to various groups including polylysine. These molecules recognize specific sequences encoded in mRNA and their hybridization prevents translation of and increases the degradation of these messages.

Antisense compositions including oligonucleotides, derivatives and analogs thereof, conjugation protocols, and antisense strategies for inhibition of transcription and translation are generally described in: Antisense Research and Applications, Crooke, S. and B. Lebleu, eds. CRC Press, Inc. Boca Raton Fla. 1993; Nucleic Acids in

Chemistry and Biology Blackburn, G. and M. J. Gait, eds. IRL Press at Oxford University Press, Inc. New York 1990; and Oligonucleotides and Analogues: A Practical Approach Eckstein, F. ed., IRL Press at Oxford University Press, Inc. New York 1991; which are each hereby incorporated herein by reference including all references cited therein which are hereby incorporated herein by reference.

Pharmaceutical Compositions

The invention provides CSTC-targeting peptides, cancer-specific isoforms of transcription modulators, polynucleotides, T cells and/or antigen presenting cells that are incorporated into pharmaceutical compositions. Pharmaceutical compositions comprise one or more such compounds and, optionally, a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an adjuvant that serves as a non-specific immune response enhancer. The adjuvant may be any substance that enhances an immune response to an exogenous antigen. Examples of adjuvants include conventional adjuvants, biodegradable microspheres (e.g., polylactic galactide), immunostimulatory oligonucleotides and liposomes (into which the compound is incorporated; see e.g., Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds that may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition can contain DNA encoding one or more of the peptides as described above, such that the peptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, Crit. Rev. Therap. Drug Carrier Systems 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., Proc. Natl. Acad. Sci. USA 86:317-321, 1989; Flexner et al., Ann. N. Y. Acad Sci. 569:86-103, 1989; Flexner et al., Vaccine 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner-Biotechniques 6:616-627, 1988; Rosenfeld et al., Science 252:431-434, 1991; Kolls et al., Proc. Natl. Acad. Sci. USA 91:215-219, 1994; Kass-Eisler et al., Proc. Natl. Acad. Sci. USA 90:11498-11502, 1993; Guzman et al., Circulation 88:2838-2848, 1993; and Guzman et al., Cir. Res. 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., Science 259:1745-1749, 1993 and reviewed by Cohen, Science 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous, intradermal or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

In addition, the carrier may contain other pharmacologically-acceptable excipients for modifying or maintaining the pH, osmolarity, viscosity, clarity, color, sterility, stability, rate of dissolution, or odor of the formulation. Similarly, the carrier may contain still other pharmacologically-acceptable excipients for modifying or maintaining the stability, rate of dissolution, release, or absorption or penetration across the blood-

brain barrier of the delivered molecule. Such excipients are those substances usually and customarily employed to formulate dosages for parenteral administration in either unit dose or multi-dose form or for direct infusion into the CSF by continuous or periodic infusion from an implanted pump.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

The compositions described herein may be administered as part of a sustained release formulation (i.e., a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site, such as a site of surgical excision of a tumor. Sustained-release formulations may contain a peptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Therapeutic and Prophylactic Methods

Treatment includes prophylaxis and therapy. Prophylaxis or therapy can be accomplished by a single direct injection at a single time point or multiple time points to a single or multiple sites. Administration can also be nearly simultaneous to multiple sites. Patients or subjects include mammals, such as human, bovine, equine, canine, feline, porcine, and ovine animals. The subject is preferably a human.

A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or

treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Cancers to be treated include, but are not limited to, melanoma, colorectal cancer, lung cancer (small and non-small cell carcinoma), hepatoma (primary liver cancer), pancreatic cancer, prostate cancer, brain tumors, including glioblastoma, astrocytoma and neuroblastoma, sarcomas, including chondrosarcoma, breast cancer, ovarian cancer, and teratocarcinoma.

Peptides or nucleic acid based drugs (e.g., antisense RNAs, siRNAs, mRNAs) can be delivered to cells via chemical means, biological means, carrier peptides, vectors, or physical delivery systems. Representative chemical means include, but are not limited to, specific chemical substances, including cationic polymers such as polyethylenimine (PEI) and cationic lipids. An example of a biological means of delivery is cell-penetrating peptides (CPPs). An exemplary carrier peptide is transportan. Vectors include plasmids and viruses, or cells. Representative physical delivery systems include, but are not limited to electrically-based systems and those using mechanical force, such as gene guns.

Isoforms of the invention can be targeted as members of protein complexes or as singular proteins by specific interaction with peptides recognizing only these isoforms. The activity of peptide in neutralizing the activity of the isoform can also be detected by using conventional proteomic methods (for example, immunoprecipitation, including chromatin immunoprecipitation (ChIP), reporter assays, immunodetection using specific antibodies) or by monitoring cellular activity.

Within certain embodiments, immunotherapy may be employed, such as active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors or infected cells with the administration of immune response-modifying agents (such as peptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8+ cytotoxic T lymphocytes and CD4+ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a

peptide provided herein. In a preferred embodiment, dendritic cells are modified *in vitro* to present the peptide, and these modified APCs are administered to the subject. T cell receptors and antibody receptors specific for the peptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The peptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Administration and Dosage

The compositions are administered in any suitable manner, often with pharmaceutically acceptable carriers. Suitable methods of administering cells in the context of the present invention to a subject are available, and, although more than one route can be used to administer a particular cell composition, a particular route can often provide a more immediate and more effective reaction than another route.

The dose administered to a patient, in the context of the present invention, should be sufficient to effect a beneficial therapeutic response in the patient over time, or to inhibit disease progression. Thus, the composition is administered to a subject in an amount sufficient to alleviate, reduce, and cure or at least partially arrest symptoms and/or complications from the disease and/or to elicit an effective immune response to the specific antigens. An amount adequate to accomplish this is defined as a "therapeutically effective dose."

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered, by injection (e.g., intracutaneous, intratumoral, intramuscular, intraperitoneal, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. In one embodiment, 2 intradermal injections of the composition are administered 10 days apart. In another embodiment, a dose is administered daily or once every 2 or 3 days over an extended period, such as weeks or months.

A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor response, and is at least 10-50% above the basal (i.e., untreated) level. Such response can be monitored, for example, by

measuring reduction in tumor size or the level of anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such therapies should also be capable of causing a response that leads to an improved clinical outcome (e.g., more frequent remissions, complete or partial or longer disease-free survival) in patients as compared to untreated patients. In general, for pharmaceutical compositions and vaccines comprising one or more peptides, the amount of each peptide present in a dose ranges from about 100 µg to 5 mg per kg of host. Suitable volumes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

Diagnostic Methods

The invention provides a method for detecting cancer in a tissue comprising contacting the tissue with a molecule that recognizes and binds a CSTC or cancer-specific isoform of a transcription modulator (or TCC) described herein. The molecule can be, for example, a CSTC-targeting peptide, an antibody directed against a CSTC or cancer-specific isoform of a transcription modulator, or an oligonucleotide probe or antisense molecule directed against a cancer-specific molecule.

The tissue can be from a mammal, such as human, bovine, equine, canine, feline, porcine, and ovine tissue. The tissue is preferably a human. The tissue can comprise a tumor specimen, tissue specimen, body fluid specimen, including blood, ductal fluid, saliva, urine, cerebrospinal fluid, or other suitable specimen.

In one embodiment, the method comprises use of an ELISA type assay. In another embodiment, the method comprises use of quantitative PCR, or other assessment of the level of isoform present in the tissue. In some embodiments, the assay makes use of a histological specimen or culture preparation. Those skilled in the art will appreciate additional variations suitable for the method of detecting cancer in tissue

through detection of a cancer-specific molecule in a specimen. Detection can be direct detection of the protein form of cancer-specific isoforms of co-regulators, or by detection of mRNA. For mRNA, typically RT-PCR based techniques are used, however, RNA can be detected also by northern blot analysis, RNase protection assay, dot blot, in situ hybridization, run-on-assays and the like. For protein-based assays, typically specific antibodies are used for immunocytochemical-histological analysis, immunoprecipitation analysis, ChiP analysis. Another option is to monitor protein activity, using cell-based assays. In one embodiment, the assay comprises determining the disappearance of the relevant protein function. For example, certain co-regulator isoforms act upon cancer cell survival. Blocking their activity would cause cancer cells stop to proliferating and induce programmed cell death.

This method can also be used to monitor levels of the cancer-specific molecule in tissue of a patient undergoing treatment for cancer. The suitability of a CSTC-targeted therapeutic regimen for initial or continued treatment can be determined by monitoring such levels using this method.

In some embodiments, the peptide and/or nucleic acid can be labeled, as desired for in vivo real-time imaging or other assays in which a detectable label facilitates identification of binding. Peptide or nucleic acids interfere with the synthesis or activity of co-regulator isoform, and this can be monitored by conventional mRNA or protein identification techniques making use a detectable label unnecessary.

The invention additionally provides a method for identifying a molecule that inhibits proliferation of cancer cells. The method comprises contacting a candidate molecule with a CSTC and determining whether the candidate molecule disrupts the biological activity of the CSTC. Disruption of the biological activity of the CSTC is indicative of a molecule that inhibits proliferation of cancer cells. Representative molecules include proteins, peptides, aptamers and nucleotides.

Kits

For use in the diagnostic and therapeutic applications described herein, kits are also within the scope of the invention. Such kits can comprise a carrier, package or container that is compartmentalized to receive one or more containers such as vials, tubes, and the like, each of the container(s) comprising one of the separate elements to be used in the method. For example, the container(s) can comprise a probe that is or can be detectably labeled. The probe can be a polypeptide or polynucleotide specific for a cancer-specific molecule of the invention. The kit can also include containers containing nucleotide(s) for amplification of a target nucleic acid sequence

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and/or a container comprising a reporter-means, such as a biotin-binding protein, e.g., avidin or streptavidin, bound to a detectable label, e.g., an enzymatic, florescent, or radioisotope label. The kit can include all or part of an amino acid sequence of the sequences described herein, or a nucleic acid molecule that encodes such amino acid sequences.

The kit of the invention will typically comprise the container described above and one or more other containers comprising materials desirable from a commercial and user standpoint, including buffers, diluents, filters, needles, syringes, and package inserts with instructions for use. In addition, a label can be provided on the container to indicate that the composition is used for a specific therapeutic or non-therapeutic application, and can also indicate directions for either *in vivo* or *in vitro* use, such as those described above. Directions and or other information can also be included on an insert which is included with the kit.

EXAMPLES

Example 1. Isolation and sequencing of mRNAs encoding for isoforms of TCC components.

Identification of isoforms of transcriptional co-regulators in melanoma cells

RNA was isolated from human cancer cell lines and primary tumors using RNA isolation KIT (Qiagen). RT-PCR was used to identify isoforms of co-regulators.

First strand cDNAs were synthesized with reverse transcriptase (SuperscriptII, Life Technologies Inc.) using 5-10 µg of mRNA from different cell lines as a template. PCR reactions were performed in the volume of 25 µl containing one tenth of RT reaction as a template and GC-Rich PCR System or the Expand. $^{TM\,Long}$ Distance PCR System kit (Roche) according to manufacturer's instructions. All amplified PCR products were sequenced and sequences analyzed to identify novel protein isoforms of componnets of TCCs.

Table 1: Protein sequences of identified isoforms of TCC components.

GTF: 51 isoforms
TAFs: 30 isoforms
SWI/SNF: 37 isoforms
MED 80: isoforms
Co-activators/Co-repressors: 6 isoforms

Full details of Table 1 are provided below.

Table 1: Protein sequences of identified isoforms of TCC components.
GTF: 51 isoforms
TAFs: 30 isoforms
SWI/SNF: 37 isoforms
MED 80: isoforms
Co-activators/Co-repressors: 6 isoforms

GTF2A2 (ID: P52657)

GTF2A2_1 (SEQ ID NO: 6)
MAYQLYRNTTLGNSLQESLDELIQILAPILQNE*

GTF2H1 (ID: P32780)

GTF2H1_1 (DA040572) (SEQ ID NO: 7)
MATSSEEVLLIVKKVRQKKQDGALYLMAERIAWAPEGKDRFTISHMYADIKCKSAILSS
DVFVCHSC*

GTF2H1_2 (BU171510) (SEQ ID NO: 8)
MATSSEEVLLIVKKVRQKKQDGALYLMAERIAWAPEGKDRFTISHMYADIKCQKISPEG
KAKIQLQLVLHAGDTTNFHFSNESTAVKERDAVKDLLQQLLPKFKRKANKELEEKNRM
LQEDPVLFQLYKDLVVSQVISAEEFWANRLNVNATDSSSTSNHKQDVGISAAFLADVR
PQTDGCNGLRYNLTSDIIESIFRTYPAVKMKYAENVPHNMTEKEFWTRFFQSHYFHRD
RLNTGSKDLFAECAKIDEKGLKTMVSLGVKNPLLDLTALEDKPLDEGYGISSVPSASNS
KSIKENSNAAIIKRFNHHSAMVLAAGLRKQEAQNEQTSEPSNMDGNSGDADCFQPAV
KRVWAKKYEPFGAQVSPNTLCDCKYCIRLFPVTQFF*

GTF2H1_3 (SEQ ID NO: 9)
MATSSEEVLLIVKKVRQKKQDGALYLMAERIAWAPEGKDRFTISHMYADIKCQKILRHF
WSCFPVNTPFLEEKVVKMKSNLERFQVTKLCPFQEKIRRQYLSTNLVSHIEEMLQTAY
NKLHTWQSRRLMKKT*

GTF2H1_4 (SEQ ID NO: 10)
MKSNLERFQVTKLCPFQEKIRRQYLSTNLVSHIEEMLQTAYNKLHTWQSRRLMKKT*

GTF2H1_5 (SEQ ID NO: 11)
MQGGTQQAINQMVPNDIQSELKHLYVAVGELLRHFWSCFPVNTPFLEEKVVKMKSNL
ERFQVTKLCPFQEKIRRQYLSTNLVSHIEEMLQTAYNKLHTWQSRRLMKKT*

GTF2H2 (ID: Q13888)

GTF2H2_1 (BG571175 etc.) (SEQ ID NO: 12)
MDEEPERTKRWEGGYERTWEILKEDESGSLKATIEDILFKAKRKRVFEHHGQVRLGM
MRHLYVVVDGSRTMEDQDLKPNRLTCTLKLLEYFVEEYFDQNPISQIGIIVTKSKRAEKL
TELSGNPRKHITSLKKAVDMTCHGEPSLYNSLSIAMQTLKLVLYIMYN*

GTF2H2_2 (SEQ ID NO: 13)
MDEEPERTKRWEGGYERTWEILKEDESGSLKATIEDILFKAKRKRVFEHHGQVRLGM
MRHLYVVVDGSRTMEDQDLKPNRLTCTLKLLEYFVEEYFDQNPISQIGIIVTKSKRAEKL
TELSGNPRKHITSLKKAVDMTCHGEPSLYNSLSIAMQTLKFCYGCQGELKDQHVYVCA
VCQNVFCVDCDVFVHDSLHCCPGCIHKIPAPSGV*

GTF2H2_3 (SEQ ID NO: 14)

MDEEPERTKRWEGGYERTWEILKEDESGSLKATIEDILFKAKRKRVFEHHGQVRLGM
VYVCAVCQNVFCVDCDVFVHDSLHCCPGCIHKIPAPSGV*

GTF2H2_4 (SEQ ID NO: 15)
MDEEPERTKRWEGGYERTWHLDGNTEPGLTLGGYFCPQCRAKYCELPVECKICGLT
LVSAPHLARSYHHLFPLDAFQEIPLEEYNGERFCYGCQGELKDQHVYVCAVCQNVFC
VDCDVFVHDSLHCCPGCIHKIPAPSGV*

GTF2H2_5 (BX460945) (SEQ ID NO: 16)
MDEEPERTKRWEGGYERTWEILKEDESGSLKATIEDILFKAKRKRVFEHHGQVRLGM
MRHLYVVVDGSRTMEDQDLKPNRLTCTLKLLEYFVEEYFDQNPISQIGIIVTKSKRAEKL
TELSGNPRKHITSLKKAVDMTCHGEPSLYNSLSIAMQTLKLVLYIMYN*

GTF2H2_6 (BX537982) (SEQ ID NO: 17)
MDEEPERTKRWEGGYERTWEILKEDESGSLKATIEDILFKAKRKRVFEHHGQVRLGM
MRHLYVVVDGSRTMEDQDLKPNRLTCTLKLLEYFVEEYFDQNPISQIGIIVTKSKRAEKL
TELSDGVLLCRQARVQWHNFGSLQSPPHGFKRFPASAS*

GTF2H3 (ID: Q13889)

GTF2H3_1 (BI550734) (SEQ ID NO: 18)
MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGDPGNPPEFNPSGSKD
GKYELLTSANEVIVEEIKDLMTKSDIKGQHTETLLAGSLAKALCYIHRMNKEVKDNQEM
KSRILVIKAAEDSALQYMNFMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
PQMPSLLQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNLIEIGYVCSVCLSIFC
NFSPICTTCETAFKISLPPVLKAKKKKLKVSA*

GTF2H3_2 (BG720598) (SEQ ID NO: 19)
MVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAVMVLGNSHLFMNRSNKLA
VIASHIQESRFLYPGKNGRLGDFFGDPGNPPEFNPSGSKDGKYELLTSANEVIVEEIKD
LMTKSDIKGQHTETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILACDITGGLYLKVPQ
MPSLLQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNLIEIGYVCSVCLSIFCNF
SPICTTCETAFKISLPPVLKAKKKKLKVSA*

GTF2H3_3 (CN263926) (SEQ ID NO: 20)
MVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAVMVLGNSHLFMNRSNKLA
VIASHIQESRFLYPGFTPFSCLSLPSSWDYYSTEPMRQKFETILPNVVKTW*

GTF2H3_4 (SEQ ID NO: 21)
MVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAVMVLGNSHLFMNRSNKLA
VIASHIQESRFLYPGKNGRLGDFFGDPGNPPESGSSL*

GTF2H3_5 (SEQ ID NO: 22)
MVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAVMVLGNSHLFMNRSNKLA
VIASHIQESRFLYPGKNGRLGDFFGDPGNPPEFNPSGSKDGKYELLTSANEVIVEEIKD
LMTKSDIKGQHTETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQYMN
FMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKVPQMPSLLQYLLWVFLPDQ
DQRSQPPK*

GTF2H3_6 (SEQ ID NO: 23)
MVSDEDELNLLVIVVDANPTWWGKQALKESQFTLSKCIDAVMVLGNSHLFMNRSNKL
AVIASHIQESRFLYPGKNGRLGDFFGDPGNPPEFNPSGSKDGKYELLTSASQVAGITTL
LNP*

GTF2H3_7 (SEQ ID NO: 24)
MVSDEDELNLLVIVVDANPIWWGKQALKESQPPK*

GTF2H3_8 (SEQ ID NO: 25)
MVSDEDELNLLVIVVDANPIWWGKQALKESQVAGITTLLNP*

GTF2H3_9 (SEQ ID NO: 26)
MVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAVMVLGNSHLFMNRSNKLA
VIASHIQESRFLYPGKNGRLGDFFGDPGNPPEFNPSGSKDGKYELLTSANEVIVEEIKD
LMTKSDIKGQHTETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILACDITGGLYLKVPQ
MPSLLQYLLWVFLPDQDQRSQLSLPSSWDYYSTEPMRQKFETILPNVVKTW*

GTF2H3_10 (SEQ ID NO: 27)
MVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAVMVLGNSHLFMNRSNKLA
VIASHIQESRFLYPGKNGRLGDFFGDPGNPPEFNPSGSKDGKYELLTSANEVIVEEIKD
LMTKSDIKGQHTETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQYMN
FMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKVPQMPSLLQYLLWVFLPDQ
DQRSQLILPPPVHVDYRAACFCHRNLIEIGYVCSVCLSIFCNFSPICTTCETAFKISQPPK
*

GTF2H3_11 (SEQ ID NO: 28)
MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGDPGNPPEFNPSGSKD
GKYELLTSANEVIVEEIKDLMTKSDIKGQHTETLLAGSLAKALCYIHRMNKEVKDNQEM
KSRILVIKAAEDSALQYMNFMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
PQMPSLLQYLLWVFLPDQDQRSQPPK*

GTF2H3_12 (DA394527) (SEQ ID NO: 29)
MVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAVMVLGNSHLFMNRSNKLA
VIASHIQESRFLYPGKNGRLGDFFGDPGNPPEFNPSGSKDGKYELLTSANEVIVEEIKD
LMTKSNNF*

GTF2H3_13 (BP281711) (SEQ ID NO: 30)
MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGDPGNPPEFNPSGSKD
GKYELLTSANEVIVEEIKDLMTKSNNF*

GTF2H4 (Q92759)

GTF2H4_1 (SEQ ID NO: 31)
MREREVMESTPSRGLNRVHLQCRNLQEFLGGLSPGVLDRLYGHPATCLAVFRELPSL
AKNWVMRMLFLEQPLPQAAVALWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGL
ILNPIFRQNLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVLHFMVGS
PSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGFQFLLLDTPAQLWYFMLQYLQTAQ
SRGMDLVEILSFLFQLSFSTLGKDYSVEGMSDSLLNFLQHLREFGLVFQRKRKSRRYY
PTRLAINLSSGVSGAGGTVHQPGFIVVETNYRLYAYTESELQIALIALFSEMLYRFPNMV
VAQVTRESVQQAIASGITAQQIIHFLRTRAHPVMLKQTPVLPPTITDQIRLWELERDRLR
FTEGVLYNQFLSQVDFELLLAHARELGVLVFENSAKRLMVVTPAGHSDVKRFWKRQK
HSS*

GTF2H4_2 (SEQ ID NO: 32)
MVVTPAGHSDVKRFWKRQKHSS*

GTF2H4_3 (SEQ ID NO: 33)

MLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDFELLLAHARELGVLVFE
NSAKRLMVVTPAGHSDVKRFWKRQKHSS*

GTF2H4_4 (SEQ ID NO: 34)
MLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDFELLLAHARELGVLVFE
NSAKRLMVVTPAGHSDVKRFWKRQKHSS*

GTF2H4_5 (SEQ ID NO: 35)
MESTPSRGLNRVHLQCRNLQEFLGGLSPGVLDRLYGHPATCLAVFREFPSLAKNWVM
RMLFLEQPLPQAAVALWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQ
NLRIAPPSPTRSGSGSWKGTDSGSLRVSCITSSCRKWTLSCCWPTRGSWACSCSRT
RPSGSWW*

GTF2H4_6 (SEQ ID NO: 36)
MESTPSRGLNRVHLQCRNLQEFLGGLSPGVLDRLYGHPATCLAVFRELPSLAKNWVM
RMLFLEQPLPQAAVALWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQ
NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVLHFMVGSPSAAVS
QDLAQLLSQAGLMKSTEPGEPPCITSAGFQFLLLDTPAQLWELERDRLRFTEGVLYNQ
FLSQVDFELLLAHARELGVLVFENSAKRLMVVTPAGHSDVKRFWKRQKHSS*

GTF2H4_7 (SEQ ID NO: 37)
MESTPSRGLNRVHLQCRNLQEFLGGLSPGVLDRLYGHPATCLAVFRELPSLAKNWVM
RMLFLEQPLPQAAVALWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQ
NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVLHFMVGSPSAAVS
QDLAQLLSQAGLMKSTEPGEPPCITSAGFQFLLLDTPAQLWYFMLQYLQTARAQRRQ
ALLEAAET*

GTF2H4_8 (SEQ ID NO: 38)
MESTPSRGLNRVHLQCRNLQEFLGGLSPGVLDRLYGHPATCLAVFRELPSLAKNWVM
RMLFLEQPLPQAAVALWVKKEFSK*

GTF2H4_9 (SEQ ID NO: 39)
MESTPSRGLNRVHLQCRNLQEFLGGLSPGVLDRLYGHPATCLAVFR*

GTF2H4_10 (BQ017927) (SEQ ID NO: 40)
MESTPSRGLNRVHLQCRNLQEFLGGLSPGVLDRLYGHPATCLAVFRELPSLAKNWVM
RMLFLEQPLPQAAVALWVKKEFSK*

ERCC2 (ID: P18074)

ERCC2_1 (AL535248) (SEQ ID NO: 41)
MRELKRTLDAKGHGVLEMPSGTGKTVSLLALIMAYQRAYPLEVTKLIYCSRTVPEIEKVI
EELRKLLNFYEKQEGEKLPFLGLALSSRKNLCIHPEVTPLRFGKDVDGKCHSLTASYVR
AQYQHDTSLPHCRFYEEFDAHGREVPLPAGIYNLDDLKALGRRQGWCPYFLARYSILH
ANVVVYSYHYLLDPKIADLVSKELARKAVVVFDEAHNIDNVCIDSMSVNLTRRTLDRCQ
GNLETLQKTVLRIKETDEQRLRDEYRRLVEGLREASAARETDAHLANPVLPDEVLQEA
VPGSIRTAEHFLGFLRRLLEYVKWRLRVQHVVQESPPAFLSGLAQRVCIQRKPLRFCA
ERLRSLLHTLEITDLADFSPLTLLANFATLVSTYAKGFTIIIEPFDDRTPTIANPILHFSCMD
ASLAIKPVFERFQSVIITSGTLSPLDIYPKILDFHPVTMATFTMTLARVCLCPMIIGRGND
QVAISSKFETREDIAVIRNYGNLLLEMSAVVPDGIVAFFTSYQYMESTVASWYEQGILE
NIQRNKLLFIETQDGAETSVALEKYQEACENGRGAILLSVARGKVSEGIDFVHHYGRAV
IMFGVPYVYTQSRILKARLEYLRDQFQIRENDFLTFDAMRHAAQCVGRAIRGKTDYGL

MVFADKRFARGDKRGKLPRWIQEHLTDANLNLTVDEGVQVAKYFLRQMAQPFHRED
QLGLSLLSLEQLESEETLKRIEQIAQQL*

ERCC2_2 (BI562139) (SEQ ID NO: 42)
MRELKRTLDAKAYPLEVTKLIYCSRTVPEIEKVIEELRKLLNFYEKQEGEKLPFLGLALSS
RKNLCIHPEVTPLRFGKDVDGKCHSLTASYVRAQYQHDTSLPHCRFYEEFDAHGREV
PLPAGIYNLDDLKALGRRQGWCPYFLARYSILHANVVVYSYHYLLDPKIADLVSKELAR
KAVVVFDEAHNIDNVCIDSMSVNLTRRTLDRCQGNLETLQKTVLRIKETDEQRLRDEYR
RLVEGLREASAARETDAHLANPVLPDEVLQEAVPGSIRTAEHFLGFLRRLLEYVKWRL
RVQHVVQESPPAFLSGLAQRVCIQRKPLRFCAERLRSLLHTLEITDLADFSPLTLLANFA
TLVSTYAKGFTIIIEPFDDRTPTIANPILHFSCMDASLAIKPVFERFQSVIITSGTLSPLDIY
PKILDFHPVTMATFTMTLARVCLCPMIIGRGNDQVAISSKFETREDIAVIRNYGNLLLEM
SAVVPDGIVAFFTSYQYMESTVASWYEQGILENIQRNKLLFIETQDGAETSVALEKYQE
ACENGRGAILLSVARGKVSEGIDFVHHYGRAVIMFGVPYVYTQSRILKARLEYLRDQFQ
IRENDFLTFDAMRHAAQCVGRAIRGKTDYGLMVFADKRFARGDKRGKLPRWIQEHLT
DANLNLTVDEGVQVAKYFLRQMAQPFHREDQLGLSLLSLEQLESEETLKRIEQIAQQL*

ERCC2_3 (BG719746 etc.) (SEQ ID NO: 43)
MRELKRTLDAKGHGVLEMPSGTGKTVSLLALIMAYQRAYPLEVTKLIYCSRTVPEIEKVI
EELRKLLNFYEKQEGEKLPFLGLALSSRKNLCIHPEVTPLRFGKDVDGKCHSLTASYVR
AQYQHDTSLPHCRFYEEFDAHGREVPLPAGIYNLDDLKALGRRQGWCPYFLARYSILH
ANVVVYSYHYLLDPKIADLVSKELARKAVVVFDEAHNIDNVCIDSMSVNLTRRTLDRCQ
GNLETLQKTVLRIKETDEQRLRDEYRRLVEGLREASAARETDAHLANPVLPDEVLQEA
VPGSIRTAEHFLGFLRRLLEYVKWRLRVQHVVQESPPAFLSGLAQRVCIQRKPLRFCA
ERLRSLLHTLEITDLADFSPLTLLANFATLVSTYAKGFTIIIEPFDDRTPTIANPILHFSCMD
ASLAIKPVFERFQSVIITSGTLSPLDIYPKILDFHPVTMATFTMTLARVCLCPMIIGRGND
QVAISSKFETREDIAVIRNYGNLLLEMSAVVPDGIVAFFTSYQYMESTVASWYEQGILE
NIQRNKLLFIETQDGAETSVALEKYQEACENGRGAILLSVARGKVSEGIDFVHHYGRAV
IMFGVPYVYTQSRILKARLEYLRDQFQIRENDFLTFDAMRHAAQCVGRAIRGKTDYGL
MVFADKRFARGDKRGKLPRWIQEHLTDANLNLTVDEGVQVAKYFLRQMAQPFHRED
QLGLSLLSLEQLESEETLKRIEQIAQQL*

ERCC3 (ID: P19447)

ERCC3_1 (CD693399) (SEQ ID NO: 44)
MQILQNFKHNPKINTIFISKVGDTSFDLPEANVLIQISSHGGSRRQEAQRLGRVLRAKKG
MVAEEYNAFFYSLVSQDTQEMAYSTKRQRFLVDQGYSFKVITKLAGMEEEDLAFSTKE
EQQQLLQKVLAATDLDAEEEVVAGEFGSRSSQASRRFGTMSSMSGADDTVYMEYHS
SRSKAPSKHVHPLFKRFRK*

MNAT1 (ID: P51948)

MNAT1_1 (AW590418) (SEQ ID NO: 45)
MDDQGCPRCKTTKYRNPSLKLMVNVCGHTLCESCVDLLFVRGAGNCPECGTPLRKS
NFRVQLFEDPTVDKEVEIRKKVLKIYNKREEDFPSLREYNDFLEEVEEIVFNLTNNVDLD
NTKKKMEIYQKENKDVIQKNKLKLTREQEELEEALEVERQENEQRRLFIQKEEQLQQIL
KRKNKQAFLDELESSDLPVALLLAQHKDRSTQLEMQLEKPKPVKPVTFSTGIKMGQHI
SLAPIHKLEEALYEYQPLQIETYGPHVPELEMLGRLGGFDTISLI*

CDK7 (ID: P50613)

CDK7_1 (SEQ ID NO: 46)

MALDVKSRAKRYEKLDFLGEGQFATVYKARDKNTNQIVAIKKIKLGHRSEAKDGINRTA
LREIKLLQELSHPNIIGVIIKDNSLVLTPSHIKAYMLMTLQGLEYLHQHWILHRDLKPNNLL
LDENGVLKLADFGLAKSFGSPNRAYTHQVVTRWYRAPELLFGARMYGVGVDMWAVG
CILAELLLRVPFLPGDSDLDQLTRIFETLGTPTEEQWPDMCSLPDYVTFKSFPGIPLHHI
FSAAGDDLLDLIQGLFLFNPCARITATQALKMKYFSNRPGPTPGCQLPRPNCPVETLKE
QSNPALAIKRKRTEALEQGGLPKKLIF*

CCNH (ID: P51946)

CCNH_1 (AB209342) (SEQ ID NO: 47)
MYHNSSQKRHWTFSSEEQLARLRADANRKFRCKAVANGKVLPNDPVFLEPHEEMTL
CKYYEKRLLEFCSVFKPAMPRSVVGTACMYFKRFYLNNSVMEYHPRIIMLTCAFLACK
VDEFNVSSPQFVGNLRESPLGQEKALEQILEYELLLIQQLNFHLIVHNPYRPFEGFLIDL
KTRYPILENPEILRKTADDFLNRIALTDAYLLYTPSQIALTAILSSASRAGITMESYLSESL
MLKENRTCLSQLLDIMKSMRNLVKKYEPPRSEEVAVLKQKLERCHSAELALNVITKKRK
GYEDDDYVSKKSKHEEVCFTPKMNSKLFLLYILV*

GTF2F1 (ID: P35269)

GTF2F1_1 (BF796638) (SEQ ID NO: 48)
MAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIY
QEEEMPESGAGSEFNRKLREEARRKFKGIKKGGVTENTSYYIFTQCPDGAFEAFPVH
NWYNFTPLARHRTLTAEEAEEEWERRNKVLNHFSIMQQRRLKDQDQDEDEEEKEKR
GRRKASELRIHDLEDDLEMSSDASDASGEEGGRVPKAKKKAPLAKGGRKKKKKKGSD
DEAFEDSDDGDFEGQEVDYMSDGSSSSQEEPESKAKAPQQEEGPKGVDEQSDSSE
ESEEEKPPEEDKEEEEEKKAPTPQEKKRRKDSSEESDSSEESDIDSEASSALFMAKKK
TPPKRERKPSGGSSRGNSRPGTPSAEGGSTSSTLRAAASKLEQGKRVSEMPAAKRL
RLDTGPQSLSGKSTPQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTK
KTGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE*

GTF2F1_2 (BG425542) (SEQ ID NO: 49)
MAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIY
QEEEKEKRGRRKASELRIHDLEDDLEMSSDASDASGEEGGRVPKAKKKAPLAKGGRK
KKKKKGSDDEAFEDSDDGDFEGQEVDYMSDGSSSSQEEPESKAKAPQQEEGPKGV
DEQSDSSEESEEEKPPEEDKEEEEEKKAPTPQEKKRRKDSSEESDSSEESDIDSEAS
SALFMAKKKTPPKRERKPSGGSSRGNSRPGTPSAEGGSTSSTLRAAASKLEQGKRVS
EMPAAKRLRLDTGPQSLSGKSTPQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKD
LLKKFQTKKTGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE*

GTF2F1_3 (BQ069267) (SEQ ID NO: 50)
MAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIY
QEEEMPESGAGSEFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIK
KGGVTENTSYYIFTQCPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVL
NHFSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMSSDASDASGEEG
GRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDSDDGDFEGQEVDYMSDGSSSSQEE
PESKAKAPQQEEGPKGVDEQSDSSEESEEEKPPEEDKEEEEEKKAPTPQEKKRRKD
SSEESDSSEESDIDSEASSAFFMAVRPSPVAGEAWASVCRLTHLPTLTSAEEEDATQE
RAEAVGRELKGQQPPRHAQRRGWQHLLHPAGGCQQTRAREAGERDACSQAVAAG
HGTPEPVWEVDTPATIRQDNTQQRRRAGD*

GTF2F1_4 (SEQ ID NO: 51)
MAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIY
QEEEMPESGAGSEFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIK
KGGVTENTSYYIFTQCPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVL

NHFSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMSSDASDASGEEG
GRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDSDDGDFEGQEVDYMSDGSSSSQEE
PESKAKAPQQEEGPKGVDEQSDSSEESEEEKPPEEDKEEEEEKKAPTPQEKKRRKD
SSEESDSSEESDIDSEASSALFMAVRPSPVAGEAWASVCRLTHLPTLTSAEEEDATQE
RAEAVGRELKGQQPPRHAQRRGWQHLLHPAGGCQQTRAR*

GTF2F1_5 (SEQ ID NO: 52)
MAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIY
QEEEMPESGAGSEFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIK
KGGVTENTSYYIFTQCPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVL
NHFSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMSSDASDASGEEG
GRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDSDDGDFEGQEVDYMSDGSSSSQEE
PESKAKAPQQEEGPKGVDEQSDTDQGPVLPTG*

GTF2F1_6 (SEQ ID NO: 53)
MAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIY
QEEEMPESGAGSEFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIK
KGGVTENTSYYIFTQCPDGAFEAFPVHNWYNFTPLARHRTLTAPSPS*

GTF2F1_7 (SEQ ID NO: 54)
MAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIY
QEEEMPESGAGSEFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIK
KGGVTENTSYYIFTQCPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVL
NHFSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMSSDASDASGEEG
GRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDSDDGDFEGQEVDYMSDGSSSSQEE
PESKAKAPQQEEGPKGVDEQSDSSEESEEEKPPEEDKEEEEEKKAPTPQEKKRRKD
SSEESDSSEESDIDSEASSAFFMAVRPSPVAGEAWASVCRLTHLPTLTSAEEEDATQE
RAEAVGRELKGQQPPRHAQRRGWQHLLHPAGGCQQTRAREAGERDACSQAVAAG
HGTPEPVWEVDTPATIRQDNTQQRVS*

GTF2F1_8 (SEQ ID NO: 55)
MAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIY
QEEEMPESGAGSEFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIK
KGGVTENTSYYIFTQCPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVL
NHFSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMSSDASDASGEEG
GRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDSDDGDFEGQEVDYMSDGSSSSQEE
PESKGLCCPLGNFYSSPFHFPKSLFSCDLSTT*

GTF2F1_9 (SEQ ID NO: 56)
MAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIY
QEEEMPESGAGSEFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIK
KGGVTENTSYYIFTQCPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVL
NHFSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMSSDASDASGEEG
GRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDSDDGDFEGQEVDYMSDGSSSSQEE
PESKAKAPQQEEGPKGVDEQSDSSEESEEEKPPEKPPPGSASLTLTKGLCCPLGNFY
SSPFHFPKSLFSCDLSTT*

TAF1 (ID: P21675)

TAF1_1 (internal 442 aa missing (125-567 aa) (SEQ ID NO: 57)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEVKDPWNLSNDEYYYPKQQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFH

RPPLKKYSFGALSQPGPHSVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTG
KDGDLILAEYSEENGPLMMQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPF
LGSLHPGQLLQAFENNLFRAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFE
VPGPNSKRANTHIRDFLQVFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLC
ADFKRTGMDSNWWVLKSDFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEK
SFFAPEEENEEDFQMKIDDEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGF
SYVKIPNKPTQQKDDKEPQPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSR
WEVIDVVRTMSTEQARSGEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSS
TEVLSTDTDSSSAEDSDFEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAA
GSAASGNNHRDDDTASVTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAY
VRIRTTKDEEFIRKFALFDEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPK
KMKERPDLKLKCGACGAIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHN
DNEELIKVEGTKIVLGKQLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNR
PHKSIHRRRTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTL
RENVRKRLYPSREEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKEDKLA
RLEKAINPLLDDDDQVAFSFILDNIVTQKMMAVPDSWPFHHPVNKKFVPDYYKVIVNPM
DLETIRKNISKHKYQSRESFLDDVNLILANSVKYNGPESQYTKTAQEIVNVCYQTLTEYD
EHLTQLEKDICTAKEAALEEAELESLDPMTPGPYTPQPPDLYDTNTSLSMSRDASVFQ
DESNMSVLDIPSATPEKQVTQEGEDGDGDLADEEEGTVQQPQASVLYEDLLMSEGED
DEEDAGSDEEGDNPFSAIQLSESGSDSDVGSGGIRPKQPRMLQENTRMDMENEESM
MSYEGDGGEASHGLEDSNISYGSYEEPDPKSNTQDTSFSSIGGYEVSEEEEDEEEEE
QRSGPSVLSQVHLSEDEEDSEDFHSIAGDSDLDSDE

TAF1_2 (BG289819) (SEQ ID NO: 58)

MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEDESRRYQQTMGSLQPLCHSDYDEDDYDADCEDIDCKLMPPPPPPPGPMKKDKDQ
DSITGEKVDFSSSSDSESEMGPQEATQAESEDGKLTLPLAGIMQHDATKLLPSVTELF
PEFRPGKVLRFLRLFGPGKNVPSVWRSARRKRKKKHRELIQEEQIQEVECSVESEVS
QKSLWNYDYAPPPPPEQCLSDDEITMMAPVESKFSQSTGDIDKVTDTKPRVAEWRYG
PARLWYDMLGVPEDGSGFDYGFKLRKTEHEPVIKSRMIEEFRKLEENNGTDLLADENF
LMVTQLHWEDDIIWDGEDVKHKGTKPQRASLAGWLPSSMTRNAMAYNVQQGFAATL
DDDKPWYSIFPIDNEDLVYGRWEDNIIWDAQAMPRLLEPPVLTLDPNDENLILEIPDEKE
EATSNSPSKESKKESSLKKSRILLGKTGVIKEEPQQNMSQPEVKDPWNLSNDEYYYPK
QQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFHRPPLKKYSFGALSQPGPH
SVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLM
MQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLF
RAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQ
VFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKS
DFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKID
DEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEP
QPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARS
GEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSD
FEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTAS
VTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALF
DEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACG
AIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGK
QLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTL
SSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSREEF
REHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKEDKLARLEKAINPLLDDDDQ
VAFSFILDNIVTQKMMAVPDSWPFHHPVNKKFVPDYYKVIVNPMDLETIRKNISKHKYQ
SRESFLDDVNLILANSVKYNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLEKDICTAK
EAALEEAELESLDPMTPGPYTPQPPDLYDTNTSLSMSRDASVFQDESNMSVLDIPSAT

PEKQVTQMRQGRGRLGEEDSDVDIEGYDDEEEDGKPKTPAPEGEDGDGDLADEEEG
TVQQPQASVLYEDLLMSEGEDDEEDAGSDEEGDNPFSAIQLSESGSDSDVGSGGIRP
KQPRMLQENTRMDMENEESMMSYEGDGGEASHGLEDSNISYGSYEEPDPKSNTQD
TSFSSIGGYEVSEEEEDEEEEEQRSGPSVLSQVHLSEDEEDSEDFHSIAGDSDLDSDE

TAF1_3 (internal 455 aa missing (105-560 aa)) (SEQ ID NO: 59)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEVKDPWNLSND
EYYYPKQQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFHRPPLKKYSFGALS
QPGPHSVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEE
NGPLMMQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAF
ENNLFRAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHI
RDFLQVFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNW
WVLKSDFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDF
QMKIDDEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKD
DKEPQPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTE
QARSGEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSA
EDSDFEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDD
DTASVTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRK
FALFDEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCG
ACGAIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIV
LGKQLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPM
VTLSSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSR
EEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKEDKLARLEKAINPLLDDD
DQVAFSFILDNIVTQKMMAVPDSWPFHHPVNKKFVPDYYKVIVNPMDLETIRKNISKHK
YQSRESFLDDVNLILANSVKYNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLEKDICT
AKEAALEEAELESLDPMTPGPYTPQPPDLYDTNTSLSMSRDASVFQDESNMSVLDIPS
ATPEKQVTQEGEDGDGDLADEEEGTVQQPQASVLYEDLLMSEGEDDEEDAGSDEEG
DNPFSAIQLSESGSDSDVGSGGIRPKQPRMLQENTRMDMENEESMMSYEGDGGEAS
HGLEDSNISYGSYEEPDPKSNTQDTSFSSIGGYEVSEEEEDEEEEEQRSGPSVLSQVH
LSEDEEDSEDFHSIAGDSDLDSDE

TAF1_4 (internal 497 aa missing (113-610 aa)) (SEQ ID NO: 60)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDIKLR
QFHRPPLKKYSFGALSQPGPHSVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQ
DLTGKDGDLILAEYSEENGPLMMQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCH
TSPFLGSLHPGQLLQAFENNLFRAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQC
PLFEVPGPNSKRANTHIRDFLQVFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRL
KLCADFKRTGMDSNWWVLKSDFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGY
GEKSFFAPEEENEEDFQMKIDDEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCG
EGFSYVKIPNKPTQQKDDKEPQPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIK
KLSRWEVIDVVRTMSTEQARSGEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNK
VLSSTEVLSTDTDSSSAEDSDFEEMGKNIENMLQNKKTSSQLSREREEQERKELQRM
LLAAGSAASGNNHRDDDTASVTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAV
IDAYVRIRTTKDEEFIRKFALFDEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEK
KPKKMKERPDLKLKCGACGAIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKT
VIHNDNEELIKVEGTKIVLGKQLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDY
LNRPHKSIHRRRTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMD
LQTLRENVRKRLYPSREEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKE
DKLARLEKAINPLLDDDDQVAFSFILDNIVTQKMMAVPDSWPFHHPVNKKFVPDYYKVI
VNPMDLETIRKNISKHKYQSRESFLDDVNLILANSVKYNGPESQYTKTAQEIVNVCYQT
LTEYDEHLTQLEKDICTAKEAALEEAELESLDPMTPGPYTPQPPDLYDTNTSLSMSRDA

SVFQDESNMSVLDIPSATPEKQVTQEGEDGDGDLADEEEGTVQQPQASVLYEDLLMS
EGEDDEEDAGSDEEGDNPFSAIQLSESGSDSDVGSGGIRPKQPRMLQENTRMDMEN
EESMMSYEGDGGEASHGLEDSNISYGSYEEPDPKSNTQDTSFSSIGGYEVSEEEEDE
EEEEQRSGPSVLSQVHLSEDEEDSEDFHSIAGDSDLDSDE

TAF1_5 (internal 531 aa missing (81- 612 aa)) (SEQ ID NO: 61)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELRQFHRPPLKKYSFGALSQPGPHSVQPLLKHIKKKAK
MREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLMMQVGMATKIKNYY
KRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLFRAPIYLHKMPETDF
LIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQVFIYRLFWKSKDRP
RRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKSDFRLPTEEEIRAMV
SPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKIDDEVRTAPWNTTRA
FIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEPQPVKKTVTGTDADL
RRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARSGEGPMSKFARGSRF
SVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSDFEEMGKNIENMLQNK
KTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTASVTSLNSSATGRCLKIY
RTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALFDEQHREEMRKERRRI
QEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACGAIGHMRTNKFCPLYYQ
TNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGKQLIESADEVRRKSLVLK
FPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTLSSILESIINDMRDLPNTY
PFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSREEFREHLELIVKNSATYNGP
KHSLTQISQSMLDLCDEKLKEKEDKLARLEKAINPLLDDDDQVAFSFILDNIVTQKMMAV
PDSWPFHHPVNKKFVPDYYKVIVNPMDLETIRKNISKHKYQSRESFLDDVNLILANSVK
YNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLEKDICTAKEAALEEAELESLDPMTPG
PYTPQPPDLYDTNTSLSMSRDASVFQDESNMSVLDIPSATPEKQVTQEGEDGDGDLA
DEEEGTVQQPQASVLYEDLLMSEGEDDEEDAGSDEEGDNPFSAIQLSESGSDSDVGS
GGIRPKQPRMLQENTRMDMENEESMMSYEGDGGEASHGLEDSNISYGSYEEPDPKS
NTQDTSFSSIGGYEVSEEEEDEEEEEQRSGPSVLSQVHLSEDEEDSEDFHSIAGDSDL
DSDE

TAF1_6 (648 aa shorter N-terminus) (SEQ ID NO: 62)
MREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLMMQVGMATKIKNYY
KRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLFRAPIYLHKMPETDF
LIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQVFIYRLFWKSKDRP
RRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKSDFRLPTEEEIRAMV
SPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKIDDEVRTAPWNTTRA
FIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEPQPVKKTVTGTDADL
RRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARSGEGPMSKFARGSRF
SVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSDFEEMGKNIENMLQNK
KTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTASVTSLNSSATGRCLKIY
RTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALFDEQHREEMRKERRRI
QEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACGAIGHMRTNKFCPLYYQ
TNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGKQLIESADEVRRKSLVLK
FPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTLSSILESIINDMRDLPNTY
PFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSREEFREHLELIVKNSATYNGP
KHSLTQISQSMLDLCDEKLKEKEDKLARLEKAINPLLDDDDQVAFSFILDNIVTQKMMAV
PDSWPFHHPVNKKFVPDYYKVIVNPMDLETIRKNISKHKYQSRESFLDDVNLILANSVK
YNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLEKDICTAKEAALEEAELESLDPMTPG
PYTPQPPDLYDTNTSLSMSRDASVFQDESNMSVLDIPSATPEKQVTQEGEDGDGDLA
DEEEGTVQQPQASVLYEDLLMSEGEDDEEDAGSDEEGDNPFSAIQLSESGSDSDVGS
GGIRPKQPRMLQENTRMDMENEESMMSYEGDGGEASHGLEDSNISYGSYEEPDPKS

NTQDTSFSSIGGYEVSEEEEDEEEEEQRSGPSVLSQVHLSEDEEDSEDFHSIAGDSDL
DSDE

TAF1_7 (internal 497 aa missing (112 - 609 aa)) (SEQ ID NO: 63)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDIKLR
QFHRPPLKKYSFGALSQPGPHSVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQ
DLTGKDGDLILAEYSEENGPLMMQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCH
TSPFLGSLHPGQLLQAFENNLFRAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQC
PLFEVPGPNSKRANTHIRDFLQVFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRL
KLCADFKRTGMDSNWWVLKSDFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGY
GEKSFFAPEEENEEDFQMKIDDEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCG
EGFSYVKIPNKPTQQKDDKEPQPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIK
KLSRWEVIDVVRTMSTEQARSGEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNK
VLSSTEVLSTDTDSSSAEDSDFEEMGKNIENMLQNKKTSSQLSREREEQERKELQRM
LLAAGSAASGNNHRDDDTASVTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAV
IDAYVRIRTTKDEEFIRKFALFDEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEK
KPKKMKERPDLKLKCGACGAIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKT
VIHNDNEELIKVEGTKIVLGKQLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDY
LNRPHKSIHRRRTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMD
LQTLRENVRKRLYPSREEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKE
DKLARLEKAINPLLDDDDQVAFSFILDNIVTQKMMAVPDSWPFHHPVNKKFVPDYYKVI
VNPMDLETIRKNISKHKYQSRESFLDDVNLILANSVKYNGPESQYTKTAQEIVNVCYQT
LTEYDEHLTQLEKDICTAKEAALEEAELESLDPMTPGPYTPQPPDLYDTNTSLSMSRDA
SVFQDESNMSVLDIPSATPEKQVTQEGEDGDGDLADEEEGTVQQPQASVLYEDLLMS
EGEDDEEDAGSDEEGDNPFSAIQLSESGSDSDVGSGGIRPKQPRMLQENTRMDMEN
EESMMSYEGDGGEASHGLEDSNISYGSYEEPDPKSNTQDTSFSSIGGYEVSEEEEDE
EEEEQRSGPSVLSQVHLSEDEEDSEDFHSIAGDSDLDSDE

TAF1_8 (internal 254 aa missing (144 - 398 aa)) (SEQ ID NO: 64)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEDESRRYQQTMGSLQPLCHSDYDEDDYDENFLMVTQLHWEDDIIWDGEDVKHKGT
KPQRASLAGWLPSSMTRNAMAYNVQQGFAATLDDDKPWYSIFPIDNEDLVYGRWED
NIIWDAQAMPRLLEPPVLTLDPNDENLILEIPDEKEEATSNSPSKESKKESSLKKSRILLG
KTGVIKEEPQQNMSQPEVKDPWNLSNDEYYYPKQQGLRGTFGGNIIQHSIPAVELRQP
FFPTHMGPIKLRQFHRPPLKKYSFGALSQPGPHSVQPLLKHIKKKAKMREQERQASG
GGEMFFMRTPQDLTGKDGDLILAEYSEENGPLMMQVGMATKIKNYYKRKPGKDPGAP
DCKYGETVYCHTSPFLGSLHPGQLLQAFENNLFRAPIYLHKMPETDFLIIRTRQGYYIRE
LVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQVFIYRLFWKSKDRPRRIRMEDIKKAF
PSHSESSIRKRLKLCADFKRTGMDSNWWVLKSDFRLPTEEEIRAMVSPEQCCAYYSMI
AAEQRLKDAGYGEKSFFAPEEENEEDFQMKIDDEVRTAPWNTTRAFIAAMKGKCLLEV
TGVADPTGCGEGFSYVKIPNKPTQQKDDKEPQPVKKTVTGTDADLRRLSLKNAKQLL
RKFGVPEEEIKKLSRWEVIDVVRTMSTEQARSGEGPMSKFARGSRFSVAEHQERYKE
ECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSDFEEMGKNIENMLQNKKTSSQLSRERE
EQERKELQRMLLAAGSAASGNNHRDDDTASVTSLNSSATGRCLKIYRTFRDEEGKEY
VRCETVRKPAVIDAYVRIRTTKDEEFIRKFALFDEQHREEMRKERRRIQEQLRRLKRNQ
EKEKLKGPPEKKPKKMKERPDLKLKCGACGAIGHMRTNKFCPLYYQTNAPPSNPVAM
TEEQEEELEKTVIHNDNEELIKVEGTKIVLGKQLIESADEVRRKSLVLKFPKQQLPPKKK
RRVGTTVHCDYLNRPHKSIHRRRTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVV
KDYYKIITRPMDLQTLRENVRKRLYPSREEFREHLELIVKNSATYNGPKHSLTQISQSML
DLCDEKLKEKEDKLARLEKAINPLLDDDDQVAFSFILDNIVTQKMMAVPDSWPFHHPVN
KKFVPDYYKVIVNPMDLETIRKNISKHKYQSRESFLDDVNLILANSVKYNGPESQYTKTA

QEIVNVCYQTLTEYDEHLTQLEKDICTAKEAALEEAELESLDPMTPGPYTPQPPDLYDT
NTSLSMSRDASVFQDESNMSVLDIPSATPEKQVTQEGEDGDGDLADEEEGTVQQPQ
ASVLYEDLLMSEGEDDEEDAGSDEEGDNPFSAIQLSESGSDSDVGSGGIRPKQPRML
QENTRMDMENEESMMSYEGDGGEASHGLEDSNISYGSYEEPDPKSNTQDTSFSSIG
GYEVSEEEEDEEEEEQRSGPSVLSQVHLSEDEEDSEDFHSIAGDSDLDSDE

TAF1_9 (internal 564 aa missing (46-610 aa)) (SEQ ID NO: 65)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNIKLRQFHRPPLKKY
SFGALSQPGPHSVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLIL
AEYSEENGPLMMQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHP
GQLLQAFENNLFRAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNS
KRANTHIRDFLQVFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTG
MDSNWWVLKSDFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEE
ENEEDFQMKIDDEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNK
PTQQKDDKEPQPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVV
RTMSTEQARSGEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTD
TDSSSAEDSDFEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGN
NHRDDDTASVTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKD
EEFIRKFALFDEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDL
KLKCGACGAIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKV
EGTKIVLGKQLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRR
RTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKR
LYPSREEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKEDKLARLEKAINP
LLDDDDQVAFSFILDNIVTQKMMAVPDSWPFHHPVNKKFVPDYYKVIVNPMDLETIRKN
ISKHKYQSRESFLDDVNLILANSVKYNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLE
KDICTAKEAALEEAELESLDPMTPGPYTPQPPDLYDTNTSLSMSRDASVFQDESNMSV
LDIPSATPEKQVTQEGEDGDGDLADEEEGTVQQPQASVLYEDLLMSEGEDDEEDAGS
DEEGDNPFSAIQLSESGSDSDVGSGGIRPKQPRMLQENTRMDMENEESMMSYEGDG
GEASHGLEDSNISYGSYEEPDPKSNTQDTSFSSIGGYEVSEEEEDEEEEEQRSGPSVL
SQVHLSEDEEDSEDFHSIAGDSDLDSDE

TAF1_10 (shorter protein, 1392 aa) (SEQ ID NO: 66)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEDESRRYQQTMGSLQPLCHSDYDEDDYDADCEDIDCKLMPPPPPPPGPMKKDKDQ
DSITGEKVDFSSSSDSESEMGPQEATQAESEDGKLTLPLAGIMQHDATKLLPSVTELF
PEFRPGKVLRFLRLFGPGKNVPSVWRSARRKRKKKHRELIQEEQIQEVECSVESEVS
QKSLWNYDYAPPPPPEQCLSDDEITMMAPVESKFSQSTGDIDKVTDTKPRVAEWRYG
PARLWYDMLGVPEDGSGFDYGFKLRKTEHEPVIKSRMIEEFRKLEENNGTDLLADENF
LMVTQLHWEDDIIWDGEDVKHKGTKPQRASLAGWLPSSMTRNAMAYNVQQGFAATL
DDDKPWYSIFPIDNEDLVYGRWEDNIIWDAQAMPRLLEPPVLTLDPNDENLILEIPDEKE
EATSNSPSKESKKESSLKKSRILLGKTGVIKEEPQQNMSQPEVKDPWNLSNDEYYYPK
QQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFHRPPLKKYSFGALSQPGPH
SVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLM
MQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLF
RAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQ
VFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKS
DFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKID
DEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEP
QPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARS
GEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSD
FEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTAS
VTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALF

DEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACG
AIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGK
QLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTL
SSILEPG*

TAF1_11 (shorter protein, 1488 aa) (SEQ ID NO: 67)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEDESRRYQQTMGSLQPLCHSDYDEDDYDADCEDIDCKLMPPPPPPPGPMKKDKDQ
DSITGEKVDFSSSSDSESEMGPQEATQAESEDGKLTLPLAGIMQHDATKLLPSVTELF
PEFRPGKVLRFLRLFGPGKNVPSVWRSARRKRKKKHRELIQEEQIQEVECSVESEVS
QKSLWNYDYAPPPPPEQCLSDDEITMMAPVESKFSQSTGDIDKVTDTKPRVAEWRYG
PARLWYDMLGVPEDGSGFDYGFKLRKTEHEPVIKSRMIEEFRKLEENNGTDLLADENF
LMVTQLHWEDDIIWDGEDVKHKGTKPQRASLAGWLPSSMTRNAMAYNVQQGFAATL
DDDKPWYSIFPIDNEDLVYGRWEDNIIWDAQAMPRLLEPPVLTLDPNDENLILEIPDEKE
EATSNSPSKESKKESSLKKSRILLGKTGVIKEEPQQNMSQPEVKDPWNLSNDEYYYPK
QQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFHRPPLKKYSFGALSQPGPH
SVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLM
MQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLF
RAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQ
VFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKS
DFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKID
DEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEP
QPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARS
GEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSD
FEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTAS
VTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALF
DEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACG
AIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGK
QLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTL
SSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSREEF
REHLDDRWRPCLKKKKKEEETWLSEYAFHKPTRGCSLPTQSQF*

TAF1_12 (shorter protein, 1425 aa) (SEQ ID NO: 68)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEDESRRYQQTMGSLQPLCHSDYDEDDYDADCEDIDCKLMPPPPPPPGPMKKDKDQ
DSITGEKVDFSSSSDSESEMGPQEATQAESEDGKLTLPLAGIMQHDATKLLPSVTELF
PEFRPGKVLRFLRLFGPGKNVPSVWRSARRKRKKKHRELIQEEQIQEVECSVESEVS
QKSLWNYDYAPPPPPEQCLSDDEITMMAPVESKFSQSTGDIDKVTDTKPRVAEWRYG
PARLWYDMLGVPEDGSGFDYGFKLRKTEHEPVIKSRMIEEFRKLEENNGTDLLADENF
LMVTQLHWEDDIIWDGEDVKHKGTKPQRASLAGWLPSSMTRNAMAYNVQQGFAATL
DDDKPWYSIFPIDNEDLVYGRWEDNIIWDAQAMPRLLEPPVLTLDPNDENLILEIPDEKE
EATSNSPSKESKKESSLKKSRILLGKTGVIKEEPQQNMSQPEVKDPWNLSNDEYYYPK
QQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFHRPPLKKYSFGALSQPGPH
SVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLM
MQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLF
RAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQ
VFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKS
DFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKID
DEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEP
QPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARS
GEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSD

FEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTAS
VTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALF
DEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACG
AIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGK
QLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTL
SSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITQPG*

TAF1_13 (shorter protein, 1432 aa) (SEQ ID NO: 69)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEDESRRYQQTMGSLQPLCHSDYDEDDYDADCEDIDCKLMPPPPPPPGPMKKDKDQ
DSITGEKVDFSSSSDSESEMGPQEATQAESEDGKLTLPLAGIMQHDATKLLPSVTELF
PEFRPGKVLRFLRLFGPGKNVPSVWRSARRKRKKKHRELIQEEQIQEVECSVESEVS
QKSLWNYDYAPPPPPEQCLSDDEITMMAPVESKFSQSTGDIDKVTDTKPRVAEWRYG
PARLWYDMLGVPEDGSGFDYGFKLRKTEHEPVIKSRMIEEFRKLEENNGTDLLADENF
LMVTQLHWEDDIIWDGEDVKHKGTKPQRASLAGWLPSSMTRNAMAYNVQQGFAATL
DDDKPWYSIFPIDNEDLVYGRWEDNIIWDAQAMPRLLEPPVLTLDPNDENLILEIPDEKE
EATSNSPSKESKKESSLKKSRILLGKTGVIKEEPQQNMSQPEVKDPWNLSNDEYYYPK
QQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFHRPPLKKYSFGALSQPGPH
SVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLM
MQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLF
RAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQ
VFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKS
DFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKID
DEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEP
QPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARS
GEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSD
FEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTAS
VTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALF
DEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACG
AIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGK
QLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTL
SSILESIINDRWRPCLKKKKKEEETWLSEYAFHKPTRGCSLPTQSQF*

TAF1_14 (shorter protein, 1466 aa) (SEQ ID NO: 70)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEDESRRYQQTMGSLQPLCHSDYDEDDYDADCEDIDCKLMPPPPPPPGPMKKDKDQ
DSITGEKVDFSSSSDSESEMGPQEATQAESEDGKLTLPLAGIMQHDATKLLPSVTELF
PEFRPGKVLRFLRLFGPGKNVPSVWRSARRKRKKKHRELIQEEQIQEVECSVESEVS
QKSLWNYDYAPPPPPEQCLSDDEITMMAPVESKFSQSTGDIDKVTDTKPRVAEWRYG
PARLWYDMLGVPEDGSGFDYGFKLRKTEHEPVIKSRMIEEFRKLEENNGTDLLADENF
LMVTQLHWEDDIIWDGEDVKHKGTKPQRASLAGWLPSSMTRNAMAYNVQQGFAATL
DDDKPWYSIFPIDNEDLVYGRWEDNIIWDAQAMPRLLEPPVLTLDPNDENLILEIPDEKE
EATSNSPSKESKKESSLKKSRILLGKTGVIKEEPQQNMSQPEVKDPWNLSNDEYYYPK
QQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFHRPPLKKYSFGALSQPGPH
SVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLM
MQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLF
RAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQ
VFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKS
DFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKID
DEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEP
QPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARS

GEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSD
FEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTAS
VTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALF
DEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACG
AIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGK
QLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTL
SSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSREEF
REHLELIVKNSATYNAGSFSI*

TAF1_15 (1485 aa, shorter protein) (SEQ ID NO: 71)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEDESRRYQQTMGSLQPLCHSDYDEDDYDADCEDIDCKLMPPPPPPPGPMKKDKDQ
DSITGEKVDFSSSSDSESEMGPQEATQAESEDGKLTLPLAGIMQHDATKLLPSVTELF
PEFRPGKVLRFLRLFGPGKNVPSVWRSARRKRKKKHRELIQEEQIQEVECSVESEVS
QKSLWNYDYAPPPPPEQCLSDDEITMMAPVESKFSQSTGDIDKVTDTKPRVAEWRYG
PARLWYDMLGVPEDGSGFDYGFKLRKTEHEPVIKSRMIEEFRKLEENNGTDLLADENF
LMVTQLHWEDDIIWDGEDVKHKGTKPQRASLAGWLPSSMTRNAMAYNVQQGFAATL
DDDKPWYSIFPIDNEDLVYGRWEDNIIWDAQAMPRLLEPPVLTLDPNDENLILEIPDEKE
EATSNSPSKESKKESSLKKSRILLGKTGVIKEEPQQNMSQPEVKDPWNLSNDEYYYPK
QQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFHRPPLKKYSFGALSQPGPH
SVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLM
MQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLF
RAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQ
VFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKS
DFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKID
DEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEP
QPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARS
GEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSD
FEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTAS
VTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALF
DEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACG
AIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGK
QLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTL
SSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSREEF
REHLELIVKNSATYNGKNQMFRDCKGHCSDPYSLLALNSD*

TAF1_16 (AI806456, 1484 aa) (SEQ ID NO: 72)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEDESRRYQQTMGSLQPLCHSDYDEDDYDADCEDIDCKLMPPPPPPPGPMKKDKDQ
DSITGEKVDFSSSSDSESEMGPQEATQAESEDGKLTLPLAGIMQHDATKLLPSVTELF
PEFRPGKVLRFLRLFGPGKNVPSVWRSARRKRKKKHRELIQEEQIQEVECSVESEVS
QKSLWNYDYAPPPPPEQCLSDDEITMMAPVESKFSQSTGDIDKVTDTKPRVAEWRYG
PARLWYDMLGVPEDGSGFDYGFKLRKTEHEPVIKSRMIEEFRKLEENNGTDLLADENF
LMVTQLHWEDDIIWDGEDVKHKGTKPQRASLAGWLPSSMTRNAMAYNVQQGFAATL
DDDKPWYSIFPIDNEDLVYGRWEDNIIWDAQAMPRLLEPPVLTLDPNDENLILEIPDEKE
EATSNSPSKESKKESSLKKSRILLGKTGVIKEEPQQNMSQPEVKDPWNLSNDEYYYPK
QQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFHRPPLKKYSFGALSQPGPH
SVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLM
MQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLF
RAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQ
VFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKS

DFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKID
DEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEP
QPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARS
GEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSD
FEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTAS
VTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALF
DEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACG
AIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGK
QLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTL
SSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSREEF
REHLELIVKNSATYNGIGIRIKHTRSIEKGHSHHHLPRE*

TAF1_17 (1460 aa, shorter protein) (SEQ ID NO: 73)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEDESRRYQQTMGSLQPLCHSDYDEDDYDADCEDIDCKLMPPPPPPPGPMKKDKDQ
DSITGEKVDFSSSSDSESEMGPQEATQAESEDGKLTLPLAGIMQHDATKLLPSVTELF
PEFRPGKVLRFLRLFGPGKNVPSVWRSARRKRKKKHRELIQEEQIQEVECSVESEVS
QKSLWNYDYAPPPPPEQCLSDDEITMMAPVESKFSQSTGDIDKVTDTKPRVAEWRYG
PARLWYDMLGVPEDGSGFDYGFKLRKTEHEPVIKSRMIEEFRKLEENNGTDLLADENF
LMVTQLHWEDDIIWDGEDVKHKGTKPQRASLAGWLPSSMTRNAMAYNVQQGFAATL
DDDKPWYSIFPIDNEDLVYGRWEDNIIWDAQAMPRLLEPPVLTLDPNDENLILEIPDEKE
EATSNSPSKESKKESSLKKSRILLGKTGVIKEEPQQNMSQPEVKDPWNLSNDEYYYPK
QQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFHRPPLKKYSFGALSQPGPH
SVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLM
MQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLF
RAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQ
VFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKS
DFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKID
DEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEP
QPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARS
GEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSD
FEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTAS
VTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALF
DEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACG
AIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGK
QLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTL
SSILESIINDMRDLPNTYPFHTPAWMTDGDPVSKRKKKKKKRGFQSMLSTSPLGVALC
PHRANSEWRGLPPRSLL*

TAF1_18 (BG289819) (SEQ ID NO: 74)
MGPGCDLLLRTAATITAAAIMSDTDSDEDSAGGGPFSLAGFLFGNINGAGQLEGESVL
DDECKKHLAGLGALGLGSLITELTANEELTGTDGALVNDEGWVRSTEDAVDYSDINEV
AEDESRRYQQTMGSLQPLCHSDYDEDDYDADCEDIDCKLMPPPPPPPGPMKKDKDQ
DSITGEKVDFSSSSDSESEMGPQEATQAESEDGKLTLPLAGIMQHDATKLLPSVTELF
PEFRPGKVLRFLRLFGPGKNVPSVWRSARRKRKKKHRELIQEEQIQEVECSVESEVS
QKSLWNYDYAPPPPPEQCLSDDEITMMAPVESKFSQSTGDIDKVTDTKPRVAEWRYG
PARLWYDMLGVPEDGSGFDYGFKLRKTEHEPVIKSRMIEEFRKLEENNGTDLLADENF
LMVTQLHWEDDIIWDGEDVKHKGTKPQRASLAGWLPSSMTRNAMAYNVQQGFAATL
DDDKPWYSIFPIDNEDLVYGRWEDNIIWDAQAMPRLLEPPVLTLDPNDENLILEIPDEKE
EATSNSPSKESKKESSLKKSRILLGKTGVIKEEPQQNMSQPEVKDPWNLSNDEYYYPK
QQGLRGTFGGNIIQHSIPAVELRQPFFPTHMGPIKLRQFHRPPLKKYSFGALSQPGPH
SVQPLLKHIKKKAKMREQERQASGGGEMFFMRTPQDLTGKDGDLILAEYSEENGPLM

MQVGMATKIKNYYKRKPGKDPGAPDCKYGETVYCHTSPFLGSLHPGQLLQAFENNLF
RAPIYLHKMPETDFLIIRTRQGYYIRELVDIFVVGQQCPLFEVPGPNSKRANTHIRDFLQ
VFIYRLFWKSKDRPRRIRMEDIKKAFPSHSESSIRKRLKLCADFKRTGMDSNWWVLKS
DFRLPTEEEIRAMVSPEQCCAYYSMIAAEQRLKDAGYGEKSFFAPEEENEEDFQMKID
DEVRTAPWNTTRAFIAAMKGKCLLEVTGVADPTGCGEGFSYVKIPNKPTQQKDDKEP
QPVKKTVTGTDADLRRLSLKNAKQLLRKFGVPEEEIKKLSRWEVIDVVRTMSTEQARS
GEGPMSKFARGSRFSVAEHQERYKEECQRIFDLQNKVLSSTEVLSTDTDSSSAEDSD
FEEMGKNIENMLQNKKTSSQLSREREEQERKELQRMLLAAGSAASGNNHRDDDTAS
VTSLNSSATGRCLKIYRTFRDEEGKEYVRCETVRKPAVIDAYVRIRTTKDEEFIRKFALF
DEQHREEMRKERRRIQEQLRRLKRNQEKEKLKGPPEKKPKKMKERPDLKLKCGACG
AIGHMRTNKFCPLYYQTNAPPSNPVAMTEEQEEELEKTVIHNDNEELIKVEGTKIVLGK
QLIESADEVRRKSLVLKFPKQQLPPKKKRRVGTTVHCDYLNRPHKSIHRRRTDPMVTL
SSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSREEF
REHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKEDKLARLEKAINPLLDDDDQ
VAFSFILDNIVTQKMMAVPDSWPFHHPVNKKFVPDYYKVIVNPMDLETIRKNISKHKYQ
SRESFLDDVNLILANSVKYNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLEKDICTAK
EAALEEAELESLDPMTPGPYTPQPPDLYDTNTSLSMSRDASVFQDESNMSVLDIPSAT
PEKQVTQMRQGRGRLGEEDSDVDIEGYDDEEEDGKPKTPAPEGEDGDGDLADEEEG
TVQQPQASVLYEDLLMSEGEDDEEDAGSDEEGDNPFSAIQLSESGSDSDVGSGGIRP
KQPRMLQENTRMDMENEESMMSYEGDGGEASHGLEDSNISYGSYEEPDPKSNTQD
TSFSSIGGYEVSEEEEDEEEEEQRSGPSVLSQVHLSEDEEDSEDFHSIAGDSDLDSDE

TAF2 (ID: O60668)

TAF2_1 (CR997208) (SEQ ID NO: 75)
MPLTGVEPARMNRKKGDKGFESPRPYKLTHQVVCINNINFQRKSVVGFVELTIFPTVA
NLNRIKLNSKQCRIYRVRINDLEAAFIYNDPTLEVCHSESKQRNLNYFSNAYAAAVSAV
DPDAGNGELCIKVPSELWKHVDELKVLKIHINFSLDQPKGGLHFVVPSVEGSMAERGA
HVFSCGYQNSTRFWFPCVDSYSELCTWKLEFTVDAAMVAVSNGDLVETVYTHDMRK
KTFHYMLTIPTAASNISLAIGPFEILVDPYMHEVTHFCLPQLLPLLKHTTSYLHEVFEFYE
EILTCRYPYSCFKTVFIDEAYVEVAAYASMSIFSTNLLHSAMIIDETPLTRRCLAQSLAQQ
FFGCFISRMSWSDEWVLKGISGYIYGLWMKKTFGVNEYRHWIKEELDKIVAYELKTGG
VLLHPIFGGGKEKDNPASHLHFSIKHPHTLSWEYYTMFQCKAHLVMRLIENRISMEFML
QVFNKLLSLASTASSQKFQSHMWSQMLVSTSGFLKSISNVSGKDIQPLIKQWVDQSGV
VKFYGSFAFNRKRNVLELEIKQDYTSPGTQKYVGPLKVTVQELDGSFNHTLQIEENSLK
HDIPCHSKSRRNKKKKIPLMNGEEVDMDLSAMDADSPLLWIRIDPDMSVLRKVEFEQA
DFMWQYQLRYERDVVAQQESILALEKFPTPASRLALTDILEQEQCFYRVRMSACFCLA
KIANSMVSTWTGPPAMKSLFTRMFCCKSCPNIVKTNNFMSFQSYFLQKTMPVAMALL
RDVHNLCPKEVLTFILDLIKYNDNRKNKFSDNYYRAEMIDALANSVTPAVSVNNEVRTL
DNLNPDVRLILEEITRFLNMEKLLPSYRHTITVSCLRAIRVLQKNGHVPSDPALFKSYAE
YGHFVDIRIAALEAVVDYTKVDRSYEELQWLLNMIQNDPVPYVRHKILNMLTKNPPFTK
NMESPLCNEALVDQLWKLMNSGTSHDWRLRCGAVDLYFTLFGLSRPSCLPLPELGLV
LNLKEKKAVLNPTIIPESVAGNQEAANNPSSHPQLVGFQNPEDDHLAKEASCNISAHQ
QGVKRKSDTPLGSPLEPGQILEKNEDSSKVKLKIRFSSSQDEEEIDMDTVHDSQAFISH
HLNMLERPSTPGLSKYRPASSRSALIPQHSAGCDSTPTTKPQWSLELARKGTGKEQA
PLEMSMHPAASAPLSVFTKESTASKHSDHHHHHHHEHKKKKKKHKHKHKHKHKHDS
KEKDKEPFTFSSPASGRSIRSPSLSD*

TAF4 (ID: O00268)

TAF4_1 (internal 432 aa missing (22-454 aa)) (SEQ ID NO: 76)
MAAGSDLLDEVFFNSEVDEKVGMVLVRSENGQLLMIPQQALAQMQAQAHAQPQTTM
APRPATPTSAPPVQISTVQAPGTPIIARQVTPTTIIKQVSQAQTTVQPSATLQRSPGVQP

QLVLGGAAQTASLGTATAVQTGTPQRTVPGATTTSSAATETMENVKKCKNFLSTLIKL
ASSGKQSTETAANVKELVQNLLDGKIEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALR
QLTPDSAAFIQQSQQQPPPPTSQATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLS
LTQPTQVGVGKQGQPTPLVIQQPPKPGALIRPPQVTLTQTPMVALRQPHNRIMLTTPQ
QIQLNPLQPVPVVKPAVLPGTKALSAVSAQAAAAQKNKLKEPGGGSFRDDDDINDVAS
MAGVNLSEESARILATNSELVGTLTRSCKDETFLLQAPLQRRILEIGKKHGITELHPDVV
SYVSHATQQRLQNLVEKISETAQQKNFSYKDDDRYEQASDVRAQLKFFEQLDQIEKQ
RKDEQEREILMRAAKSRSRQEDPEQLRLKQKAKEMQQQELAQMRQRDANLTALAAIG
PRKKRKVDCPGPGSGAEGSGPGSVVPGSSGVGTPRQFTRQRITRVNLRDLIFCLENE
RETSHSLLLYKAFLK*

TAF5L (ID: O75529)

TAF5L_1 (shorter protein, 85 aa) (SEQ ID NO: 77)
MKRVRTEQIQMAVSCYLKRRQYVDSDGPLKQGLRLSQTAEEMAANLTVQSESGCANI
VSAAPCQAEPQQYEVQFGRLRNFLTGCL*

TAF6L (ID: Q9Y6J9)

TAF6L_1 (different C-terminus after 460 aa) (SEQ ID NO: 78)
MSEREERRFVEIPRESVRLMAESTGLELSDEVAALLAEDVCYRLREATQNSSQFMKHT
KRRKLTVEDFNRALRWSSVEAVCGYGSQEALPMRPAREGELYFPEDREVNLVELALA
TNIPKGCAETAVRVHVSYLDGKGNLAPQGSVPSAVSSLTDDLLKYYHQVTRAVLGDDP
QLMKVALQDLQTNSKIGALLPYFVYVVSGVKSVSHDLEQLHRLLQVARSLFRNPHLCL
GPYVRCLVGSVLYCVLEPLAASINPLNDHWTLRDGAALLLSHIFWTHGDLVSGLYQHIL
LSLQKILADPVRPLCCHYGAVVGLHALGWKAVERVLYPHLSTYWTNLQAVLDDYSVSN
AQVKADGHKVYGAILVAVERLLKMKAQAAEPNRGGPGGRGCRRLDDLPWDSLLFQE
SSSGGGAEPSFGSGLPLPPGGAGPEDPSLSVTLADIYRELYAFFGDSLATRFGTGLAL
RAETAHDRPYQPPRPPVGALGLLAVLAALSQWPLRSL*

TAF6L_2 (316 aa protein, different sequence after 292 aa) (SEQ ID NO: 79)
MSEREERRFVEIPRESVRLMAESTGLELSDEVAALLAEDVCYRLREATQNSSQFMKHT
KRRKLTVEDFNRALRWSSVEAVCGYGSQEALPMRPAREGELYFPEDREVNLVELALA
TNIPKGCAETAVRVHVSYLDGKGNLAPQGSVPSAVSSLTDDLLKYYHQVTRAVLGDDP
QLMKVALQDLQTNSKIGALLPYFVYVVSGVKSVSHDLEQLHRLLQVARSLFRNPHLCL
GPYVRCLVGSVLYCVLEPLAASINPLNDHWTLRDGAALLLSHIFWTHGDLVSGLYQHIL
LSRPPVGALGLLAVLAALSQWPLRSL*

TAF7L (ID: Q5H9L6)

TAF7L_1 (AK026810) (SEQ ID NO: 80)
MSESQDEVPDEVENQFILRLPLEHACTVRNLARSQSVKMKDKLKIDLLPDGRHAVVEV
EDVPLAAKLVDLPCVIESLRTLDKKTFYKTADISQMLVCTADGDIHLSPEEPAASTDPNI
VRKKERGREEKCVWKHGITPPLKNVRKKRFRKTQKKVPDVKEMEKSSFTEYIESPDVE
NEVKRLLRSDAEAVSTRWEVIAEDGTKEIESQGSIPGFLISSGMSSHKQGHTSSVMEIQ
KQIEKKEKKLHKIQNKAQRQKDLIMKVENLTLKNHFQSVLEQLELQEKQKNEKLISLQE
QLQRFLKK*

TAF7L_2 (different sequence after 135 aa) (SEQ ID NO: 81)
MSESQDEVPDEVENQFILRLPLEHACTVRNLARSQSVKMKDKLKIDLLPHFPTGTVAAF
SEEVRRAIGVAHKPWIHHPDCRLDETVHVFVPSVALC*

TAF8 (ID: Q7Z7C8)

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TAF8_1 (different C-terminus after 164 aa) (SEQ ID NO: 82)
MADAAATAGAGGSGTRSGSKQSTNPADNYHLARRRTLQVVVSSLLTEAGFESAEKAS
VETLTEMLQSYISEIGRSAKSYCEHTARTQPTLSDIVVTLVEMGFNVDTLPAYAKRSQR
MVITAPPVTNQPVTPKALTAGQNRPHPPHIPSHFPEFPDPHTYIKTPEDSGAEKENTSV
LQQNPSLSGSRNGEENIIDNPYLRPVKKPKIRRKKPDTF*

TAF15 (ID: Q92804)

TAF15_1 (different C-terminus after 393aa) (SEQ ID NO: 83)
MSDSGSYGQSGGEQQSYSTYGNPGSQGYGQASQSYSGYGQTTDSSYGQNYSGYS
SYGQSQSGYSQSYGGYENQKQSSYSQQPYNNQGQQQNMESSGSQGGRAPSYDQP
DYGQQDSYDQQSGYDQHQGSYDEQSNYDQQHDSYSQNQQSYHSQRENYSHHTQD
DRRDVSRYGEDNRGYGGSQGGGRGRGGYDKDGRGPMTGSSGGDRGGFKNFGGH
RDYGPRTDADSESDNSDNNTIFVQGLGEGVSTDQVGEFFKQIGIIKTNKKTGKPMINLY
TDKDTGKPKGEATVSFDDPPSAKAAIDWFDGKEFHGNIIKVSFATRRPEFMRGGGSG
GGRRGRGGYRGRGGFQGRGGDPKSGDWVCPNPSCGNMNFARRNSCNQCNEPRP
EDSRPSGGETTTEMISATDHTDDCFECSFVSDMIHSEIARVLPAAFLVASSWVVKLSDI
WIFIWVGGLGQFFF*

TAF15_2 (internal 112 aa missing (439-551 aa)) (SEQ ID NO: 84)
MSDSGSYGQSGGEQQSYSTYGNPGSQGYGQASQSYSGYGQTTDSSYGQNYSGYS
SYGQSQSGYSQSYGGYENQKQSSYSQQPYNNQGQQQNMESSGSQGGRAPSYDQP
DYGQQDSYDQQSGYDQHQGSYDEQSNYDQQHDSYSQNQQSYHSQRENYSHHTQD
DRRDVSRYGEDNRGYGGSQGGGRGRGGYDKDGRGPMTGSSGGDRGGFKNFGGH
RDYGPRTDADSESDNSDNNTIFVQGLGEGVSTDQVGEFFKQIGIIKTNKKTGKPMINLY
TDKDTGKPKGEATVSFDDPPSAKAAIDWFDGKEFHGNIIKVSFATRRPEFMRGGGSG
GGRRGRGGYRGRGGFQGRGGDPKSGDWVCPNPSCGNMNFARRNSCNQCNEPRP
EDSRPSGGDFRGRGYGGERGYRGRGGRGGDRGGYGGDRSGGGYGGDRSSGGGY
SGDRSGGGYGGDRGGGYGGDRGGYGGKMGGRNDYRNDQRNRPY*

TAF15_3 (internal 60 aa missing (469-529 aa)) (SEQ ID NO: 85)
MSDSGSYGQSGGEQQSYSTYGNPGSQGYGQASQSYSGYGQTTDSSYGQNYSGYS
SYGQSQSGYSQSYGGYENQKQSSYSQQPYNNQGQQQNMESSGSQGGRAPSYDQP
DYGQQDSYDQQSGYDQHQGSYDEQSNYDQQHDSYSQNQQSYHSQRENYSHHTQD
DRRDVSRYGEDNRGYGGSQGGGRGRGGYDKDGRGPMTGSSGGDRGGFKNFGGH
RDYGPRTDADSESDNSDNNTIFVQGLGEGVSTDQVGEFFKQIGIIKTNKKTGKPMINLY
TDKDTGKPKGEATVSFDDPPSAKAAIDWFDGKEFHGNIIKVSFATRRPEFMRGGGSG
GGRRGRGGYRGRGGFQGRGGDPKSGDWVCPNPSCGNMNFARRNSCNQCNEPRP
EDSRPSGGDFRGRGYGGERGYRGRGGRGGDRGGYGGDRSGGGYGGDRSSGGGY
SGDRSGGGYGGDRSGGGYGGDRGGGYGGDRGGGYGGDRGGGSGYGGDRSGGY
GGDRSGGGYGGDRGGGYGGDRGGYGGKMGGRNDYRNDQRNRPY*

TAF15_4 (BU192829) (SEQ ID NO: 86)
MSDSGSYGQSGGEQQSYSTYGNPGSQGYGQASQSYSGYGQTTDSSYGQNYSGYS
SYGQSQSGYSQSYGGYENQKQSSYSQQPYNNQGQQQNMESSGSQGGRAPSYDQP
DYGQQDSYDQQSGYDQHQGSYDEQSNYDQQHDSYSQNQQSYHSQRENYSHHTQD
DRRDVSRYGEDNRGYDKDGRGPMTGSSGGDRGGFKNFGGHRDYGPRTDADSESD
NSDNNTIFVQGLGEGVSTDQVGEFFKQIGIIKTNKKTGKPMINLYTDKDTGKPKGEATV
SFDDPPSAKAAIDWFDGKEFHGNIIKVSFATRRPEFMRGGGSGGGRRGRGGYRGRG
GFQGRGGDPKSGDWVCPNPSCGNMNFARRNSCNQCNEPRPEDSRPSGGDFRGRG
YGGERGYRGRGGRGGDRGGYGGDRSGGGYGGDRSSGGGYSGDRSGGGYGGDR
SGGGYGGDRGGGYGGDRGGGYGGDRGGGYGGDRGGYGGDRGGGYGGDRGGYG

GDRGGYGGDRGGYGGDRGGYGGDRSRGGYGGDRGGGSGYGGDRSGGYGGDRS
GGGYGGDRGGGYGGDRGGYGGKMGGRNDYRNDQRNRPY

MED1 (ID: Q15648)

MED1_1 (internal 421 aa missing (203-624 aa)) (SEQ ID NO: 87)
MKAQGETEESEKLSKMSSLLERLHAKFNQNRPWSETIKLVRQVMEKRVVMSSGGHQ
HLVSCLETLQKALKVTSLPAMTDRLESIARQNGLGSHLSASGTECYITSDMFYVEVQLD
PAGQLCDVKVAHHGENPVSCPELVQQLREKNFDEFSKHLKGLVNLYNLPGDNKLKTK
MYLALQSLEQDLSKMAIMYWKATNAGPLDKIPHHTPPPVSSMAGNTKNHPMLMNLLK
DNPAQDFSTLYGSSPLERQNSSSGSPRMEICSGSNKTKKKKSSRLPPEKPKHQTEDD
FQRELFSMDVDSQNPIFDVNMTADTLDTPHITPAPSQCSTPPTTYPQPVPHPQPSIQR
MVRLSSSDSIGPDVTDILSDIAEEASKLPSTSDDCPAIGTPLRDSSSSGHSQSTLFDSD
VFQTNNNENPYTDPADLIADAAGSPSSDSPTNHFFHDGVDFNPDLLNSQSQSGFGEE
YFDESSQSGDNDDFKGFASQALNTLGVPMLGGDNGETKFKGNNQADTVDFSIISVAG
KALAPADLMEHHSGSQGPLLTTGDLGKEKTQKRVKEGNGTSNSTLSGPGLDSKPGKR
SRTPSNDGKSKDKPPKRKKADTEGKSPSHSSSNRPFTPPTSTGGSKSPGSAGRSQT
PPGVATPPIPKITIQIPKGTVMVGKPSSHSQYTSSGSVSSSGSKSHHSHSSSSSSSAST
SGKMKSSKSEGSSSSKLSSSMYSSQGSSGSSQSKNSSQSGGKPGSSPITKHGLSSG
SSSTKMKPQGKPSSLMNPSLSKPNISPSHSRPPGGSDKLASPMKPVPGTPPSSKAKS
PISSGSGGSHMSGTSSSSGMKSSSGLGSSGSLSQKTPPSSNSCTASSSSFSSSGSS
MSSSQNQHGSSKGKSPSRNKKPSLTAVIDKLKHGVVTSGPGGEDPLDGQMGVSTNS
SSHPMSSKHNMSGGEFQGKREKSDKDKSKVSTSGSSVDSSKKTSESKNVGSTGVAK
IIISKHDGGSPSIKAKVTLQKPGESSGEGLRPQMASSKNYGSPLISGSTPKHERGSPSH
SKSPAYTPQNLDSESESGSSIAEKSYQNSPSSDDGIRPLPEYSTEKHKKHKKEKKKVK
DKDRDRDRDKDRDKKKSHSIKPESWSKSPISSDQSLSMTSNTILSADRPSRLSPDFMI
GEEDDDLMDVALIGN

MED1_2 (78 aa protein, different sequence after 62 aa) (SEQ ID NO: 88)
MKAQGETEESEKLSKMSSLLERLHAKFNQNRPWSETIKLVRQVMEKRVVMSSGGHQ
HLVSCLFDGRQHQEPPDAHEPS*

MED1_3 (584 aa protein, different sequence after 547 aa) (SEQ ID NO: 4)
MKAQGETEESEKLSKMSSLLERLHAKFNQNRPWSETIKLVRQVMEKRVVMSSGGHQ
HLVSCLETLQKALKVTSLPAMTDRLESIARQNGLGSHLSASGTECYITSDMFYVEVQLD
PAGQLCDVKVAHHGENPVSCPELVQQLREKNFDEFSKHLKGLVNLYNLPGDNKLKTK
MYLALQSLEQDLSKMAIMYWKATNAGPLDKILHGSVGYLTPRSGGHLMNLKYYVSPS
DLLDDKTASPIILHENNVSRSLGMNASVTIEGTSAVYKLPIAPLIMGSHPVDNKWTPSFS
SITSANSVDLPACFFLKFPQPIPVSRAFVQKLQNCTGIPLFETQPTYAPLYELITQFELSK
DPDPIPLNHNMRFYAALPGQQHCYFLNKDAPLPDGRSLQGTLVSKITFQHPGRVPLILN
LIRHQVAYNTLIGSCVKRTILKEDSPGLLQFEVCPLSESRFSVSFQHPVNDSLVCVVMD
VQDSTHVSCKLYKGLSDALICTDDFIAKVVQRCMSIPVTMRAIRRKAETIQADTPALSLI
AETVEDMVKKNLPPASSPGERGVYHWLESDPSSSHAATCLFDGRQHQEPPDAHEPS*

MED1_4 (311 aa missing (1148-1459 aa)) (SEQ ID NO: 89)
MKAQGETEESEKLSKMSSLLERLHAKFNQNRPWSETIKLVRQVMEKRVVMSSGGHQ
HLVSCLETLQKALKVTSLPAMTDRLESIARQNGLGSHLSASGTECYITSDMFYVEVQLD
PAGQLCDVKVAHHGENPVSCPELVQQLREKNFDEFSKHLKGLVNLYNLPGDNKLKTK
MYLALQSLEQDLSKMAIMYWKATNAGPLDKILHGSVGYLTPRSGGHLMNLKYYVSPS
DLLDDKTASPIILHENNVSRSLGMNASVTIEGTSAVYKLPIAPLIMGSHPVDNKWTPSFS
SITSANSVDLPACFFLKFPQPIPVSRAFVQKLQNCTGIPLFETQPTYAPLYELITQFELSK
DPDPIPLNHNMRFYAALPGQQHCYFLNKDAPLPDGRSLQGTLVSKITFQHPGRVPLILN
LIRHQVAYNTLIGSCVKRTILKEDSPGLLQFEVCPLSESRFSVSFQHPVNDSLVCVVMD

VQDSTHVSCKLYKGLSDALICTDDFIAKVVQRCMSIPVTMRAIRRKAETIQADTPALSLI
AETVEDMVKKNLPPASSPGYGMTTGNNPMSGTTTSTNTFPGGPIATLFNMSMSIKDR
HESVGHGEDFSKVSQNPILTSLLQITGNGGSTIGSSPTPPHHTPPPVSSMAGNTKNHP
MLMNLLKDNPAQDFSTLYGSSPLERQNSSSGSPRMEICSGSNKTKKKKSSRLPPEKP
KHQTEDDFQRELFSMDVDSQNPIFDVNMTADTLDTPHITPAPSQCSTPPTTYPQPVPH
PQPSIQRMVRLSSSDSIGPDVTDILSDIAEEASKLPSTSDDCPAIGTPLRDSSSSGHSQ
STLFDSDVFQTNNNENPYTDPADLIADAAGSPSSDSPTNHFFHDGVDFNPDLLNSQSQ
SGFGEEYFDESSQSGDNDDFKGFASQALNTLGVPMLGGDNGETKFKGNNQADTVDF
SIISVAGKALAPADLMEHHSGSQGPLLTTGDLGKEKTQKRVKEGNGTSNSTLSGPGLD
SKPGKRSRTPSNDGKSKDKPPKRKKADTEGKSPSHSSSNRPFTPPTSTGGSKSPGSA
GRSQTPPGVATPPIPKITIQIPKGTVMVGKPSSHSQYTSSGSVSSSGSKSHHSHSSSS
SSSASTSGKMKSSKSEGSSSSKLSSSMYSSQGSSGSSQSKNSSQNLDSESESGSSIA
EKSYQNSPSSDDGIRPLPEYSTEKHKKHKKEKKKVKDKDRDRDRDKDRDKKKSHSIK
PESWSKSPISSDQSLSMTSNTILSADRPSRLSPDFMIGEEDDDLMDVALIGN

MED1_5 (internal 26 aa missing (167-193 aa)) (SEQ ID NO: 90)
MKAQGETEESEKLSKMSSLLERLHAKFNQNRPWSETIKLVRQVMEKRVVMSSGGHQ
HLVSCLETLQKALKVTSLPAMTDRLESIARQNGLGSHLSASGTECYITSDMFYVEVQLD
PAGQLCDVKVAHHGENPVSCPELVQQLREKNFDEFSKHLKGLVNLYNLPGDKKATNA
GPLDKILHGSVGYLTPRSGGHLMNLKYYVSPSDLLDDKTASPIILHENNVSRSLGMNAS
VTIEGTSAVYKLPIAPLIMGSHPVDNKWTPSFSSITSANSVDLPACFFLKFPQPIPVSRA
FVQKLQNCTGIPLFETQPTYAPLYELITQFELSKDPDPIPLNHNMRFYAALPGQQHCYF
LNKDAPLPDGRSLQGTLVSKITFQHPGRVPLILNLIRHQVAYNTLIGSCVKRTILKEDSP
GLLQFEVCPLSESRFSVSFQHPVNDSLVCVVMDVQDSTHVSCKLYKGLSDALICTDDF
IAKVVQRCMSIPVTMRAIRRKAETIQADTPALSLIAETVEDMVKKNLPPASSPGYGMTT
GNNPMSGTTTSTNTFPGGPIATLFNMSMSIKDRHESVGHGEDFSKVSQNPILTSLLQIT
GNGGSTIGSSPTPPHHTPPPVSSMAGNTKNHPMLMNLLKDNPAQDFSTLYGSSPLER
QNSSSGSPRMEICSGSNKTKKKKSSRLPPEKPKHQTEDDFQRELFSMDVDSQNPIFD
VNMTADTLDTPHITPAPSQCSTPPTTYPQPVPHPQPSIQRMVRLSSSDSIGPDVTDILS
DIAEEASKLPSTSDDCPAIGTPLRDSSSSGHSQSTLFDSDVFQTNNNENPYTDPADLIA
DAAGSPSSDSPTNHFFHDGVDFNPDLLNSQSQSGFGEEYFDESSQSGDNDDFKGFA
SQALNTLGVPMLGGDNGETKFKGNNQADTVDFSIISVAGKALAPADLMEHHSGSQGP
LLTTGDLGKEKTQKRVKEGNGTSNSTLSGPGLDSKPGKRSRTPSNDGKSKDKPPKRK
KADTEGKSPSHSSSNRPFTPPTSTGGSKSPGSAGRSQTPPGVATPPIPKITIQIPKGTV
MVGKPSSHSQYTSSGSVSSSGSKSHHSHSSSSSSSASTSGKMKSSKSEGSSSSKLS
SSMYSSQGSSGSSQSKNSSQSGGKPGSSPITKHGLSSGSSSTKMKPQGKPSSLMNP
SLSKPNISPSHSRPPGGSDKLASPMKPVPGTPPSSKAKSPISSGSGGSHMSGTSSSS
GMKSSSGLGSSGSLSQKTPPSSNSCTASSSSFSSSGSSMSSSQNQHGSSKGKSPSR
NKKPSLTAVIDKLKHGVVTSGPGGEDPLDGQMGVSTNSSSHPMSSKHNMSGGEFQG
KREKSDKDKSKVSTSGSSVDSSKKTSESKNVGSTGVAKIIISKHDGGSPSIKAKVTLQK
PGESSGEGLRPQMASSKNYGSPLISGSTPKHERGSPSHSKSPAYTPQNLDSESESGS
SIAEKSYQNSPSSDDGIRPLPEYSTEKHKKHKKEKKKVKDKDRDRDRDKDRDKKKSH
SIKPESWSKSPISSDQSLSMTSNTILSADRPSRLSPDFMIGEEDDDLMDVALIGN

MED1_6 (internal 25 aa missing (143-168 aa)) (SEQ ID NO: 91)
MKAQGETEESEKLSKMSSLLERLHAKFNQNRPWSETIKLVRQVMEKRVVMSSGGHQ
HLVSCLETLQKALKVTSLPAMTDRLESIARQNGLGSHLSASGTECYITSDMFYVEVQLD
PAGQLCDVKVAHHGENPVSCPELVQQLSKLKTKMYLALQSLEQDLSKMAIMYWKATN
AGPLDKILHGSVGYLTPRSGGHLMNLKYYVSPSDLLDDKTASPIILHENNVSRSLGMNA
SVTIEGTSAVYKLPIAPLIMGSHPVDNKWTPSFSSITSANSVDLPACFFLKFPQPIPVSR
AFVQKLQNCTGIPLFETQPTYAPLYELITQFELSKDPDPIPLNHNMRFYAALPGQQHCY
FLNKDAPLPDGRSLQGTLVSKITFQHPGRVPLILNLIRHQVAYNTLIGSCVKRTILKEDSP
GLLQFEVCPLSESRFSVSFQHPVNDSLVCVVMDVQDSTHVSCKLYKGLSDALICTDDF

IAKVVQRCMSIPVTMRAIRRKAETIQADTPALSLIAETVEDMVKKNLPPASSPGYGMTT
GNNPMSGTTTSTNTFPGGPIATLFNMSMSIKDRHESVGHGEDFSKVSQNPILTSLLQIT
GNGGSTIGSSPTPPHHTPPPVSSMAGNTKNHPMLMNLLKDNPAQDFSTLYGSSPLER
QNSSSGSPRMEICSGSNKTKKKKSSRLPPEKPKHQTEDDFQRELFSMDVDSQNPIFD
VNMTADTLDTPHITPAPSQCSTPPTTYPQPVPHPQPSIQRMVRLSSSDSIGPDVTDILS
DIAEEASKLPSTSDDCPAIGTPLRDSSSSGHSQSTLFDSDVFQTNNNENPYTDPADLIA
DAAGSPSSDSPTNHFFHDGVDFNPDLLNSQSQSGFGEEYFDESSQSGDNDDFKGFA
SQALNTLGVPMLGGDNGETKFKGNNQADTVDFSIISVAGKALAPADLMEHHSGSQGP
LLTTGDLGKEKTQKRVKEGNGTSNSTLSGPGLDSKPGKRSRTPSNDGKSKDKPPKRK
KADTEGKSPSHSSSNRPFTPPTSTGGSKSPGSAGRSQTPPGVATPPIPKITIQIPKGTV
MVGKPSSHSQYTSSGSVSSSGSKSHHSHSSSSSSSASTSGKMKSSKSEGSSSSKLS
SSMYSSQGSSGSSQSKNSSQSGGKPGSSPITKHGLSSGSSSTKMKPQGKPSSLMNP
SLSKPNISPSHSRPPGGSDKLASPMKPVPGTPPSSKAKSPISSGSGGSHMSGTSSSS
GMKSSSGLGSSGSLSQKTPPSSNSCTASSSSFSSSGSSMSSSQNQHGSSKGKSPSR
NKKPSLTAVIDKLKHGVVTSGPGGEDPLDGQMGVSTNSSmSHPMSSKHNMSGGEFQ
GKREKSDKDKSKVSTSGSSVDSSKKTSESKNVGSTGVAKIIISKHDGGSPSIKAKVTLQ
KPGESSGEGLRPQMASSKNYGSPLISGSTPKHERGSPSHSKSPAYTPQNLDSESESG
SSIAEKSYQNSPSSDDGIRPLPEYSTEKHKKHKKEKKKVKDKDRDRDRDKDRDKKKS
HSIKPESWSKSPISSDQSLSMTSNTILSADRPSRLSPDFMIGEEDDDLMDVALIGN

MED1_7 (different sequence after 547 aa) (SEQ ID NO: 92)
MKAQGETEESEKLSKMSSLLERLHAKFNQNRPWSETIKLVRQVMEKRVVMSSGGHQ
HLVSCLETLQKALKVTSLPAMTDRLESIARQNGLGSHLSASGTECYITSDMFYVEVQLD
PAGQLCDVKVAHHGENPVSCPELVQQLREKNFDEFSKHLKGLVNLYNLPGDNKLKTK
MYLALQSLEQDLSKMAIMYWKATNAGPLDKILHGSVGYLTPRSGGHLMNLKYYVSPS
DLLDDKTASPIILHENNVSRSLGMNASVTIEGTSAVYKLPIAPLIMGSHPVDNKWTPSFS
SITSANSVDLPACFFLKFPQPIPVSRAFVQKLQNCTGIPLFETQPTYAPLYELITQFELSK
DPDPIPLNHNMRFYAALPGQQHCYFLNKDAPLPDGRSLQGTLVSKITFQHPGRVPLILN
LIRHQVAYNTLIGSCVKRTILKEDSPGLLQFEVCPLSESRFSVSFQHPVNDSLVCVVMD
VQDSTHVSCKLYKGLSDALICTDDFIAKVVQRCMSIPVTMRAIRRKAETIQADTPALSLI
AETVEDMVKKNLPPASSPGERGVYHWLESDPSSSHAATCLFDGRQHQEPPDAHEPS*

MED1_8 (1150 aa protein (C-terminus shorter)) (SEQ ID NO: 93)
MKAQGETEESEKLSKMSSLLERLHAKFNQNRPWSETIKLVRQVMEKRVVMSSGGHQ
HLVSCLETLQKALKVTSLPAMTDRLESIARQNGLGSHLSASGTECYITSDMFYVEVQLD
PAGQLCDVKVAHHGENPVSCPELVQQLREKNFDEFSKHLKGLVNLYNLPGDNKLKTK
MYLALQSLEQDLSKMAIMYWKATNAGPLDKILHGSVGYLTPRSGGHLMNLKYYVSPS
DLLDDKTASPIILHENNVSRSLGMNASVTIEGTSAVYKLPIAPLIMGSHPVDNKWTPSFS
SITSANSVDLPACFFLKFPQPIPVSRAFVQKLQNCTGIPLFETQPTYAPLYELITQFELSK
DPDPIPLNHNMRFYAALPGQQHCYFLNKDAPLPDGRSLQGTLVSKITFQHPGRVPLILN
LIRHQVAYNTLIGSCVKRTILKEDSPGLLQFEVCPLSESRFSVSFQHPVNDSLVCVVMD
VQDSTHVSCKLYKGLSDALICTDDFIAKVVQRCMSIPVTMRAIRRKAETIQADTPALSLI
AETVEDMVKKNLPPASSPGYGMTTGNNPMSGTTTSTNTFPGGPIATLFNMSMSIKDR
HESVGHGEDFSKVSQNPILTSLLQITGNGGSTIGSSPTPPHHTPPPVSSMAGNTKNHP
MLMNLLKDNPAQDFSTLYGSSPLERQNSSSGSPRMEICSGSNKTKKKKSSRLPPEKP
KHQTEDDFQRELFSMDVDSQNPIFDVNMTADTLDTPHITPAPSQCSTPPTTYPQPVPH
PQPSIQRMVRLSSSDSIGPDVTDILSDIAEEASKLPSTSDDCPAIGTPLRDSSSSGHSQ
STLFDSDVFQTNNNENPYTDPADLIADAAGSPSSDSPTNHFFHDGVDFNPDLLNSQSQ
SGFGEEYFDESSQSGDNDDFKGFASQALNTLGVPMLGGDNGETKFKGNNQADTVDF
SIISVAGKALAPADLMEHHSGSQGPLLTTGDLGKEKTQKRVKEGNGTSNSTLSGPGLD
SKPGKRSRTPSNDGKSKDKPPKRKKADTEGKSPSHSSSNRPFTPPTSTGGSKSPGSA
GRSQTPPGVATPPIPKITIQIPKGTVMVGKPSSHSQYTSSGSVSSSGSKSHHSHSSSS
SSSASTSGKMKSSKSEGSSSSKLSSSMYSSQGSSGSSQSKNSSQTL*

MED4 (ID: Q9NPJ6)

MED4_1 (BG771094) (SEQ ID NO: 94)
MAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLEVLSRELIEMLAISRNQKLLQ
AGEENQVLELLIHRDGEFQELMKLALNQGKIHHEMQVLEKEVEKRDSDIQQLQKQLKE
AEQILATAVYQAKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWVPGDPRRPY
PTDLEMRSGLLGQMNNPSTNGVNGHLPGDALAAGRLPDVLAPQYPWQSNDMSMNM
LPPNHSSDFLLEPPGHNKENEDDVEIMSTDSSSSSSESD

MED6 (ID: O75586)

MED6_1 (BM802752; 257aa, C-terminus 12 aa longer) (SEQ ID NO: 95)
MAAVDIRDNLLGISWVDSSWIPILNSGSVLDYFSERSNPFYDRTCNNEVVKMQRLTLE
HLNQMVGIEYILLHAQEPILFIIRKQQRQSPAQVIPLADYYIIAGVIYQAPDLGSVINSRVL
TAVHGIQSAFDEAMSYCRYHPSKGYWWHFKDHEEQDKVRPKAKRKEEPSSIFQRQR
VDALLLDLRQKFPPKFVQLKPGEKPVPVDQTKKEAEPIPETVKPEEKETTKNVQQTVS
AKGPPEKRMRLHYIILSIKINSC*

MED6_2 (BP350015; 97 aa protein) (SEQ ID NO: 96)
MAAVDIRDNLLGISWVDSSWIPILNSGSVLDYFSERSNPFYDRTCNNEVVKMQRLTLE
HLNQMVGIEYILLHAQEPILFIIRKQQRQSPAQGKMCKL

MED6_3 (different sequence after 205 aa) (SEQ ID NO: 97)
MAAVDIRDNLLGISWVDSSWIPILNSGSVLDYFSERSNPFYDRTCNNEVVKMQRLTLE
HLNQMVGIEYILLHAQEPILFIIRKQQRQSPAQVIPLADYYIIAGVIYQAPDLGSVINSRVL
TAVHGIQSAFDEAMSYCRYHPSKGYWWHFKDHEEQDKVRPKAKRKEEPSSIFQRQR
VDALLLDLRQKFPPKFVQLKPGEKPVPVDHLRSEVQDQPDQYGETPSLLKIQKLAGRG
GGRP*

MED10 (ID: Q8N2G1)

MED10_1 (BI462618; 69 aa protein) (SEQ ID NO: 98)
MAEKFDHLEEHLEKFVENIRQLGIIVSDFQPSSQAGLNQKLNFIVTGLQDIDKCRQQLH
DITVPLEVFE*

MED11 (ID: Q6NS89)

MED11_1 (AL534685; 93 aa protein, different sequence after 74 aa) (SEQ ID NO: 99)
MATYSLANERLRALEDIEREIGAILQNAGTVILELSKEKTNERLLDRQAAAFTASVQHVE
AELSAQIRYLTQVGVSGGFCERTPALGQSLRLG*

MED12 (ID: Q7Z3Z5)

MED12_1 (96 aa missing (1904-2000 aa)) (SEQ ID NO: 100)
MKQSMPSLHTKKILFCYFHLTNSWCLRRYGLGKMAAFGILSYEHRPLKRPRPRLGPPD
VYPQDPKQKEDELTALNVKQGFNNQPAVSGDEHGSAKNVSFNPAKISSNFSSIIAEKL
RCNTLPDTGRRKPQVNQKDNFWLVTARSQSAINTWFTDLAGTKPLTQLAKKVPIFSKK
EEVFGYLAKYTVPVMRAAWLIKMTCAYYAAISETKVKKRHVDPFMEWTQIITKYLWEQL
QKMAEYYRPGPAGSGGCGSTIGPLPHDVEVAIRQWDYTEKLAMFMFQDGMLDRHEF
LTWVLECFEKIRPGEDELLKLLLPLLLRYSGEFVQSAYLSRRLAYFCTRRLALQLDGVS
SHSSHVISAQSTSTLPTTPAPQPPTSSTPSTPFSDLLMCPQHRPLVFGLSCILQTILLCC
PSALVWHYSLTDSRIKTGSPLDHLPIAPSNLPMPEGNSAFTQQVRAKLREIEQQIKERG

QAVEVRWSFDKCQEATAGFTIGRVLHTLEVLDSHSFERSDFSNSLDSLCNRIFGLGPS
KDGHEISSDDDAVVSLLCEWAVSCKRSGRHRAMVVAKLLEKRQAEIEAERCGESEAA
DEKGSIASGSLSAPSAPIFQDVLLQFLDTQAPMLTDPRSESERVEFFNLVLLFCELIRHD
VFSHNMYTCTLISRGDLAFGAPGPRPPSPFDDPADDPEHKEAEGSSSSKLEDPGLSE
SMDIDPSSSVLFEDMEKPDFSLFSPTMPCEGKGSPSPEKPDVEKEVKPPPKEKIEGTL
GVLYDQPRHVQYATHFPIPQEESCSHECNQRLVVLFGVGKQRDDARHAIKKITKDILKV
LNRKGTAETDQLAPIVPLNPGDLTFLGGEDGQKRRRNRPEAFPTAEDIFAKFQHLSHY
DQHQVTAQVSRNVLEQITSFALGMSYHLPLVQHVQFIFDLMEYSLSISGLIDFAIQLLNE
LSVVEAELLLKSSDLVGSYTTSLCLCIVAVLRHYHACLILNQDQMAQVFEGLCGVVKHG
MNRSDGSSAERCILAYLYDLYTSCSHLKNKFGELFSDFCSKVKNTIYCNVEPSESNMR
WAPEFMIDTLENPAAHTFTYTGLGKSLSENPANRYSFVCNALMHVCVGHHDPDRVND
IAILCAELTGYCKSLSAEWLGVLKALCCSSNNGTCGFNDLLCNVDVSDLSFHDSLATFV
AILIARQCLLLEDLIRCAAIPSLLNAACSEQDSEPGARLTCRILLHLFKTPQLNPCQSDGN
KPTVGIRSSCDRHLLAASQNRIVDGAVFAVLKAVFVLGDAELKGSGFTVTGGTEELPEE
EGGGGSGGRRQGGRNISVETASLDVYAKYVLRSICQQEWVGERCLKSLCEDSNDLQ
DPVLSSAQAQRLMQLICYPHRLLDNEDGENPQRQRIKRILQNLDQWTMRQSSLELQL
MIKQTPNNEMNSLLENIAKATIEVFQRSAETGSSSGSTASNMPSSSKTKPVLSSLERSG
VWLVAPLIAKLPTSVQGHVLKAAGEELEKGQHLGSSSRKERDRQKQKSMSLLSQQPF
LSLVLTCLKGQDEQREGLLTSLYSQVHQIVNNWRDDQYLDDCKPKQLMHEALKLRLNL
VGGMFDTVQRSTQQTTEWAMLLLEIIISGTVDMQSNNELFTTVLDMLSVLINGTLAADM
SSISQGSMEENKRAYMNLAKKLQKELGERQSDSLEKVRQLLPLPKQTRDVITCEPQGS
LIDTKGNKIAGFDSIFKKEGLQVSTKQKISPWDLFEGLKPSAPLSWGWFGTVRVDRRV
ARGEEQQRLLLYHTHLRPRPRAYYLEPLPLPPEDEEPPAPTLLEPEKKAPEPPKTDKP
GAAPPSTEERKKKSTKGKKRSQPATKTEDYGMGPGRSGPYGVTVPPDLLHHPNPGSI
THLNYRQGSIGLYTQNQPLPAGGPRVDPYRPVRLPMQKLPPSYSSQPYQSTHPSTNP
TLVDPTRHLQQRPSGYVHQQAPTYGHGLTSTQRFSHQTLQQTPMISTMTPMSAQGV
QAGVRSTAILPEQQQQQQQQQQQQQQQQQQQQQQQQQQQQYHIRQQQQQQILRQQQ
QQQQQQQQQQQQQQQQQQQQQQQQQHQQQQQQQAAPPQPQPQSQPQFQRQGLQ
QTQQQQQTAALVRQLQQQLSNTQPQPSTNIFGRY*

MED12_2 (25 aa missing (1996-2021 aa)) (SEQ ID NO: 101)
MKQSMPSLHTKKILFCYFHLTNSWCLRRYGLGKMAAFGILSYEHRPLKRPRPRLGPPD
VYPQDPKQKEDELTALNVKQGFNNQPAVSGDEHGSAKNVSFNPAKISSNFSSIIAEKL
RCNTLPDTGRRKPQVNQKDNFWLVTARSQSAINTWFTDLAGTKPLTQLAKKVPIFSKK
EEVFGYLAKYTVPVMRAAWLIKMTCAYYAAISETKVKKRHVDPFMEWTQIITKYLWEQL
QKMAEYYRPGPAGSGGCGSTIGPLPHDVEVAIRQWDYTEKLAMFMFQDGMLDRHEF
LTWVLECFEKIRPGEDELLKLLLPLLLRYSGEFVQSAYLSRRLAYFCTRRLALQLDGVS
SHSSHVISAQSTSTLPTTPAPQPPTSSTPSTPFSDLLMCPQHRPLVFGLSCILQTILLCC
PSALVWHYSLTDSRIKTGSPLDHLPIAPSNLPMPEGNSAFTQQVRAKLREIEQQIKERG
QAVEVRWSFDKCQEATAGFTIGRVLHTLEVLDSHSFERSDFSNSLDSLCNRIFGLGPS
KDGHEISSDDDAVVSLLCEWAVSCKRSGRHRAMVVAKLLEKRQAEIEAERCGESEAA
DEKGSIASGSLSAPSAPIFQDVLLQFLDTQAPMLTDPRSESERVEFFNLVLLFCELIRHD
VFSHNMYTCTLISRGDLAFGAPGPRPPSPFDDPADDPEHKEAEGSSSSKLEDPGLSE
SMDIDPSSSVLFEDMEKPDFSLFSPTMPCEGKGSPSPEKPDVEKEVKPPPKEKIEGTL
GVLYDQPRHVQYATHFPIPQEESCSHECNQRLVVLFGVGKQRDDARHAIKKITKDILKV
LNRKGTAETDQLAPIVPLNPGDLTFLGGEDGQKRRRNRPEAFPTAEDIFAKFQHLSHY
DQHQVTAQVSRNVLEQITSFALGMSYHLPLVQHVQFIFDLMEYSLSISGLIDFAIQLLNE
LSVVEAELLLKSSDLVGSYTTSLCLCIVAVLRHYHACLILNQDQMAQVFEGLCGVVKHG
MNRSDGSSAERCILAYLYDLYTSCSHLKNKFGELFSDFCSKVKNTIYCNVEPSESNMR
WAPEFMIDTLENPAAHTFTYTGLGKSLSENPANRYSFVCNALMHVCVGHHDPDRVND
IAILCAELTGYCKSLSAEWLGVLKALCCSSNNGTCGFNDLLCNVDVSDLSFHDSLATFV
AILIARQCLLLEDLIRCAAIPSLLNAACSEQDSEPGARLTCRILLHLFKTPQLNPCQSDGN
KPTVGIRSSCDRHLLAASQNRIVDGAVFAVLKAVFVLGDAELKGSGFTVTGGTEELPEE

EGGGGSGGRRQGGRNISVETASLDVYAKYVLRSICQQEWVGERCLKSLCEDSNDLQ
DPVLSSAQAQRLMQLICYPHRLLDNEDGENPQRQRIKRILQNLDQWTMRQSSLELQL
MIKQTPNNEMNSLLENIAKATIEVFQRSAETGSSSGSTASNMPSSSKTKPVLSSLERSG
VWLVAPLIAKLPTSVQGHVLKAAGEELEKGQHLGSSSRKERDRQKQKSMSLLSQQPF
LSLVLTCLKGQDEQREGLLTSLYSQVHQIVNNWRDDQYLDDCKPKQLMHEALKLRLNL
VGGMFDTVQRSTQQTTEWAMLLLEIIISGTVDMQSNNELFTTVLDMLSVLINGTLAADM
SSISQGSMEENKRAYMNLAKKLQKELGERQSDSLEKVRQLLPLPKQTRDVITCEPQGS
LIDTKGNKIAGFDSIFKKEGLQVSTKQKISPWDLFEGLKPSAPLSWGWFGTVRVDRRV
ARGEEQQRLLLYHTHLRPRPRAYYLEPLPLPPEDEEPPAPTLLEPEKKAPEPPKTDKP
GAAPPSTEERKKKSTKGKKRSQPATKTEDYGMGPGRSGPYGVTVPPDLLHHPNPGSI
THLNYRQGSIGLYTQNQPLPAGGPRVDPYRPVRLPMQKLPTRPTYPGVLPTTMTGVM
GLEPSSYKTSVYRQQQPAVPQGQRLRQQLQAKIQSQGMLGQSSVHQMTPSSSYGLQ
TSQGYTPYVSHVGLQQHTGPADPTRHLQQRPSGYVHQQAPTYGHGLTSTQRFSHQT
LQQTPMISTMTPMSAQGVQAGVRSTAILPEQQQQQQQQQQQQQQQQQQQQQQQQQ
QQYHIRQQQQQQILRQQQQQQQQQQQQQQQQQQQQQQQQQQQQHQQQQQQQAAP
PQPQPQSQPQFQRQGLQQTQQQQQTAALVRQLQQQLSNTQPQPSTNIFGRY*

MED12_3 (2047 aa protein, different seq after 2014 aa) (SEQ ID NO: 102)
MKQSMPSLHTKKILFCYFHLTNSWCLRRYGLGKMAAFGILSYEHRPLKRPRPRLGPPD
VYPQDPKQKEDELTALNVKQGFNNQPAVSGDEHGSAKNVSFNPAKISSNFSSIIAEKL
RCNTLPDTGRRKPQVNQKDNFWLVTARSQSAINTWFTDLAGTKPLTQLAKKVPIFSKK
EEVFGYLAKYTVPVMRAAWLIKMTCAYYAAISETKVKKRHVDPFMEWTQIITKYLWEQL
QKMAEYYRPGPAGSGGCGSTIGPLPHDVEVAIRQWDYTEKLAMFMFQDGMLDRHEF
LTWVLECFEKIRPGEDELLKLLLPLLLRYSGEFVQSAYLSRRLAYFCTRRLALQLDGVS
SHSSHVISAQSTSTLPTTPAPQPPTSSTPSTPFSDLLMCPQHRPLVFGLSCILQTILLCC
PSALVWHYSLTDSRIKTGSPLDHLPIAPSNLPMPEGNSAFTQQVRAKLREIEQQIKERG
QAVEVRWSFDKCQEATAGFTIGRVLHTLEVLDSHSFERSDFSNSLDSLCNRIFGLGPS
KDGHEISSDDDAVVSLLCEWAVSCKRSGRHRAMVVAKLLEKRQAEIEAERCGESEAA
DEKGSIASGSLSAPSAPIFQDVLLQFLDTQAPMLTDPRSESERVEFFNLVLLFCELIRHD
VFSHNMYTCTLISRGDLAFGAPGPRPPSPFDDPADDPEHKEAEGSSSSKLEDPGLSE
SMDIDPSSSVLFEDMEKPDFSLFSPTMPCEGKGSPSPEKPDVEKEVKPPPKEKIEGTL
GVLYDQPRHVQYATHFPIPQEESCSHECNQRLVVLFGVGKQRDDARHAIKKITKDILKV
LNRKGTAETDQLAPIVPLNPGDLTFLGGEDGQKRRRNRPEAFPTAEDIFAKFQHLSHY
DQHQVTAQVSRNVLEQITSFALGMSYHLPLVQHVQFIFDLMEYSLSISGLIDFAIQLLNE
LSVVEAELLLKSSDLVGSYTTSLCLCIVAVLRHYHACLILNQDQMAQVFEGLCGVVKHG
MNRSDGSSAERCILAYLYDLYTSCSHLKNKFGELFSDFCSKVKNTIYCNVEPSESNMR
WAPEFMIDTLENPAAHTFTYTGLGKSLSENPANRYSFVCNALMHVCVGHHDPDRVND
IAILCAELTGYCKSLSAEWLGVLKALCCSSNNGTCGFNDLLCNVDVSDLSFHDSLATFV
AILIARQCLLLEDLIRCAAIPSLLNAACSEQDSEPGARLTCRILLHLFKTPQLNPCQSDGN
KPTVGIRSSCDRHLLAASQNRIVDGAVFAVLKAVFVLGDAELKGSGFTVTGGTEELPEE
EGGGGSGGRRQGGRNISVETASLDVYAKYVLRSICQQEWVGERCLKSLCEDSNDLQ
DPVLSSAQAQRLMQLICYPHRLLDNEDGENPQRQRIKRILQNLDQWTMRQSSLELQL
MIKQTPNNEMNSLLENIAKATIEVFQRSAETGSSSGSTASNMPSSSKTKPVLSSLERSG
VWLVAPLIAKLPTSVQGHVLKAAGEELEKGQHLGSSSRKERDRQKQKSMSLLSQQPF
LSLVLTCLKGQDEQREGLLTSLYSQVHQIVNNWRDDQYLDDCKPKQLMHEALKLRLNL
VGGMFDTVQRSTQQTTEWAMLLLEIIISGTVDMQSNNELFTTVLDMLSVLINGTLAADM
SSISQGSMEENKRAYMNLAKKLQKELGERQSDSLEKVRQLLPLPKQTRDVITCEPQGS
LIDTKGNKIAGFDSIFKKEGLQVSTKQKISPWDLFEGLKPSAPLSWGWFGTVRVDRRV
ARGEEQQRLLLYHTHLRPRPRAYYLEPLPLPPEDEEPPAPTLLEPEKKAPEPPKTDKP
GAAPPSTEERKKKSTKGKKRSQPATKTEDYGMGPGRSGPYGVTVPPDLLHHPNPGSI
THLNYRQGSIGLYTQNQPLPAGGPRVDPYRPVRLPMQKLPTRPTYPGVLPTTMTGVM
GLEPSSYKTSVYRQQQPAVPQGQRLRQQLQAKIQSQGMLGQSSVHQMTPSSSYGLQ

TSQGYTPYVSHVGLQQHTGPAGTMVPPSYSSQPYQSTHPFLLIPNPIPGLAPVVVGAL
PSGSIFNKFLVFLLM*

MED12_4 (internal 504 aa missing (1387-1891 aa)) (SEQ ID NO: 103)
MKQSMPSLHTKKILFCYFHLTNSWCLRRYGLGKMAAFGILSYEHRPLKRPRPRLGPPD
VYPQDPKQKEDELTALNVKQGFNNQPAVSGDEHGSAKNVSFNPAKISSNFSSIIAEKL
RCNTLPDTGRRKPQVNQKDNFWLVTARSQSAINTWFTDLAGTKPLTQLAKKVPIFSKK
EEVFGYLAKYTVPVMRAAWLIKMTCAYYAAISETKVKKRHVDPFMEWTQIITKYLWEQL
QKMAEYYRPGPAGSGGCGSTIGPLPHDVEVAIRQWDYTEKLAMFMFQDGMLDRHEF
LTWVLECFEKIRPGEDELLKLLLPLLLRYSGEFVQSAYLSRRLAYFCTRRLALQLDGVS
SHSSHVISAQSTSTLPTTPAPQPPTSSTPSTPFSDLLMCPQHRPLVFGLSCILQTILLCC
PSALVWHYSLTDSRIKTGSPLDHLPIAPSNLPMPEGNSAFTQQVRAKLREIEQQIKERG
QAVEVRWSFDKCQEATAGFTIGRVLHTLEVLDSHSFERSDFSNSLDSLCNRIFGLGPS
KDGHEISSDDDAVVSLLCEWAVSCKRSGRHRAMVVAKLLEKRQAEIEAERCGESEAA
DEKGSIASGSLSAPSAPIFQDVLLQFLDTQAPMLTDPRSESERVEFFNLVLLFCELIRHD
VFSHNMYTCTLISRGDLAFGAPGPRPPSPFDDPADDPEHKEAEGSSSSKLEDPGLSE
SMDIDPSSSVLFEDMEKPDFSLFSPTMPCEGKGSPSPEKPDVEKEVKPPPKEKIEGTL
GVLYDQPRHVQYATHFPIPQEESCSHECNQRLVVLFGVGKQRDDARHAIKKITKDILKV
LNRKGTAETDQLAPIVPLNPGDLTFLGGEDGQKRRRNRPEAFPTAEDIFAKFQHLSHY
DQHQVTAQVSRNVLEQITSFALGMSYHLPLVQHVQFIFDLMEYSLSISGLIDFAIQLLNE
LSVVEAELLLKSSDLVGSYTTSLCLCIVAVLRHYHACLILNQDQMAQVFEGLCGVVKHG
MNRSDGSSAERCILAYLYDLYTSCSHLKNKFGELFSDFCSKVKNTIYCNVEPSESNMR
WAPEFMIDTLENPAAHTFTYTGLGKSLSENPANRYSFVCNALMHVCVGHHDPDRVND
IAILCAELTGYCKSLSAEWLGVLKALCCSSNNGTCGFNDLLCNVDVSDLSFHDSLATFV
AILIARQCLLLEDLIRCAAIPSLLNAACSEQDSEPGARLTCRILLHLFKTPQLNPCQSDGN
KPTVGIRSSCDRHLLAASQNRIVDGAVFAVLKAVFVLGDAELKGSGFTVTGGTEELPEE
EGGGGSGGRRQGGRNISVETASLDVYAKYVLRSICQQEWVGERCLKSLCEDSNDLQ
DPVLSSAQAQRLMQLICYPHRLLDNEDGENPQRQRIKRILQNLDPYRPVRLPMQKLPT
RPTYPGVLPTTMTGVMGLEPSSYKTSVYRQQQPAVPQGQRLRQQLQQSQGMLGQS
SVHQMTPSSSYGLQTSQGYTPYVSHVGLQQHTGPAGTMVPPSYSSQPYQSTHPSTN
PTLVDPTRHLQQRPSGYVHQQAPTYGHGLTSTQRFSHQTLQQTPMISTMTPMSAQG
VQAGVRSTAILPEQQQQQQQQQQQQQQQQQQQQQQQQQQQQYHIRQQQQQQILRQQ
QQQQQQQQQQQQQQQQQQQQQQQQQQHQQQQQQQAAPPQPQPQSQPQFQRQGL
QQTQQQQQTAALVRQLQQQLSNTQPQPSTNIFGRY*

MED12_5 (397 aa missing (1769-2166 aa)) (SEQ ID NO: 104)
MKQSMPSLHTKKILFCYFHLTNSWCLRRYGLGKMAAFGILSYEHRPLKRPRPRLGPPD
VYPQDPKQKEDELTALNVKQGFNNQPAVSGDEHGSAKNVSFNPAKISSNFSSIIAEKL
RCNTLPDTGRRKPQVNQKDNFWLVTARSQSAINTWFTDLAGTKPLTQLAKKVPIFSKK
EEVFGYLAKYTVPVMRAAWLIKMTCAYYAAISETKVKKRHVDPFMEWTQIITKYLWEQL
QKMAEYYRPGPAGSGGCGSTIGPLPHDVEVAIRQWDYTEKLAMFMFQDGMLDRHEF
LTWVLECFEKIRPGEDELLKLLLPLLLRYSGEFVQSAYLSRRLAYFCTRRLALQLDGVS
SHSSHVISAQSTSTLPTTPAPQPPTSSTPSTPFSDLLMCPQHRPLVFGLSCILQTILLCC
PSALVWHYSLTDSRIKTGSPLDHLPIAPSNLPMPEGNSAFTQQVRAKLREIEQQIKERG
QAVEVRWSFDKCQEATAGFTIGRVLHTLEVLDSHSFERSDFSNSLDSLCNRIFGLGPS
KDGHEISSDDDAVVSLLCEWAVSCKRSGRHRAMVVAKLLEKRQAEIEAERCGESEAA
DEKGSIASGSLSAPSAPIFQDVLLQFLDTQAPMLTDPRSESERVEFFNLVLLFCELIRHD
VFSHNMYTCTLISRGDLAFGAPGPRPPSPFDDPADDPEHKEAEGSSSSKLEDPGLSE
SMDIDPSSSVLFEDMEKPDFSLFSPTMPCEGKGSPSPEKPDVEKEVKPPPKEKIEGTL
GVLYDQPRHVQYATHFPIPQEESCSHECNQRLVVLFGVGKQRDDARHAIKKITKDILKV
LNRKGTAETDQLAPIVPLNPGDLTFLGGEDGQKRRRNRPEAFPTAEDIFAKFQHLSHY
DQHQVTAQVSRNVLEQITSFALGMSYHLPLVQHVQFIFDLMEYSLSISGLIDFAIQLLNE
LSVVEAELLLKSSDLVGSYTTSLCLCIVAVLRHYHACLILNQDQMAQVFEGLCGVVKHG

MNRSDGSSAERCILAYLYDLYTSCSHLKNKFGELFSDFCSKVKNTIYCNVEPSESNMR
WAPEFMIDTLENPAAHTFTYTGLGKSLSENPANRYSFVCNALMHVCVGHHDPDRVND
IAILCAELTGYCKSLSAEWLGVLKALCCSSNNGTCGFNDLLCNVDVSDLSFHDSLATFV
AILIARQCLLLEDLIRCAAIPSLLNAACSEQDSEPGARLTCRILLHLFKTPQLNPCQSDGN
KPTVGIRSSCDRHLLAASQNRIVDGAVFAVLKAVFVLGDAELKGSGFTVTGGTEELPEE
EGGGGSGGRRQGGRNISVETASLDVYAKYVLRSICQQEWVGERCLKSLCEDSNDLQ
DPVLSSAQAQRLMQLICYPHRLLDNEDGENPQRQRIKRILQNLDQWTMRQSSLELQL
MIKQTPNNEMNSLLENIAKATIEVFQRSAETGSSSGSTASNMPSSSKTKPVLSSLERSG
VWLVAPLIAKLPTSVQGHVLKAAGEELEKGQHLGSSSRKERDRQKQKSMSLLSQQPF
LSLVLTCLKGQDEQREGLLTSLYSQVHQIVNNWRDDQYLDDCKPKQLMHEALKLRLNL
VGGMFDTVQRSTQQTTEWAMLLLEIIISGTVDMQSNNELFTTVLDMLSVLINGTLAADM
SSISQGSMEENKRAYMNLAKKLQKELGERQSDSLEKVRQLLPLPKQTRDVITCEPQGS
LIDTKGNKIAGFDSIFKKEGLQVSTKQKISPWDLFEGLKPSAPLSWGWFGTVRVDRRV
ARGEEQQRLLLYHTHLRPRPQSQPQFQRQGLQQTQQQQQTAALVRQLQQQLSNTQ
PQPSTNIFGRY*

MED13 (ID: Q9UHV7)

MED13_1 (internal 37 aa missing (392-429 aa)) (SEQ ID NO: 105)
MSASFVPNGASLEDCHCNLFCLADLTGIKWKKYVWQGPTSAPILFPVTEEDPILSSFSR
CLKADVLGVWRRDQRPGRRELWIFWWGEDPVLLTLFTMTYQKKKMECGRMDFPMN
AVLCFSKAVHNLLERCLMNRNFVRIGKWFVKPYEKDEKPINKSEHLSCSFTFFLHGDS
NVCTSVEINQHQPVYLLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK
LIGEWKQFYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVRMIYPACFVLVPQS
DIPTPSPVGSTHCSSSCLGVHQVPASTRDPAMSSVTLTPPTSPEEVQTVDPQSVQKW
VKFSSVSDGFNSDSTSHHGGKIPRKLANHVVDRVWQECNMNRAQNKHKNLKSRNAG
QQGQAPSLGQQQQILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMDADSAS
QRLVISAPDSQVRFSNIRTNDVAKTPQMHGTEMANSPQPPPLSPHPCDVVDEGVTKT
PSTPQSQHFYQMPTPDPLVPSKPMEDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEE
DEANIAWKYYKFPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKKPLK
VSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEFLFPDKKDRQNSEREAGK
KHKVEDGTSSVTVLSHEEDAMSLFSPSIKQDAPRPTSHARPPSTSLIYDSDLAVSYTDL
DNLFNSDEDELTPGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPSLE
QHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIEVDEGFCSPKPSEIKDF
SYVYKPENCQILVGCSMFAPLKTLPSQYLPLIKLPEECIYRQSWTVGKLELLSSGPSMP
FIKEGDGSNMDQEYGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP
RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEPATVPSIPEAHSLYV
NLILSESVMNLFKDCNSDSCCICVCNMNIKGADVGVYIPDPTQEAQYRCTCGFSAVMN
RKFGNNSGLFLEDELDIIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLIL
LLQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLALEHGRQFMDNM
SGGKVDEALVKSSCLHPWSKRNDVSMQCSQDILRMLLSLQPVLQDAIQKKRTVRPWG
VQGPLTWQQFHKMAGRGSYGTDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLML
EPYGSQRDIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLLTDGIMRVG
STASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQVCRYDLGPYLASLPLDSSLLSQP
NLVAPTSQSLITPPQMTNTGNANTPSATLASAASSTMTVTSGVAISTSVATANSTLTTA
STSSSSSSNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQQTSAL
QTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSHAVTYPPAIVVYIIDPFTYENT
DESTNSSSVWTLGLLRCFLEMVQTLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHL
KSLAFSAFTQCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPPFILAPVK
DKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASCTDLYGELLETCIINIDVPNRAR
RKKSSARKFGLQKLWEWCLGLVQMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRNL
QSLSKRLKDMCRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGSVFGRSTTLN
MQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDLAFNPNNDGADGMGIFDLL

29aa

DTGDDLDPDIINILPASPTGSPVHSPGSHYPHGGDAGKGQSTDRLLSTEPHEEVPNILQ
QPLALGYFVSTAKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVPSVQSDELLHSKH
SHPLDSNQTSDVLRFVLEQYNALSWLTCDPATQDRRSCLPIHFVVLNQLYNFIMNML

MED13_2 (internal 228 aa missing (429 - 657 aa)) (SEQ ID NO: 106)
MSASFVPNGASLEDCHCNLFCLADLTGIKWKKYVWQGPTSAPILFPVTEEDPILSSFSR
CLKADVLGVWRRDQRPGRRELWIFWWGEDPVLLTLFTMTYQKKKMECGRMDFPMN
AVLCFSKAVHNLLERCLMNRNFVRIGKWFVKPYEKDEKPINKSEHLSCSFTFFLHGDS
NVCTSVEINQHQPVYLLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK
LIGEWKQFYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVRMIYPACFVLVPQS
DIPTPSPVGSTHCSSSCLGVHQVPASTRDPAMSSVTLTPPTSPEEVQTVDPQSVQKW
VKFSSVSDGFNSDSTSHHGGKIPRKLANHVVDRVWQECNMNRAQNKKKYSASSGGL
CEEATAAKVASWDFVEATQRTNCSCLRLMVQCKKPLKVSDELVQQYQIKNQCLSAIAS
DAEQEPKIDPYAFVEGDEEFLFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDA
MSLFSPSIKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELTPGSKKSAN
GSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPSLEQHIMGFSPMNMNNKEYGSM
DTTPGGTVLEGNSSSIGAQFKIEVDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAP
LKTLPSQYLPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQEYGTAYTP
QTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTPRTPRTPRGAGGPASAQGSVK
YENSDLYSPASTPSTCRPLNSVEPATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCI
CVCNMNIKGADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFLEDELDIIGRNT
DCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILLLQDQCTNLFSPFGAADQDPF
PKSGVISNWVRVEERDCCNDCYLALEHGRQFMDNMSGGKVDEALVKSSCLHPWSKR
NDVSMQCSQDILRMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG
TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQRDIAYVVLCPENEALL
NGAKSFFRDLTAIYESCRLGQHRPVSRLLTDGIMRVGSTASKKLSEKLVAEWFSQAAD
GNNEAFSKLKLYAQVCRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGN
ANTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSSSNLNSGVSSNKLPS
FPPFGSMNSNAAGSMSTQANTVQSGQLGGQQTSALQTAGISGESSSLPTQPHPDVS
ESTMDRDKVGIPTDGDSHAVTYPPAIVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLE
MVQTLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAFTQCRRPLPTSTNV
KTLTGFGPGLAMETALRSPDRPECIRLYAPPFILAPVKDKQTELGETFGEAGQKYNVLF
VGYCLSHDQRWILASCTDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCLG
LVQMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRNLQSLSKRLKDMCRMCGISAADS
PSILSACLVAMEPQGSFVIMPDSVSTGSVFGRSTTLNMQTSQLNTPQDTSCTHILVFPT
SASVQVASATYTTENLDLAFNPNNDGADGMGIFDLLDTGDDLDPDIINILPASPTGSPV
HSPGSHYPHGGDAGKGQSTDRLLSTEPHEEVPNILQQPLALGYFVSTAKAGPLPDWF
WSACPQAQYQCPLFLKASLHLHVPSVQSDELLHSKHSHPLDSNQTSDVLRFVLEQYN
ALSWLTCDPATQDRRSCLPIHFVVLNQLYNFIMNML

MED14 (ID: O60244)

MED14_1 (BQ325013; internal 44 aa missing (1045-1089 aa)) (SEQ ID NO: 107)
MAPVQLENHQLVPPGGGGGGSGGPPSAPAPPPPGAAVAAAAAAAASPGYRLSTLIEF
LLHRAYSELMVLTDLLPRKSDVERKIEIVQFASRTRQLFVRLLALVKWANNAGKVEKCA
MISSFLDQQAILFVDTADRLASLARDALVHARLPSFAIPYAIDVLTTGSYPRLPTCIRDKII
PPDPITKIEKQATLHQLNQILRHRLVTTDLPPQLANLTVANGRVKFRVEGEFEATLTVM
GDDPDVPWRLLKLEILVEDKETGDGRALVHSMQISFIHQLVQSRLFADEKPLQDMYNC
LHSFCLSLQLEVLHSQTLMLIRERWGDLVQVERYHAGKCLSLSVWNQQVLGRKTGTA
SVHKVTIKIDENDVSKPLQIFHDPPLPASDSKLVERAMKIDHLSIEKLLIDSVHARAHQKL
QELKAILRGFNANENSSIETALPALVVPILEPCGNSECLHIFVDLHSGMFQLMLYGLDQA
TLDDMEKSVNDDMKRIIPWIQQLKFWLGQQRCKQSIKHLPTISSETLQLSNYSTHPIGN
LSKNKLFIKLTRLPQYYIVVEMLEVPNKPTQLSYKYYFMSVNAADREDSPAMALLLQQF

KENIQDLVFRTKTGKQTRTNAKRKLSDDPCPVESKKTKRAGEMCAFNKVLAHFVAMC
DTNMPFVGLRLELSNLEIPHQGVQVEGDGFSHAIRLLKIPPCKGITEETQKALDRSLLD
CTFRLQGRNNRTWVAELVFANCPLNGTSTREQGPSRHVYLTYENLLSEPVGGRKVVE
MFLNDWNSIARLYECVLEFARSLPDIPAHLNIFSEVRVYNYRKLILCYGTTKGSSISIQW
NSIHQKFHISLGTVGPNSGCSNCHNTILHQLQEMFNKTPNVVQLLQVLFDTQAPLNAIN
KLPTVPMLGLTQRTNTAYQCFSILPQSSTHIRLAFRNMYCIDIYCRSRGVVAIRDGAYSL
FDNSKLVEGFYPAPGLKTFLNMFVDSNQDARRRSVNEDDNPPSPIGGDMMDSLISQL
QPPPQQQPFPKQPGTSGAYPLTSPPTSYHSTVNQSPSMMHTQSPGTLDPSSPYTMV
SPSGRAGNWPGSPQVSGPSPAARMPGMSPANPSLHSPVPDASHSPRAGTSSQTMP
TNMPPPRKLPQRSWAASIPTILTHSALNILLLPSPTPGLVPGLAGSYLCSPLERFLGSVI
MRRHLQRIIQQETLQLINSNEPGVIMFKTDALKCRVALSPKTNQTLQLKLTPENAGQWK
PDELQVLEKFFETRVAGPPFKANTLIAFTKLLGAPTHILRDCVHIMKLELFPDQATQLKW
NVQFCLTIPPSAPPIAPPGTPAVVLKSKMLFFLQLTQKTSVPPQEPVSIIVPIIYDMASGT
TQQADIPRQQNSSVAAPMMVSNILKRFAEMNPPRQGECTIFAAVRDLMANLTLPPVGR
P

MED14_2 (CN282118; 116 aa shorter N-terminus) (SEQ ID NO: 108)
MISSFLDQQAILFVDTADRLASLARDALVHARLPSFAIPYAIDVLTTGSYPRLPTCIRDKII
PPDPITKIEKQATLHQLNQILRHRLVTTDLPPQLANLTVANGRVKFRVEGEFEATLTVM
GDDPDVPWRLLKLEILVEDKETGDGRALVHSMQISFIHQLVQSRLFADEKPLQDMYNC
LHSFCLSLQLEVLHSQTLMLIRERWGDLVQVERYHAGKCLSLSVWNQQVLGRKTGTA
SVHKVTIKIDENDVSKPLQIFHDPPLPASDSKLVERAMKIDHLSIEKLLIDSVHARAHQKL
QELKAILRGFNANENSSIETALPALVVPILEPCGNSECLHIFVDLHSGMFQLMLYGLDQA
TLDDMEKSVNDDMKRIIPWIQQLKFWLGQQRCKQSIKHLPTISSETLQLSNYSTHPIGN
LSKNKLFIKLTRLPQYYIVVEMLEVPNKPTQLSYKYYFMSVNAADREDSPAMALLLQQF
KENIQDLVFRTKTGKQTRTNAKRKLSDDPCPVESKKTKRAGEMCAFNKVLAHFVAMC
DTNMPFVGLRLELSNLEIPHQGVQVEGDGFSHAIRLLKIPPCKGITEETQKALDRSLLD
CTFRLQGRNNRTWVAELVFANCPLNGTSTREQGPSRHVYLTYENLLSEPVGGRKVVE
MFLNDWNSIARLYECVLEFARSLPDIPAHLNIFSEVRVYNYRKLILCYGTTKGSSISIQW
NSIHQKFHISLGTVGPNSGCSNCHNTILHQLQEMFNKTPNVVQLLQVLFDTQAPLNAIN
KLPTVPMLGLTQRTNTAYQCFSILPQSSTHIRLAFRNMYCIDIYCRSRGVVAIRDGAYSL
FDNSKLVEGFYPAPGLKTFLNMFVDSNQDARRRSVNEDDNPPSPIGGDMMDSLISQL
QPPPQQQPFPKQPGTSGAYPLTSPPTSYHSTVNQSPSMMHTQSPGNLHAASSPSGA
LRAPSPASFVPTPPPSSHGISIGPGASFASPHGTLDPSSPYTMVSPSGRAGNWPGSP
QVSGPSPAARMPGMSPANPSLHSPVPDASHSPRAGTSSQTMPTNMPPPRKLPQRS
WAASIPTILTHSALNILLLPSPTPGLVPGLAGSYLCSPLERFLGSVIMRRHLQRIIQQETL
QLINSNEPGVIMFKTDALKCRVALSPKTNQTLQLKLTPENAGQWKPDELQVLEKFFET
RVAGPPFKANTLIAFTKLLGAPTHILRDCVHIMKLELFPDQATQLKWNVQFCLTIPPSAP
PIAPPGTPAVVLKSKMLFFLQLTQKTSVPPQEPVSIIVPIIYDMASGTTQQADIPRQQNS
SVAAPMMVSNILKRFAEMNPPRQGECTIFAAVRDLMANLTLPPVGRP

MED14_3 (AI436571; short protein, 118 aa) (SEQ ID NO: 109)
MAPVQLENHQLVPPGGGGGGSGGPPSAPAPPPPGAAVAAAAAAAASPGYRLSTLIEF
LLHRAYSELMVLTDLLPRKSDVERKIEIVQFASRTRQLFVRLLALVKWANNAGKVEKCA
VS*

MED14_4 (BF196217; different C-terminus after 1431 aa) (SEQ ID NO: 110)
MAPVQLENHQLVPPGGGGGGSGGPPSAPAPPPPGAAVAAAAAAAASPGYRLSTLIEF
LLHRAYSELMVLTDLLPRKSDVERKIEIVQFASRTRQLFVRLLALVKWANNAGKVEKCA
MISSFLDQQAILFVDTADRLASLARDALVHARLPSFAIPYAIDVLTTGSYPRLPTCIRDKII
PPDPITKIEKQATLHQLNQILRHRLVTTDLPPQLANLTVANGRVKFRVEGEFEATLTVM
GDDPDVPWRLLKLEILVEDKETGDGRALVHSMQISFIHQLVQSRLFADEKPLQDMYNC
LHSFCLSLQLEVLHSQTLMLIRERWGDLVQVERYHAGKCLSLSVWNQQVLGRKTGTA

SVHKVTIKIDENDVSKPLQIFHDPPLPASDSKLVERAMKIDHLSIEKLLIDSVHARAHQKL
QELKAILRGFNANENSSIETALPALVVPILEPCGNSECLHIFVDLHSGMFQLMLYGLDQA
TLDDMEKSVNDDMKRIIPWIQQLKFWLGQQRCKQSIKHLPTISSETLQLSNYSTHPIGN
LSKNKLFIKLTRLPQYYIVVEMLEVPNKPTQLSYKYYFMSVNAADREDSPAMALLLQQF
KENIQDLVFRTKTGKQTRTNAKRKLSDDPCPVESKKTKRAGEMCAFNKVLAHFVAMC
DTNMPFVGLRLELSNLEIPHQGVQVEGDGFSHAIRLLKIPPCKGITEETQKALDRSLLD
CTFRLQGRNNRTWVAELVFANCPLNGTSTREQGPSRHVYLTYENLLSEPVGGRKVVE
MFLNDWNSIARLYECVLEFARSLPDIPAHLNIFSEVRVYNYRKLILCYGTTKGSSISIQW
NSIHQKFHISLGTVGPNSGCSNCHNTILHQLQEMFNKTPNVVQLLQVLFDTQAPLNAIN
KLPTVPMLGLTQRTNTAYQCFSILPQSSTHIRLAFRNMYCIDIYCRSRGVVAIRDGAYSL
FDNSKLVEGFYPAPGLKTFLNMFVDSNQDARRRSVNEDDNPPSPIGGDMMDSLISQL
QPPPQQQPFPKQPGTSGAYPLTSPPTSYHSTVNQSPSMMHTQSPGNLHAASSPSGA
LRAPSPASFVPTPPPSSHGISIGPGASFASPHGTLDPSSPYTMVSPSGRAGNWPGSP
QVSGPSPAARMPGMSPANPSLHSPVPDASHSPRAGTSSQTMPTNMPPPRKLPQRS
WAASIPTILTHSALNILLLPSPTPGLVPGLAGSYLCSPLERFLGSVIMRRHLQRIIQQETL
QLINSNEPGVIMFKTDALKCRVALSPKTNQTLQLKLTPENAGQWKPDELQVLEKFFET
RVAGPPFKANTLIAFTKLLGAPTHILRDCVHIMKLELFPDQATQLKWNVQFCLTIPPSAP
PIAPPGTPAVVLKSKMLFFLQLTQKTSVPPQEPVSIIVPIIYDMASGTTQQADIPRQQNS
SVAAPMMVSNILKRFAEMNPPRQGSIKGTGCPSDFL*

MED15 (ID: Q96RN5)

MED15_1 (CB156495; 26 aa shorter N-terminus) (SEQ ID NO: 111)
MRKAGVAHSKSSKDMESHVFLKAKTRDEYLSLVARLIIHFRDIHNKKSQASVSDPMNA
LQSLTGGPAAGAAGIGMPPRGPGQSLGGMGSLGAMGQPMSLSGQPPPGTSGMAPH
SMAVVSTATPQTQLQLQQVALQQQQQQQQFQQQQQAALQQQQQQQQQQQFQAQ
QSAMQQQFQAVVQQQQQLQQQQQQQQHLIKLHHQNQQQIQQQQQQLQRIAQLQLQ
QQQQQQQQQQQQQQQQALQAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQ
PPPQPQQPPVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQ
PPVQPQVQQQQTAVQTAQAAQMVAPGVQMITEALAQGGMHIRARFPPTTAVSAIPSS
SIPLGRQPMAQVSQSSLPMLSSPSPGQQVQTPQSMPPPPQPSPQPGQPSSQPNSNV
SSGPAPSPSSFLPSPSPQPSQSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQ
AEEQQYLDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILTDPSKRCPLKTLQ
KCEIALEKLKNDMAVPTPPPPPVPPTKQQYLCQPLLDAVLANIRSPVFNHSLYRTFVPA
MTAIHGPPITAPVVCTRKRRLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGT
VHLICKLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSVHRCMTSRLL
QLPDKHSVTALLNTWAQSVHQACLSAA

MED15_2 (CN336649; internal 82 aa missing (71-152 aa)) (SEQ ID NO: 112)
MDVSGQETDWRSTAFRQKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYL
SLVARLIIHFRDIPQLQLQQVALQQQQQQQQFQQQQQAALQQQQQQQQQQQFQAQ
QSAMQQQFQAVVQQQQQLQQQQQQQQHLIKLHHQNQQQIQQQQQQLQRIAQLQLQ
QQQQQQQQQQQQQQQQALQAQPPIQQPPMQQPQPPPSQALPQQLQQMHHTQHHQ
PPPQPQQPPVAQNQPSQLPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQ
PPVQPQVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTPQSMPPP
PQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTARTPQNFSVPSPG
PLNTPVNPSSVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSK
MKSLLDILTDPSKRCPLKTLQKCEIALEKLKNDMAVPTPPPPPVPPTKQQYLCQPLLDA
VLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKRRLEDDERQSIPSVLQGEVA
RLDPKFLVNLDPSHCSNNGTVHLICKLDDKDLPSVPPLELSVPADYPAQSPLWIDRQW
QYDANPFLQSVHRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA

MED15_3 (BF983466; different C-terminus after 670 aa) (SEQ ID NO: 113)

MDVSGQETDWRSTAFRQKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYL
SLVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAAGIGMPPRGPGQSLGGMG
SLGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQVALQQQQQQQQF
QQQQQAALQQQQQQQQQQQFQAQQSAMQQQFQAVVQQQQQLQQQQQQQQHLIK
LHHQNQQQIQQQQQQLQRIAQLQLQQQQQQQQQQQQQQQQQALQAQPPIQQPPMQ
QPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQPLVSQA
QALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMVAPGVQMI
TEALAQGGMHIRARFPPTTAVSAIPSSSIPLGRQPMAQVSQSSLPMLSSPSPGQQVQT
PQSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTARTPQN
FSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMINKIDKNED
RKKDLSKMKSLLDILTDPSKRCPLKTLQKCEIALEKLKNDMAVPTPPPPPVPPTKQQYL
CQPLLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKRRLEDDERQSIPSV
LQGEVARLDPKFLVNLDPSHCSNNGTVHLICKLGECPEGRDWCGKAGPDRSPRTLPS
KPDGTAPRTHPVFTPRQAVCSILTHTGLQTAWPCLSPHCQSPHTLTSPTQMWLCLPG
P*

MED15_4 (694 aa protein, different C-terminus after 656 aa) (SEQ ID NO: 114)
MDVSGQETDWRSTAFRQKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYL
SLVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAAGIGMPPRGPGQSLGGMG
SLGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQVALQQQQQQQQF
QQQQQAALQQQQQQQQQQQFQAQQSAMQQQFQAVVQQQQQLQQQQQQQQHLIK
LHHQNQQQIQQQQQQLQRIAQLQLQQQQQQQQQQQQQQQQQALQAQPPIQQPPMQ
QPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQLPPQSQTQPLVSQA
QALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMVAPGVQMI
TEALAQGGMHIRARFPPTTAVSAIPSSSIPLGRQPMAQVSQSSLPMLSSPSPGQQVQT
PQSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTARTPQN
FSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMINKIDKNED
RKKDLSKMKSLLDILTDPSKRCPLKTLQKCEIALEKLKNDMAVPTPPPPPVPPTKQQYL
CQPLLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITYVQLGWALRRAASPGPRVPG
VVTMPPPQGPSGVHPEAQA*

MED15_5 (106 aa missing (198-304 aa)) (SEQ ID NO: 115)
MDVSGQETDWRSTAFRQKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYL
SLVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAAGIGMPPRGPGQSLGGMG
SLGAMGQPMSLSGQPPPGTSGMAPHSMAVVSTATPQTQLQLQQVALQQQQQQQQF
QQQQQAALQQQQQQQQQQQFQAQQSAMQQPQQPPVAQNQPSQLPPQSQTQPLV
SQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQPQVQQQQTAVQTAQAAQMVAPGV
QMITEALAQGGMHIRARFPPTTAVSAIPSSSIPLGRQPMAQVSQSSLPMLSSPSPGQQ
VQTPQSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTART
PQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQYLDKLKQLSKYIEPLRRMINKIDK
NEDRKKDLSKMKSLLDILTDPSKRCPLKTLQKCEIALEKLKNDMAVPTPPPPPVPPTKQ
QYLCQPLLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKRRLEDDERQSI
PSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLICKLDDKDLPSVPPLELSVPADYPAQ
SPLWIDRQWQYDANPFLQSVHRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA

MED16 (ID: Q9Y2X0) - Anri

MED16_1 (internal 778 aa missing (5-783 aa)) (SEQ ID NO: 116)
MCDLRRLHLGACPTEECKACTRCGCVTMLKSPNRTTAVKQWEQRWIKNCLAVEGRG
PDACVTSRASEEAPAFVQLGPQSTHHSPRTPRSLDHLHPEDRP

MED16_2 (internal 640 aa missing (146-786 aa)) (SEQ ID NO: 117)

MCDLRRPAAGGMMDLAYVCEWEKWSKSTHCPSVPLACAWSCRNLIAFTMDLRSDD
QDLTRMIHILDTEHPWDLHSIPSEHHEAITCLEWDQSGSRLLSADADGQIKCWSMADH
LANSWESSVGSLVEGDPIVALSWLHNGVKLALHLGACPTEECKACTRCGCVTMLKSP
NRTTAVKQWEQRWIKNCLAVEGRGPDACVTSRASEEAPAFVQLGPQSTHHSPRTPR
SLDHLHPEDRP

MED16_3 (509 aa missing (44-553 aa)) (SEQ ID NO: 118)
MCDLRRPAAGGMMDLAYVCEWEKWSKSTHCPSVPLACAWSCRNLIAISSTLKSLLRP
HFLNTPDKSPGDRLTEICTKITDVDIDKVMINLKTEEFVLDMNTLQALQQLLQWVGDFV
LYLLASLPNQGSLLRPGHSFLRDGTSLGMLRELMVVIRIWGLLKPSCLPVYTATSDTQD
SMSLLFRLLTKLWICCRDEGPASEPDEALVDECCLLPSQLLIPSLDWLPASDGLVSRLQ
PKQPLRLQFGRAPTLPGSAATLQLDGLARAPGQPKIDHLRRLHLGACPTEECKACTRC
GCVTMLKSPNRTTAVKQWEQRWIKNCLAVEGRGPDACVTSRASEEAPAFVQLGPQS
THHSPRTPRSLDHLHPEDRP

MED16_4 (239 aa missing (143-382 aa)) (SEQ ID NO: 119)
MCDLRRPAAGGMMDLAYVCEWEKWSKSTHCPSVPLACAWSCRNLIAFTMDLRSDD
QDLTRMIHILDTEHPWDLHSIPSEHHEAITCLEWDQSGSRLLSADADGQIKCWSMADH
LANSWESSVGSLVEGDPIVALSWLHNGVKLALAFHDGSVHIVHRLSLQTMAVFYSSAA
PRPVDEPAMKRPRTAGPAVHLKAMQLSWTSLALVGIDSHGKLSVLRLSPSMGHPLEV
GLALRHLLFLLEYCMVTGYDWWDILLHVQPSMVQSLVEKLHEEYTRQTAALQQVLSTR
ILAMKASLCKLSPCTVTRVCDYHTKLFLIAISSTLKSLLRPHFLNTPDKSPGDRLTEICTKI
TDVDIDKVMINLKTEEFVLDMNTLQALQQLLQWVGDFVLYLLASLPNQGSLLRPGHSFL
RDGTSLGMLRELMVVIRIWGLLKPSCLPVYTATSDTQDSMSLLFRLLTKLWICCRDEGP
ASEPDEALVDECCLLPSQLLIPSLDWLPASDGLVSRLQPKQPLRLQFGRAPTLPGSAA
TLQLDGLARAPGQPKIDHLRRLHLGACPTEECKACTRCGCVTMLKSPNRTTAVKQWE
QRWIKNCLAVEGRGPDACVTSRASEEAPAFVQLGPQSTHHSPRTPRSLDHLHPEDRP

MED16_5 (595 aa shorter N-terminus) (SEQ ID NO: 120)
MINLKTEEFVLDMNTLQALQQLLQWVGDFVLYLLASLPNQGSLLRPGHSFLRDGTSLG
MLRELMVVIRIWGLLKPSCLPVYTATSDTQDSMSLLFRLLTKLWICCRDEGPASEPDEA
LVDECCLLPSQLLIPSLDWLPASDGLVSRLQPKQPLRLQFGRAPTLPGSAATLQLDGLA
RAPGQPKIDHLRRLHLGACPTEECKACTRCGCVTMLKSPNRTTAVKQWEQRWIKNCL
AVEGRGPDACVTSRASEEAPAFVQLGPQSTHHSPRTPRSLDHLHPEDRP

MED16_6 (147 aa, different sequence after 114 aa) (SEQ ID NO: 121)
MCDLRRPAAGGMMDLAYVCEWEKWSKSTHCPSVPLACAWSCRNLIAFTMDLRSDD
QDLTRMIHILDTEHPWDLHSIPSEHHEAITCLEWDQSGSRLLSADADGQIKCWSMADH
PAAARATARPGLSSARLTSARPAGLLKAVGRTPA*

MED16_7 (469 aa missing (17-486 aa)) (SEQ ID NO: 122)
MCDLRRPAAGGMMDLAYDWWDILLHVQPSMVQSLVEKLHEEYTRQTAALQQVLSTRI
LAMKASLCKLSPCTVTRVCDYHTKLFLIAISSTLKSLLRPHFLNTPDKSPGDRLTEICTKI
TDVDIDKVMINLKTEEFVLDMNTLQALQQLLQWVGDFVLYLLASLPNQGSLLRPGHSFL
RDGTSLGMLRELMVVIRIWGLLKPSCLPVYTATSDTQDSMSLLFRLLTKLWICCRDEGP
ASEPDEALVDECCLLPSQLLIPSLDWLPASDGLVSRLQPKQPLRLQFGRAPTLPGSAA
TLQLDGLARAPGQPKIDHLRRLHLGACPTEECKACTRCGCVTMLKSPNRTTAVKQWE
QRWIKNCLAVEGRGPDACVTSRASEEAPAFVQLGPQSTHHSPRTPRSLDHLHPEDRP
*

MED16_8 (512 aa missing (51-563 aa)) (SEQ ID NO: 123)
MCDLRRPAAGGMMDLAYVCEWEKWSKSTHCPSVPLACAWSCRNLIAFTMDLLRPHF
LNTPDKSPGDRLTEICTKITDVDIDKVMINLKTEEFVLDMNTLQALQQLLQWVGDFVLYL

LASLPNQGSLLRPGHSFLRDGTSLGMLRELMVVIRIWGLLKPSCLPVYTATSDTQDSM
SLLFRLLTKLWICCRDEGPASEPDEALVDECCLLPSQLLIPSLDWLPASDGLVSRLQPK
QPLRLQFGRAPTLPGSAATLQLDGLARAPGQPKIDHLRRLHLGACPTEECKACTRCG
CVTMLKSPNRTTAVKQWEQRWIKNCLAVEGRGPDACVTSRASEEAPAFVQLGPQST
HHSPRTPRSLDHLHPEDRP

MED16_9 (380 aa missing (78-458 aa)) (SEQ ID NO: 124)
MCDLRRPAAGGMMDLAYVCEWEKWSKSTHCPSVPLACAWSCRNLIAFTMDLRSDD
QDLTRMIHILDTEHPWDLHSIPSPSMGHPLEVGLALRHLLFLLEYCMVTGYDWWDILLH
VQPSMVQSLVEKLHEEYTRQTAALQQVLSTRILAMKASLCKLSPCTVTRVCDYHTKLF
LIAISSTLKSLLRPHFLNTPDKSPGDRLTEICTKITDVDIDKVMINLKTEEFVLDMNTLQAL
QQLLQWVGDFVLYLLASLPNQGSLLRPGHSFLRDGTSLGMLRELMVVIRIWGLLKPSC
LPVYTATSDTQDSMSLLFRLLTKLWICCRDEGPASEPDEALVDECCLLPSQLLIPSLDW
LPASDGLVSRLQPKQPLRLQFGRAPTLPGSAATLQLDGLARAPGQPKIDHLRRLHLGA
CPTEECKACTRCGCVTMLKSPNRTTAVKQWEQRWIKNCLAVEGRGPDACVTSRASE
EAPAFVQLGPQSTHHSPRTPRSLDHLHPEDRP

MED16_10 (internal 69 aa missing (452-521 aa)) (SEQ ID NO: 125)
MCDLRRPAAGGMMDLAYVCEWEKWSKSTHCPSVPLACAWSCRNLIAFTMDLRSDD
QDLTRMIHILDTEHPWDLHSIPSEHHEAITCLEWDQSGSRLLSADADGQIKCWSMADH
LANSWESSVGSLVEGDPIVALSWLHNGVKLALHVEKSGASSFGEKFSRVKFSPSLTLF
GGKPMEGWIAVTVSGLVTVSLLKPSGQVLTSTESLCRLRGRVALADIAFTGGGNIVVAT
ADGSSASPVQFYKVCVSVVSEKCRIDTEILPSLFMRCTTDLNRKDKFPAITHLKFLARD
MSEQVLLCASSQTSSIVECWSLRKEGLPVNNIFQQISPVVGDKQPTILKWRILSATNDL
DRVSAVALPKLPISLTNTDLKVASDTQFYPGLGLALAFHDGSVHIVHRLSLQTMAVFYS
SAAPRPVDEPAMKRPRTAGPAVHLKAMQLSWTSLALVGIDSHGKVLSTRILAMKASLC
KLSPCTVTRVCDYHTKLFLIAISSTLKSLLRPHFLNTPDKSPGDRLTEICTKITDVDIDKV
MINLKTEEFVLDMNTLQALQQLLQWVGDFVLYLLASLPNQGSLLRPGHSFLRDGTSLG
MLRELMVVIRIWGLLKPSCLPVYTATSDTQDSMSLLFRLLTKLWICCRDEGPASEPDEA
LVDECCLLPSQLLIPSLDWLPASDGLVSRLQPKQPLRLQFGRAPTLPGSAATLQLDGLA
RAPGQPKIDHLRRLHLGACPTEECKACTRCGCVTMLKSPNRTTAVKQWEQRWIKNCL
AVEGRGPDACVTSRASEEAPAFVQLGPQSTHHSPRTPRSLDHLHPEDRP

MED16_11 (internal 412 aa missing (149-561 aa)) (SEQ ID NO: 126)
MCDLRRPAAGGMMDLAYVCEWEKWSKSTHCPSVPLACAWSCRNLIAFTMDLRSDD
QDLTRMIHILDTEHPWDLHSIPSEHHEAITCLEWDQSGSRLLSADADGQIKCWSMADH
LANSWESSVGSLVEGDPIVALSWLHNGVKLALHVEKSLLRPHFLNTPDKSPGDRLTEI
CTKITDVDIDKVMINLKTEEFVLDMNTLQALQQLLQWVGDFVLYLLASLPNQGSLLRPG
HSFLRDGTSLGMLRELMVVIRIWGLLKPSCLPVYTATSDTQDSMSLLFRLLTKLWICCR
DEGPASEPDEALVDECCLLPSQLLIPSLDWLPASDGLVSRLQPKQPLRLQFGRAPTLP
GSAATLQLDGLARAPGQPKIDHLRRLHLGACPTEECKACTRCGCVTMLKSPNRTTAV
KQWEQRWIKNCLAVEGRGPDACVTSRASEEAPAFVQLGPQSTHHSPRTPRSLDHLH
PEDRP

MED16_12 (528 aa shorter N-terminus) (SEQ ID NO: 127)
MKASLCKLSPCTVTRVCDYHTKLFLIAISSTLKSLLRPHFLNTPDKSPGDRLTEICTKITD
VDIDKVMINLKTEEFVLDMNTLQALQQLLQWVGDFVLYLLASLPNQGSLLRPGHSFLR
DGTSLGMLRELMVVIRIWGLLKPSCLPVYTATSDTQDSMSLLFRLLTKLWICCRDEGPA
SEPDEALVDECCLLPSQLLIPSLDWLPASDGLVSRLQPKQPLRLQFGRAPTLPGSAATL
QLDGLARAPGQPKIDHLRRLHLGACPTEECKACTRCGCVTMLKSPNRTTAVKQWEQR
WIKNCLAVEGRGPDACVTSRASEEAPAFVQLGPQSTHHSPRTPRSLDHLHPEDRP

MED16_13 (internal 369 aa missing (14-383 aa)) (SEQ ID NO: 128)

MCDLRRPAAGGMMALAFHDGSVHIVHRLSLQTMAVFYSSAAPRPVDEPAMKRPRTA
GPAVHLKAMQLSWTSLALVGIDSHGKLSVLRLSPSMGHPLEVGLALRHLLFLLEYCMV
TGYDWWDILLHVQPSMVQSLVEKLHEEYTRQTAALQQVLSTRILAMKASLCKLSPCTV
TRVCDYHTKLFLIAISSTLKSLLRPHFLNTPDKSPGDRLTEICTKITDVDIDKVMINLKTEE
FVLDMNTLQALQQLLQWVGDFVLYLLASLPNQGSLLRPGHSFLRDGTSLGMLRELMV
VIRIWGLLKPSCLPVYTATSDTQDSMSLLFRLLTKLWICCRDEGPASEPDEALVDECCL
LPSQLLIPSLDWLPASDGLVSRLQPKQPLRLQFGRAPTLPGSAATLQLDGLARAPGQP
KIDHLRRLHLGACPTEECKACTRCGCVTMLKSPNRTTAVKQWEQRWIKNCLAVEGRG
PDACVTSRASEEAPAFVQLGPQSTHHSPRTPRSLDHLHPEDRP

MED17 (ID: Q9NVC6)

MED17_1 (505 aa; different sequence after 382 aa) (SEQ ID NO: 129)
MSGVRAVRISIESACEKQVHEVGLDGTETYLPPLSMSQNLARLAQRIDFSQGSGSEEE
EAAGTEGDAQEWPGAGSSADQDDEEGVVKFQPSLWPWDSVRNNLRSALTEMCVLY
DVLSIVRDKKFMTLDPVSQDALPPKQNPQTLQLISKKKSLAGAAQILLKGAERLTKSVTE
NQENKLQRDFNSELLRLRQHWKLRKVGDKILGDLSYRSAGSLFPHHGTFEVIKNTDLD
LDKKIPEDYCPLDVQIPSDLEGSAYIKVSIQKQAPDIGDLGTVNLFKRPLPKSKPGSPHW
QTKLEAAQNVLLCKEIFAQLSREAVQIKSQVPHIVVKNQIISQPFPSLQLSISLCHSSNDK
KSQKFATEKQCPEDHLYVLEHNLHLLIREFVMDLKVAARLWFSFLVTNVKTFQKVMFY
KITNGVIFVGHSKKFSGIKWKVEILFIKWSCLCLHLALVYYDFFQMFPKEVSRNFDLKCL
QINYKHKEEITSKRVLFLKIIIRKCLFSTFKLFTL*

MED19 (ID: Q8IV02)

MED19_1 (AY148462; 50 aa longer C-terminus) (SEQ ID NO: 130)
MRELPGSTELTGSTNLITHYNLEQAYNKFCGKKVKEKLSNFLPDLPGMIDLPGSHDNS
SLRSLIEKPPILSSSFNPITGTMLAGFRLHTGPLPEQCRLMHIQPPKKKNKHKHKQSRT
QDPVPPETPSDSDHKKKKKKKEEDPERKRKKKEKKKKKNRHSPDHPGMGSSQASSS
SSLR*

MED19_2 (BM926711; 18 aa longer C-terminus) (SEQ ID NO: 131)
MENFTALFGAQADPPPPPTALGFGPGKPPPPPPPPAGGGPGTAPPPTAATAPPGADK
SGAGCGPFYLMRELPGSTELTGSTNLITHYNLEQAYNKFCGKKVKEKLSNFLPDLPGM
IDLPGSHDNSSLRSLIEKPPILSSSFNPITGTMLAGFRLHTGPLPEQCRLMHIQPPKKKN
KHKHKQSRTQDPVPPGKKQFYSKQKKKKKKKNLTF*

MED19_3 (CB990038; different C-terminus after 158 aa) (SEQ ID NO: 132)
MENFTALFGAQADPPPPPTALGFGPGKPPPPPPPPAGGGPGTAPPPTAATAPPGADK
SGAGCGPFYLMRELPGSTELTGSTNLITHYNLEQAYNKFCGKKVKEKLSNFLPDLPGM
IDLPGSHDNSSLRSLIEKPPILSSSFNPITGTMLAGFRLHTGPVSPVGGRRQMGRPKHG
DGFSLQVCSFIMEQNG*

MED20 (ID: Q9H944)

MED20_1 (8 aa shorter N-terminus) (SEQ ID NO: 133)
MPVAEGKSVQQTVELLTRKLEMLGAEKQGTFCVDCETYHTAASTLGSQGQTGKLMYV
MHNSEYPLSCFALFENGPCLIADTNFDVLMVKLKGFFQSAKASKIETRGTRYQYCDFL
VKVGTVTMGPSARGISVEVEYGPCVVASDCWSLLLEFLQSFLGSHTPGAPAVFGNRH
DAVYGPADTMVQYMELFNKIRKQQQVPVAGIR

MED20_2 (BX366933; shorter protein, 145 aa) (SEQ ID NO: 134)

MGVTCVSQMPVAEGKSVQQTVELLTRKLEMLGAEKQGTFCVDCETYHTAASTLGSQ
GQTGKLMYVMHNSEYPLSCFALFENGPCLIADTNFDVLMVKLKGFFQSAKASKIETRG
TRYQYCDFLVKVGTVTMGPSARGISVEVRPW*

MED21 (ID: Q13503)

MED21_1 (BP213142; longer protein (159 aa), different sequence after 135 aa) (SEQ ID NO: 135)
MADRLTQLQDAVNSLADQFCNAIGVLQQCGPPASFNNIQTAINKDQPANPTEEYAQLF
AALIARTAKDIDVLIDSLPSEESTAALQAASLYKLEEENHEAATCLEDVVYRGDMLLEKI
QSALADIAQSQLKTRSGEVSVTQAEVQFCDHGSLQLHPGFR*

MED22 (ID: Q15528)

MED22_1 (DA228337; 53 aa protein, different sequence after 41 aa) (SEQ ID NO: 136)
MAQQRALPQSKETLLQSYNKRLKDDIKSIMDNFTEIIKTAKVGVGWPTKGSRV*

MED23 (ID: Q9ULK4) - Anri

MED23_1 ()

MED24 (ID: O75448)

MED24_1 (AI815881; extra 19 aa in the middle of protein sequence, after 188 aa) (SEQ ID NO: 5)
MKVVNLKQAILQAWKERWSDYQWAINMKKFFPKGATWDILNLADALLEQAMIGPSPN
PLILSYLKYAISSQMVSYSSVLTAISKFDDFSRDLCVQALLDIMDMFCDRLSCHGKAEEC
IGLCRALLSALHWLLRCTAASAERLREGLEAGTPAAGEKQLAMCLQRLEKTLSSTKNR
ALLHIAKLEEASLHTSQGLGQGGTRANQPTASWTAIEHSLLKLGEILANLSNPQLRSQA
EQCGTLIRSIPTMLSVHAEQMHKTGFPTVHAVILLEGTMNLTGETQSLVEQLTMVKRM
QHIPTPLFVLEIWKACFVGLIESPEGTEELKWTAFTFLKIPQVLVKLKKYSHGDKDFTED
VNCAFEFLLKLTPLLDKADQRCNCDCTNFLLQECGKQGLLSEASVNNLMAKRKADRE
HAPQQKSGENANIQPNIQLILRAEPTVTNILKTMDADHSKSPEGLLGVLGHMLSGKSLD
LLLAAAAATGKLKSFARKFINLNEFTTYGSEESTKPASVRALLFDISFLMLCHVAQTYGS
EVILSESRTGAEVPFFETWMQTCMPEEGKILNPDHPCFRPDSTKVESLVALLNNSSEM
KLVQMKWHEACLSISAAILEILNAWENGVLAFESIQKITDNIKGKVCSLAVCAVAWLVAH
VRMLGLDEREKSLQMIRQLAGPLFSENTLQFYNERVVIMNSILERMCADVLQQTATQIK
FPSTGVDTMPYWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRSIHIFDTLLHMGGVYWFC
NNLIKELLKETRKEHTLRAVELLYSIFCLDMQQVTLVLLGHILPGLLTDSSKWHSLMDPP
GTALAKLAVWCALSSYSSHKGQASTRQKKRHREDIEDYISLFPLDDVQPSKLMRLLSS
NEDDANILSSPTDRSMSSSLSASQLHTVNMRDPLNRVLANLFLLISSILGSRTAGPHTQ
FVQWFMEECVDCLEQGGRGSVLQFMPFTTVSELVKVSAMSSPKVVLAITDLSLPLGR
QVAAKAIAAL

MED24_2 (AK022508; internal 12 aa missing (72-84 aa)) (SEQ ID NO: 137)
MKVVNLKQAILQAWKERWSDYQWAINMKKFFPKGATWDILNLADALLEQAMIGPSPN
PLILSYLKYAISSQFDDFSRDLCVQALLDIMDMFCDRLSCHGKAEECIGLCRALLSALH
WLLRCTAASAERLREGLEAGTPAAGEKQLAMCLQRLEKTLSSTKNRALLHIAKLEEAS
SWTAIEHSLLKLGEILANLSNPQLRSQAEQCGTLIRSIPTMLSVHAEQMHKTGFPTVHA
VILLEGTMNLTGETQSLVEQLTMVKRMQHIPTPLFVLEIWKACFVGLIESPEGTEELKW
TAFTFLKIPQVLVKLKKYSHGDKDFTEDVNCAFEFLLKLTPLLDKADQRCNCDCTNFLL

QECGKQGLLSEASVNNLMAKRKADREHAPQQKSGENANIQPNIQLILRAEPTVTNILKT
MDADHSKSPEGLLGVLGHMLSGKSLDLLLAAAAATGKLKSFARKFINLNEFTTYGSEE
STKPASVRALLFDISFLMLCHVAQTYGSEVILSESRTGAEVPFFETWMQTCMPEEGKIL
NPDHPCFRPDSTKVESLVALLNNSSEMKLVQMKWHEACLSISAAILEILNAWENGVLAF
ESIQKITDNIKGKVCSLAVCAVAWLVAHVRMLGLDEREKSLQMIRQLAGPLFSENTLQF
YNERVVIMNSILERMCADVLQQTATQIKFPSTGVDTMPYWNLLPPKRPIKEVLTDIFAKV
LEKGWVDSRSIHIFDTLLHMGGVYWFCNNLIKELLKETRKEHTLRAVELLYSIFCLDMQ
QVTLVLLGHILPGLLTDSSKWHSLMDPPGTALAKLAVWCALSSYSSHKGQASTRQKKR
HREDIEDYISLFPLDDVQPSKLMRLLSSNEDDANILSSPTDRSMSSSLSASQLHTVNMR
DPLNRVLANLFLLISSILGSRTAGPHTQFVQWFMEECVDCLEQGGRGSVLQFMPFTTV
SELVKVSAMSSPKVVLAITDLSLPLGRQVAAKAIAAL*

MED24_3 (internal 13 aa missing (71-84 aa), extra 19 aa after 187 aa) (SEQ ID NO: 138)

MKVVNLKQAILQAWKERWSDYQWAINMKKFFPKGATWDILNLADALLEQAMIGPSPN
PLILSYLKYAISSQFDDFSRDLCVQALLDIMDMFCDRLSCHGKAEECIGLCRALLSALH
WLLRCTAASAERLREGLEAGTPAAGEKQLAMCLQRLEKTLSSTKNRALLHIAKLEEASL
HTSQGLGQGGTRANQPTASWTAIEHSLLKLGEILANLSNPQLRSQAEQCGTLIRSIPTM
LSVHAEQMHKTGFPTVHAVILLEGTMNLTGETQSLVEQLTMVKRMQHIPTPLFVLEIWK
ACFVGLIESPEGTEELKWTAFTFLKIPQVLVKLKKYSHGDKDFTEDVNCAFEFLLKLTPL
LDKADQRCNCDCTNFLLQECGKQGLLSEASVNNLMAKRKADREHAPQQKSGENANI
QPNIQLILRAEPTVTNILKTMDADHSKSPEGLLGVLGHMLSGKSLDLLLAAAAATGKLKS
FARKFINLNEFTTYGSEESTKPASVRALLFDISFLMLCHVAQTYGSEVILSESRTGAEVP
FFETWMQTCMPEEGKILNPDHPCFRPDSTKVESLVALLNNSSEMKLVQMKWHEACLS
ISAAILEILNAWENGVLAFESIQKITDNIKGKVCSLAVCAVAWLVAHVRMLGLDEREKSL
QMIRQLAGPLFSENTLQFYNERVVIMNSILERMCADVLQQTATQIKFPSTGVDTMPYW
NLLPPKRPIKEVLTDIFAKVLEKGWVDSRSIHIFDTLLHMGGVYWFCNNLIKELLKETRK
EHTLRAVELLYSIFCLDMQQVTLVLLGHILPGLLTDSSKWHSLMDPPGTALAKLAVWCA
LSSYSSHKGQASTRQKKRHREDIEDYISLFPLDDVQPSKLMRLLSSNEDDANILSSPTD
RSMSSSLSASQLHTVNMRDPLNRVLANLFLLISSILGSRTAGPHTQFVQWFMEECVDC
LEQGGRGSVLQFMPFTTVSELVKVSAMSSPKVVLAITDLSLPLGRQVAAKAIAAL

MED24_4 (CN307366; extra 44 aa after 874 aa) (SEQ ID NO: 139)

MKVVNLKQAILQAWKERWSDYQWAINMKKFFPKGATWDILNLADALLEQAMIGPSPN
PLILSYLKYAISSQMVSYSSVLTAISKFDDFSRDLCVQALLDIMDMFCDRLSCHGKAEEC
IGLCRALLSALHWLLRCTAASAERLREGLEAGTPAAGEKQLAMCLQRLEKTLSSTKNR
ALLHIAKLEEASSWTAIEHSLLKLGEILANLSNPQLRSQAEQCGTLIRSIPTMLSVHAEQ
MHKTGFPTVHAVILLEGTMNLTGETQSLVEQLTMVKRMQHIPTPLFVLEIWKACFVGLI
ESPEGTEELKWTAFTFLKIPQVLVKLKKYSHGDKDFTEDVNCAFEFLLKLTPLLDKADQ
RCNCDCTNFLLQECGKQGLLSEASVNNLMAKRKADREHAPQQKSGENANIQPNIQLIL
RAEPTVTNILKTMDADHSKSPEGLLGVLGHMLSGKSLDLLLAAAAATGKLKSFARKFIN
LNEFTTYGSEESTKPASVRALLFDISFLMLCHVAQTYGSEVILSESRTGAEVPFFETWM
QTCMPEEGKILNPDHPCFRPDSTKVESLVALLNNSSEMKLVQMKWHEACLSISAAILEI
LNAWENGVLAFESIQKITDNIKGKVCSLAVCAVAWLVAHVRMLGLDEREKSLQMIRQL
AGPLFSENTLQFYNERVVIMNSILERMCADVLQQTATQIKFPSTGVDTMPYWNLLPPK
RPIKEVLTDIFAKVLEKGWVDSRSIHIFDTLLHMGGVYWFCNNLIKELLKETRKEHTLRA
VELLYSIFCLDMQQVTLVLLGHILPGLLTDSSKWHSLMDPPGTALAKLAVWCALSSYSS
HKGQASTRQKKRHREDIEDYISLFPLDDVQPSKLMRLLSSNEDDANILSSPRSSLGSPC
TSYLRWVKVGLGHPRGAPLLHSAGCFPALHLLRPTADRSMSSSLSASQLHTVNMRDP
LNRVLANLFLLISSILGSRTAGPHTQFVQWFMEECVDCLEQGGRGSVLQFMPFTTVSE
LVKVSAMSSPKVVLAITDLSLPLGRQVAAKAIAAL*

MED24_5 (internal 503 aa missing (80-583 aa)) (SEQ ID NO: 140)

MKVVNLKQAILQAWKERWSDYQWAINMKKFFPKGATWDILNLADALLEQAMIGPSPN
PLILSYLKYAISSQMVSYSSVLTAILEILNAWENGVLAFESIQKITDNIKGKVCSLAVCAVA
WLVAHVRMLGLDEREKSLQMIRQLAGPLFSENTLQFYNERVVIMNSILERMCADVLQQ
TATQIKFPSTGVDTMPYWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRSIHIFDTLLHMGG
VYWFCNNLIKELLKETRKEHTLRAVELLYSIFCLDMQQVTLVLLGHILPGLLTDSSKWHS
LMDPPGTALAKLAVWCALSSYSSHKGQASTRQKKRHREDIEDYISLFPLDDVQPSKLM
RLLSSNEDDANILSSPTDRSMSSSLSASQLHTVNMRDPLNRVLANLFLLISSILGSRTAG
PHTQFVQWFMEECVDCLEQGGRGSVLQFMPFTTVSELVKVSAMSSPKVVLAITDLSL
PLGRQVAAKAIAAL

MED24_6 (internal 276 aa missing (180-456 aa)) (SEQ ID NO: 141)
MKVVNLKQAILQAWKERWSDYQWAINMKKFFPKGATWDILNLADALLEQAMIGPSPN
PLILSYLKYAISSQMVSYSSVLTAISKFDDFSRDLCVQALLDIMDMFCDRLSCHGKAEEC
IGLCRALLSALHWLLRCTAASAERLREGLEAGTPAAGEKQLAMCLQRLEKTLSSTKNR
ALLHIATGKLKSFARKFINLNEFTTYGSEESTKPASVRALLFDISFLMLCHVAQTYGSEVI
LSESRTGAEVPFFETWMQTCMPEEGKILNPDHPCFRPDSTKVESLVALLNNSSEMKLV
QMKWHEACLSISAAILEILNAWENGVLAFESIQKITDNIKGKVCSLAVCAVAWLVAHVR
MLGLDEREKSLQMIRQLAGPLFSENTLQFYNERVVIMNSILERMCADVLQQTATQIKFP
STGVDTMPYWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRSIHIFDTLLHMGGVYWFCN
NLIKELLKETRKEHTLRAVELLYSIFCLDMQQVTLVLLGHILPGLLTDSSKWHSLMDPPG
TALAKLAVWCALSSYSSHKGQASTRQKKRHREDIEDYISLFPLDDVQPSKLMRLLSSN
EDDANILSSPTDRSMSSSLSASQLHTVNMRDPLNRVLANLFLLISSILGSRTAGPHTQF
VQWFMEECVDCLEQGGRGSVLQFMPFTTVSELVKVSAMSSPKVVLAITDLSLPLGRQ
VAAKAIAAL

MED24_7 (internal 413 aa missing (265-678 aa)) (SEQ ID NO: 142)
MKVVNLKQAILQAWKERWSDYQWAINMKKFFPKGATWDILNLADALLEQAMIGPSPN
PLILSYLKYAISSQMVSYSSVLTAISKFDDFSRDLCVQALLDIMDMFCDRLSCHGKAEEC
IGLCRALLSALHWLLRCTAASAERLREGLEAGTPAAGEKQLAMCLQRLEKTLSSTKNR
ALLHIAKLEEASSWTAIEHSLLKLGEILANLSNPQLRSQAEQCGTLIRSIPTMLSVHAEQ
MHKTGFPTVHAVILLEGTMNLTGETQSLVEQQTATQIKFPSTGVDTMPYWNLLPPKRPI
KEVLTDIFAKVLEKGWVDSRSIHIFDTLLHMGGVYWFCNNLIKELLKETRKEHTLRAVEL
LYSIFCLDMQQVTLVLLGHILPGLLTDSSKWHSLMDPPGTALAKLAVWCALSSYSSHK
GQASTRQKKRHREDIEDYISLFPLDDVQPSKLMRLLSSNEDDANILSSPTDRSMSSSLS
ASQLHTVNMRDPLNRVLANLFLLISSILGSRTAGPHTQFVQWFMEECVDCLEQGGRG
SVLQFMPFTTVSELVKVSAMSSPKVVLAITDLSLPLGRQVAAKAIAAL

MED24_8 (shorter C-terminus (837 aa)) (SEQ ID NO: 143)
MKVVNLKQAILQAWKERWSDYQWAINMKKFFPKGATWDILNLADALLEQAMIGPSPN
PLILSYLKYAISSQMVSYSSVLTAISKFDDFSRDLCVQALLDIMDMFCDRLSCHGKAEEC
IGLCRALLSALHWLLRCTAASAERLREGLEAGTPAAGEKQLAMCLQRLEKTLSSTKNR
ALLHIAKLEEASSWTAIEHSLLKLGEILANLSNPQLRSQAEQCGTLIRSIPTMLSVHAEQ
MHKTGFPTVHAVILLEGTMNLTGETQSLVEQLTMVKRMQHIPTPLFVLEIWKACFVGLI
ESPEGTEELKWTAFTFLKIPQVLVKLKKYSHGDKDFTEDVNCAFEFLLKLTPLLDKADQ
RCNCDCTNFLLQECGKQGLLSEASVNNLMAKRKADREHAPQQKSGENANIQPNIQLIL
RAEPTVTNILKTMDADHSKSPEGLLGVLGHMLSGKSLDLLLAAAAATGKLKSFARKFIN
LNEFTTYGSEESTKPASVRALLFDISFLMLCHVAQTYGSEVILSESRTGAEVPFFETWM
QTCMPEEGKILNPDHPCFRPDSTKVESLVALLNNSSEMKLVQMKWHEACLSISAAILEI
LNAWENGVLAFESIQKITDNIKGKVCSLAVCAVAWLVAHVRMLGLDEREKSLQMIRQL
AGPLFSENTLQFYNERVVIMNSILERMCADVLQQTATQIKFPSTGVDTMPYWNLLPPK
RPIKEVLTDIFAKVLEKGWVDSRSIHIFDTLLHMGGVYWFCNNLIKELLKETRKEHTLRA
VELLYSIFCLDMQQVTLVLLGHILPGLLTDSSKWHSLMDPPGTALAKLAVWCALSSYSS
HKGQASTRQKKRHL*

MED24_9 (shorter protein (852 aa), different seq after 848 aa) (SEQ ID NO: 144)
MKVVNLKQAILQAWKERWSDYQWAINMKKFFPKGATWDILNLADALLEQAMIGPSPN
PLILSYLKYAISSQMVSYSSVLTAISKFDDFSRDLCVQALLDIMDMFCDRLSCHGKAEEC
IGLCRALLSALHWLLRCTAASAERLREGLEAGTPAAGEKQLAMCLQRLEKTLSSTKNR
ALLHIAKLEEASSWTAIEHSLLKLGEILANLSNPQLRSQAEQCGTLIRSIPTMLSVHAEQ
MHKTGFPTVHAVILLEGTMNLTGETQSLVEQLTMVKRMQHIPTPLFVLEIWKACFVGLI
ESPEGTEELKWTAFTFLKIPQVLVKLKKYSHGDKDFTEDVNCAFEFLLKLTPLLDKADQ
RCNCDCTNFLLQECGKQGLLSEASVNNLMAKRKADREHAPQQKSGENANIQPNIQLIL
RAEPTVTNILKTMDADHSKSPEGLLGVLGHMLSGKSLDLLLAAAAATGKLKSFARKFIN
LNEFTTYGSEESTKPASVRALLFDISFLMLCHVAQTYGSEVILSESRTGAEVPFFETWM
QTCMPEEGKILNPDHPCFRPDSTKVESLVALLNNSSEMKLVQMKWHEACLSISAAILEI
LNAWENGVLAFESIQKITDNIKGKVCSLAVCAVAWLVAHVRMLGLDEREKSLQMIRQL
AGPLFSENTLQFYNERVVIMNSILERMCADVLQQTATQIKFPSTGVDTMPYWNLLPPK
RPIKEVLTDIFAKVLEKGWVDSRSIHIFDTLLHMGGVYWFCNNLIKELLKETRKEHTLRA
VELLYSIFCLDMQQVTLVLLGHILPGLLTDSSKWHSLMDPPGTALAKLAVWCALSSYSS
HKGQASTRQKKRHREDIEDYISLFPAPDS*

MED24_10 (312 aa shorter N-terminus) (SEQ ID NO: 145)
MPLVPRWCPTLLSSQPSIPQVLVKLKKYSHGDKDFTEDVNCAFEFLLKLTPLLDKADQ
RCNCDCTNFLLQECGKQGLLSEASVNNLMAKRKADREHAPQQKSGENANIQPNIQLIL
RAEPTVTNILKTMDADHSKSPEGLLGVLGHMLSGKSLDLLLAAAAATGKLKSFARKFIN
LNEFTTYGSEESTKPASVRALLFDISFLMLCHVAQTYGSEVILSES

MED24_11 (498 aa shorter N-terminus) (SEQ ID NO: 146)
MLCHVAQTYGSEVILSESRTGAEVPFFETWMQTCMPEEGKILNPDHPCFRPDSTKVE
SLVALLNNSSEMKLVQMKWHEACLSISAAILEILNAWENGVLAFESIQKITDNIKGKVCS
LAVCAVAWLVAHVRMLGLDEREKSLQMIRQLAGPLFSENTLQFYNERVVIMNSILERM
CADVLQQTATQIKFPSTGVDTMPYWNLLPPKRPIKEVLTDIFAKVLEKGWVDSRSIHIFD
TLLHMGGVYWFCNNLIKELLKETRKEHTLRAVELLYSIFCLDMQQVTLVLLGHILPGLLT
DSSKWHSLMDPPGTALAKLAVWCALSSYSSHKGQASTRQKKRHREDIEDYISLFPLD
DVQPSKLMRLLSSNEDDANILSSPTDRSMSSSLSASQLHTVNMRDPLNRVLANLFLLIS
SILGSRTAGPHTQFVQWFMEECVDCLEQGGRGSVLQFMPFTTVSELVKVSAMSSPKV
VLAITDLSLPLGRQVAAKAIAAL

MED25 (ID: Q6P143) - Anri

MED25_1 (213 aa missing (61-274 aa)) (SEQ ID NO: 147)
MVPGSEGPARAGSVVADVVFVIEGTANLGPYFEGLRKHYLLPAIEYFNGGPPAETDFG
GDVPGNLSAAQVAAQNAVEAAKNQKAGLGPRFSPITPLQQAAPGVGPPFSQAPAPQL
PPGPPGAPKPPPASQPSLVSTVAPGSGLAPTAQPGAPSMAGTVAPGGVSGPSPAQL
GAPALGGQQSVSNKLLAWSGVLEWQEKPKPASVDANTKLTRSLPCQVYVNHGENLK
TEQWPQKLIMQLIPQQLLTTLGPLFRNSRMVQFHFTNKDLESLKGLYRIMGNGFAGCV
HFPHTAPCEVRVLMLLYSSKKKIFMGLIPYDQSGFVNGIRQVITNHKQVQQQKLEQQQ
RGMGGQQAPPGLGPILEDQARPSQNLLQLRPPQPQPQGTVGASGATGQPQPQGTA
QPPPGAPQGPPGAASGPPPPGPILRPQNPGANPQLRSLLLNPPPPQTGVPPPQASLH
HLQPPGAPALLPPPHQGLGQPQLGPPLLHPPPAQSWPAQLPPRAPLPGQMLLSGGP
RGPVPQPGLQPSVMEDDILMDLI*

MED25_2 (616 aa missing (26-642 aa)) (SEQ ID NO: 148)
MVPGSEGPARAGSVVADVVFVIEGTANPQLRSLLLNPPPPQTGVPPPQASLHHLQPP
GAPALLPPPHQGLGQPQLGPPLLHPPPAQSWPAQLPPRAPLPGQMLLSGGPRGPVP
QPGLQPSVMEDDILMDLI*

MED25_3 (579 aa missing (51-630 aa)) (SEQ ID NO: 149)
MVPGSEGPARAGSVVADVVFVIEGTANLGPYFEGLRKHYLLPAIEYFNGGPPGPILRP
QNPGANPQLRSLLLNPPPPQTGVPPPQASLHHLQPPGAPALLPPPHQGLGQPQLGPP
LLHPPPAQSWPAQLPPRAPLPGQMLLSGGPRGPVPQPGLQPSVMEDDILMDLI*

MED26 (ID: O95402)

MED26_1 (BC105952; 92 aa protein, different sequence after 76 aa) (SEQ ID NO: 150)
MTAAPASPQQIRDRLLQAIDPQSNIRNMVAVLEVISSLEKYPITKEALEETRLGKLINDVR
KKTKNEELAKRAKKLPGWQWACRPRGQPPGA*

MED26_2 (internal 86 aa missing (61-147 aa)) (SEQ ID NO: 151)
MTAAPASPQQIRDRLLQAIDPQSNIRNMVAVLEVISSLEKYPITKEALEETRLGKLINDVR
KRRGDQRDLGHPGPPPKVSKASHDPLVPNSSPLPTNGISGSPESFASSLDGSGHAGP
EGSRLERDENDKHSGKIPVNAVRPHTSSPGLGKPPGPCLQPKASVLQQLDRVDETPG
PPHPKGPPRCSFSPRNSRHEGSFARQQSLYAPKGSVPSPSPRPQALDATQVPSPLPL
AQPSTPPVRRLELLPSAESPVCWLEQPESHQRLAGPGCKAGLSPAEPLLSRAGFSPD
SSKADSDAASSGGSDSKKKKRYRPRDYTVNLDGQVAEAGVKPVRLKERKLTFDPMTR
QIKPLTQKEPVRADSPVHMEQQSRTELDKQEAKASLQSPFEQTNWKELSRNEIIQSYL
SRQSSLLSSSGAQTPGAHHFMSEYLKQEESTRQGARQLHVLVPQSPPTDLPGLTREV
TQDDLDRIQASQWPGVNGCQDTQGNWYDWTQCISLDPHGDDGRLNILPYVCLD

MED27 (ID: Q6P2C8)

MED27_1 (BC070331; shorter protein, 195 aa) (SEQ ID NO: 152)
MADVINVSVNLEAFSQAISAIQALRSSVSRVFDCLKDGMRNKETLEGREKAFIAHFQDN
LHSVNRDLNELERLSNLVGKPSENHPLHNSGLLSLDPVQDKTPLYSQLLQAYKWSNKL
QYHAGLASGLLNQQSLKRSANQMGVSAKRRPKAQPTTLVLPPQYVDDVISRIDRMFP
EMSIHLSRPNGTSAMLLVRSA*

MED28 (ID: Q9H204)

MED28_1 (AF317678; 4 aa longer C-terminus) (SEQ ID NO: 153)
MAAPLGGMFSGQPPGPPQAPPGLPGQASLLQAAPGAPRPSSSTLVDELESSFEACFA
SLVSQDYVNGTDQEEIRTGVDQCIQKFLDIARQTECFFLQKRLQLSVQKPEQVIKEDVS
ELRNELQRKDALVQKHLTKLRHWQQVLEDINVQHKKPADIPQGSLAYLEQASANIPAP
LKPTHLTG*

MED28_2 (shorter protein (125 aa), different sequence after 113 aa) (SEQ ID NO: 154)
MAAPLGGMFSGQPPGPPQAPPGLPGQASLLQAAPGAPRPSSSTLVDELESSFEACFA
SLVSQDYVNGTDQEEIRTGVDQCIQKFLDIARQTECFFLQKRLQLSVQKPEQVIKEVFL
LRKKKTTCP*

MED30 (ID: Q96HR3)

MED30_1 (AA811383; shorter protein, different sequence after 112 aa) (SEQ ID NO: 155)
MSTPPLAASGMAPGPFAGPQAQQAAREVNTASLCRIGQETVQDIVYRTMEIFQLLRN
MQLPNGVTYHTGTYQDRLTKLQDNLRQLSVLFRKLRLVYDKCNENCGGMDPIPVEVIF
CDRGRMNIRCELVSRQLLIFFLSLLF*
MED30_2 (AW371008; shorter protein, 153 aa) (SEQ ID NO: 156)

MSTPPLAASGMAPGPFAGPQAQQAAREVNTASLCRIGQETVQDIVYRTMEIFQLLRN
MQLPNGVTYHTGTYQDRLTKLQDNLRQLSVLFRKLRLVYDKCNENCGGMDPIPVEQLI
PYVEEDGSKNDDRAGPPRFASEERREIAEVNKVLGEAF*

MED30_3 (157 aa protein, different sequence from 147 aa) (SEQ ID NO: 157)
MSTPPLAASGMAPGPFAGPQAQQAAREVNTASLCRIGQETVQDIVYRTMEIFQLLRN
MQLPNGVTYHTGTYQDRLTKLQDNLRQLSVLFRKLRLVYDKCNENCGGMDPIPVEQLI
PYVEEDGSKNDDRAGPPRFASEERREIAEVNKALSSVPEFLP*

MED31 (ID: Q9Y3C7)

MED31_1 (AK130946; 43 aa protein) (SEQ ID NO: 158)
MAAAVAMETDDAGNRLRFQLELEFVQCLANPNYLNCTLSVYTC*

MED31_2 (BU678904; 74 aa shorter N-terminus) (SEQ ID NO: 159)
MLELLQYEHFRKELVNAQCAKFIDEQQILHWQHYSRKRMRLQQALAEQQQQNNTSGK
*

MED31_3 (BX489859; short protein, 44 aa) (SEQ ID NO: 160)
MAAAVAMETDDAGNRLRFQLELEFVQCLANPNYLNCKLLSTSLN*

CDK8 (ID: P49336)

CDK8_1 (BE884669; internal 48 aa missing (216 - 264 aa)) (SEQ ID NO: 161)
MDYDFKVKLSSERERVEDLFEYEGCKVGRGTYGHVYKAKRKDGKDDKDYALKQIEGT
GISMSACREIALLRELKHPNVISLQKVFLSHADRKVWLLFDYAEHDLWHIIKFHRASKAN
KKPVQLPRGMVKSLLYQILDGIHYLHANWVLHRDLKPANILVMGEGPERGRVKIADMG
FARLFNSPLKPLADLDPVVVTFWYRAPELLLGARHYTKAIDKDWEDIKKMPEHSTLMK
DFRRNTYTNCSLIKYMEKHKVKPDSKAFHLLQKLLTMDPIKRITSEQAMQDPYFLEDPL
PTSDVFAGCQIPYPKREFLTEEEPDDKGDKKNQQQQQGNNHTNGTGHPGNQDSSHT
QGPPLKKVRVVPPTTTSGGLIMTSDYQRSNPHAAYPNPGPSTSQPQSSMGYSATSQ
QPPQYSHQTHRY

CCNC (ID: P24863)

CCNC_1 (BC026272; shorter protein (163 aa), different sequece after 135 aa) (SEQ ID NO: 162)
MVAPRPLRRVVLFYQGKLCSMAGNFWQSSHYLQWILDKQDLLKERQKDLKFLSEEEY
WKLQIFFTNVIQALGEHLKLRQQVIATATVYFKRFYARYSLKSIDPVLMAPTCVFLASKV
EEFGVVSNTRLIAAATSVCKCKKYICFKDVILKKAPEYIDFFFFSL*

CCNC_2 (BX387621; short protein, 50 aa) (SEQ ID NO: 163)
MAGNFWQSSHYLQWILDKQDLLKERQKDLKFLSEEEYWKLQIFFTNGKLF*

CCNC_3 (AI479346; different sequence after 285 aa) (SEQ ID NO: 164)
MVAPRPLRRVVLFYQGKLCSMAGNFWQSSHYLQWILDKQDLLKERQKDLKFLSEEEY
WKLQIFFTNVIQALGEHLKLRQQVIATATVYFKRFYARYSLKSIDPVLMAPTCVFLASKV
EEFGVVSNTRLIAAATSVLKTRFSYAFPKEFPYRMNHILECEFYLLELMDCCLIVYHPYR
PLLQYVQDMGQEDMLLPLAWRIVNDTYRTDLCLLYPPFMIALACLHVACVVQQKDARQ
WFAELSVDMEKILEIIRVILKLYEQWKNFDERKEMATILSKMPKPKPPPNRNSLSDSPLV
AGPEAAR*

SMARCA1 (ID: P28370)

SMARCA1_1 (BC051825; internal 12 aa missing (467 - 477 aa)) (SEQ ID NO: 165)
MDPEYEEKMKADRAKRFEFLLKQTELFAHFIQPSAQKSPTSPLNMKLGRPRIKKDEKQ
SLISAGDYRHRRTEQEEDEELLSESRKTSNVCIRFEVSPSYVKGGPLRDYQIRGLNWLI
SLYENGVNGILADEMGLGKTLQTIALLGYLKHYRNIPGPHMVLVPKSTLHNWMNEFKR
WVPSLRVICFVGDKDARAAFIRDEMMPGEWDVCVTSYEMVIKEKSVFKKFHWRYLVID
EAHRIKNEKSKLSEIVREFKSTNRLLLTGTPLQNNLHELWALLNFLLPDVFNSADDFDS
WFDTKNCLGDQKLVERLHAVLKPFLLRRIKTDVEKSLPPKKEIKIYLGLSKMQREWYTKI
LMKDIDVLNSSGKMDKMRLLNILMQLRKCCNHPYLFDGAEPGPPYTTDEHIVSNSGKM
VVLDKLLAKLKEQGSRVLIFSQMTRLLDILEDYCMWRGYEYCRLDGQTPHEEREEAIE
AFNAPNSSKFIFMLSTRAGGLGINLASADVVILYDSDWNPQVDLQAMDRAHRIGQKKP
VRVFRLITDNTVEERIVERAEIKLRLDSIVIQQGRLIDQQSNKLAKEEMLQMIRHGATHVF
ASKESELTDEDITTILERGEKKTAEMNERLQKMGESSLRNFRMDIEQSLYKFEGEDYR
EKQKLGMVEWIEPPKRERKANYAVDAYFREALRVSEPKIPKAPRPPKQPNVQDFQFF
PPRLFELLEKEILYYRKTIGYKVPRNPDIPNPALAQREEQKKIDGAEPLTPEETEEKEKLL
TQGFTNWTKRDFNQFIKANEKYGRDDIDNIAREVEGKSPEEVMEYSAVFWERCNELQ
DIEKIMAQIERGEARIQRRISIKKALDAKIARYKAPFHQLRIQYGTSKGKNYTEEEDRFLI
CMLHKMGFDRENVYEELRQCVRNAPQFRFDWFIKSRTAMEFQRRCNTLISLIEKENM
EIEERERAEKKKRATKTPMVKFSAFS*

SMARCA1_2 (internal 139 aa missing (463 - 602 aa)) (SEQ ID NO: 166)
MDPEYEEKMKADRAKRFEFLLKQTELFAHFIQPSAQKSPTSPLNMKLGRPRIKKDEKQ
SLISAGDYRHRRTEQEEDEELLSESRKTSNVCIRFEVSPSYVKGGPLRDYQIRGLNWLI
SLYENGVNGILADEMGLGKTLQTIALLGYLKHYRNIPGPHMVLVPKSTLHNWMNEFKR
WVPSLRVICFVGDKDARAAFIRDEMMPGEWDVCVTSYEMVIKEKSVFKKFHWRYLVID
EAHRIKNEKSKLSEIVREFKSTNRLLLTGTPLQNNLHELWALLNFLLPDVFNSADDFDS
WFDTKNCLGDQKLVERLHAVLKPFLLRRIKTDVEKSLPPKKEIKIYLGLSKMQREWYTKI
LMKDIDVLNSSGKMDKMRLLNILMQLRKCCNHPYLFDGAEPGPPYTTDEHIVSNSGKM
VVLDKLLAKLKEQGSRVLIFSQMTRLLDILEDYCMWRGYEYCRLDGQTPHEERESELT
DEDITTILERGEKKTAEMNERLQKMGESSLRNFRMDIEQSLYKFEGEDYREKQKLGMV
EWIEPPKRERKANYAVDAYFREALRVSEPKIPKAPRPPKQPNVQDFQFFPPRLFELLE
KEILYYRKTIGYKVPRNPDIPNPALAQREEQKKIDGAEPLTPEETEEKEKLLTQGFTNWT
KRDFNQFIKANEKYGRDDIDNIAREVEGKSPEEVMEYSAVFWERCNELQDIEKIMAQIE
RGEARIQRRISIKKALDAKIARYKAPFHQLRIQYGTSKGKNYTEEEDRFLICMLHKMGFD
RENVYEELRQCVRNAPQFRFDWFIKSRTAMEFQRRCNTLISLIEKENMEIEERERAEK
KKRATKTPMVKFSAFS

SMARCA2 (ID: P51531)

SMARCA2_1 (isoform 2, internal 18 aa missing (1400-1418)) (SEQ ID NO: 167)
MSTPTDPGAMPHPGPSPGPGPSPGPILGPSPGPGPSPGSVHSMMGPSPGPPSVSHP
MPTMGSTDFPQEGMHQMHKPIDGIHDKGIVEDIHCGSMKGTGMRPPHPGMGPPQSP
MDQHSQGYMSPHPSPLGAPEHVSSPMSGGGPTPPQMPPSQPGALIPGDPQAMSQP
NRGPSPFSPVQLHQLRAQILAYKMLARGQPLPETLQLAVQGKRTLPGLQQQQQQQQ
QQQQQQQQQQQQQQQPQQQPPQPQTQQQQQPALVNYNRPSGPGPELSGPSTPQ
KLPVPAPGGRPSPAPPAAAQPPAAAVPGPSVPQPAPGQPSPVLQLQQKQSRISPIQK
PQGLDPVEILQEREYRLQARIAHRIQELENLPGSLPPDLRTKATVELKALRLLNFQRQL
RQEVVACMRRDTTLETALNSKAYKRSKRQTLREARMTEKLEKQQKIEQERKRRQKHQ
EYLNSILQHAKDFKEYHRSVAGKIQKLSKAVATWHANTEREQKKETERIEKERMRRLM
AEDEEGYRKLIDQKKDRRLAYLLQQTDEYVANLTNLVWEHKQAQAAKEKKKRRRRKK
KAEENAEGGESALGPDGEPIDESSQMSDLPVKVTHTETGKVLFGPEAPKASQLDAWL
EMNPGYEVAPRSDSEESDSDYEEEDEEEESSRQETEEKILLDPNSEEVSEKDAKQIIET

AKQDVDDEYSMQYSARGSQSYYTVAHAISERVEKQSALLINGTLKHYQLQGLEWMVS
LYNNNLNGILADEMGLGKTIQTIALITYLMEHKRLNGPYLIIVPLSTLSNWTYEFDKWAPS
VVKISYKGTPAMRRSLVPQLRSGKFNVLLTTYEYIIKDKHILAKIRWKYMIVDEGHRMKN
HHCKLTQVLNTHYVAPRRILLTGTPLQNKLPELWALLNFLLPTIFKSCSTFEQWFNAPF
AMTGERVDLNEEETILIIRRLHKVLRPFLLRRLKKEVESQLPEKVEYVIKCDMSALQKILY
RHMQAKGILLTDGSEKDKKGKGGAKTLMNTIMQLRKICNHPYMFQHIEESFAEHLGYS
NGVINGAELYRASGKFELLDRILPKLRATNHRVLLFCQMTSLMTIMEDYFAFRNFLYLRL
DGTTKSEDRAALLKKFNEPGSQYFIFLLSTRAGGLGLNLQAADTVVIFDSDWNPHQDL
QAQDRAHRIGQQNEVRVLRLCTVNSVEEKILAAAKYKLNVDQKVIQAGMFDQKSSSHE
RRAFLQAILEHEEENEEEDEVPDDETLNQMIARREEEFDLFMRMDMDRRREDARNPK
RKPRLMEEDELPSWIIKDDAEVERLTCEEEEEKIFGRGSRQRRDVDYSDALTEKQWLR
AIEDGNLEEMEEEVRLKKRKRRRNVDKDPAKEDVEKAKKRRGRPPAEKLSPNPPKLT
KQMNAIIDTVINYKDSSGRQLSEVFIQLPSRKELPEYYELIRKPVDFPLSTLSNWTYEFD
KWAPSVVKISYKGTPAMRRSLVPQLRSGKFNVLLTTYEYIIKDKHILAKIRWKYMIVDEG
HRMKNHHCKLTQVLNTHYVAPRRILLTGTPLQNKLPELWALLNFLLPTIFKSCSTFEQW
FNAPFAMTGERVDLNEEETILIIRRLHKVLRPFLLRRLKKEVESQLPEKVEYVIKCDMSA
LQKILYRHMQAKGILLTDGSEKDKKGKGGAKTLMNTIMQLRKICNHPYMFQHIEESFAE
HLGYSNGVINGAELYRASGKFELLDRILPKLRATNHRVLLFCQMTSLMTIMEDYFAFRN
FLYLRLDGTTKSEDRAALLKKFNEPGSQYFIFLLSTRAGGLGLNLQAADTVVIFDSDWN
PHQDLQAQDRAHRIGQQNEVRVLRLCTVNSVEEKILAAAKYKLNVDQKVIQAGMFDQK
SSSHERRAFLQAILEHEEENEEEDEVPDDETLNQMIARREEEFDLFMRMDMDRRRED
ARNPKRKPRLMEEDELPSWIIKDDAEVERLTCEEEEEKIFGRGSRQRRDVDYSDALTE
KQWLRAIEDGNLEEMEEEVRLKKRKRRRNVDKDPAKEDVEKAKKRRGRPPAEKLSPN
PPKLTKQMNAIIDTVINYKDRCNVEKVPSNSQLEIEGNSSGRQLSEVFIQLPSRKELPEY
YELIRKPVDFKKIKERIRNHKYRSLGDLEKDVMLLCHNAQTFNLEGSQIYEDSIVLQSVF
KSARQKIAKEEESEDESNEEEEEEDEEESESEAKSVKVKIKLNKKDDKGRDKGKGKKR
PNRGKAKPVVSDFDSDEEQDEREQSEGSGTDDE*

SMARCA2_2 (isoform 2 but 50 aa shorter C-terminus (different seq after 1509 aa)
(SEQ ID NO: 168)
MSTPTDPGAMPHPGPSPGPGPSPGPILGPSPGPGPSPGSVHSMMGPSPGPPSVSHP
MPTMGSTDFPQEGMHQMHKPIDGIHDKGIVEDIHCGSMKGTGMRPPHPGMGPPQSP
MDQHSQGYMSPHPSPLGAPEHVSSPMSGGGPTPPQMPPSQPGALIPGDPQAMSQP
NRGPSPFSPVQLHQLRAQILAYKMLARGQPLPETLQLAVQGKRTLPGLQQQQQQQQ
QQQQQQQQQQQQQQPPQPQTQQQQQPALVNYNRPSGPGPELSGPSTPQKLPVP
APGGRPSPAPPAAAQPPAAAVPGPSVPQPAPGQPSPVLQLQQKQSRISPIQKPQGLD
PVEILQEREYRLQARIAHRIQELENLPGSLPPDLRTKATVELKALRLLNFQRQLRQEVVA
CMRRDTTLETALNSKAYKRSKRQTLREARMTEKLEKQQKIEQERKRRQKHQEYLNSIL
QHAKDFKEYHRSVAGKIQKLSKAVATWHANTEREQKKETERIEKERMRRLMAEDEEG
YRKLIDQKKDRRLAYLLQQTDEYVANLTNLVWEHKQAQAAKEKKKRRRRKKKAEENA
EGGESALGPDGEPIDESSQMSDLPVKVTHTETGKVLFGPEAPKASQLDAWLEMNPGY
EVAPRSDSEESDSDYEEEDEEEESSRQETEEKILLDPNSEEVSEKDAKQIIETAKQDVD
DEYSMQYSARGSQSYYTVAHAISEWVEKQSALLINGTLKHYQLQGLEWMVSLYNNNL
NGILADEMGLGKTIQTIALITYLMEHKRLNGPYLIIVPLSTLSNWTYEFDKWAPSVVKISY
KGTPAMRRSLVPQLRSGKFNVLLTTYEYIIKDKHILAKIRWKYMIVDEGHRMKNHHCKL
TQVLNTHYVAPRRILLTGTPLQNKLPELWALLNFLLPTIFKSCSTFEQWFNAPFAMTGE
RVDLNEEETILIIRRLHKVLRPFLLRRLKKEVESQLPEKVEYVIKCDMSALQKILYRHMQA
KGILLTDGSEKDKKGKGGAKTLMNTIMQLRKICNHPYMFQHIEESFAEHLGYSNGVING
AELYRASGKFELLDRILPKLRATNHRVLLFCQMTSLMTIMEDYFAFRNFLYLRLDGTTK
SEDRAALLKKFNEPGSQYFIFLLSTRAGGLGLNLQAADTVVIFDSDWNPHQDLQAQDR
AHRIGQQNEVRVLRLCTVNSVEEKILAAAKYKLNVDQKVIQAGMFDQKSSSHERRAFL
QAILEHEEENEEEDEVPDDETLNQMIARREEEFDLFMRMDMDRRREDARNPKRKPRL
MEEDELPSWIIKDDAEVERLTCEEEEEKIFGRGSRQRRDVDYSDALTEKQWLRAIEDG

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NLEEMEEEVRLKKRKRRRNVDKDPAKEDVEKAKKRRGRPPAEKLSPNPPKLTKQMNA
IIDTVINYKDSSGRQLSEVFIQLPSRKELPEYYELIRKPVDFKKIKERIRNHKYRSLGDLE
KDVMLLCHNAQTFNLEGSQIYEDSIVLQSVFKSARQKIAKEEESEDESNEEEEEEDEEE
SESEGTVRRKWDG*

SMARCA2_3 (different sequence after 1400 aa) (SEQ ID NO: 169)
MSTPTDPGAMPHPGPSPGPGPSPGPILGPSPGPGPSPGSVHSMMGPSPGPPSVSHP
MPTMGSTDFPQEGMHQMHKPIDGIHDKGIVEDIHCGSMKGTGMRPPHPGMGPPQSP
MDQHSQGYMSPHPSPLGAPEHVSSPMSGGGPTPPQMPPSQPGALIPGDPQAMSQP
NRGPSPFSPVQLHQLRAQILAYKMLARGQPLPETLQLAVQGKRTLPGLQQQQQQQQ
QQQQQQQQQQQQQQQPQQQPPQPQTQQQQQPALVNYNRPSGPGPELSGPSTPQ
KLPVPAPGGRPSPAPPAAAQPPAAAVPGPSVPQPAPGQPSPVLQLQQKQSRISPIQK
PQGLDPVEILQEREYRLQARIAHRIQELENLPGSLPPDLRTKATVELKALRLLNFQRQL
RQEVVACMRRDTTLETALNSKAYKRSKRQTLREARMTEKLEKQQKIEQERKRRQKHQ
EYLNSILQHAKDFKEYHRSVAGKIQKLSKAVATWHANTEREQKKETERIEKERMRRLM
AEDEEGYRKLIDQKKDRRLAYLLQQTDEYVANLTNLVWEHKQAQAAKEKKKRRRRKK
KAEENAEGGESALGPDGEPIDESSQMSDLPVKVTHTETGKVLFGPEAPKASQLDAWL
EMNPGYEVAPRSDSEESDSDYEEEDEEEESSRQETEEKILLDPNSEEVSEKDAKQIIET
AKQDVDDEYSMQYSARGSQSYYTVAHAISERVEKQSALLINGTLKHYQLQGLEWMVS
LYNNNLNGILADEMGLGKTIQTIALITYLMEHKRLNGPYLIIVPLSTLSNWTYEFDKWAPS
VVKISYKGTPAMRRSLVPQLRSGKFNVLLTTYEYIIKDKHILAKIRWKYMIVDEGHRMKN
HHCKLTQVLNTHYVAPRRILLTGTPLQNKLPELWALLNFLLPTIFKSCSTFEQWFNAPF
AMTGERVDLNEEETILIIRRLHKVLRPFLLRRLKKEVESQLPEKVEYVIKCDMSALQKILY
RHMQAKGILLTDGSEKDKKGKGGAKTLMNTIMQLRKICNHPYMFQHIEESFAEHLGYS
NGVINGAELYRASGKFELLDRILPKLRATNHRVLLFCQMTSLMTIMEDYFAFRNFLYLRL
DGTTKSEDRAALLKKFNEPGSQYFIFLLSTRAGGLGLNLQAADTVVIFDSDWNPHQDL
QAQDRAHRIGQQNEVRVLRLCTVNSVEEKILAAAKYKLNVDQKVIQAGMFDQKSSSHE
RRAFLQAILEHEEENEEEDEVPDDETLNQMIARREEEFDLFMRMDMDRRREDARNPK
RKPRLMEEDELPSWIIKDDAEVERLTCEEEEEKIFGRGSRQRRDVDYSDALTEKQWLR
AIEDGNLEEMEEEVRLKKRKRRRNVDKDPAKEDVEKAKKRRGRPPAEKLSPNPPKLT
KQMNAIIDTVINYKDRNSQKEVGRMMSDQYGPFSLVELNSFLPCLISTQ*

SMARCA4 (ID: P5153)

SMARCA4_1 (internal 33 aa missing (1259-1292 aa)) (SEQ ID NO: 170)
MSTPDPPLGGTPRPGPSPGPGPSPGAMLGPSPGPSPGSAHSMMGPSPGPPSAGHPI
PTQGPGGYPQDNMHQMHKPMESMHEKGMSDDPRYNQMKGMGMRSGGHAGMGP
PPSPMDQHSQGYPSPLGGSEHASSPVPASGPSSGPQMSSGPGGAPLDGADPQALG
QQNRGPTPFNQNQLHQLRAQIMAYKMLARGQPLPDHLQMAVQGKRPMPGMQQQM
PTLPPPSVSATGPGPGPGPGPGPGPGPAPPNYSRPHGMGGPNMPPPGPSGVPPGM
PGQPPGGPPKPWPEGPMANAAAPTSTPQKLIPPQPTGRPSPAPPAVPPAASPVMPP
QTQSPGQPAQPAPMVPLHQKQSRITPIQKPRGLDPVEILQEREYRLQARIAHRIQELEN
LPGSLAGDLRTKATIELKALRLLNFQRQLRQEVVVCMRRDTALETALNAKAYKRSKRQ
SLREARITEKLEKQQKIEQERKRRQKHQEYLNSILQHAKDFKEYHRSVTGKIQKLTKAV
ATYHANTEREQKKENERIEKERMRRLMAEDEEGYRKLIDQKKDKRLAYLLQQTDEYVA
NLTELVRQHKAAQVAKEKKKKKKKKKAENAEGQTPAIGPDGEPLDETSQMSDLPVKVI
HVESGKILTGTDAPKAGQLEAWLEMNPGYEVAPRSDSEESGSEEEEEEEEEEQPQAA
QPPTLPVEEKKKIPDPDSDDVSEVDARHIIENAKQDVDDEYGVSQALARGLQSYYAVA
HAVTERVDKQSALMVNGVLKQYQIKGLEWLVSLYNNNLNGILADEMGLGKTIQTIALIT
YLMEHKRINGPFLIIVPLSTLSNWAYEFDKWAPSVVKVSYKGSPAARRAFVPQLRSGK
FNVLLTTYEYIIKDKHILAKIRWKYMIVDEGHRMKNHHCKLTQVLNTHYVAPRRLLLTGT
PLQNKLPELWALLNFLLPTIFKSCSTFEQWFNAPFAMTGEKVDLNEEETILIIRRLHKVL
RPFLLRRLKKEVEAQLPEKVEYVIKCDMSALQRVLYRHMQAKGVLLTDGSEKDKKGK

GGTKTLMNTIMQLRKICNHPYMFQHIEESFSEHLGFTGGIVQGLDLYRASGKFELLDRI
LPKLRATNHKVLLFCQMTSLMTIMEDYFAYRGFKYLRLDGTTKAEDRGMLLKTFNEPG
SEYFIFLLSTRAGGLGLNLQSADTVIIFDSDWNPHQDLQAQDRAHRIGQQNEVRVLRLC
TVNSVEEKILAAAKYKLNVDQKVIQAGMFDQKSSSHERRAFLQAILEHEEQDEEEDEV
PDDETVNQMIARHEEEFDLFMRMDLDRRREEARNPKRKPRLMEEDELPSWIIKDDAE
VERLTCEEEEEKMFGRGSRHRKEVDYSDSLTEKQWLKAIEEGTLEEIEEEVRQKKSSR
KRKRDSDAGSSTPTTSTRSRDKDDESKKQKKRGRPPAEKLSPNPPNLTKKMKKIVDA
VIKYKDSSSGRQLSEVFIQLPSRKELPEYYELIRKPVDFKKIKERIRNHKYRSLNDLEKD
VMLLCQNAQTFNLEGSLIYEDSIVLQSVFTSVRQKIEKEDDSEGEESEEEEEGEEEGSE
SESRSVKVKIKLGRKEKAQDRLKGGRRRPSRGSRAKPVVSDDDSEEEQEEDRSGSG
SEED*

SMARCA4_2 (internal 213 aa missing (615-828 aa)) (SEQ ID NO: 171)
MSTPDPPLGTPRPGPSPGPGPSPGAMLGPSPGPSPGSAHSMMGPSPGPPSAGHPIP
TQGPGGYPQDNMHQMHKPMESMHEKGMSDPRYNQMKGMGMRSGGHAGMGPPPS
PMDQHSQGYPSPLGGSEHASSPVPASGPSSGPQMSSGPGGAPLDGADPQALGQQN
RGPTPFNQNQLHQLRAQIMAYKMLARGQPLPDHLQMAVQGKRPMPGMQQQMPTLP
PPSVSATGPGPGPGPGPGPGPGPAPPNYSRPHGMGGPNMPPPGPSGVPPGMPGQ
PPGGPPKPWPEGPMANAAAPTSTPQKLIPPQPTGRPSPAPPAVPPAASPVMPPQTQS
PGQPAQPAPMVPLHQKQSRITPIQKPRGLDPVEILQEREYRLQARIAHRIQELENLPGS
LAGDLRTKATIELKALRLLNFQRQLRQEVVVCMRRDTALETALNAKAYKRSKRQSLRE
ARITEKLMEKQQKIEQERKRRQKHQEYLNSILQHAKDFKEYHRSVTGKIQKLTKAVATY
HANTEREQKKENERIEKERMRRLMAEDEEGYRKLIDQKKDKRLAYLLQQTDEYVANLT
ELVRQHKAAQVAKEKKKKKKKKKAENAEGQTPAIGPDGEPLDETSQMSDLPVKVSYK
GSPAARRAFVPQLRSGKFNVLLTTYEYIIKDKHILAKIRWKYMIVDEGHRMKNHHCKLT
QVLNTHYVAPRRLLLTGTPLQNKLPELWALLNFLLPTIFKSCSTFEQWFNAPFAMTGEK
VDLNEEETILIIRRLHKVLRPFLLRRLKKEVEAQLPEKVEYVIKCDMSALQRVLYRHMQA
KGVLLTDGSEKDKKGKGGTKTLMNTIMQLRKICNHPYMFQHIEESFSEHLGFTGGIVQ
GLDLYRASGKFELLDRILPKLRATNHKVLLFCQMTSLMTIMEDYFAYRGFKYLRLDGTT
KAEDRGMLLKTFNEPGSEYFIFLLSTRAGGLGLNLQSADTVIIFDSDWNPHQDLQAQD
RAHRIGQQNEVRVLRLCTVNSVEEKILAAAKYKLNVDQKVIQAGMFDQKSSSHERRAF
LQAILEHEEQDESRHCSTGSGSASFAHTAPPPAGVNPDLEEPPLKEEDEVPDDETVN
QMIARHEEEFDLFMRMDLDRRREEARNPKRKPRLMEEDELPSWIIKDDAEVERLTCEE
EEEKMFGRGSRHRKEVDYSDSLTEKQWLKAIEEGTLEEIEEEVRQKKSSRKRKRDSD
AGSSTPTTSTRSRDKDDESKKQKKRGRPPAEKLSPNPPNLTKKMKKIVDAVIKYKDSS
SGRQLSEVFIQLPSRKELPEYYELIRKPVDFKKIKERIRNHKYRSLNDLEKDVMLLCQNA
QTFNLEGSLIYEDSIVLQSVFTSVRQKIEKEDDSEGEESEEEEEGEEEGSESESRSVKV
KIKLGRKEKAQDRLKGGRRRPSRGSRAKPVVSDDDSEEEQEEDRSGSGSEED
SMARCA4_3 (277 aa missing (527 - 804 aa)) (SEQ ID NO: 172)
MSTPDPPLGTPRPGPSPGPGPSPGAMLGPSPGPSPGSAHSMMGPSPGPPSAGHPIP
TQGPGGYPQDNMHQMHKPMESMHEKGMSDPRYNQMKGMGMRSGGHAGMGPPPS
PMDQHSQGYPSPLGGSEHASSPVPASGPSSGPQMSSGPGGAPLDGADPQALGQQN
RGPTPFNQNQLHQLRAQIMAYKMLARGQPLPDHLQMAVQGKRPMPGMQQQMPTLP
PPSVSATGPGPGPGPGPGPGPGPAPPNYSRPHGMGGPNMPPPGPSGVPPGMPGQ
PPGGPPKPWPEGPMANAAAPTSTPQKLIPPQPTGRPSPAPPAVPPAASPVMPPQTQS
PGQPAQPAPMVPLHQKQSRITPIQKPRGLDPVEILQEREYRLQARIAHRIQELENLPGS
LAGDLRTKATIELKALRLLNFQRQLRQEVVVCMRRDTALETALNAKAYKRSKRQSLRE
ARITEKLEKQQKIEQERKRRQKHQEYLNSILQHAKDFKEYHRSVTGKIQKLTKAVATYH
ANTEREQKKENERIEKERMRRLIIVPLSTLSNWAYEFDKWAPSVVKVSYKGSPAARRA
FVPQLRSGKFNVLLTTYEYIIKDKHILAKIRWKYMIVDEGHRMKNHHCKLTQVLNTHYVA
PRRLLLTGTPLQNKLPELWALLNFLLPTIFKSCSTFEQWFNAPFAMTGEKVDLNEEETIL
IIRRLHKVLRPFLLRRLKKEVEAQLPEKVEYVIKCDMSALQRVLYRHMQAKGVLLTDGS
EKDKKGKGGTKTLMNTIMQLRKICNHPYMFQHIEESFSEHLGFTGGIVQGLDLYRASG

KFELLDRILPKLRATNHKVLLFCQMTSLMTIMEDYFAYRGFKYLRLDGTTKAEDRGMLL
KTFNEPGSEYFIFLLSTRAGGLGLNLQSADTVIIFDSDWNPHQDLQAQDRAHRIGQQN
EVRVLRLCTVNSVEEKILAAAKYKLNVDQKVIQAGMFDQKSSSHERRAFLQAILEHEEQ
DESRHCSTGSGSASFAHTAPPPAGVNPDLEEPPLKEEDEVPDDETVNQMIARHEEEF
DLFMRMDLDRRREEARNPKRKPRLMEEDELPSWIIKDDAEVERLTCEEEEEKMFGRG
SRHRKEVDYSDSLTEKQWLKAIEEGTLEEIEEEVRQKKSSRKRKRDSDAGSSTPTTST
RSRDKDDESKKQKKRGRPPAEKLSPNPPNLTKKMKKIVDAVIKYKDSSSGRQLSEVFI
QLPSRKELPEYYELIRKPVDFKKIKERIRNHKYRSLNDLEKDVMLLCQNAQTFNLEGSLI
YEDSIVLQSVFTSVRQKIEKEDDSEGEESEEEEEGEEEGSESESRSVKVKIKLGRKEKA
QDRLKGGRRRPSRGSRAKPVVSDDDSEEEQEEDRSGSGSEED

SMARCA4_4 (internal 296 aa missing (1126-1422 aa)) (SEQ ID NO: 173)
MSTPDPPLGTPRPGPSPGPGPSPGAMLGPSPGPSPGSAHSMMGPSPGPPSAGHPIP
TQGPGGYPQDNMHQMHKPMESMHEKGMSDPRYNQMKGMGMRSGGHAGMGPPPS
PMDQHSQGYPSPLGGSEHASSPVPASGPSSGPQMSSGPGGAPLDGADPQALGQQN
RGPTPFNQNQLHQLRAQIMAYKMLARGQPLPDHLQMAVQGKRPMPGMQQQMPTLP
PPSVSATGPGPGPGPGPGPGPGPAPPNYSRPHGMGGPNMPPPGPSGVPPGMPGQ
PPGGPPKPWPEGPMANAAAPTSTPQKLIPPQPTGRPSPAPPAVPPAASPVMPPQTQS
PGQPAQPAPMVPLHQKQSRITPIQKPRGLDPVEILQEREYRLQARIAHRIQELENLPGS
LAGDLRTKATIELKALRLLNFQRQLRQEVVVCMRRDTALETALNAKAYKRSKRQSLRE
ARITEKLEKQQKIEQERKRRQKHQEYLNSILQHAKDFKEYHRSVTGKIQKLTKAVATYH
ANTEREQKKENERIEKERMRRLMAEDEEGYRKLIDQKKDKRLAYLLQQTDEYVANLTE
LVPQHKAAQVAKEKKKKKKKKKAENAEGQTPAIGPDGEPLDETSQMSDLPVKVIHVES
GKILTGTDAPKAGQLEAWLEMNPGYEVAPRSDSEESGSEEEEEEEEEEQPQAAQPPT
LPVEEKKKIPDPDSDDVSEVDARHIIENAKQDVDDEYGVSQALARGLQSYYAVAHAVT
ERVDKQSALMVNGVLKQYQIKGLEWLVSLYNNNLNGILADEMGLGKTIQTIALITYLME
HKRINGPFLIIVPLSTLSNWAYEFDKWAPSVVKVSYKGSPAARRAFVPQLRSGKFNVLL
TTYEYIIKDKHILAKIRWKYMIVDEGHRMKNHHCKLTQVLNTHYVAPRRLLLTGTPLQNK
LPELWALLNFLLPTIFKSCSTFEQWFNAPFAMTGEKVDLNEEETILIIRRLHKVLRPFLLR
RLKKEVEAQLPEKVEYVIKCDMSALQRVLYRHMQAKGVLLTDGSEKDKKGKGGTKTL
MNTIMQLRKICNHPYMFQHIEESFSEHLGFTGGIVQGLDLYRASGKFELLDRILPKLRAT
NHKVLLFCQMTSLMTIMEDYFAYRGFKYLRLDGTTSTRSRDKDDESKKQKKRGRPPA
EKLSPNPPNLTKKMKKIVDAVIKYKDSSSGRQLSEVFIQLPSRKELPEYYELIRKPVDFK
KIKERIRNHKYRSLNDLEKDVMLLCQNAQTFNLEGSLIYEDSIVLQSVFTSVRQKIEKED
DSEGEESEEEEEGEEEGSESESRSVKVKIKLGRKEKAQDRLKGGRRRPSRGSRAKPV
VSDDDSEEEQEEDRSGSGSEED

SMARCA4_5 (internal 209 aa missing (198-407 aa)) (SEQ ID NO: 174)
MSTPDPPLGTPRPGPSPGPGPSPGAMLGPSPGPSPGSAHSMMGPSPGPPSAGHPIP
TQGPGGYPQDNMHQMHKPMESMHEKGMSDPRYNQMKGMGMRSGGHAGMGPPPS
PMDQHSQGYPSPLGGSEHASSPVPASGPSSGPQMSSGPGGAPLDGADPQALGQQN
RGPTPFNQNQLHQLRAQIMAYKMLARGQPLPDHLLNFQRQLRQEVVVCMRRDTALET
ALNAKAYKRSKRQSLREARITEKLEKQQKIEQERKRRQKHQEYLNSILQHAKDFKEYH
RSVTGKIQKLTKAVATYHANTEREQKKENERIEKERMRRLMAEDEEGYRKLIDQKKDK
RLAYLLQQTDEYVANLTELVPQHKAAQVAKEKKKKKKKKKAENAEGQTPAIGPDGEPL
DETSQMSDLPVKVIHVESGKILTGTDAPKAGQLEAWLEMNPGYEVAPRSDSEESGSE
EEEEEEEEEQPQAAQPPTLPVEEKKKIPDPDSDDVSEVDARHIIENAKQDVDDEYGVS
QALARGLQSYYAVAHAVTERVDKQSALMVNGVLKQYQIKGLEWLVSLYNNNLNGILAD
EMGLGKTIQTIALITYLMEHKRINGPFLIIVPLSTLSNWAYEFDKWAPSVVKVSYKGSPA
ARRAFVPQLRSGKFNVLLTTYEYIIKDKHILAKIRWKYMIVDEGHRMKNHHCKLTQVLN
THYVAPRRLLLTGTPLQNKLPELWALLNFLLPTIFKSCSTFEQWFNAPFAMTGEKVDLN
EEETILIIRRLHKVLRPFLLRRLKKEVEAQLPEKVEYVIKCDMSALQRVLYRHMQAKGVL

LTDGSEKDKKGKGGTKTLMNTIMQLRKICNHPYMFQHIEESFSEHLGFTGGIVQGLDL
YRASGKFELLDRILPKLRATNHKVLLFCQMTSLMTIMEDYFAYRGFKYLRLDGTTKAED
RGMLLKTFNEPGSEYFIFLLSTRAGGLGLNLQSADTVIIFDSDWNPHQDLQAQDRAHRI
GQQNEVRVLRLCTVNSVEEKILAAAKYKLNVDQKVIQAGMFDQKSSSHERRAFLQAIL
EHEEQDESRHCSTGSGSASFAHTAPPPAGVNPDLEEPPLKEEDEVPDDETVNQMIAR
HEEEFDLFMRMDLDRRREEARNPKRKPRLMEEDELPSWIIKDDAEVERLTCEEEEEK
MFGRGSRHRKEVDYSDSLTEKQWLKAIEEGTLEEIEEEVRQKKSSRKRKRDSDAGSS
TPTTSTRSRDKDDESKKQKKRGRPPAEKLSPNPPNLTKKMKKIVDAVIKYKDSSSGRQ
LSEVFIQLPSRKELPEYYELIRKPVDFKKIKERIRNHKYRSLNDLEKDVMLLCQNAQTFN
LEGSLIYEDSIVLQSVFTSVRQKIEKEDDSEGEESEEEEEGEEEGSESESRSVKVKIKL
GRKEKAQDRLKGGRRRPSRGSRAKPVVSDDDSEEEQEEDRSGSGSEED

SMARCA4_6 (internal 259 aa missing (203-462 aa)) (SEQ ID NO: 175)
MSTPDPPLGTPRPGPSPGPGPSPGAMLGPSPGPSPGSAHSMMGPSPGPPSAGHPIP
TQGPGGYPQDNMHQMHKPMESMHEKGMSDPRYNQMKGMGMRSGGHAGMGPPPS
PMDQHSQGYPSPLGGSEHASSPVPASGPSSGPQMSSGPGGAPLDGADPQALGQQN
RGPTPFNQNQLHQLRAQIMAYKMLARGQPLPDHLQMAVQERKRRQKHQEYLNSILQ
HAKDFKEYHRSVTGKIQKLTKAVATYHANTEREQKKENERIEKERMRRLMAEDEEGY
RKLIDQKKDKRLAYLLQQTDEYVANLTELVPQHKAAQVAKEKKKKKKKKKAENAEGQT
PAIGPDGEPLDETSQMSDLPVKVIHVESGKILTGTDAPKAGQLEAWLEMNPGYEVAPR
SDSEESGSEEEEEEEEEEQPQAAQPPTLPVEEKKKIPDPDSDDVSEVDARHIIENAKQ
DVDDEYGVSQALARGLQSYYAVAHAVTERVDKQSALMVNGVLKQYQIKGLEWLVSLY
NNNLNGILADEMGLGKTIQTIALITYLMEHKRINGPFLIIVPLSTLSNWAYEFDKWAPSVV
KVSYKGSPAARRAFVPQLRSGKFNVLLTTYEYIIKDKHILAKIRWKYMIVDEGHRMKNH
HCKLTQVLNTHYVAPRRLLLTGTPLQNKLPELWALLNFLLPTIFKSCSTFEQWFNAPFA
MTGEKVDLNEEETILIIRRLHKVLRPFLLRRLKKEVEAQLPEKVEYVIKCDMSALQRVLY
RHMQAKGVLLTDGSEKDKKGKGGTKTLMNTIMQLRKICNHPYMFQHIEESFSEHLGFT
GGIVQGLDLYRASGKFELLDRILPKLRATNHKVLLFCQMTSLMTIMEDYFAYRGFKYLR
LDGTTKAEDRGMLLKTFNEPGSEYFIFLLSTRAGGLGLNLQSADTVIIFDSDWNPHQDL
QAQDRAHRIGQQNEVRVLRLCTVNSVEEKILAAAKYKLNVDQKVIQAGMFDQKSSSHE
RRAFLQAILEHEEQDESRHCSTGSGSASFAHTAPPPAGVNPDLEEPPLKEEDEVPDDE
TVNQMIARHEEEFDLFMRMDLDRRREEARNPKRKPRLMEEDELPSWIIKDDAEVERLT
CEEEEEKMFGRGSRHRKEVDYSDSLTEKQWLKAIEEGTLEEIEEEVRQKKSSRKRKR
DSDAGSSTPTTSTRSRDKDDESKKQKKRGRPPAEKLSPNPPNLTKKMKKIVDAVIKYK
DSSSGRQLSEVFIQLPSRKELPEYYELIRKPVDFKKIKERIRNHKYRSLNDLEKDVMLLC
QNAQTFNLEGSLIYEDSIVLQSVFTSVRQKIEKEDDSEGEESEEEEEGEEEGSESESRS
VKVKIKLGRKEKAQDRLKGGRRRPSRGSRAKPVVSDDDSEEEQEEDRSGSGSEED

SMARCA4_7 (AB209313; different C-terminus after 1183 aa) (SEQ ID NO: 176)
MSTPDPPLGTPRPGPSPGPGPSPGAMLGPSPGPSPGSAHSMMGPSPGPPSAGHPIP
TQGPGGYPQDNMHQMHKPMESMHEKGMSDPRYNQMKGMGMRSGGHAGMGPPPS
PMDQHSQGYPSPLGGSEHASSPVPASGPSSGPQMSSGPGGAPLDGADPQALGQQN
RGPTPFNQNQLHQLRAQIMAYKMLARGQPLPDHLQMAVQGKRPMPGMQQQMPTLP
PPSVSATGPGPGPGPGPGPGPGPAPPNYSRPHGMGGPNMPPPGPSGVPPGMPGQ
PPGGPPKPWPEGPMANAAAPTSTPQKLIPPQPTGRPSPAPPAVPPAASPVMPPQTQS
PGQPAQPAPMVPLHQKQSRITPIQKPRGLDPVEILQEREYRLQARIAHRIQELENLPGS
LAGDLRTKATIELKALRLLNFQRQLRQEVVVCMRRDTALETALNAKAYKRSKRQSLRE
ARITEKLEKQQKIEQERKRRQKHQEYLNSILQHAKDFKEYHRSVTGKIQKLTKAVATYH
ANTEREQKKENERIEKERMRRLMAEDEEGYRKLIDQKKDKRLAYLLQQTDEYVANLTE
LVPQHKAAQVAKEKKKKKKKKKAENAEGQTPAIGPDGEPLDETSQMSDLPVKVIHVES
GKILTGTDAPKAGQLEAWLEMNPGYEVAPRSDSEESGSEEEEEEEEEEQPQAAQPPT
LPVEEKKKIPDPDSDDVSEVDARHIIENAKQDVDDEYGVSQALARGLQSYYAVAHAVT
ERVDKQSALMVNGVLKQYQIKGLEWLVSLYNNNLNGILADEMGLGKTIQTIALITYLME

HKRINGPFLIIVPLSTLSNWAYEFDKWAPSVVKVSYKGSPAARRAFVPQLRSGKFNVLL
TTYEYIIKDKHILAKIRWKYMIVDEGHRMKNHHCKLTQVLNTHYVAPRRLLLTGTPLQNK
LPELWALLNFLLPTIFKSCSTFEQWFNAPFAMTGEKVDLNEEETILIIRRLHKVLRPFLLR
RLKKEVEAQLPEKVEYVIKCDMSALQRVLYRHMQAKGVLLTDGSEKDKKGKGGTKTL
MNTIMQLRKICNHPYMFQHIEESFSEHLGFTGGIVQGLDLYRASGKFELLDRILPKLRAT
NHKVLLFCQMTSLMTIMEDYFAYRGFKYLRLDGTTKAEDRGMLLKTFNEPGSEYFIFLL
STRAGGLGLNLQSADTVIIFDSDWNPHQVKAGRAPGRGEGRGCLQNLEETALA*

SMARCC2 (ID: Q8TAQ2)

SMARCC2_1 (internal 495 aa missing (41-536 aa) + 31 aa missing (551-582 aa)) (SEQ ID NO: 177)
MAVRKKDGGPNVKYYEAADTVTQFDNVRLWLGKNYKKYIQADTPSGLVPLQPKTPQQ
TSASQQMLNFPDKGKEKPTDMQNFGLRTDMYTKKNVPSKSKAAASATREWTEQETL
LLLEALEMYKDDWNKVSEHVGSRTQDECILHFLRLPIEDPYLEDSEASLGPLAYQPIPF
SQSGNPVMSTVAFLASVVDPRVASAAAKSALEEFSKMKEEVPTALVEAHVRKVEEAA
KVTGKADPAFGLESSGIAGTTSDEPERIEESGNDEARVEGQATDEKKEPKEPREGGG
AIEEEAKEKTSEAPKKDEEKGKEGDSEKESEKSDGDPIVDPEKEKEPKEGQEEVLKEV
VESEGERKTKVERDIGEGNLSTAAAAALAAAAVKAKHLAAVEERKIKSLVALLVETQMK
KLEIKLRHFEELETIMDREREALEYQRQQLLADRQAFHMEQLKYAEMRARQQHFQQM
HQQQQQPPPALPPGSQPIPPTGAAGPPAVHGLAVAPASVVPAPAGSGAPPGSLGPSE
QIGQAGSTAGPQQQQPAGAPQPGAVPPGVPPPGPHGPSPFPNQQTPPSMMPGAVP
GSGHPGVAGNAPLGLPFGMPPPPPPPAPSIIPFGSLADSISINLPAPPNLHGHHHHLPF
APGTLPPPNLPVSMANPLHPNLPATTTMPSSLPLGPGLGSAAAQSPAIVAAVQGNLLP
SASPLPDPGTPLPPDPTAPSPGTVTPVPPPQ

SMARCC2_2 (internal 449 aa missing (103-552 aa)) (SEQ ID NO: 178)
MAVRKKDGGPNVKYYEAADTVTQFDNVRLWLGKNYKKYIQAEPPTNKSLSSLVVQLL
QFQEEVFGKHVSNAPLTKLPIKCFLDFKAGGSLCHILAAAYKFKSDQVDADTKAGRKG
KELDDLVPETAKGKPELQTSASQQMLNFPDKGKEKPTDMQNFGLRTDMYTKKNVPSK
SKAAASATREWTEQETLLLLEALEMYKDDWNKVSEHVGSRTQDECILHFLRLPIEDPY
LEDSEASLGPLAYQPIPFSQSGNPVMSTVAFLASVVDPRVASAAAKSALEEFSKMKEE
VPTALVEAHVRKVEEAAKVTGKADPAFGLESSGIAGTTSDEPERIEESGNDEARVEGQ
ATDEKKEPKEPREGGGAIEEEAKEKTSEAPKKDEEKGKEGDSEKESEKSDGDPIVDPE
KEKEPKEGQEEVLKEVVESEGERKTKVERDIGEGNLSTAAAAALAAAAVKAKHLAAVE
ERKIKSLVALLVETQMKKLEIKLRHFEELETIMDREREALEYQRQQLLADRQAFHMEQL
KYAEMRARQQHFQQMHQQQQQPPPALPPGSQPIPPTGAAGPPAVHGLAVAPASVVP
APAGSGAPPGSLGPSEQIGQAGSTAGPQQQQPAGAPQPGAVPPGVPPPGPHGPSPF
PNQQTPPSMMPGAVPGSGHPGVAGNAPLGLPFGMPPPPPPPAPSIIPFGSLADSISIN
LPAPPNLHGHHHHLPFAPGTLPPPNLPVSMANPLHPNLPATTTMPSSLPLGPGLGSAA
AQSPAIVAAVQGNLLPSASPLPDPGTPLPPDPTAPSPGTVTPVPPPQ

SMARCC2_3 (NM_003075.2; 31 aa missing (551-582 aa)) (SEQ ID NO: 179)
MAVRKKDGGPNVKYYEAADTVTQFDNVRLWLGKNYKKYIQAEPPTNKSLSSLVVQLL
QFQEEVFGKHVSNAPLTKLPIKCFLDFKAGGSLCHILAAAYKFKSDQGWRRYDFQNPS
RMDRNVEMFMTIEKSLVQNNCLSRPNIFLCPEIEPKLLGKLKDIIKRHQGTVTEDKNNA
SHVVYPVPGNLEEEEWVRPVMKRDKQVLLHWGYYPDSYDTWIPASEIEASVEDAPTP
EKPRKVHAKWILDTDTFNEWMNEEDYEVNDDKNPVSRRKKISAKTLTDEVNSPDSDR
RDKKGGNYKKRKRSPSPSPTPEAKKKNAKKGPSTPYTKSKRGHREEEQEDLTKDMD
EPSPVPNVEEVTLPKTVNTKKDSESAPVKGGTMTDLDEQEDESMETTGKDEDENSTG
NKGEQTKNPDLHEDNVTEQTHHIIIPSYAAWFDYNSVHAIERRALPEFFNGKNKSKTPE
IYLAYRNFMIDTYRLNPQEYLTSTACRRNLAGDVCAIMRVHAFLEQWGLINYQVDAESR
PTPMGPPPTSHFHVLADTPSGLVPLQPKTPQQTSASQQMLNFPDKGKEKPTDMQNF

GLRTDMYTKKNVPSKSKAAASATREWTEQETLLLLEALEMYKDDWNKVSEHVGSRTQ
DECILHFLRLPIEDPYLEDSEASLGPLAYQPIPFSQSGNPVMSTVAFLASVVDPRVASA
AAKSALEEFSKMKEEVPTALVEAHVRKVEEAAKVTGKADPAFGLESSGIAGTTSDEPE
RIEESGNDEARVEGQATDEKKEPKEPREGGGAIEEEAKEKTSEAPKKDEEKGKEGDS
EKESEKSDGDPIVDPEKEKEPKEGQEEVLKEVVESEGERKTKVERDIGEGNLSTAAAA
ALAAAAVKAKHLAAVEERKIKSLVALLVETQMKKLEIKLRHFEELETIMDRREREALEYQR
QQLLADRQAFHMEQLKYAEMRARQQHFQQMHQQQQQPPPALPPGSQPIPPTGAAG
PPAVHGLAVAPASVVPAPAGSGAPPGSLGPSEQIGQAGSTAGPQQQQPAGAPQPGA
VPPGVPPPGPHGPSPFPNQQTPPSMMPGAVPGSGHPGVAGNAPLGLPFGMPPPPP
PPAPSIIPFGSLADSISINLPAPPNLHGHHHHLPFAPGTLPPPNLPVSMANPLHPNLPAT
TTMPSSLPLGPGLGSAAAQSPAIVAAVQGNLLPSASPLPDPGTPLPPDPTAPSPGTVT
PVPPPQ

SMARCC2_4 (extra 82 aa after 1105 aa, different 16 aa after 1090 aa) (SEQ ID NO: 180)
MAVRKKDGGPNVKYYEAADTVTQFDNVRLWLGKNYKKYIQAEPPTNKSLSSLVVQLL
QFQEEVFGKHVSNAPLTKLPIKCFLDFKAGGSLCHILAAAYKFKSDQGWRRYDFQNPS
RMDRNVEMFMTIEKSLVQNNCLSRPNIFLCPEIEPKLLGKLKDIIKRHQGTVTEDKNNA
SHVVYPVPGNLEEEEWVRPVMKRDKQVLLHWGYYPDSYDTWIPASEIEASVEDAPTP
EKPRKVHAKWILDTDTFNEWMNEEDYEVNDDKNPVSRRKKISAKTLTDEVNSPDSDR
RDKKGGNYKKRKRSPSPSPTPEAKKKNAKKGPSTPYTKSKRGHREEEQEDLTKDMD
EPSPVPNVEEVTLPKTVNTKKDSESAPVKGGTMTDLDEQEDESMETTGKDEDENSTG
NKGEQTKNPDLHEDNVTEQTHHIIIPSYAAWFDYNSVHAIERRALPEFFNGKNKSKTPE
IYLAYRNFMIDTYRLNPQEYLTSTACRRNLAGDVCAIMRVHAFLEQWGLINYQVDAESR
PTPMGPPPTSHFHVLADTPSGLVPLQPKTPQQTSASQQMLNFPDKGKEKPTDMQNF
GLRTDMYTKKNVPSKSKAAASATREWTEQETLLLLEALEMYKDDWNKVSEHVGSRTQ
DECILHFLRLPIEDPYLEDSEASLGPLAYQPIPFSQSGNPVMSTVAFLASVVDPRVASA
AAKSALEEFSKMKEEVPTALVEAHVRKVEEAAKVTGKADPAFGLESSGIAGTTSDEPE
RIEESGNDEARVEGQATDEKKEPKEPREGGGAIEEEAKEKTSEAPKKDEEKGKEGDS
EKESEKSDGDPIVDPEKEKEPKEGQEEVLKEVVESEGERKTKVERDIGEGNLSTAAAA
ALAAAAVKAKHLAAVEERKIKSLVALLVETQMKKLEIKLRHFEELETIMDRREREALEYQR
QQLLADRQAFHMEQLKYAEMRARQQHFQQMHQQQQQPPPALPPGSQPIPPTGAAG
PPAVHGLAVAPASVVPAPAGSGAPPGSLGPSEQIGQAGSTAGPQQQQPAGAPQPGA
VPPGVPPPGPHGPSPFPNQQTPPPAPSIIPFGSLADSISINLPAPPNLHGHHHHLPFAP
GTLPPPNLPVSMANPLHPNLPATTTMPSSLPLGPGLGSAAAQSPAIVAAVQGNLLPSA
SPLPDPGTPLPPDPTAPSPGTVTPVPPPQ*

SMARCC2_5 (internal 31 aa missing (550-581 aa), different sequence after 621 aa, shorter protein (634 aa)) (SEQ ID NO: 181)
MAVRKKDGGPNVKYYEAADTVTQFDNVRLWLGKNYKKYIQAEPPTNKSLSSLVVQLL
QFQEEVFGKHVSNAPLTKLPIKCFLDFKAGGSLCHILAAAYKFKSDQGWRRYDFQNPS
RMDRNVEMFMTIEKSLVQNNCLSRPNIFLCPEIEPKLLGKLKDIIKRHQGTVTEDKNNA
SHVVYPVPGNLEEEEWVRPVMKRDKQVLLHWGYYPDSYDTWIPASEIEASVEDAPTP
EKPRKVHAKWILDTDTFNEWMNEEDYEVNDDKNPVSRRKKISAKTLTDEVNSPDSDR
RDKKGGNYKKRKRSPSPSPTPEAKKKNAKKGPSTPYTKSKRGHREEEQEDLTKDMD
EPSPVPNVEEVTLPKTVNTKKDSESAPVKGGTMTDLDEQEDESMETTGKDEDENSTG
NKGEQTKNPDLHEDNVTEQTHHIIIPSYAAWFDYNSVHAIERRALPEFFNGKNKSKTPE
IYLAYRNFMIDTYRLNPQEYLTSTACRRNLAGDVCAIMRVHAFLEQWGLINYQVDAESR
PTPMGPPPTSHFHVLADTPSGLVPLQPKTPQQTSASQQMLNFPDKGKEKPTDMQNF
GLRTDMYTKKNVPSKLLHFLWIKKKKKK*

SMARCC2_6 (internal 105 aa missing (1090-1195 aa) (SEQ ID NO: 182)

MAVRKKDGGPNVKYYEAADTVTQFDNVRLWLGKNYKKYIQAEPPTNKSLSSLVVQLL
QFQEEVFGKHVSNAPLTKLPIKCFLDFKAGGSLCHILAAAYKFKSDQGWRRYDFQNPS
RMDRNVEMFMTIEKSLVQNNCLSRPNIFLCPEIEPKLLGKLKDIIKRHQGTVTEDKNNA
SHVVYPVPGNLEEEEWVRPVMKRDKQVLLHWGYYPDSYDTWIPASEIEASVEDAPTP
EKPRKVHAKWILDTDTFNEWMNEEDYEVNDDKNPVSRRKKISAKTLTDEVNSPDSDR
RDKKGGNYKKRKRSPSPSPTPEAKKKNAKKGPSTPYTKSKRGHREEEQEDLTKDMD
EPSPVPNVEEVTLPKTVNTKKDSESAPVKGGTMTDLDEQEDESMETTGKDEDENSTG
NKGEQTKNPDLHEDNVTEQTHHIIIPSYAAWFDYNSVHAIERRALPEFFNGKNKSKTPE
IYLAYRNFMIDTYRLNPQEYLTSTACRRNLAGDVCAIMRVHAFLEQWGLINYQVDAESR
PTPMGPPPTSHFHVLADTPSGLVPLQPKTPQQTSASQQMLNFPDKGKEKPTDMQNF
GLRTDMYTKKNVPSKSKAAASATREWTEQETLLLLEALEMYKDDWNKVSEHVGSRTQ
DECILHFLRLPIEDPYLEDSEASLGPLAYQPIPFSQSGNPVMSTVAFLASVVDPRVASA
AAKSALEEFSKMKEEVPTALVEAHVRKVEEAAKVTGKADPAFGLESSGIAGTTSDEPE
RIEESGNDEARVEGQATDEKKEPKEPREGGGAIEEEAKEKTSEAPKKDEEKGKEGDS
EKESEKSDGDPIVDPEKEKEPKEGQEEVLKEVVESEGERKTKVERDIGEGNLSTAAAA
ALAAAAVKAKHLAAVEERKIKSLVALLVETQMKKLEIKLRHFEELETIMDREREALEYQR
QQLLADRQAFHMEQLKYAEMRARQQHFQQMHQQQQQPPPALPPGSQPIPPTGAAG
PPAVHGLAVAPASVVPAPAGSGAPPGSLGPSEQIGQAGSTAGPQQQQPAGAPQPGA
VPPGVPPPGPHGPSPFPNQQTPPSMMPGAVPGSGHPGVAGNAPLGLPFGMPPPPP
PPDPTAPSPGTVTPVPPPQ*

SMARCC2_7 (internal 25 aa missing (1088 - 1113 aa)) (SEQ ID NO: 183)
MAVRKKDGGPNVKYYEAADTVTQFDNVRLWLGKNYKKYIQAEPPTNKSLSSLVVQLL
QFQEEVFGKHVSNAPLTKLPIKCFLDFKAGGSLCHILAAAYKFKSDQGWRRYDFQNPS
RMDRNVEMFMTIEKSLVQNNCLSRPNIFLCPEIEPKLLGKLKDIIKRHQGTVTEDKNNA
SHVVYPVPGNLEEEEWVRPVMKRDKQVLLHWGYYPDSYDTWIPASEIEASVEDAPTP
EKPRKVHAKWILDTDTFNEWMNEEDYEVNDDKNPVSRRKKISAKTLTDEVNSPDSDR
RDKKGGNYKKRKRSPSPSPTPEAKKKNAKKGPSTPYTKSKRGHREEEQEDLTKDMD
EPSPVPNVEEVTLPKTVNTKKDSESAPVKGGTMTDLDEQEDESMETTGKDEDENSTG
NKGEQTKNPDLHEDNVTEQTHHIIIPSYAAWFDYNSVHAIERRALPEFFNGKNKSKTPE
IYLAYRNFMIDTYRLNPQEYLTSTACRRNLAGDVCAIMRVHAFLEQWGLINYQVDAESR
PTPMGPPPTSHFHVLADTPSGLVPLQPKTPQQTSASQQMLNFPDKGKEKPTDMQNF
GLRTDMYTKKNVPSKSKAAASATREWTEQETLLLLEALEMYKDDWNKVSEHVGSRTQ
DECILHFLRLPIEDPYLEDSEASLGPLAYQPIPFSQSGNPVMSTVAFLASVVDPRVASA
AAKSALEEFSKMKEEVPTALVEAHVRKVEEAAKVTGKADPAFGLESSGIAGTTSDEPE
RIEESGNDEARVEGQATDEKKEPKEPREGGGAIEEEAKEKTSEAPKKDEEKGKEGDS
EKESEKSDGDPIVDPEKEKEPKEGQEEVLKEVVESEGERKTKVERDIGEGNLSTAAAA
ALAAAAVKAKHLAAVEERKIKSLVALLVETQMKKLEIKLRHFEELETIMDREREALEYQR
QQLLADRQAFHMEQLKYAEMRARQQHFQQMHQQQQQPPPALPPGSQPIPPTGAAG
PPAVHGLAVAPASVVPAPAGSGAPPGSLGPSEQIGQAGSTAGPQQQQPAGAPQPGA
VPPGVPPPGPHGPSPFPNQQTPPSMMPGAVPGSGHPGVAGNAPLGLPFGMPPPPN
LHGHHHHLPFAPGTLPPPNLPVSMANPLHPNLPATTTMPSSLPLGPGLGSAAAQSPAI
VAAVQGNLLPSASPLPDPGTPLPPDPTAPSPGTVTPVPPPQ*

SMARCC2_8 (NM_003075) (SEQ ID NO: 184)
MAVRKKDGGPNVKYYEAADTVTQFDNVRLWLGKNYKKYIQAEPPTNKSLSSLVVQLL
QFQEEVFGKHVSNAPLTKLPIKCFLDFKAGGSLCHILAAAYKFKSDQGWRRYDFQNPS
RMDRNVEMFMTIEKSLVQNNCLSRPNIFLCPEIEPKLLGKLKDIIKRHQGTVTEDKNNA
SHVVYPVPGNLEEEEWVRPVMKRDKQVLLHWGYYPDSYDTWIPASEIEASVEDAPTP
EKPRKVHAKWILDTDTFNEWMNEEDYEVNDDKNPVSRRKKISAKTLTDEVNSPDSDR
RDKKGGNYKKRKRSPSPSPTPEAKKKNAKKGPSTPYTKSKRGHREEEQEDLTKDMD
EPSPVPNVEEVTLPKTVNTKKDSESAPVKGGTMTDLDEQEDESMETTGKDEDENSTG
NKGEQTKNPDLHEDNVTEQTHHIIIPSYAAWFDYNSVHAIERRALPEFFNGKNKSKTPE

IYLAYRNFMIDTYRLNPQEYLTSTACRRNLAGDVCAIMRVHAFLEQWGLINYQVDAESR
PTPMGPPPTSHFHVLADTPSGLVPLQPKTPQQTSASQQMLNFPDKGKEKPTDMQNF
GLRTDMYTKKNVPSKSKAAASATREWTEQETLLLLEALEMYKDDWNKVSEHVGSRTQ
DECILHFLRLPIEDPYLEDSEASLGPLAYQPIPFSQSGNPVMSTVAFLASVVDPRVASA
AAKSALEEFSKMKEEVPTALVEAHVRKVEEAAKVTGKADPAFGLESSGIAGTTSDEPE
RIEESGNDEARVEGQATDEKKEPKEPREGGGAIEEEAKEKTSEAPKKDEEKGKEGDS
EKESEKSDGDPIVDPEKEKEPKEGQEEVLKEVVESEGERKTKVERDIGEGNLSTAAAA
ALAAAAVKAKHLAAVEERKIKSLVALLVETQMKKLEIKLRHFEELETIMDREREALEYQR
QQLLADRQAFHMEQLKYAEMRARQQHFQQMHQQQQQPPPALPPGSQPIPPTGAAG
PPAVHGLAVAPASVVPAPAGSGAPPGSLGPSEQIGQAGSTAGPQQQQPAGAPQPGA
VPPGVPPPGPHGPSPFPNQQTPPSMMPGAVPGSGHPGVAGNAPLGLPFGMPPPPP
PPAPSIIPFGSLADSISINLPAPPNLHGHHHHLPFAPGTLPPPNLPVSMANPLHPNLPAT
TTMPSSLPLGPGLGSAAAQSPAIVAAVQGNLLPSASPLPDPGTPLPPDPTAPSPGTVT
PVPPPQ*

SMARCD1 (ID: Q96GM5)

SMARCD1_1 (DA534102; 23 aa shorter N-terminus) (SEQ ID NO: 185)
MLPGSRMTPQGPSMGPPGYGGNPSVRPGLAQSGMDQSRKRPAPQQIQQVQQQAV
QNRNHNAKKKKMADKILPQRIRELVPESQAYMDLLAFERKLDQTIMRKRLDIQEALKRP
IKQKRKLRIFISNTFNPAKSDAEDGEGTVASWELRVEGRLLEDSALSKYDATKQKRKFS
SFFKSLVIELDKDLYGPDNHLVEWHRTATTQETDGFQVKRPGDVNVRCTVLLMLDYQ
PPQFKLDPRLARLLGIHTQTRPVIIQALWQYIKTHKLQDPHEREFVICDKYLQQIFESQR
MKFSEIPQRLHALLMPPEPIIINHVISVDPNDQKKTACYDIDVEVDDTLKTQMNSFLLSTA
SQQEIATLDNKIHETIETINQLKTQREFMLSFARDPQGFINDWLQSQCRDLKTMTDVVG
NPEEERRAEFYFQPWAQEAVCRYFYSKVQQRRQELEQALGIRNT

SMARCD1_2 (AL540421; internal 80 aa missing (178-258 aa)) (SEQ ID NO: 186)
MAARAGFQSVAPSGGAGASGGAGAAAALGPGGTPGPPVRMGPAPGQGLYRSPMPG
AAYPRPGMLPGSRMTPQGPSMGPPGYGGNPSVRPGLAQSGMDQSRKRPAPQQIQQ
VQQQAVQNRNHNAKKKKMADKILPQRIRELVPESQAYMDLLAFERKLDQTIMRKRLDI
QEALKRPIKWHRTATTQETDGFQVKRPGDVNVRCTVLLMLDYQPPQFKLDPRLARLL
GIHTQTRPVIIQALWQYIKTHKLQDPHEREFVICDKYLQQIFESQRMKFSEIPQRLHALL
MPPEPIIINHVISVDPNDQKKTACYDIDVEVDDTLKTQMNSFLLSTASQQEIATLDNKIHE
TIETINQLKTQREFMLSFARDPQGFINDWLQSQCRDLKTMTDVVGNPEEERRAEFYFQ
PWAQEAVCRYFYSKVQQRRQELEQALGIRNT

SMARCD1_3 (BX384720; internal 41 aa missing (139 - 180 aa) (SEQ ID NO: 187)
MAARAGFQSVAPSGGAGASGGAGAAAALGPGGTPGPPVRMGPAPGQGLYRSPMPG
AAYPRPGMLPGSRMTPQGPSMGPPGYGGNPSVRPGLAQSGMDQSRKRPAPQQIQQ
VQQQAVQNRNHNAKKKKMADKILPQRIRELVPESQAYMDLLAFERKLDQTIMRKRLDI
QEALKRPIKSALSKYDATKQKRKFSSFFKSLVIELDKDLYGPDNHLVEWHRTATTQETD
GFQVKRPGDVNVRCTVLLMLDYQPPQFKLDPRLARLLGIHTQTRPVIIQALWQYIKTHK
LQDPHEREFVICDKYLQQIFESQRMKFSEIPQRLHALLMPPEPIIINHVISVDPNDQKKTA
CYDIDVEVDDTLKTQMNSFLLSTASQQEIATLDNKIHETIETINQLKTQREFMLSFARDP
QGFINDWLQSQCRDLKTMTDVVGNPEEERRAEFYFQPWAQEAVCRYFYSKVQQRR
QELEQALGIRNT

SMARCD2 (ID: Q92925)

SMARCD2_1 (213 aa protein, different sequence after 178 aa) (SEQ ID NO: 188)
MSPGNRMPMARLAGGTPCWLPIWCSSSASTWHPTHHDGSIPKTPACAPAQPPMPAQ
RRGLKRRKMADKVLPQRIRELVPESQAYMDLLAFERKLDQTIARKRMEIQEAIKKPLTQ

KRKLRIYISNTFSPSKAEGDSAGTAGTPGGTPAGDKVASWELRVEGKLLDDPSKQKRK
FSSFFSFLNLCKRLWPPSSPGMPEGCLSSGLGRGGDTPVL*

SMARCD2_2 (261 aa protein, different sequence after 168 aa) (SEQ ID NO: 189)
MSPGNRMPMARLAGGTPCWLPIWCSSSASTWHPTHHDGSIPKTPACAPAQPPMPAQ
RRGLKRRKMADKVLPQRIRELVPESQAYMDLLAFERKLDQTIARKRMEIQEAIKKPLTQ
KRKLRIYISNTFSPSKAEGDSAGTAGTPGGTPAGDKVASWELRVEGKLLDDPSLSKPK
FFAIPTSPALLLVFSFPLGICTILGASFLCGSHFFCTGVSWGFSGSLLGASFFSFLNLCK
RLWPPSSPGMPEGCLSSGLGRGGDTPVL*

SMARCD2_3 (153 aa protein, different sequence after 146 aa) (SEQ ID NO: 190)
MSPGNRMPMARLAGGTPCWLPIWCSSSASTWHPTHHDGSIPKTPACAPAQPPMPAQ
RRGLKRRKMADKVLPQRIRELVPESQAYMDLLAFERKLDQTIARKRMEIQEAIKKPLTQ
KRKLRIYISNTFSPSKAEGDSAGTAGTPGGTHVEARVR*

SMARCD2_4 (207 aa protein, different sequence after 149 aa) (SEQ ID NO: 191)
MSPGNRMPMARLAGGTPCWLPIWCSSSASTWHPTHHDGSIPKTPACAPAQPPMPAQ
RRGLKRRKMADKVLPQRIRELVPESQAYMDLLAFERKLDQTIARKRMEIQEAIKKPLTQ
KRKLRIYISNTFSPSKAEGDSAGTAGTPGGTPAGEPVRCLLLFFPQSMQAALAAIISWD
ARGLPLQRLGPGRGHSSSLAWPEVWGMCMWRPG*

SMARCD2_5 (internal 328 aa missing (71-399 aa)) (SEQ ID NO: 192)
MLPGPALRGPGPAQYQRPGMSPGNRMPMARLAGGTPCWLPIWCSSSASTWHPTHH
DGSIPKTPACAPAQPPMPAQRRGLKRRKMADKVLPQRRDLKIITDVIGNPEEERRAAF
YHQPWAQEAVGRHIFAKVQQRRQELEQVLGIRLT*

SMARCD2_6 (148 aa protein, different sequence after 69 aa) (SEQ ID NO: 193)
MLPGPALRGPGPAQYQRPGMSPGNRMPMARLAGGTPCWLPIWCSSSASTWHPTHH
DGSIPKTPACAPAQPPMPAQRRGLKRRKMADKVFREPVRCLLLFFPQSMQAALAAIIS
WDARGLPLQRLGPGRGHSSSLAWPEVWGMCMWRPG*

SMARCD3 (ID: Q6STE5)

SMARCD3_1 (426 aa protein, different sequence after 413 aa) (SEQ ID NO: 194)
MAADEVAGGARKATKSKLFEFLVHGVRPGMPSGARMPHQGAPMGPPGSPYMGSPA
VRPGLAPAGMEPARKRAAPPPGQSQAQSQGQPVPTAPARSRSAKRRKMADKILPQRI
RELVPESQAYMDLLAFERKLDQTIMRKRVDIQEALKRPMKQKRKLRLYISNTFNPAKPD
AEDSDGSIASWELRVEGKLLDDPSKQKRKFSSFFKSLVIELDKDLYGPDNHLVEWHRT
PTTQETDGFQVKRPGDLSVRCTLLLMLDYQPPQFKLDPRLARLLGLHTQSRSAIVQAL
WQYVKTNRLQDSHDKEYINGDKYFQQIFDCPRLKFSEIPQRLTALLLPPDPIVINHVISV
DPSDQKKTACYDIDVEVEEPLKGQMSSFLLSTANQQEISALDSKIHETIESINQLKIQRD
FMLSFSSITPLPPWGVGLD*

SMARCD3_2 (451 aa protein, different sequence after 432 aa) (SEQ ID NO: 195)
MAADEVAGGARKATKSKLFEFLVHGVRPGMPSGARMPHQGAPMGPPGSPYMGSPA
VRPGLAPAGMEPARKRAAPPPGQSQAQSQGQPVPTAPARSRSAKRRKMADKILPQRI
RELVPESQAYMDLLAFERKLDQTIMRRVDIQEALKRPMKQKRKLRLYISNTFNPAKPDA
EDSDGSIASWELRVEGKLLDDPSKQKRKFSSFFKSLVIELDKDLYGPDNHLVEWHRTP
TTQETDGFQVKRPGDLSVRCTLLLMLDYQPPQFKLDPRLARLLGLHTQSRSAIVQALW
QYVKTNRLQDSHDKEYINGDKYFQQIFDCPRLKFSEIPQRLTALLLPPDPIVINHVISVDP
SDQKKTACYDIDVEVEEPLKGQMSSFLLSTANQQEISALDSKIHETIESINQLKIQRDFM
LSFSRDPKGYVQDLLRSQSRDLKVKRETQGVQNTDTCSCSHFL*

SMARCE1 (ID: Q969G3)

SMARCE1_1 (BC047731; 77 aa protein, different C-terminus after 52aa) (SEQ ID NO: 196)
MSKRPSYAPPPTPAPATQMPSTPGFVGYNPYSHLAYNNYRLGGNPGTNSRVTVGES
TITASGKQLELTRNAFRIRSF*

SMARCE1_2 (CR600221; internal 35 aa missing (17 – 52 aa)) (SEQ ID NO: 197)
MSKRPSYAPPPTPAPATASSGITIPKPPKPPDKPLMPYMRYSRKVWDQVKASNPDLKL
WEIGKIIGGMWRDLTDEEKQEYLNEYEAEKIEYNESMKAYHNSPAYLAYINAKSRAEAA
LEEESRQRQSRMEKGEPYMSIQPAEDPDDYDDGFSMKHTATARFQRNHRLISEILSES
VVPDVRSVVTTARMQVLKRQVQSLMVHQRKLEAELLQIEERHQEKKRKFLESTDSFN
NELKRLCGLKVEVDMEKIAAEIAQAEEQARKRQEEREKEAAEQAERSQSSIVPEEEQA
ANKGEEKKDDENIPMETEETHLEETTESQQNGEEGTSTPEDKESGQEGVDSMAEEGT
SDSNTGSESNSATVEEPPTDPIPEDEKKE*

SMARCE1_3 (BY796605; 70 aa shorter N-terminus) (SEQ ID NO: 198)
MPYMRYSRKVWDQVKASNPDLKLWEIGKIIGGMWRDLTDEEKQEYLNEYEAEKIEYN
ESMKAYHNSPAYLAYINAKSRAEAALEEESRQRQSRMEKGEPYMSIQPAEDPDDYDD
GFSMKHTATARFQRNHRLISEILSESVVPDVRSVVTTARMQVLKRQVQSLMVHQRKLE
AELLQIEERHQEKKRKFLESTDSFNNELKRLCGLKVEVDMEKIAAEIAQAEEQARKRQE
EREKEAAEQAERSQSSIVPEEEQAANKGEEKKDDENIPMETEETHLEETTESQQNGE
EGTSTPEDKESGQEGVDSMAEEGTSDSNTGSESNSATVEEPPTDPIPEDEKKE*

SMARCE1_4 (218 aa protein, different sequence after 180 aa) (SEQ ID NO: 199)
MSKRPSYAPPPTPAPATQMPSTPGFVGYNPYSHLAYNNYRLGGNPGTNSRVTASSGI
TIPKPPKPPDKPLMPYMRYSRKVWDQVKASNPDLKLWEIGKIIGGMWRDLTDEEKQE
YLNEYEAEKIEYNESMKAYHNSPAYLAYINAKSRAEAALEEESRQRQSRMEKGEPYMS
IQPAEDPDGKRKKVGFCLCFLCELRYEKSLKYKFLFLILNGKESII*

SMARCE1_5 (18 aa shorter N-terminus) (SEQ ID NO: 200)
MPSTPGFVGYNPYSHLAYNNYRLGGNPGTNSRVTASSGITIPKPPKPPDKPLMPYMR
YSRKVWDQVKASNPDLKLWEIGKIIGGMWRDLTDEEKQEYLNEYEAEKIEYNESMKAY
HNSPAYLAYINAKSRAEAALEEESRQRQSRMEKGEPYMSIQPAEDPDDYDDGFSMKH
TATARFQRNHRLISEILSESVVPDVRSVVTTARMQVLKRQVQSLMVHQRKLEAELLQIE
ERHQEKKRKFLESTDSFNNELKRLCGLKVEVDMEKIAAEIAQAEEQARKRQEEREKEA
AEQAERSQSSIVPEEEQAANKGEEKKDDENIPMETEETHLEETTESQQNGEEGTSTPE
DKESGQEGVDSMAEEGTSDSNTGSESNSATVEEPPTDPIPEDEKKE

BAF250a (ID: O14497)

BAF250a_1 (56 aa missing (751-807 aa)) (SEQ ID NO: 201)
MAAQVAPAAASSLGNPPPPPPSELKKAEQQQREEAGGEAAAAAAAERGEMKAAAGQ
ESEGPAVGPPQPLGKELQDGAESNGGGGGGGAGSGGGPGAEPDLKNSNGNAGPR
PALNNNLTEPPGGGGGGSSDGVGAPPHSAAAALPPPAYGFGQPYGRSPSAVAAAAA
AVFHQQHGGQQSPGLAALQSGGGGGLEPYAGPQQNSHDHGFPNHQYNSYYPNRSA
YPPPAPAYALSSPRGGTPGSGAAAAAGSKPPPSSSASASSSSSSFAQQRFGAMGGG
GPSAAGGGTPQPTATPTLNQLLTSPSSARGYQGYPGGDYSGGPQDGGAGKGPADM
ASQCWGAAAAAAAAAAASGGAQQRSHHAPMSPGSSGGGGQPLARTPQPSSPMDQ
MGKMRPQPYGGTNPYSQQQGPPSGPQQGHGYPGQPYGSQTPQRYPMTMQGRAQ
SAMGGLSYTQQIPPYGQQGPSGYGQQGQTPYYNQQSPHPQQQQPPYSQQPPSQTP
HAQPSYQQQPQSQPPQLQSSQPPYSQQPSQPPHQQSPAPYPSQQSTTQQHPQSQP
PYSQPQAQSPYQQQQPQQPAPSTLSQQAAYPQPQSQQSQQTAYSQQRFPPPQELS
QDSFGSQASSAPSMTSSKGGQEDMNLSLQSRPSSLPDLSGSIDDLPMGTEGALSPGV

STSGISSSQGEQSNPAQSPFSPHTSPHLPGIRGPSPSPVGSPASVAQSRSGPLSPAAV
PGNQMPPRPPSGQSDSIMHPSMNQSSIAQDRGGYPRQPNYNALPNANYPSAGMAG
GINPMGAGGQMHGQPGIPPYGTLPPGRMSHASMGNRPYGPNMANMPPQVGSGMC
PPPGGMNRKTQETAVAMHVAANSIQNRPPGYPNMNQGGMMGTGPPYGQGINSMAG
MINPQGPPYSMGGTMANNSAGMAASPEMMGLGDVKLTPATKMNNKADGTPKTESKS
KKSSSSTTTNEKITKLYELGGEPERKMWVDRYLAFTEEKAMGMTNLPAVGRKPLDLYR
LYVSVKEIGGLTQVNKNKKWRELATNLNVGTSSSAASSLKKQYIQCLYAFECKIERGED
PPPDIFAAADSKKSQPKIQPPSPAGSGSMQGPQTPQSTSSSMAEGGDLKPPTPASTP
HSQIPPLPGMSRSNSVGIQDAFNDGSDSTFQKRNSMTPNPGYQPSMNTSDMMGRMS
YEPNKDPYGSMRKAPGSDPFMSSGQGPNGGMGDPYSRAAGPGLGNVAMGPRQHY
PYGGPYDRVRTEPGIGPEGNMSTGAPQPNLMPSNPDSGMYSPSRYPPQQQQQQQQ
RHDSYGNQFSTQGTPSGSPFPSQQTTMYQQQQQNYKRPMDGTYGPPAKRHEGEM
YSVPYSTGQGQPQQQQLPPAQPQPASQQQAAQPSPQQDVYNQYGNAYPATATAAT
ERRPAGGPQNQFPFQFGRDRVSAPPGTNAQQNMPPQMMGGPIQASAEVAQQGTM
WQGRNDMTYNYANRQSTGSAPQGPAYHGVNRTDEMLHTDQRANHEGSWPSHGTR
QPPYGPSAPVPPMTRPPPSNYQPPPSMQNHIPQVSSPAPLPRPMENRTSPSKSPFLH
SGMKMQKAGPPVPASHIAPAPVQPPMIRRDITFPPGSVEATQPVLKQRRRLTMKDIGT
PEAWRVMMSLKSGLLAESTWALDTINILLYDDNSIMTFNLSQLPGLLELLVEYFRRCLIE
IFGILKEYEVGDPGQRTLLDPGRFSKVSSPAPMEGGEEEEELLGPKLEEEEEEEVVEN
DEEIAFSGKDKPASENSEEKLISKFDKLPVKIVQKNDPFVVDCSDKLGRVQEFDSGLLH
WRIGGGDTTEHIQTHFESKTELLPSRPHAPCPPAPRKHVTTAEGTPGTTDQEGPPPD
GPPEKRITATMDDMLSTRSSTLTEDGAKSSEAIKESSKFPFGISPAQSHRNIKILEDEPH
SKDETPLCTLLDWQDSLAKRCVCVSNTIRSLSFVPGNDFEMSKHPGLLLILGKLILLHHK
HPERKQAPLTYEKEEEQDQGVSCNKVEWWWDCLEMLRENTLVTLANISGQLDLSPY
PESICLPVLDGLLHWAVCPSAEAQDPFSTLGPNAVLSPQRLVLETLSKLSIQDNNVDLIL
ATPPFSRLEKLYSTMVRFLSDRKNPVCREMAVVLLANLAQGDSLAARAIAVQKGSIGN
LLGFLEDSLAATQFQQSQASLLHMQNPPFEPTSVDMMRRAARALLALAKVDENHSEF
TLYESRLLDISVSPLMNSLVSQVICDVLFLIGQS

NCOA6 (ID: Q14686)

NCOA6_1 (CN348777; internal 993 aa missing (972-1965 aa)) (SEQ ID NO: 202)
MVLDDLPNLEDIYTSLCSSTMEDSEMDFDSGLEDDDTKSDSILEDSTIFVAFKGNIDDK
DFKWKLDAILKNVPNLLHMESSKLKVQKVEPWNSVRVTFNIPREAAERLRILAQSNNQ
QLRDLGILSVQIEGEGAINLALAQNRSQDVRMNGPMGAGNSVRMEAGFPMASGPGIIR
MNNPATVMIPPGGNVSSSMMAPGPNPELQPRTPRPASQSDAMDPLLSGLHIQQQSH
PSGSLAPPHHPMQPVSVNRQMNPANFPQLQQQQQQQQQQQQQQQQQQQQQQQQQ
QLQARPPQQHQQQQPQGIRPQFTAPTQVPVPPGWNQLPSGALQPPPAQGSLGTMT
ANQGWKKAPLPGPMQQQLQARPSLATVQTPSHPPPPYPFGSQQASQAHTNFPQMS
NPGQFTAPQMKSLQGGPSRVPTPLQQPHLTNKSPASSPSSFQQGSPASSPTVNQTQ
QQMGPRPPQNNPLPQGFQQPVSSPGRNPMVQQGNVPPNFMVMQQQPPNQGPQSL
HPGLGGMPKRLPPGFSAGQANPNFMQGQVPSTTATTPGNSGAPQLQANQNVQHAG
GQGAGPPQNQMQVSHGPPNMMQPSLMGIHGNMNNQQAGTSGVPQVNLSNMQGQ
PQQGPPSQLMGMHQQIVPSQGQMVQQQGTLNPQNPMILSRAQLMPQGQMMVNPP
SQNLGPSPQRMTPPKQMLSQQGPQMMAPHNQMMGPQGQVLLQQNPMIEQIMTNQ
MQGNKQQFNTQNQSNVMPGPAQIMRGPTPNMQGNMVQFTGQMSGQMLPQQGPV
NNSPSQVMGIQGQVLRPPGPSPHMAQQHGDPATTANNDVSLSQMMPDVSIQQTNM
VPPHVQAMQGNSASGNHFSGHGMSFNAPFSGAPNGNQMSCGQNPGFPVNKDVTLT
SPLLVNLLQSDISAGHFGVNNKQNNTNANKPKKKKPPRKKKNSQQDLNTPDTRPAGL
EEADQPPLPGEQGINLDNSGPKLPEFSNRPPAPSQNLVSKETSTTALQASVARPELEV
NAAIVSGQSSEPKEIVEKSKIPGRRNSRTEEPTVASESVENGHRKRSSRPASASSSTK
DITSAVQSKRRKSK*

29aaa

2008259792 07 May 2012

NCOR1 (ID: O75376)

NCOR1_1 (DA914568; 120 aa missing (1841 - 1961 aa)) (SEQ ID NO: 203)
MSSSGYPPNQGAFSTEQSRYPPHSVQYTFPNTRHQQEFAVPDYRSSHLEVSQASQL
LQQQQQQQLRRRPSLLSEFHPGSDRPQERRTSYEPFHPGPSPVDHDSLESKRPRLE
QVSDSHFQRVSAAVLPLVHPLPEGLRASADAKKDPAFGGKHEAPSSPISGQPCGDDQ
NASPSKLSKEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEEAAKPPEPEKPVSPPPV
EQKHRSIVQIIYDENRKKAEEAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRK
KLILFFKRRNHARKQREQKICQRYDQLMEAWEKKVDRIENNPRRKAKESKTREYYEKQ
FPEIRKQREQQERFQRVGQRGAGLSATIARSEHEISEIIDGLSEQENNEKQMRQLSVIP
PMMFDAEQRRVKFINMNGLMEDPMKVYKDRQFMNVWTDHEKEIFKDKFIQHPKNFGL
IASYLERKSVPDCVLYYYLTKKNENYKALVRRNYGKRRGRNQQIARPSQEEKVEEKEE
DKAEKTEKKEEEKKDEEEKDEKEDSKENTKEKDKIDGTAEETEEREQATPRGRKTANS
QGRRKGRITRSMTNEAAAASAAAAAATEEPPPPLPPPPEPISTEPVETSRWTEEEMEV
AKKGLVEHGRNWAAIAKMVGTKSEAQCKNFYFNYKRRHNLDNLLQQHKQKTSRKPR
EERDVSQCESVASTVSAQEDEDIEASNEEENPEDSEVEAVKPSEDSPENATSRGNTE
PAVELEPTTETAPSTSPSLAVPSTKPAEDESVETQVNDSISAETAEQMDVDQQEHSAE
EGSVCDPPPATKADSVDVEVRVPENHASKVEGDNTKERDLDRASEKVEPRDEDLVVA
QQINAQRPEPQSDNDSSATCSADEDVDGEPERQRMFPMDSKPSLLNPTGSILVSSPL
KPNPLDLPQLQHRAAVIPPMVSCTPCNIPIGTPVSGYALYQRHIKAMHESALLEEQRQR
QEQIDLECRSSTSPCGTSKSPNREWEVLQPAPHQVITNLPEGVRLPTTRPTRPPPPLIP
SSKTTVASEKPSFIMGGSISQGTPGTYLTSHNQASYTQETPKPSVGSISLGLPRQQES
AKSATLPYIKQEEFSPRSQNSQPEGLLVRAQHEGVVRGTAGAIQEGSITRGTPTSKISV
ESIPSLRGSITQGTPALPQTGIPTEALVKGSISRMPIEDSSPEKGREEAASKGHVIYEGK
SGHILSYDNIKNAREGTRSPRTAHEISLKRSYESVEGNIKQGMSMRESPVSAPLEGLIC
RALPRGSPHSDLKERTVLSGSIMQGTPRATTESFEDGLKYPKQIKRESPPIRAFEGAIT
KGKPYDGITTIKEMGRSIHEIPRQDILTQESRKTPEVVQSTRPIIEGSISQGTPIKFDNNS
GQSAIKHNVKSLITGPSKLSRGMPPLEIVPENIKVVERGKYEDVKAGETVRSRHTSVVS
SGPSVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTISSN
KSTNHERKSTLTPTQRESIPAKSPVPGVDPVVSHSPFDPHHRGSTAGEVYRSHLPTHL
DPAMPFHRALDPAAAAYLFQRQLSPTPGYPSQYQLYAMENTRQTILNDYITSQQMQV
NLRPDVARGLSPREQPLGLPYPATRGIIDLTNMPPTILVPHPGGTSTPPMDRITYIPGTQ
ITFPPRPYNSASMSPGHPTHLAAAASAERERERERERERERIAAASSDLYLRPGSE
QPGRPGSHGYVRSPSPSVRTQETMLQQRPSVFQGTNGTSVITPLDPTAQLRIMPLPA
GGPSISQGLPASRYNTAADALAALVDAAASAPQMDVSKTKEISSHRYETPSDAIEVISP
ASSPAPPQEKLQTYQPEVVKANQAENDPTRQYEGPLHHYRPQQESPSPQQQLPPSS
QAEGMGQVPRTHRLITLADHICQIITQDFARNQVSSQTPQQPPTSTFQNSPSALVSTPV
RTKTSNRYSPESQAQSVHHQRPGSRVSPENLVDKSRGSRPGKSPERSHVSSEPYEPI
SPPQVPVVHEKQDSLLLLSQRGAEPAEQRNDARSPGSISYLPSFFTKLENTSPMVKSK
KQEIFRKLNSSGGGDSDMAAAQPGTEIFNLPAVTTSGSVSSRGHSFADPASNLGLEDII
RKALMGSFDDKVEDHGVVMSQPMGVVPGTANTSVVTSGETRREEGDPSPHSGGVC
KPKLISKSNSRKSKSPIPGQGYLGTERPSSVSSVHSEGDYHRQTPGWAWEDRPSSTG
STQFPYNPLTMRMLSSTPPTPIACAPSAVNQAAPHQQNRIWEREPAPLLSAQYETLSD
SDD

NCOR2 (ID: Q9Y618)

NCOR2_1 (different sequence after 2051 aa) (SEQ ID NO: 204)
MSGSTQLVAQTWRATEPRYPPHSLSYPVQIARTHTDVGLLEYQHHSRDYASHLSPGSI
IQPQRRRPSLLSEFQPGNERSQELHLRPESHSYLPELGKSEMEFIESKRPRLELLPDPL
LRPSPLLATGQPAGSEDLTKDRSLTGKLEPVSPPSPPHTDPELELVPPRLSKEELIQNM
DRVDREITMVEQQISKLKKKQQQLEEEAAKPPEPEKPVSPPPIESKHRSLVQIIYDENR
KKAEAAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQ

WKQKFCQRYDQLMEALEKKVERIENNPRRRAKESKVREYYEKQFPEIRKQRELQERM
QSRVGQRGSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMLYDADQQRIK
FINMNGLMADPMKVYKDRQVMNMWSEQEKETFREKFMQHPKNFGLIASFLERKTVAE
CVLYYYLTKKNENYKSLVRRSYRRRGKSQQQQQQQQQQQQQQQQQPMPRSSQEE
KDEKEKEKEAEKEEEKPEVENDKEDLLKEKTDDTSGEDNDEKEAVASKGRKTANSQG
RRKGRITRSMANEANSEEAITPQQSAELASMELNESSRWTEEEMETAKKGLLEHGRN
WSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQQHKLKMEKERNARRKKKKAPAAA
SEEAAFPPVVEDEEMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPATVNNSS
DTESIPSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPPRRTSRAPIEPTPASEATG
APTPPPAPPSPSAPPPVVPKEEKEEETAAAPPVEEGEEQKPPAAEELAVDTGKAEEPV
KSECTEEAEEGPAKGKDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDSDSSA
TCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANASPQKPLDLKQLKQRAAAIPPIQ
VTKVHEPPREDAAPTKPAPPAPPPPQNLQPESDAPQQPGSSPRGKSRSPAPPADKEA
FAAEAQKLPGDPPCWTSGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTA
RPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTMG
LPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTALGSVPGGSI
TKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVI
YEGKKGHVLSYEGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSA
SIEGLMGRAIPPERHSPHHLKEQHHIRGSITQGIPRSYVEAQEDYLRREAKLLKREGTP
PPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAP
RPLKEGSITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALER
ACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSP
VTMREPTPRLQEGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHPISPYEHLLRG
VSGVDLYRSHIPLAFDPTSIPRGIPLDAAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDTA
ALENRQTIINDYITSQQMHHNTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQ
VPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSSS
ERERDRDRERDRDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSSGGGGGSSSR
PASHSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKPTVLRSTSTSSPVR
PAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPAR
SGLEPASSPSKGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASASDPHRE
KTQSKPFSIQELELRSLGYHGSSYSPQCARSGPHRLPQPTRLLETKSGQVGGQKGQV
RPGGNGCSEDWTVFFTHRCRSGGKERQM*

BAZ1A (ID: Q9NRL2)

BAZ1A_1 (internal 32 aa missing (504-536 aa)) (SEQ ID NO: 205)
MPLLHRKPFVRQKPPADLRPDEEVFYCKVTNEIFRHYDDFFERTILCNSLVWSCAVTG
RPGLTYQEALESEKKARQNLQSFPEPLIIPVLYLTSLTHRSRLHEICDDIFAYVKDRYFV
EETVEVIRNNGARLQCRILEVLPPSHQNGFANGHVNSVDGETIIISDSDDSETQSCSFQ
NGKKKDAIDPLLFKYKVQPTKKELHESAIVKATQISRRKHLFSRDKLKLFLKQHCEPQD
GVIKIKASSLSTYKIAEQDFSYFFPDDPPTFIFSPANRRRGRPPKRIHISQEDNVANKQT
LASYRSKATKERDKLLKQEEMKSLAFEKAKLKREKADALEAKKKEKEDKEKKREELKKI
VEEERLKKKEEKERLKVEREKEREKLREEKRKYVEYLKQWSKPREDMECDDLKELPE
PTPVKTRLPPEIFGDALMVLEFLNAFGELFDLQDEFPDGVTLEVLEEALVGNDSEGPLC
ELLFFFLTAIFQAIAEEEEEVAKEQLTDADTKGCSLKSLDLDSCTLSEILRLHILASGADV
TSANAKYRYQKRGGFDATDDACMELRLSNPSLVKKLSSTSVYDLTPGEKMKILHALCG
KLLTLVSTRDFIEDYVDILRQAKQEFRELKAEQHRKEREEAAARIRKRKEEKLKEQEQK
MKEKQEKLKEDEQRNSTADISIGEEEREDFDTSIESKDTEQKELDQDMVTEDEDDPGS
HKRGRRGKRGQNGFKEFTRQEQINCVTREPLTADEEEALKQEHQRKEKELLEKIQSAI
ACTNIFPLGRDRMYRRYWIFPSIPGLFIEEDYSGLTEDMLLPRPSSFQNNVQSQDPQV
STKTGEPLMSESTSNIDQGPRDHSVQLPKPVHKPNRWCFYSSCEQLDQLIEALNSRG
HRESALKETLLQEKSRICAQLARFSEEKFHFSDKPQPDSKPTYSRGRSSNAYDPSQM
CAEKQLELRLRDFLLDIEDRIYQGTLGAIKVTDRHIWRSALESGRYELLSEENKENGIIKT

VNEDVEEMEIDEQTKVIVKDRLLGIKTETPSTVSTNASTPQSVSSVVHYLAMALFQIEQ
GIERRFLKAPLDASDSGRSYKTVLDRWRESLLSSASLSQVFLHLSTLDRSVIWSKSILN
ARCKICRKKGDAENMVLCDGCDRGHHTYCVRPKLKTVPEGDWFCPECRPKQRSRRL
SSRQRPSLESDEDVEDSMGGEDDEVDGDEEEGQSEEEEYEVEQDEDDSQEEEEVSL
PKRGRPQVRLPVKTRGKLSSSFSSRGQQQEPGRYPSRSQQSTPKTTVSSKTGRSLR
KINSAPPTETKSLRIASRSTRHSHGPLQADVFVELLSPRRKRRGRKSANKTPENSPNF
PNFRVIATKSSEQSRSVNIASKLSLQESESKRRCKKRQSPEPSPVTLGRRSSGRQGGV
HELSAFEQLVVELVRHDDSWPFLKLVSKIQVPDYYDIIKKPIALNIIREKVNKCEYKLASE
FIDDIELMFSNCFEYNPRNTSEAKAGTRLQAFFHIQAQKLGLHVTPSNVDQVSTPPAAK
KSRI

BAZ1A_2 (internal 242 aa missing (504-746 aa)) (SEQ ID NO: 206)
MPLLHRKPFVRQKPPADLRPDEEVFYCKVTNEIFRHYDDFFERTILCNSLVWSCAVTG
RPGLTYQEALESEKKARQNLQSFPEPLIIPVLYLTSLTHRSRLHEICDDIFAYVKDRYFV
EETVEVIRNNGARLQCRILEVLPPSHQNGFANGHVNSVDGETIIISDSDDSETQSCSFQ
NGKKKDAIDPLLFKYKVQPTKKELHESAIVKATQISRRKHLFSRDKLKLFLKQHCEPQD
GVIKIKASSLSTYKIAEQDFSYFFPDDPPTFIFSPANRRRGRPPKRIHISQEDNVANKQT
LASYRSKATKERDKLLKQEEMKSLAFEKAKLKREKADALEAKKKEKEDKEKKREELKKI
VEEERLKKKEEKERLKVEREKEREKLREEKRKYVEYLKQWSKPREDMECDDLKELPE
PTPVKTRLPPEIFGDALMVLEFLNAFGELFDLQDEFPDGVTLEVLEEALVGNDSEGPLC
ELLFFFLTAIFQAIAEEEEEVAKEQLTDADTKGKRGQNGFKEFTRQEQINCVTREPLTA
DEEEALKQEHQRKEKELLEKIQSAIACTNIFPLGRDRMYRRYWIFPSIPGLFIEEDYSGL
TEDMLLPRPSSFQNNVQSQDPQVSTKTGEPLMSESTSNIDQGPRDHSVQLPKPVHKP
NRWCFYSSCEQLDQLIEALNSRGHRESALKETLLQEKSRICAQLARFSEEKFHFSDKP
QPDSKPTYSRGRSSNAYDPSQMCAEKQLELRLRDFLLDIEDRIYQGTLGAIKVTDRHI
WRSALESGRYELLSEENKENGIIKTVNEDVEEMEIDEQTKVIVKDRLLGIKTETPSTVST
NASTPQSVSSVVHYLAMALFQIEQGIERRFLKAPLDASDSGRSYKTVLDRWRESLLSS
ASLSQVFLHLSTLDRSVIWSKSILNARCKICRKKGDAENMVLCDGCDRGHHTYCVRPK
LKTVPEGDWFCPECRPKQRSRRLSSRQRPSLESDEDVEDSMGGEDDEVDGDEEEG
QSEEEEYEVEQDEDDSQEEEEVSLPKRGRPQVRLPVKTRGKLSSSFSSRGQQQEPG
RYPSRSQQSTPKTTVSSKTGRSLRKINSAPPTETKSLRIASRSTRHSHGPLQADVFVEL
LSPRRKRRGRKSANKTPENSPNFPNFRVIATKSSEQSRSVNIASKLSLQESESKRRCK
KRQSPEPSPVTLGRRSSGRQGGVHELSAFEQLVVELVRHDDSWPFLKLVSKIQVPDY
YDIIKKPIALNIIREKVNKCEYKLASEFIDDIELMFSNCFEYNPRNTSEAKAGTRLQAFFHI
QAQKLGLHVTPSNVDQVSTPPAAKKSRI

BAZ1A_3 (93 aa missing (38-131 aa)) (SEQ ID NO: 207)
MPLLHRKPFVRQKPPADLRPDEEVFYCKVTNEIFRHYELQCRILEVLPPSHQNGFANG
HVNSVDGETIIISDSDDSETQSCSFQNGKKKDAIDPLLFKYKVQPTKKELHESAIVKATQ
ISRRKHLFSRDKLKLFLKQHCEPQDGVIKIKASSLSTYKIAEQDFSYFFPDDPPTFIFSPA
NRRRGRPPKRIHISQEDNVANKQTLASYRSKATKERDKLLKQEEMKSLAFEKAKLKRE
KADALEAKKKEKEDKEKKREELKKIVEEERLKKKEEKERLKVEREKEREKLREEKRKYV
EYLKQWSKPREDMECDDLKELPEPTPVKTRLPPEIFGDALMVLEFLNAFGELFDLQDE
FPDGVTLEVLEEALVGNDSEGPLCELLFFFLTAIFQAIAEEEEEVAKEQLTDADTKDLTE
ALDEDADPTKSALSAVASLAAAWPQLHQGCSLKSLDLDSCTLSDILRLHILASGADVTS
ANAKYRYQKRGGFDATDDACMELRLSNPSLVKKLSSTSVYDLTPGEKMKILHALCGKL
LTLVSTRDFIEDYVDILRQAKQEFRELKAEQHRKEREEAAARIRKRKEEKLKEQEQKMK
EKQEKLKEDEQRNSTADISIGEEEREDFDTSIESKDTEQKELDQDMVTEDEDDPGSHK
RGRRGKRGQNGFKEFTRQEQINCVTREPLTADEEEALKQEHQRKEKELLEKIQSAIAC
TNIFPLGRDRMYRRYWIFPSIPGLFIEEDYSGLTEDMLLPRPSSFQNNVQSQDPQVSTK
TGEPLMSESTSNIDQGPRDHSVQLPKPVHKPNRWCFYSSCEQLDQLIEALNSRGHRE
SALKETLLQEKSRICAQLARFSEEKFHFSDKPQPDSKPTYSRGRSSNAYDPSQMCAEK
QLELRLRDFLLDIEDRIYQGTLGAIKVTDRHIWRSALESGRYELLSEENKENGIIKTVNED

VEEMEIDEQTKVIVKDRLLGIKTETPSTVSTNASTPQSVSSVVHYLAMALFQIEQGIERR
FLKAPLDASDSGRSYKTVLDRWRESLLSSASLSQVFLHLSTLDRSVIWSKSILNARCKI
CRKKGDAENMVLCDGCDRGHHTYCVRPKLKTVPEGDWFCPECRPKQRSRRLSSRQ
RPSLESDEDVEDSMGGEDDEVDGDEEEGQSEEEEYEVEQDEDDSQEEEEVSLPKRG
RPQVRLPVKTRGKLSSSFSSRGQQQEPGRYPSRSQQSTPKTTVSSKTGRSLRKINSA
PPTETKSLRIASRSTRHSHGPLQADVFVELLSPRRKRRGRKSANKTPENSPNFPNFRV
IATKSSEQSRSVNIASKLSLQESESKRRCKKRQSPEPSPVTLGRRSSGRQGGVHELSA
FEQLVVELVRHDDSWPFLKLVSKIQVPDYYDIIKKPIALNIIREKVNKCEYKLASEFIDDIE
LMFSNCFEYNPRNTSEAKAGTRLQAFFHIQAQKLGLHVTPSNVDQVSTPPAAKKSRI

Example 2. Identification of isoforms in transcriptional complexes: MudPIT analysis.

Nuclear extracts were prepared according to the method of Dignam et al. (1983) from parental HeLa cells and six HeLa cell lines stably expressing mammalian Mediator subunits human Nut2 (MED10) (Malik et al., 2000), mouse Med25 (MED9) (Tomomori-Sato et al., 2003), human Intersex (MED29) (Sato et al., 2003a), human LCMR1 (MED19) (Sato et al., 2003a), human AK007855 (MED28), or human CRSP70 (MED26), all with N-terminal FLAG epitope tags. Nuclear extracts were subjected to anti-FLAG agarose immunoaffinity chromatography performed essentially as described for purification of the TRAP/SMCC Mediator complex from FLAG-Nut2-expressing HeLa cells (Malik et al., 2000)

Phosphocellulose Chromatography

HeLa cell nuclear extracts (30 ml) were prepared according to the method of Dignam et al. (1983) and dialyzed against HEG buffer [20 mM HEPES-NaOH (pH 7.6), 0.1 mM EDTA, 1 mM DTT, and 10% (v/v) glycerol, 1 mM benzamidine, 0.25 mM PMSF, 2 g/ml aprotinin] to a conductivity equivalent to that of HEG containing 0.1 M KCl.

Following centrifugation for 30 min at 40,000 rpm in a Ti-45 rotor, the supernatant (130 mg of protein) was applied at two packed column volumes per hour to a phosphocellulose column (10 mg of protein per ml packed column bed volume) equilibrated in HEG containing 0.1 M KCl. The column was washed at the same flow rate with HEG containing 0.1 M KCl and eluted stepwise with HEG containing 0.3, 0.5, and 1.0 M KCl. One-fifth column volume fractions were collected. Protein eluted from the column with 0.5 M KCl and 1.0 M KCl was subjected to FLAG immunopurification as described above.

Identification of Mediator subunits and Mediator-associated proteins was accomplished using a modification of the MudPIT procedure described by Washburn et al. (2001). For each analysis, 60 µl aliquots of anti-FLAG agarose eluates were used.

Results

MudPIT analysis identified following isoforms of MED complex components from immunoprecipitated MED complexes:

MED1.3 (SEQ ID NO: 4).

MKAQGETEESEKLSKMSSLLERLHAKFNQNRPWSETIKLVRQVMEKRVVMSSGGH
QHLVSCLETLQKALKVTSLPAMTDRLESIARQNGLGSHLSASGTECYITSDMFYVEV

QLDPAGQLCDVKVAHHGENPVSCPELVQQLREKNFDEFSKHLKGLVNLYNLPGDN
KLKTKMYLALQSLEQDLSKMAIMYWKATNAGPLDKILHGSVGYLTPRSGGHLMNLK
YYVSPSDLLDDKTASPIILHENNVSRSLGMNASVTIEGTSAVYKLPIAPLIMGSHPVD
NKWTPSFSSITSANSVDLPACFFLKFPQPIPVSRAFVQKLQNCTGIPLFETQPTYAPL
YELITQFELSKDPDPIPLNHNMRFYAALPGQQHCYFLNKDAPLPDGRSLQGTLVSKI
TFQHPGRVPLILNLIRHQVAYNTLIGSCVKRTILKEDSPGLLQFEVCPLSESRFSVSF
QHPVNDSLVCVVMDVQDSTHVSCKLYKGLSDALICTDDFIAKVVQRCMSIPVTMRAI
RRKAETIQADTPALSLIAETVEDMVKKNLPPASSPGERGVYHWLESDPSSSHAATC
LFDGRQHQEPPDAHEPS*

MED24.1 (SEQ ID NO: 5).

MKVVNLKQAILQAWKERWSDYQWAINMKKFFPKGATWDILNLADALLEQAMIGPSP
NPLILSYLKYAISSQMVSYSSVLTAISKFDDFSRDLCVQALLDIMDMFCDRLSCHGKA
EECIGLCRALLSALHWLLRCTAASAERLREGLEAGTPAAGEKQLAMCLQRLEKTLS
STKNRALLHIAKLEEASLHTSQGLGQGGTRANQPTASWTAIEHSLLKLGEILANLSN
PQLRSQAEQCGTLIRSIPTMLSVHAEQMHKTGFPTVHAVILLEGTMNLTGETQSLVE
QLTMVKRMQHIPTPLFVLEIWKACFVGLIESPEGTEELKWTAFTFLKIPQVLVKLKKY
SHGDKDFTEDVNCAFEFLLKLTPLLDKADQRCNCDCTNFLLQECGKQGLLSEASVN
NLMAKRKADREHAPQQKSGENANIQPNIQLILRAEPTVTNILKTMDADHSKSPEGLL
GVLGHMLSGKSLDLLLAAAAATGKLKSFARKFINLNEFTTYGSEESTKPASVRALLF
DISFLMLCHVAQTYGSEVILSESRTGAEVPFFETWMQTCMPEEGKILNPDHPCFRP
DSTKVESLVALLNNSSEMKLVQMKWHEACLSISAAILEILNAWENGVLAFESIQKITD
NIKGKVCSLAVCAVAWLVAHVRMLGLDEREKSLQMIRQLAGPLFSENTLQFYNERV
VIMNSILERMCADVLQQTATQIKFPSTGVDTMPYWNLLPPKRPIKEVLTDIFAKVLEK
GWVDSRSIHIFDTLLHMGGVYWFCNNLIKELLKETRKEHTLRAVELLYSIFCLDMQQ
VTLVLLGHILPGLLTDSSKWHSLMDPPGTALAKLAVWCALSSYSSHKGQASTRQKK
RHREDIEDYISLFPLDDVQPSKLMRLLSSNEDDANILSSPTDRSMSSSLSASQLHTV
NMRDPLNRVLANLFLLISSILGSRTAGPHTQFVQWFMEECVDCLEQGGRGSVLQF
MPFTTVSELVKVSAMSSPKVVLAITDLSLPLGRQVAAKAIAAL

Example 3. Identification of isoforms in transcriptional complexes: biochemical fractionation.

Materials and methods.

Preparation of Nuclear Extracts from Mammalian Cells

Collect cells from monolayer cultures.

1. Remove the culture medium from confluent monolayer cultures. Wash the cells by pipetting sufficient PBS to cover them, swirling gently, and pouring off the PBS. Scrape the cells into fresh PBS and pool in a graduated conical centrifuge tube.

2. Pellet the cells by centrifuging 10 min at 3000 rpm.

3. Decant the supernatants and discard. Using the graduations on the tube, measure the pcv.

4. Rapidly resuspend the cell pellets in a volume of hypotonic buffer 5 times the pcv.

Centrifuge the cells 5 min 3000 rpm and discard supernatant. Do this step quickly because proteins can leak out of the cell at this point and be discarded with the supernatant. This step removes salt from the PBS solution so that efficient swelling can occur in the next step; however, some swelling will occur during this step.

5. Resuspend the packed cells in hypotonic buffer to a final volume of 3 times the original pcv (step 3) and allow to swell on ice 10 min. For example, if an original pcv of 10 ml has swelled to 20 ml in step 4, only 10 ml of additional buffer is required at this step. The cells should swell at least 2-fold.

6. Transfer the cells to an Insulin syringe. Homogenize with ten up-and-down strokes. Perform the homogenization slowly, especially the down strokes.

7. Transfer cells to centrifuge tubes. Collect the nuclei by centrifuging 15 min at 4000 rpm (3300 g). Remove the supernatant and save for S-100 cytoplasmic extract preparation.

Extraction of chromatin complexes

8. Using the graduations on the tubes, measure the packed nuclear volume (pnv) from step 7. Resuspend the nuclei in a volume of low-salt buffer equal to 1/2 pnv. Resuspension of the nuclei with a small volume of low-salt buffer allows thorough rapid mixing of the nuclei during the addition of the high-salt buffer (step 9)

9. In a dropwise fashion, while stirring gently, add a volume of high-salt buffer equal to ~12 the pnv (from step 8). The high-salt buffer must be added dropwise with frequent or continuous mixing. If it is added too quickly, local concentration of salt can become high and some nuclei will lyse. The final concentration of potassium chloride should be ~300 mM.

10. Allow the nuclei to extract for 30 min with continuous gentle mixing. Mixing can be done using very gentle stirring on a magnetic stirrer or by tilting on a tiltboard.

11. Pellet the extracted nuclei by centrifuging 30 min at 14,500 rpm (25,000~ g). Draw off the resulting supernatant. This is the nuclear extract.

Dialyze and store the extract

12. Place the nuclear extract in dialysis tubing. Dialyze against 50 vol of dialysis buffer until the extract reaches 100 mM KCl.

13. Remove the extract from the dialysis bag. Centrifuge the extract 20 min at 14,500 rpm. Discard the pellet. This will remove protein and nucleic acid that precipitates when the potassium chloride concentration is lowered during dialysis.

14. Determine the protein concentration of the supernatant. Aliquot into tubes if desired and rapidly freeze by submerging in liquid nitrogen. Store the extracts at ~80°C.

Dialysis buffer

20 mM HEPES, pH 7.9 at 4°C
20% glycerol
100 mM KCl
0.2 mM EDTA
0.2 mM PMSF*
0.5 mM DTT*

High-salt buffer

20 mM HEPES, pH 7.9 at 4°C
25% glycerol
1.5 mM MgCl2
0.8, 1.0, 1.2, 1.4 or 1.6 M KCl
0.2 mM EDTA
0.2 mM PMSF*
0.5 mM DTT*

*Add ingredients immediately before use (see introductory note to reagents and solutions).

Hypotonic buffer

10 mM HEPES, pH 7.9 at 4°C

1.5 mM MgCl2

10 mM KCl

0.2 mM PMSF*

0.5 mM DTT*

Low-salt buffer

Prepare high-salt buffer, substituting 0.02 M KCl for 1.2 M KCl.

*Add ingredients immediately before use (see introductory note to reagents and solutions).

Fractionation of chromatin complexes.

Pre-cycling of P11 resin

1. Stir resin into 25 volumes of 0,5 M NaOH for 5 minutes.
2. Wash with mQ until the filtrate pH is 11.0.
3. Stir resin into 25 volumes of 0,5 M HCl for 5 minutes.
4. Wash with mQ until the filtrate pH is above 3.0.
5. Transfer the pre-cycled PC immediately into 20 volumes of 5x concentrated buffer solution:

   100 mM Hepes pH 7.9

   20 % v/v glycerol

   2.5 mM DTT

   1.0 mM EDTA

   0.5 M KCl
6. Titrate the slurry to the correct pH
7. Decant the supernatant.
8. Stir the PC into 20 volumes of the starting elution buffer
9. Leave for 3-4 minutes.
10. Repeat washing until pH is correct and storage at +4°C for week.

Batch purification of transcription complexes.

For 25 mg of protein it is necessary 1 ml bed volume of packed resin.

11. Add appropriate quality of pre-cycling resin to cell nuclear extract.
12. Rotate about 1 hour at +4°C.
13. Centrifuge 3 minutes at 2000 rpm at +4°C.

14. Supernatant – is flow through fraction, keep it at -80°C until analysis.
15. Wash resin step by step increasing KCl concentration of elution buffer from 0,2 to 1,0 M, adding 2 volumes of buffer to 1 bed volume of PC. At every stage rotate resin for 30 minutes at +4°C and pull down for 3 minutes at 2000 rpm. Collect fractions.

Elution buffer:

20 mM Hepes pH 7.9
20 % glycerol
0.2 mM EDTA
0.5 mM DTT
1x PIC
KCl 0.2 M-1.0 M

Western blot analysis.

Western blot analysis was performed according to the protocol published in Ali Sadra, Tomas Cinek and John B. Imboden. "Multiple Probing of an Immunoblot Membrane Using a Non-Block Technique: Advantages in Speed and Sensitivity." *Analytical Biochemistry* , **278**, 2000, p. 235-237

Briefly, 15 µg of protein samples were solubilized in SDS sample buffer and were subjected to 10% SDS–polyacrylamide gel electrophoresis. The proteins were then transferred onto PVDF membranes (Amersham) using Bio-Rad semi-dry blotter and standard Towbin buffer (10 x concentrate (0.25 M Tris and 1.92 M Glycine in aqueous solution)). For further analysis the non-block technique was used, after the transfer of proteins onto the PVDF membrane, the membrane was air-dried for 15 min and went through three cycles of 50 % methanol–water hydration. The blotted membrane was then left in 100 % methanol for 2 min and allowed to dry completely in an incubator for 10 min at 37°C. After the membrane was dry, it was incubated with the primary antibody solution (made in 3% nonfat milk–TBS-T) overnight at +4°C. The membrane was then washed 3 times with TBS-T for 10 min per each wash, followed by incubation with the secondary antibody solution (made in 3% nonfat milk–TBS-T) for 30 min at room temperature and with gentle shaking. Following three washes of 20 min each with TBS-T, the ECL detection (Amersham) of the signals of the target proteins was performed.

Antibodies:

Primary antibodies:

- Baf57 (C-20) against an epitope within the internal region of human Baf57, (Santa Cruz), dilution 1:500;
- P62/THIIH1 (mouse monoclonal, MAb 3C9, kind gift of J.M.Egly), dilution 1:10 000;
- Med-16/TRAP 95 (C-19) against an epitope within the C-terminus of human TRAP 95, dilution 1:500.

Secondary antibodies (anti-goat for Baf57 and Med-16/TRAP 95, anti anti-mouse for p62/THIIH1), dilution 1:100 000.

Results.

Fractionation of nuclear extracts following Western blotting to detect isoforms of TCCs clearly showed that isoforms are present in transcription complexes and can be fractionated similar to wild type isoforms.

BAF complexes

Fractionation of BAF complexes was analyzed using P11 phosphocellulose. Western blot analysis of BAF fractions identified isoforms and wild type BAF57 in the same fractions that is an indication that BAF57 isoforms are present in the active BAF57 complex.

Figure 1 shows the results of analysis of BAF complexes from HeLa and human melanoma SK-Mel 28 and WM266-4 cells. Aliquots of HeLa, SKMel28 and WM 266-4 cell nuclear extracts were chromatographed on ion-exchange PE11 column containing. After washing the column extensively with buffer containing 0.1M KCl, bound proteins were eluted with buffer containing 0.2 (lanes 2, 8 and 14), 0.3M KCl (lanes 3, 9 and 15), 0.5M KCl (lanes 4, 10 and 16), 0.75MKCl (lanes 5, and 11) and 1.0M KCl (lanes 6, and 12). Initial "flow through" is depicted on lanes 1, 7 and 13.

GTF Complex

Fractionation of GTF complexes was analyzed using P11 phosphocellulose. Western blot analysis of TFIIH subunit p62 identified isoforms and wild type p62 in the same fractions that is an indication that TFIIH subunit isoforms are present in the active complex.

Figure 2 shows the results of analysis of fractionation of GTF complex by detecting p62 (TFIIH subunit) using Western blot detection from HeLa cells and human melanoma SK-Mel 28 and WM266-4 cells. Aliquots of HeLa, SKMel28 and WM 266-4 cell nuclear extracts were chromatographed on ion-exchange PE11 column. After washing the column extensively with buffer containing 0.1M KCl, bound proteins

were eluted with buffer containing 0.2 (lanes 2, 8 and 14), 0.3M KCl (lanes 3, 9 and 15), 0.5M KCl (lanes 4, 10 and 16), 0.75MKCl (lanes 5, 11 and 17) and 1.0M KCl (lanes 6, 12 and 18). Initial "flow through" is depicted on lanes 1, 7 and 13.

MED Complex

Fractionation of MED complex was analyzed using P11 phosphocellulose. Western blot analysis of MED subunit MED16 identified isoforms and wild type MED16 in the same fractions that is an indication that MED subunit isoforms are present in the active complex.

Figure 3 shows results of assessment of mediator complex purification conditions by detecting MED-16 in NER fractions from HeLa cells as compared to melanoma SK-Mel 28 cells. Aliquots of HeLa and SKMel28 cell nuclear extracts were chromatographed on ion-exchange PE11 column. After washing the column extensively with buffer containing 0.1M KCl, bound proteins were eluted with buffer containing 0.2 (lanes 2 and 8), 0.3M KCl (lanes 3 and 9), 0.5M KCl (lanes 4 and 10), 0.75MKCl (lanes 5 and 11) and 1.0M KCl (lanes 6and 12). Initial "flow through" is depicted on lanes 1 and 7.

Example 4. Binding of peptide BAF57p12 to isoform of BAF57iso.

Materials and methods

Protein purification. We have cloned and expressed BAF57, BAF57 iso, into pGEX-4T-1 (N-terminal GST) expression vector and expressed both wild type and isoform of BAF57

Expression of proteins was induced 8 hours at 300C with 1 mM IPTG. Following induction cells were pelleted and washed in native extraction buffer:

10 mM Na2HPO4, 1.8 mM KH2PO4 (pH7.3)

140mM NaCl

2.7 mM KCl

1% Triton X100

Protease inhibitor cocktail (Roch Diagnostics, complete, cat # 11 836 145 001)

GST-Baf57 and GST-BAF57iso protein purification: Cells were lysed using sonication: 3x15 sec on ice, letting lysate to cool between sonications.

Lysate was centrifuged 10 min at 11 000xg to remove insoluble material. Supernatant was transferred to new tube.

100 µl of a 50% slurry of Glutathione Sepharose 4B (GE Healthcare) was added to each lysate supernatant and mixed gently for 5 min at RT.

500 µl of 1x extraction buffer without Triton X100 was added, vortexed briefly and centrifuged for 1 min to sediment the sepharose beads.

Supernatants were discarded and washing was repeated 2 times for a total of 3 washes.

The fusion protein was eluted by the addition of 30 µl of glutathione elution buffer (10 mM reduced glutathione, 50 mM Tris-HCl, pH 8.0) and incubated for 5 min RT

Solutions were centrifuged for 5 min max rpm and supernatant transferred to fresh tubes.

Purity proteins was analyzed using SDS PAGE and Western blot using antibodies against BAF57 that recognize both wild type and isoform of BAF57.

Binding studies. We used GST-BAF57 and GST-BAF57iso proteins extracted and purified using native conditions to conduct binding studies.

Initially fluorescein labeled peptide BAF57p12 was used to analyze its binding to GST-BAF57 and GST-BAF57iso bound to glutathione sepharose or in solution following binding to glutathione sepharose. Both protocols gave us similar results, peptide BAF57p12 binds to BAF57iso with high affinity but it also binds to BAF57, however the affinity is lower (Fig.4). These experiments were done using peptides that were synthesized 1.5 years previously.

Binding of peptide to matrix bound proteins. Matrix bound proteins (10 µg/50µl) were incubated with different concentrations of labeled peptides (0.01 nM – 10 µM) in binding buffer (10mM phosphate, 50mM NaCl, 5 mM MgCl2, 2 mM spermidine, 0.3 mM DDT, pH 7.9) for 15 min at room temperature. Following incubation, matrix was washed with an incubation buffer 3 times of 10 volumes. Bound fluorescence was detected following release of protein from the matrix using 10 mM reduced glutathione, 50 mM Tris-HCl, pH 8.0.

Binding of peptides to proteins in solution. Purified proteins at concentration 10 µg/100µl were mixed with labeled peptides (0.01 nM – 10 µM) in binding buffer (10mM phosphate, 50mM NaCl, 5 mM MgCl2, 2 mM spermidine, 0.3 mM DDT, pH 7.9) for 15 min at room temperature.. Following incubation a capture reagent (50µl, Glutathione Sepharose 4B (GE Healthcare) was added and incubate for 20 min at room temperature. Following washing (5 times) with binding buffer bound proteins was released using 10 mM reduced glutathione, 50 mM Tris-HCl, pH 8.0.

Surface Plasmon Resonance analysis. To analyze binding of BAF57p12 to GST-BAF57 and GST-BAF57iso purified proteins we also used Surface Plasmon Resonance analysis using Biacore 3000 system at University of Helsinki (Finland). With this system, molecules of interest (ligands – proteins GST-BAF57 and GST-BAF57iso) were immobilized on a sensor surface, and binding partners (analytes – peptide BAF57p12) were then passed over it in a mobile aqueous phase. Their interaction on the sensor surface can subsequently be monitored in real time without the use of labels. Proteins GST-BAF57 and GST-BAF57iso were immobilized by amine coupling methods, according to the instruction manual for the Biacore 3000 CM5 sensor chip, which utilizes a primary amino group of proteins for covalent attachment to the matrix. To estimate protein-peptide interactions, the affinity of the interaction (the equilibrium dissociation constant (KD), was determined from the level of binding at equilibrium as a function of the sample concentrations by BIAevalution version 4.1 software (Biacore, Inc.). Peptide BAF57p12 was dissolved in running (binding buffer) buffer, and binding experiments were performed at 25 °C in running buffer with a flow rate of 20 µl/min. Our preliminary analysis results show that BAF57p12 binding to GST-BAFiso has a Kd value of 5.5 x 10-7 M and BAF57p12 binding to GST-BAF has a Kd value of 3 x 10-4 M. These results confirm our data obtained by using fluorescein labeled peptides.

Example 5. Expression of isoforms in various cancers.

This example demonstrates the expression of isoforms of transcription factor complex (TCC) components in various types of cancer. Expression was determined by RT-PCR analysis of clinical cancer samples as well as numerous cell lines. Semiquantitative RT-PCR analysis was followed by DNA sequence analysis of PCR fragments. Analysis of normal tissues and non-cancerous cell lines revealed no expression of these isoforms, indicating that their expression is cancer-specific. Table 2 below lists the types of cancers shown to express various isoform genes.

Table 2. Expression of isoforms of TCC components in different cancer types

Gene	Expression of isoforms in cancers
MED24	melanoma, colorectal cancer, glioblastoma
MED1	melanoma, colorectal, glioma, lung
MED4	melanoma, colorectal, lung, glioma
MED12	melanoma, colorectal, breast, glioma
MED13	lung, breast
MED14	ovarian, breast, liver
MED15	chondrosarcoma, prostate,

MED28	colorectal, breast
MED30	colorectal, breast, neuroblastoma, glioma
BAF57	melanoma, colorectal cancer, glioblastoma
BAF250	colorectal, breast, neuroblastoma, glioma
BAF155	lung, breast, prostate
BAF170	lung, breast, prostate
BAF60	lung, teratocarcinoma
BAF53	colorectal, breast
BAF47	glioma, neuroblastoma, prostate
TAF1	lung, hepatoma
TAF4	neuroblastoma, glioma, pancreatic
TAF7L	breast, prostate

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

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CLAIMS

1. An isolated isoform of a transcriptional co-regulator wherein the isoform is an isoform of MED as set forth in SEQ ID NO: 4-5, 87-93, 95-99, 105-107 and 109-164 or a sequence fully complementary thereto.

2. An isolated peptide of at least 6 amino acids in length that specifically binds to an isoform of claim 1.

3. The peptide of claim 2 that is at least 12 amino acids in length.

4. A fusion protein comprising an isoform of claim 1 or a peptide of claim 2 or claim 3 fused with a heterologous peptide.

5. The fusion protein of claim 4, wherein the heterologous peptide is selected from the group consisting of SEQ ID NO: 1-3.

6. An isolated antibody that specifically binds an isoform of claim 1.

7. The antibody of claim 6, which is labeled with a detectable marker.

8. An isolated polynucleotide that encodes an isoform of claim 1 or a complement thereof.

9. A composition comprising an isoform of claim 1, a peptide of claim 2 or claim 3, a protein of claim 4 or claim 5, or an antibody of claim 6 or claim 7, and a pharmaceutically acceptable carrier.

10. A method for detecting cancer in a tissue specimen comprising detecting the presence of an isoform of claim 1 in the tissue specimen, wherein presence of the isoform is indicative of cancer.

11. The method of claim 10, wherein the detecting comprises contacting the tissue specimen with a detectable molecule that specifically binds an isoform of claim 1 and detecting binding of the detectable molecule, wherein binding of the detectable molecule is indicative of cancer.

12. A method for monitoring cancer in a subject, the method comprising:

(a) assaying a tissue specimen obtained from the subject to measure the amount of an isoform of claim 1 present in the specimen; and

(b) comparing the amount of the isoform present in the specimen to the amount of isoform determined under a previous condition, wherein a change in the amount of the isoform is indicative of a change in the progression of the cancer.

13. The method of claim 12, wherein the assaying comprises contacting the specimen with a detectable molecule that specifically binds an isoform of claim 1, wherein a change in the level of binding of the detectable molecule is indicative of a change in the progression of the cancer.

14. The method of claim 12, wherein the assaying of step (a) comprises determining the percentage of cancer cells in the tissue specimen to which the isoform binds and/or determining the quantity of binding of the detectable molecule in the tissue specimen.

15. The method of any one of claims 10 to 14, wherein the cancer is melanoma, colorectal cancer, lung cancer, hepatoma, pancreatic cancer, prostate cancer, gliomas, glioblastoma, neuroblastoma, sarcoma, chondrosarcoma, breast cancer, ovarian cancer, or teratocarcinoma.

16. The method of any one of claims 10 to 15, wherein the molecule that specifically binds the isoform is an antibody.

17. The method of claim 16, wherein the antibody is labeled with a detectable marker.

18. A method of killing cancer cells, the method comprising contacting the cancer cells with the peptide of claim 2 or claim 3 or the fusion protein of claim 4 or claim 5.

19. A method of treating cancer in a subject, the method comprising administering to the subject an effective amount of an isoform of claim 1; a peptide of claim 2 or claim 3; a protein of claim 4 or claim 5; an antibody of claim 6 or claim 7; or a composition of claim 9.

20. Use of an isoform of claim 1; a peptide of claim 2 or claim 3; a protein of claim 4 or claim 5; an antibody of claim 6 or claim 7; or a composition of claim 9, in the manufacture of a medicament for the treatment of cancer.

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21. A kit for detecting cancer in a tissue specimen comprising an antibody of claim 6 or claim 7.

22. An isolated isoform according to claim 1; an isolated peptide according to claim 2; a fusion protein according to claim 4; an isolated antibody according to claim 6; an isolated polynucleotide according to claim 8; a composition according to claim 9; a method according to any one of claims 10, 12, 18 or 19; use according to claim 20; or a kit according to claim 21, substantially as herein described with reference to any one or more of the examples but excluding comparative examples.

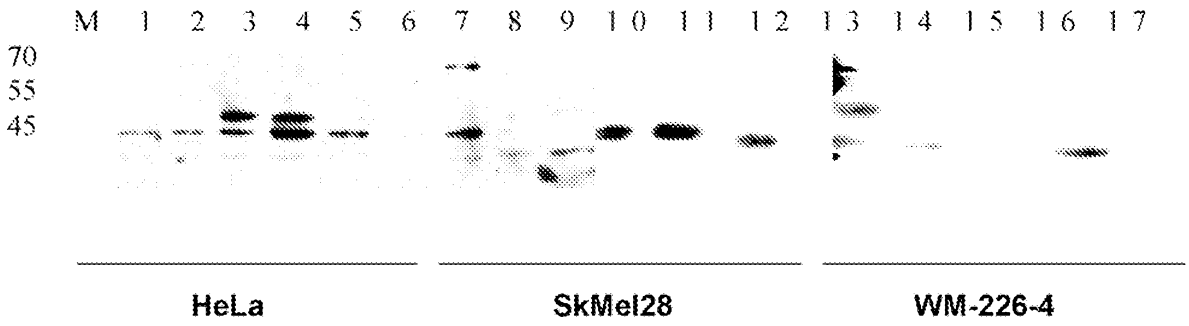

Figure 1

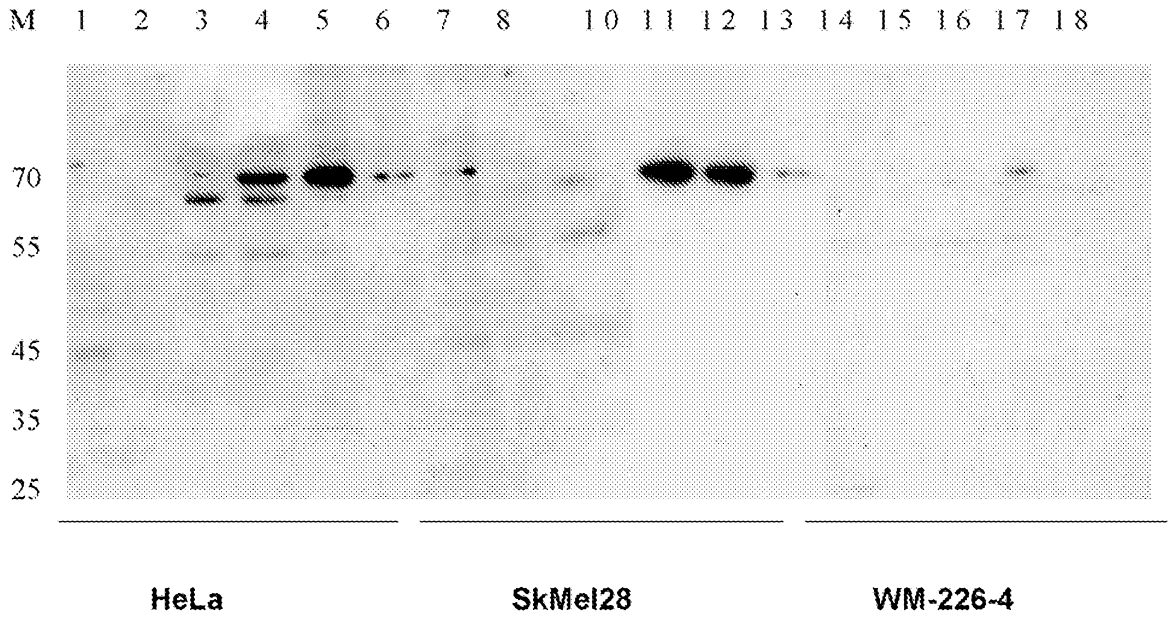

Figure 2

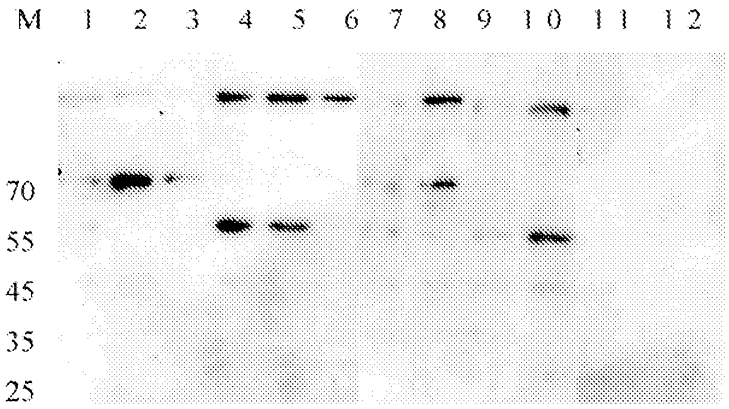

Figure 3

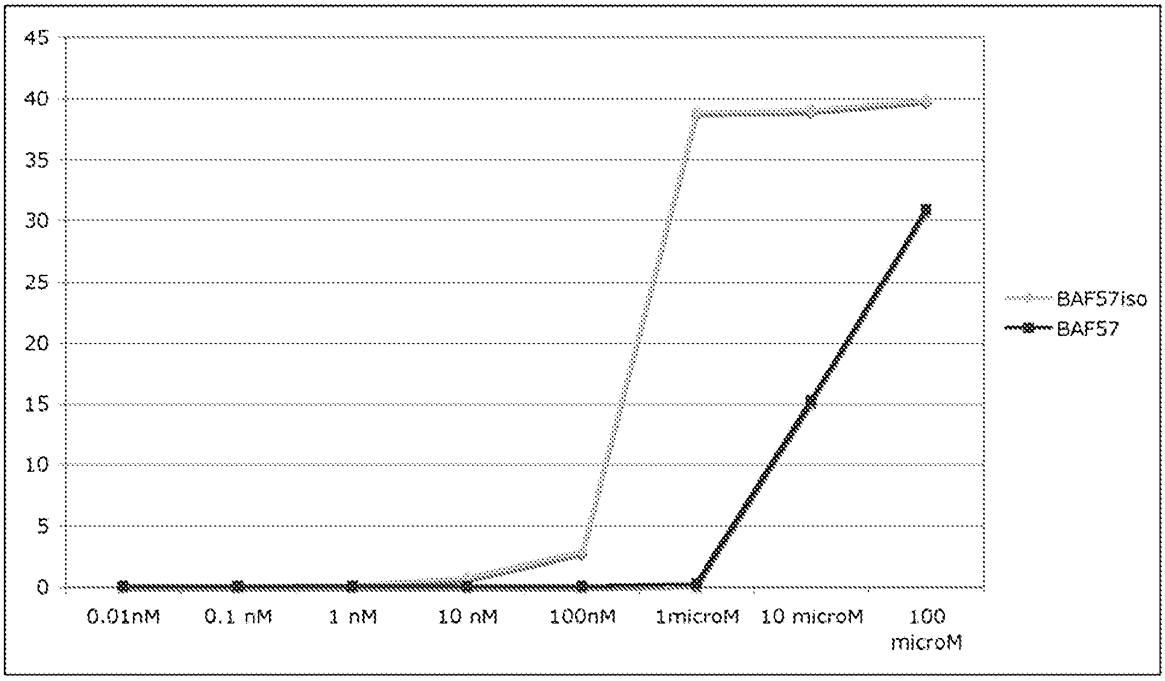

Figure 4

20082597792 07 May 2012

<110> ONCOTX, INC.

<120> CANCER RELATED ISOFORMS OF COMPONENTS OF TRANSCRIPTION FACTOR COMPLEXES AS BIOMARKERS AND DRUG TARGETS

<130> ONC.2-WO-U2

<140>
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<150> 60/941,747
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<170> PatentIn version 3.3

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<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 1
Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 2
<211> 7
<212> PRT
<213> Artificial Sequence

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

<400> 2
Pro Pro Lys Lys Arg Lys Val
1 5

<210> 3
<211> 6
<212> PRT
<213> Artificial Sequence

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

<400> 3
Pro Lys Lys Arg Lys Val
1 5

<210> 4
<211> 584
<212> PRT
<213> Homo sapiens

<400> 4

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Met Lys Ala Gln Gly Glu Thr Glu Glu Ser Glu Lys Leu Ser Lys Met
1               5                  10                  15

Ser Ser Leu Leu Glu Arg Leu His Ala Lys Phe Asn Gln Asn Arg Pro
            20                  25                  30

Trp Ser Glu Thr Ile Lys Leu Val Arg Gln Val Met Glu Lys Arg Val
        35                  40                  45

Val Met Ser Ser Gly Gly His Gln His Leu Val Ser Cys Leu Glu Thr
    50                  55                  60

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

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

Ser Gly Thr Glu Cys Tyr Ile Thr Ser Asp Met Phe Tyr Val Glu Val
            100                 105                 110

Gln Leu Asp Pro Ala Gly Gln Leu Cys Asp Val Lys Val Ala His His
        115                 120                 125

Gly Glu Asn Pro Val Ser Cys Pro Glu Leu Val Gln Gln Leu Arg Glu
    130                 135                 140

Lys Asn Phe Asp Glu Phe Ser Lys His Leu Lys Gly Leu Val Asn Leu
145                 150                 155                 160

Tyr Asn Leu Pro Gly Asp Asn Lys Leu Lys Thr Lys Met Tyr Leu Ala
                165                 170                 175

Leu Gln Ser Leu Glu Gln Asp Leu Ser Lys Met Ala Ile Met Tyr Trp
            180                 185                 190

Lys Ala Thr Asn Ala Gly Pro Leu Asp Lys Ile Leu His Gly Ser Val
        195                 200                 205

Gly Tyr Leu Thr Pro Arg Ser Gly Gly His Leu Met Asn Leu Lys Tyr
    210                 215                 220

Tyr Val Ser Pro Ser Asp Leu Leu Asp Asp Lys Thr Ala Ser Pro Ile
225                 230                 235                 240

Ile Leu His Glu Asn Asn Val Ser Arg Ser Leu Gly Met Asn Ala Ser
                245                 250                 255

Val Thr Ile Glu Gly Thr Ser Ala Val Tyr Lys Leu Pro Ile Ala Pro
            260                 265                 270
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Leu Ile Met Gly Ser His Pro Val Asp Asn Lys Trp Thr Pro Ser Phe
275 280 285

Ser Ser Ile Thr Ser Ala Asn Ser Val Asp Leu Pro Ala Cys Phe Phe
290 295 300

Leu Lys Phe Pro Gln Pro Ile Pro Val Ser Arg Ala Phe Val Gln Lys
305 310 315 320

Leu Gln Asn Cys Thr Gly Ile Pro Leu Phe Glu Thr Gln Pro Thr Tyr
325 330 335

Ala Pro Leu Tyr Glu Leu Ile Thr Gln Phe Glu Leu Ser Lys Asp Pro
340 345 350

Asp Pro Ile Pro Leu Asn His Asn Met Arg Phe Tyr Ala Ala Leu Pro
355 360 365

Gly Gln Gln His Cys Tyr Phe Leu Asn Lys Asp Ala Pro Leu Pro Asp
370 375 380

Gly Arg Ser Leu Gln Gly Thr Leu Val Ser Lys Ile Thr Phe Gln His
385 390 395 400

Pro Gly Arg Val Pro Leu Ile Leu Asn Leu Ile Arg His Gln Val Ala
405 410 415

Tyr Asn Thr Leu Ile Gly Ser Cys Val Lys Arg Thr Ile Leu Lys Glu
420 425 430

Asp Ser Pro Gly Leu Leu Gln Phe Glu Val Cys Pro Leu Ser Glu Ser
435 440 445

Arg Phe Ser Val Ser Phe Gln His Pro Val Asn Asp Ser Leu Val Cys
450 455 460

Val Val Met Asp Val Gln Asp Ser Thr His Val Ser Cys Lys Leu Tyr
465 470 475 480

Lys Gly Leu Ser Asp Ala Leu Ile Cys Thr Asp Asp Phe Ile Ala Lys
485 490 495

Val Val Gln Arg Cys Met Ser Ile Pro Val Thr Met Arg Ala Ile Arg
500 505 510

Arg Lys Ala Glu Thr Ile Gln Ala Asp Thr Pro Ala Leu Ser Leu Ile
515 520 525

Ala Glu Thr Val Glu Asp Met Val Lys Lys Asn Leu Pro Pro Ala Ser
530 535 540

Ser Pro Gly Glu Arg Gly Val Tyr His Trp Leu Glu Ser Asp Pro Ser

545 550 555 560

Ser Ser His Ala Ala Thr Cys Leu Phe Asp Gly Arg Gln His Gln Glu
565 570 575

Pro Pro Asp Ala His Glu Pro Ser
580

<210> 5
<211> 1008
<212> PRT
<213> Homo sapiens

<400> 5
Met Lys Val Val Asn Leu Lys Gln Ala Ile Leu Gln Ala Trp Lys Glu
1 5 10 15

Arg Trp Ser Asp Tyr Gln Trp Ala Ile Asn Met Lys Lys Phe Phe Pro
20 25 30

Lys Gly Ala Thr Trp Asp Ile Leu Asn Leu Ala Asp Ala Leu Leu Glu
35 40 45

Gln Ala Met Ile Gly Pro Ser Pro Asn Pro Leu Ile Leu Ser Tyr Leu
50 55 60

Lys Tyr Ala Ile Ser Ser Gln Met Val Ser Tyr Ser Ser Val Leu Thr
65 70 75 80

Ala Ile Ser Lys Phe Asp Asp Phe Ser Arg Asp Leu Cys Val Gln Ala
85 90 95

Leu Leu Asp Ile Met Asp Met Phe Cys Asp Arg Leu Ser Cys His Gly
100 105 110

Lys Ala Glu Glu Cys Ile Gly Leu Cys Arg Ala Leu Leu Ser Ala Leu
115 120 125

His Trp Leu Leu Arg Cys Thr Ala Ala Ser Ala Glu Arg Leu Arg Glu
130 135 140

Gly Leu Glu Ala Gly Thr Pro Ala Ala Gly Glu Lys Gln Leu Ala Met
145 150 155 160

Cys Leu Gln Arg Leu Glu Lys Thr Leu Ser Ser Thr Lys Asn Arg Ala
165 170 175

Leu Leu His Ile Ala Lys Leu Glu Glu Ala Ser Leu His Thr Ser Gln
180 185 190

Gly Leu Gly Gln Gly Gly Thr Arg Ala Asn Gln Pro Thr Ala Ser Trp
195 200 205

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Thr Ala Ile Glu His Ser Leu Leu Lys Leu Gly Glu Ile Leu Ala Asn
    210                 215                 220

Leu Ser Asn Pro Gln Leu Arg Ser Gln Ala Glu Gln Cys Gly Thr Leu
225                 230                 235                 240

Ile Arg Ser Ile Pro Thr Met Leu Ser Val His Ala Glu Gln Met His
                245                 250                 255

Lys Thr Gly Phe Pro Thr Val His Ala Val Ile Leu Leu Glu Gly Thr
            260                 265                 270

Met Asn Leu Thr Gly Glu Thr Gln Ser Leu Val Glu Gln Leu Thr Met
        275                 280                 285

Val Lys Arg Met Gln His Ile Pro Thr Pro Leu Phe Val Leu Glu Ile
    290                 295                 300

Trp Lys Ala Cys Phe Val Gly Leu Ile Glu Ser Pro Glu Gly Thr Glu
305                 310                 315                 320

Glu Leu Lys Trp Thr Ala Phe Thr Phe Leu Lys Ile Pro Gln Val Leu
                325                 330                 335

Val Lys Leu Lys Lys Tyr Ser His Gly Asp Lys Asp Phe Thr Glu Asp
            340                 345                 350

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

Lys Ala Asp Gln Arg Cys Asn Cys Asp Cys Thr Asn Phe Leu Leu Gln
    370                 375                 380

Glu Cys Gly Lys Gln Gly Leu Leu Ser Glu Ala Ser Val Asn Asn Leu
385                 390                 395                 400

Met Ala Lys Arg Lys Ala Asp Arg Glu His Ala Pro Gln Gln Lys Ser
                405                 410                 415

Gly Glu Asn Ala Asn Ile Gln Pro Asn Ile Gln Leu Ile Leu Arg Ala
            420                 425                 430

Glu Pro Thr Val Thr Asn Ile Leu Lys Thr Met Asp Ala Asp His Ser
        435                 440                 445

Lys Ser Pro Glu Gly Leu Leu Gly Val Leu Gly His Met Leu Ser Gly
    450                 455                 460

Lys Ser Leu Asp Leu Leu Leu Ala Ala Ala Ala Ala Thr Gly Lys Leu
465                 470                 475                 480

Lys Ser Phe Ala Arg Lys Phe Ile Asn Leu Asn Glu Phe Thr Thr Tyr
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485 490 495

Gly Ser Glu Glu Ser Thr Lys Pro Ala Ser Val Arg Ala Leu Leu Phe
500 505 510

Asp Ile Ser Phe Leu Met Leu Cys His Val Ala Gln Thr Tyr Gly Ser
515 520 525

Glu Val Ile Leu Ser Glu Ser Arg Thr Gly Ala Glu Val Pro Phe Phe
530 535 540

Glu Thr Trp Met Gln Thr Cys Met Pro Glu Glu Gly Lys Ile Leu Asn
545 550 555 560

Pro Asp His Pro Cys Phe Arg Pro Asp Ser Thr Lys Val Glu Ser Leu
565 570 575

Val Ala Leu Leu Asn Asn Ser Ser Glu Met Lys Leu Val Gln Met Lys
580 585 590

Trp His Glu Ala Cys Leu Ser Ile Ser Ala Ala Ile Leu Glu Ile Leu
595 600 605

Asn Ala Trp Glu Asn Gly Val Leu Ala Phe Glu Ser Ile Gln Lys Ile
610 615 620

Thr Asp Asn Ile Lys Gly Lys Val Cys Ser Leu Ala Val Cys Ala Val
625 630 635 640

Ala Trp Leu Val Ala His Val Arg Met Leu Gly Leu Asp Glu Arg Glu
645 650 655

Lys Ser Leu Gln Met Ile Arg Gln Leu Ala Gly Pro Leu Phe Ser Glu
660 665 670

Asn Thr Leu Gln Phe Tyr Asn Glu Arg Val Val Ile Met Asn Ser Ile
675 680 685

Leu Glu Arg Met Cys Ala Asp Val Leu Gln Gln Thr Ala Thr Gln Ile
690 695 700

Lys Phe Pro Ser Thr Gly Val Asp Thr Met Pro Tyr Trp Asn Leu Leu
705 710 715 720

Pro Pro Lys Arg Pro Ile Lys Glu Val Leu Thr Asp Ile Phe Ala Lys
725 730 735

Val Leu Glu Lys Gly Trp Val Asp Ser Arg Ser Ile His Ile Phe Asp
740 745 750

Thr Leu Leu His Met Gly Gly Val Tyr Trp Phe Cys Asn Asn Leu Ile
755 760 765

Lys Glu Leu Leu Lys Glu Thr Arg Lys Glu His Thr Leu Arg Ala Val
770 775 780

Glu Leu Leu Tyr Ser Ile Phe Cys Leu Asp Met Gln Gln Val Thr Leu
785 790 795 800

Val Leu Leu Gly His Ile Leu Pro Gly Leu Leu Thr Asp Ser Ser Lys
805 810 815

Trp His Ser Leu Met Asp Pro Pro Gly Thr Ala Leu Ala Lys Leu Ala
820 825 830

Val Trp Cys Ala Leu Ser Ser Tyr Ser Ser His Lys Gly Gln Ala Ser
835 840 845

Thr Arg Gln Lys Lys Arg His Arg Glu Asp Ile Glu Asp Tyr Ile Ser
850 855 860

Leu Phe Pro Leu Asp Asp Val Gln Pro Ser Lys Leu Met Arg Leu Leu
865 870 875 880

Ser Ser Asn Glu Asp Asp Ala Asn Ile Leu Ser Ser Pro Thr Asp Arg
885 890 895

Ser Met Ser Ser Ser Leu Ser Ala Ser Gln Leu His Thr Val Asn Met
900 905 910

Arg Asp Pro Leu Asn Arg Val Leu Ala Asn Leu Phe Leu Leu Ile Ser
915 920 925

Ser Ile Leu Gly Ser Arg Thr Ala Gly Pro His Thr Gln Phe Val Gln
930 935 940

Trp Phe Met Glu Glu Cys Val Asp Cys Leu Glu Gln Gly Gly Arg Gly
945 950 955 960

Ser Val Leu Gln Phe Met Pro Phe Thr Thr Val Ser Glu Leu Val Lys
965 970 975

Val Ser Ala Met Ser Ser Pro Lys Val Val Leu Ala Ile Thr Asp Leu
980 985 990

Ser Leu Pro Leu Gly Arg Gln Val Ala Ala Lys Ala Ile Ala Ala Leu
995 1000 1005

<210> 6
<211> 33
<212> PRT
<213> Homo sapiens

<400> 6
Met Ala Tyr Gln Leu Tyr Arg Asn Thr Thr Leu Gly Asn Ser Leu Gln

1 5 10 15

Glu Ser Leu Asp Glu Leu Ile Gln Ile Leu Ala Pro Ile Leu Gln Asn
20 25 30

Glu

<210> 7
<211> 67
<212> PRT
<213> Homo sapiens

<400> 7
Met Ala Thr Ser Ser Glu Glu Val Leu Leu Ile Val Lys Lys Val Arg
1 5 10 15

Gln Lys Lys Gln Asp Gly Ala Leu Tyr Leu Met Ala Glu Arg Ile Ala
20 25 30

Trp Ala Pro Glu Gly Lys Asp Arg Phe Thr Ile Ser His Met Tyr Ala
35 40 45

Asp Ile Lys Cys Lys Ser Ala Ile Leu Ser Ser Asp Val Phe Val Cys
50 55 60

His Ser Cys
65

<210> 8
<211> 385
<212> PRT
<213> Homo sapiens

<400> 8
Met Ala Thr Ser Ser Glu Glu Val Leu Leu Ile Val Lys Lys Val Arg
1 5 10 15

Gln Lys Lys Gln Asp Gly Ala Leu Tyr Leu Met Ala Glu Arg Ile Ala
20 25 30

Trp Ala Pro Glu Gly Lys Asp Arg Phe Thr Ile Ser His Met Tyr Ala
35 40 45

Asp Ile Lys Cys Gln Lys Ile Ser Pro Glu Gly Lys Ala Lys Ile Gln
50 55 60

Leu Gln Leu Val Leu His Ala Gly Asp Thr Thr Asn Phe His Phe Ser
65 70 75 80

Asn Glu Ser Thr Ala Val Lys Glu Arg Asp Ala Val Lys Asp Leu Leu
85 90 95

Gln Gln Leu Leu Pro Lys Phe Lys Arg Lys Ala Asn Lys Glu Leu Glu
100 105 110

Glu Lys Asn Arg Met Leu Gln Glu Asp Pro Val Leu Phe Gln Leu Tyr
115 120 125

Lys Asp Leu Val Val Ser Gln Val Ile Ser Ala Glu Glu Phe Trp Ala
130 135 140

Asn Arg Leu Asn Val Asn Ala Thr Asp Ser Ser Ser Thr Ser Asn His
145 150 155 160

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

Gln Thr Asp Gly Cys Asn Gly Leu Arg Tyr Asn Leu Thr Ser Asp Ile
180 185 190

Ile Glu Ser Ile Phe Arg Thr Tyr Pro Ala Val Lys Met Lys Tyr Ala
195 200 205

Glu Asn Val Pro His Asn Met Thr Glu Lys Glu Phe Trp Thr Arg Phe
210 215 220

Phe Gln Ser His Tyr Phe His Arg Asp Arg Leu Asn Thr Gly Ser Lys
225 230 235 240

Asp Leu Phe Ala Glu Cys Ala Lys Ile Asp Glu Lys Gly Leu Lys Thr
245 250 255

Met Val Ser Leu Gly Val Lys Asn Pro Leu Leu Asp Leu Thr Ala Leu
260 265 270

Glu Asp Lys Pro Leu Asp Glu Gly Tyr Gly Ile Ser Ser Val Pro Ser
275 280 285

Ala Ser Asn Ser Lys Ser Ile Lys Glu Asn Ser Asn Ala Ala Ile Ile
290 295 300

Lys Arg Phe Asn His His Ser Ala Met Val Leu Ala Ala Gly Leu Arg
305 310 315 320

Lys Gln Glu Ala Gln Asn Glu Gln Thr Ser Glu Pro Ser Asn Met Asp
325 330 335

Gly Asn Ser Gly Asp Ala Asp Cys Phe Gln Pro Ala Val Lys Arg Val
340 345 350

Trp Ala Lys Lys Tyr Glu Pro Phe Gly Ala Gln Val Ser Pro Asn Thr
355 360 365

Leu Cys Asp Cys Lys Tyr Cys Ile Arg Leu Phe Pro Val Thr Gln Phe
370 375 380

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Phe
385

<210> 9
<211> 132
<212> PRT
<213> Homo sapiens

<400> 9
Met Ala Thr Ser Ser Glu Glu Val Leu Leu Ile Val Lys Lys Val Arg
1 5 10 15

Gln Lys Lys Gln Asp Gly Ala Leu Tyr Leu Met Ala Glu Arg Ile Ala
20 25 30

Trp Ala Pro Glu Gly Lys Asp Arg Phe Thr Ile Ser His Met Tyr Ala
35 40 45

Asp Ile Lys Cys Gln Lys Ile Leu Arg His Phe Trp Ser Cys Phe Pro
50 55 60

Val Asn Thr Pro Phe Leu Glu Glu Lys Val Val Lys Met Lys Ser Asn
65 70 75 80

Leu Glu Arg Phe Gln Val Thr Lys Leu Cys Pro Phe Gln Glu Lys Ile
85 90 95

Arg Arg Gln Tyr Leu Ser Thr Asn Leu Val Ser His Ile Glu Glu Met
100 105 110

Leu Gln Thr Ala Tyr Asn Lys Leu His Thr Trp Gln Ser Arg Arg Leu
115 120 125

Met Lys Lys Thr
130

<210> 10
<211> 56
<212> PRT
<213> Homo sapiens

<400> 10
Met Lys Ser Asn Leu Glu Arg Phe Gln Val Thr Lys Leu Cys Pro Phe
1 5 10 15

Gln Glu Lys Ile Arg Arg Gln Tyr Leu Ser Thr Asn Leu Val Ser His
20 25 30

Ile Glu Glu Met Leu Gln Thr Ala Tyr Asn Lys Leu His Thr Trp Gln
35 40 45

Ser Arg Arg Leu Met Lys Lys Thr
50 55

<210> 11
<211> 108
<212> PRT
<213> Homo sapiens

<400> 11
Met Gln Gly Gly Thr Gln Gln Ala Ile Asn Gln Met Val Pro Asn Asp
1 5 10 15

Ile Gln Ser Glu Leu Lys His Leu Tyr Val Ala Val Gly Glu Leu Leu
20 25 30

Arg His Phe Trp Ser Cys Phe Pro Val Asn Thr Pro Phe Leu Glu Glu
35 40 45

Lys Val Val Lys Met Lys Ser Asn Leu Glu Arg Phe Gln Val Thr Lys
50 55 60

Leu Cys Pro Phe Gln Glu Lys Ile Arg Arg Gln Tyr Leu Ser Thr Asn
65 70 75 80

Leu Val Ser His Ile Glu Glu Met Leu Gln Thr Ala Tyr Asn Lys Leu
85 90 95

His Thr Trp Gln Ser Arg Arg Leu Met Lys Lys Thr
100 105

<210> 12
<211> 165
<212> PRT
<213> Homo sapiens

<400> 12
Met Asp Glu Glu Pro Glu Arg Thr Lys Arg Trp Glu Gly Gly Tyr Glu
1 5 10 15

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

Thr Ile Glu Asp Ile Leu Phe Lys Ala Lys Arg Lys Arg Val Phe Glu
35 40 45

His His Gly Gln Val Arg Leu Gly Met Met Arg His Leu Tyr Val Val
50 55 60

Val Asp Gly Ser Arg Thr Met Glu Asp Gln Asp Leu Lys Pro Asn Arg
65 70 75 80

Leu Thr Cys Thr Leu Lys Leu Leu Glu Tyr Phe Val Glu Glu Tyr Phe
85 90 95

Asp Gln Asn Pro Ile Ser Gln Ile Gly Ile Ile Val Thr Lys Ser Lys
100 105 110

Arg Ala Glu Lys Leu Thr Glu Leu Ser Gly Asn Pro Arg Lys His Ile

115 120 125

Thr Ser Leu Lys Lys Ala Val Asp Met Thr Cys His Gly Glu Pro Ser
130 135 140

Leu Tyr Asn Ser Leu Ser Ile Ala Met Gln Thr Leu Lys Leu Val Leu
145 150 155 160

Tyr Ile Met Tyr Asn
165

<210> 13
<211> 209
<212> PRT
<213> Homo sapiens

<400> 13
Met Asp Glu Glu Pro Glu Arg Thr Lys Arg Trp Glu Gly Gly Tyr Glu
1 5 10 15

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

Thr Ile Glu Asp Ile Leu Phe Lys Ala Lys Arg Lys Arg Val Phe Glu
35 40 45

His His Gly Gln Val Arg Leu Gly Met Met Arg His Leu Tyr Val Val
50 55 60

Val Asp Gly Ser Arg Thr Met Glu Asp Gln Asp Leu Lys Pro Asn Arg
65 70 75 80

Leu Thr Cys Thr Leu Lys Leu Leu Glu Tyr Phe Val Glu Glu Tyr Phe
85 90 95

Asp Gln Asn Pro Ile Ser Gln Ile Gly Ile Ile Val Thr Lys Ser Lys
100 105 110

Arg Ala Glu Lys Leu Thr Glu Leu Ser Gly Asn Pro Arg Lys His Ile
115 120 125

Thr Ser Leu Lys Lys Ala Val Asp Met Thr Cys His Gly Glu Pro Ser
130 135 140

Leu Tyr Asn Ser Leu Ser Ile Ala Met Gln Thr Leu Lys Phe Cys Tyr
145 150 155 160

Gly Cys Gln Gly Glu Leu Lys Asp Gln His Val Tyr Val Cys Ala Val
165 170 175

Cys Gln Asn Val Phe Cys Val Asp Cys Asp Val Phe Val His Asp Ser
180 185 190

Leu His Cys Cys Pro Gly Cys Ile His Lys Ile Pro Ala Pro Ser Gly
195 200 205

Val

<210> 14
<211> 96
<212> PRT
<213> Homo sapiens

<400> 14
Met Asp Glu Glu Pro Glu Arg Thr Lys Arg Trp Glu Gly Gly Tyr Glu
1 5 10 15

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

Thr Ile Glu Asp Ile Leu Phe Lys Ala Lys Arg Lys Arg Val Phe Glu
35 40 45

His His Gly Gln Val Arg Leu Gly Met Val Tyr Val Cys Ala Val Cys
50 55 60

Gln Asn Val Phe Cys Val Asp Cys Asp Val Phe Val His Asp Ser Leu
65 70 75 80

His Cys Cys Pro Gly Cys Ile His Lys Ile Pro Ala Pro Ser Gly Val
85 90 95

<210> 15
<211> 140
<212> PRT
<213> Homo sapiens

<400> 15
Met Asp Glu Glu Pro Glu Arg Thr Lys Arg Trp Glu Gly Gly Tyr Glu
1 5 10 15

Arg Thr Trp His Leu Asp Gly Asn Thr Glu Pro Gly Leu Thr Leu Gly
20 25 30

Gly Tyr Phe Cys Pro Gln Cys Arg Ala Lys Tyr Cys Glu Leu Pro Val
35 40 45

Glu Cys Lys Ile Cys Gly Leu Thr Leu Val Ser Ala Pro His Leu Ala
50 55 60

Arg Ser Tyr His His Leu Phe Pro Leu Asp Ala Phe Gln Glu Ile Pro
65 70 75 80

Leu Glu Glu Tyr Asn Gly Glu Arg Phe Cys Tyr Gly Cys Gln Gly Glu
85 90 95

Leu Lys Asp Gln His Val Tyr Val Cys Ala Val Cys Gln Asn Val Phe

100 105 110

Cys Val Asp Cys Asp Val Phe Val His Asp Ser Leu His Cys Cys Pro
115 120 125

Gly Cys Ile His Lys Ile Pro Ala Pro Ser Gly Val
130 135 140

<210> 16
<211> 165
<212> PRT
<213> Homo sapiens

<400> 16
Met Asp Glu Glu Pro Glu Arg Thr Lys Arg Trp Glu Gly Gly Tyr Glu
1 5 10 15

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

Thr Ile Glu Asp Ile Leu Phe Lys Ala Lys Arg Lys Arg Val Phe Glu
35 40 45

His His Gly Gln Val Arg Leu Gly Met Met Arg His Leu Tyr Val Val
50 55 60

Val Asp Gly Ser Arg Thr Met Glu Asp Gln Asp Leu Lys Pro Asn Arg
65 70 75 80

Leu Thr Cys Thr Leu Lys Leu Leu Glu Tyr Phe Val Glu Glu Tyr Phe
85 90 95

Asp Gln Asn Pro Ile Ser Gln Ile Gly Ile Ile Val Thr Lys Ser Lys
100 105 110

Arg Ala Glu Lys Leu Thr Glu Leu Ser Gly Asn Pro Arg Lys His Ile
115 120 125

Thr Ser Leu Lys Lys Ala Val Asp Met Thr Cys His Gly Glu Pro Ser
130 135 140

Leu Tyr Asn Ser Leu Ser Ile Ala Met Gln Thr Leu Lys Leu Val Leu
145 150 155 160

Tyr Ile Met Tyr Asn
165

<210> 17
<211> 155
<212> PRT
<213> Homo sapiens

<400> 17
Met Asp Glu Glu Pro Glu Arg Thr Lys Arg Trp Glu Gly Gly Tyr Glu
1 5 10 15

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

Thr Ile Glu Asp Ile Leu Phe Lys Ala Lys Arg Lys Arg Val Phe Glu
35 40 45

His His Gly Gln Val Arg Leu Gly Met Met Arg His Leu Tyr Val Val
50 55 60

Val Asp Gly Ser Arg Thr Met Glu Asp Gln Asp Leu Lys Pro Asn Arg
65 70 75 80

Leu Thr Cys Thr Leu Lys Leu Leu Glu Tyr Phe Val Glu Glu Tyr Phe
85 90 95

Asp Gln Asn Pro Ile Ser Gln Ile Gly Ile Ile Val Thr Lys Ser Lys
100 105 110

Arg Ala Glu Lys Leu Thr Glu Leu Ser Asp Gly Val Leu Leu Cys Arg
115 120 125

Gln Ala Arg Val Gln Trp His Asn Phe Gly Ser Leu Gln Ser Pro Pro
130 135 140

His Gly Phe Lys Arg Phe Pro Ala Ser Ala Ser
145 150 155

<210> 18
<211> 267
<212> PRT
<213> Homo sapiens

<400> 18
Met Val Leu Gly Asn Ser His Leu Phe Met Asn Arg Ser Asn Lys Leu
1 5 10 15

Ala Val Ile Ala Ser His Ile Gln Glu Ser Arg Phe Leu Tyr Pro Gly
20 25 30

Lys Asn Gly Arg Leu Gly Asp Phe Phe Gly Asp Pro Gly Asn Pro Pro
35 40 45

Glu Phe Asn Pro Ser Gly Ser Lys Asp Gly Lys Tyr Glu Leu Leu Thr
50 55 60

Ser Ala Asn Glu Val Ile Val Glu Glu Ile Lys Asp Leu Met Thr Lys
65 70 75 80

Ser Asp Ile Lys Gly Gln His Thr Glu Thr Leu Leu Ala Gly Ser Leu
85 90 95

Ala Lys Ala Leu Cys Tyr Ile His Arg Met Asn Lys Glu Val Lys Asp

100 105 110

Asn Gln Glu Met Lys Ser Arg Ile Leu Val Ile Lys Ala Ala Glu Asp
115 120 125

Ser Ala Leu Gln Tyr Met Asn Phe Met Asn Val Ile Phe Ala Ala Gln
130 135 140

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

Leu Leu Gln Gln Ala Cys Asp Ile Thr Gly Gly Leu Tyr Leu Lys Val
165 170 175

Pro Gln Met Pro Ser Leu Leu Gln Tyr Leu Leu Trp Val Phe Leu Pro
180 185 190

Asp Gln Asp Gln Arg Ser Gln Leu Ile Leu Pro Pro Pro Val His Val
195 200 205

Asp Tyr Arg Ala Ala Cys Phe Cys His Arg Asn Leu Ile Glu Ile Gly
210 215 220

Tyr Val Cys Ser Val Cys Leu Ser Ile Phe Cys Asn Phe Ser Pro Ile
225 230 235 240

Cys Thr Thr Cys Glu Thr Ala Phe Lys Ile Ser Leu Pro Pro Val Leu
245 250 255

Lys Ala Lys Lys Lys Lys Leu Lys Val Ser Ala
260 265

<210> 19
<211> 265
<212> PRT
<213> Homo sapiens

<400> 19
Met Val Ser Asp Glu Asp Glu Leu Asn Leu Leu Val Ile Val Val Asp
1 5 10 15

Ala Asn Pro Ile Trp Trp Gly Lys Gln Ala Leu Lys Glu Ser Gln Phe
20 25 30

Thr Leu Ser Lys Cys Ile Asp Ala Val Met Val Leu Gly Asn Ser His
35 40 45

Leu Phe Met Asn Arg Ser Asn Lys Leu Ala Val Ile Ala Ser His Ile
50 55 60

Gln Glu Ser Arg Phe Leu Tyr Pro Gly Lys Asn Gly Arg Leu Gly Asp
65 70 75 80

Phe Phe Gly Asp Pro Gly Asn Pro Pro Glu Phe Asn Pro Ser Gly Ser
85 90 95

Lys Asp Gly Lys Tyr Glu Leu Leu Thr Ser Ala Asn Glu Val Ile Val
100 105 110

Glu Glu Ile Lys Asp Leu Met Thr Lys Ser Asp Ile Lys Gly Gln His
115 120 125

Thr Glu Thr Leu Leu Ala Gly Ser Leu Ala Lys Ala Leu Cys Tyr Ile
130 135 140

His Arg Met Asn Lys Glu Val Lys Asp Asn Gln Glu Met Lys Ser Arg
145 150 155 160

Ile Leu Ala Cys Asp Ile Thr Gly Gly Leu Tyr Leu Lys Val Pro Gln
165 170 175

Met Pro Ser Leu Leu Gln Tyr Leu Leu Trp Val Phe Leu Pro Asp Gln
180 185 190

Asp Gln Arg Ser Gln Leu Ile Leu Pro Pro Pro Val His Val Asp Tyr
195 200 205

Arg Ala Ala Cys Phe Cys His Arg Asn Leu Ile Glu Ile Gly Tyr Val
210 215 220

Cys Ser Val Cys Leu Ser Ile Phe Cys Asn Phe Ser Pro Ile Cys Thr
225 230 235 240

Thr Cys Glu Thr Ala Phe Lys Ile Ser Leu Pro Pro Val Leu Lys Ala
245 250 255

Lys Lys Lys Lys Leu Lys Val Ser Ala
260 265

<210> 20
<211> 109
<212> PRT
<213> Homo sapiens

<400> 20
Met Val Ser Asp Glu Asp Glu Leu Asn Leu Leu Val Ile Val Val Asp
1 5 10 15

Ala Asn Pro Ile Trp Trp Gly Lys Gln Ala Leu Lys Glu Ser Gln Phe
20 25 30

Thr Leu Ser Lys Cys Ile Asp Ala Val Met Val Leu Gly Asn Ser His
35 40 45

Leu Phe Met Asn Arg Ser Asn Lys Leu Ala Val Ile Ala Ser His Ile
50 55 60

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Gln Glu Ser Arg Phe Leu Tyr Pro Gly Phe Thr Pro Phe Ser Cys Leu
65 70 75 80

Ser Leu Pro Ser Ser Trp Asp Tyr Tyr Ser Thr Glu Pro Met Arg Gln
85 90 95

Lys Phe Glu Thr Ile Leu Pro Asn Val Val Lys Thr Trp
100 105

<210> 21
<211> 95
<212> PRT
<213> Homo sapiens

<400> 21
Met Val Ser Asp Glu Asp Glu Leu Asn Leu Leu Val Ile Val Val Asp
1 5 10 15

Ala Asn Pro Ile Trp Trp Gly Lys Gln Ala Leu Lys Glu Ser Gln Phe
20 25 30

Thr Leu Ser Lys Cys Ile Asp Ala Val Met Val Leu Gly Asn Ser His
35 40 45

Leu Phe Met Asn Arg Ser Asn Lys Leu Ala Val Ile Ala Ser His Ile
50 55 60

Gln Glu Ser Arg Phe Leu Tyr Pro Gly Lys Asn Gly Arg Leu Gly Asp
65 70 75 80

Phe Phe Gly Asp Pro Gly Asn Pro Pro Glu Ser Gly Ser Ser Leu
85 90 95

<210> 22
<211> 243
<212> PRT
<213> Homo sapiens

<400> 22
Met Val Ser Asp Glu Asp Glu Leu Asn Leu Leu Val Ile Val Val Asp
1 5 10 15

Ala Asn Pro Ile Trp Trp Gly Lys Gln Ala Leu Lys Glu Ser Gln Phe
20 25 30

Thr Leu Ser Lys Cys Ile Asp Ala Val Met Val Leu Gly Asn Ser His
35 40 45

Leu Phe Met Asn Arg Ser Asn Lys Leu Ala Val Ile Ala Ser His Ile
50 55 60

Gln Glu Ser Arg Phe Leu Tyr Pro Gly Lys Asn Gly Arg Leu Gly Asp
65 70 75 80

Phe Phe Gly Asp Pro Gly Asn Pro Pro Glu Phe Asn Pro Ser Gly Ser
85 90 95

Lys Asp Gly Lys Tyr Glu Leu Leu Thr Ser Ala Asn Glu Val Ile Val
100 105 110

Glu Glu Ile Lys Asp Leu Met Thr Lys Ser Asp Ile Lys Gly Gln His
115 120 125

Thr Glu Thr Leu Leu Ala Gly Ser Leu Ala Lys Ala Leu Cys Tyr Ile
130 135 140

His Arg Met Asn Lys Glu Val Lys Asp Asn Gln Glu Met Lys Ser Arg
145 150 155 160

Ile Leu Val Ile Lys Ala Ala Glu Asp Ser Ala Leu Gln Tyr Met Asn
165 170 175

Phe Met Asn Val Ile Phe Ala Ala Gln Lys Gln Asn Ile Leu Ile Asp
180 185 190

Ala Cys Val Leu Asp Ser Asp Ser Gly Leu Leu Gln Gln Ala Cys Asp
195 200 205

Ile Thr Gly Gly Leu Tyr Leu Lys Val Pro Gln Met Pro Ser Leu Leu
210 215 220

Gln Tyr Leu Leu Trp Val Phe Leu Pro Asp Gln Asp Gln Arg Ser Gln
225 230 235 240

Pro Pro Lys

<210> 23
<211> 119
<212> PRT
<213> Homo sapiens

<400> 23
Met Val Ser Asp Glu Asp Glu Leu Asn Leu Leu Val Ile Val Val Asp
1 5 10 15

Ala Asn Pro Thr Trp Trp Gly Lys Gln Ala Leu Lys Glu Ser Gln Phe
20 25 30

Thr Leu Ser Lys Cys Ile Asp Ala Val Met Val Leu Gly Asn Ser His
35 40 45

Leu Phe Met Asn Arg Ser Asn Lys Leu Ala Val Ile Ala Ser His Ile
50 55 60

Gln Glu Ser Arg Phe Leu Tyr Pro Gly Lys Asn Gly Arg Leu Gly Asp
65 70 75 80

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Phe Phe Gly Asp Pro Gly Asn Pro Pro Glu Phe Asn Pro Ser Gly Ser
85 90 95

Lys Asp Gly Lys Tyr Glu Leu Leu Thr Ser Ala Ser Gln Val Ala Gly
100 105 110

Ile Thr Thr Leu Leu Asn Pro
115

<210> 24
<211> 34
<212> PRT
<213> Homo sapiens

<400> 24
Met Val Ser Asp Glu Asp Glu Leu Asn Leu Leu Val Ile Val Val Asp
1 5 10 15

Ala Asn Pro Ile Trp Trp Gly Lys Gln Ala Leu Lys Glu Ser Gln Pro
20 25 30

Pro Lys

<210> 25
<211> 41
<212> PRT
<213> Homo sapiens

<400> 25
Met Val Ser Asp Glu Asp Glu Leu Asn Leu Leu Val Ile Val Val Asp
1 5 10 15

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

Ala Gly Ile Thr Thr Leu Leu Asn Pro
35 40

<210> 26
<211> 227
<212> PRT
<213> Homo sapiens

<400> 26
Met Val Ser Asp Glu Asp Glu Leu Asn Leu Leu Val Ile Val Val Asp
1 5 10 15

Ala Asn Pro Ile Trp Trp Gly Lys Gln Ala Leu Lys Glu Ser Gln Phe
20 25 30

Thr Leu Ser Lys Cys Ile Asp Ala Val Met Val Leu Gly Asn Ser His
35 40 45

Leu Phe Met Asn Arg Ser Asn Lys Leu Ala Val Ile Ala Ser His Ile
50 55 60

Gln Glu Ser Arg Phe Leu Tyr Pro Gly Lys Asn Gly Arg Leu Gly Asp
65 70 75 80

Phe Phe Gly Asp Pro Gly Asn Pro Pro Glu Phe Asn Pro Ser Gly Ser
85 90 95

Lys Asp Gly Lys Tyr Glu Leu Leu Thr Ser Ala Asn Glu Val Ile Val
100 105 110

Glu Glu Ile Lys Asp Leu Met Thr Lys Ser Asp Ile Lys Gly Gln His
115 120 125

Thr Glu Thr Leu Leu Ala Gly Ser Leu Ala Lys Ala Leu Cys Tyr Ile
130 135 140

His Arg Met Asn Lys Glu Val Lys Asp Asn Gln Glu Met Lys Ser Arg
145 150 155 160

Ile Leu Ala Cys Asp Ile Thr Gly Gly Leu Tyr Leu Lys Val Pro Gln
165 170 175

Met Pro Ser Leu Leu Gln Tyr Leu Leu Trp Val Phe Leu Pro Asp Gln
180 185 190

Asp Gln Arg Ser Gln Leu Ser Leu Pro Ser Ser Trp Asp Tyr Tyr Ser
195 200 205

Thr Glu Pro Met Arg Gln Lys Phe Glu Thr Ile Leu Pro Asn Val Val
210 215 220

Lys Thr Trp
225

<210> 27
<211> 296
<212> PRT
<213> Homo sapiens

<400> 27
Met Val Ser Asp Glu Asp Glu Leu Asn Leu Leu Val Ile Val Val Asp
1 5 10 15

Ala Asn Pro Ile Trp Trp Gly Lys Gln Ala Leu Lys Glu Ser Gln Phe
20 25 30

Thr Leu Ser Lys Cys Ile Asp Ala Val Met Val Leu Gly Asn Ser His
35 40 45

Leu Phe Met Asn Arg Ser Asn Lys Leu Ala Val Ile Ala Ser His Ile
50 55 60

Gln Glu Ser Arg Phe Leu Tyr Pro Gly Lys Asn Gly Arg Leu Gly Asp

65 70 75 80

Phe Phe Gly Asp Pro Gly Asn Pro Pro Glu Phe Asn Pro Ser Gly Ser
85 90 95

Lys Asp Gly Lys Tyr Glu Leu Leu Thr Ser Ala Asn Glu Val Ile Val
100 105 110

Glu Glu Ile Lys Asp Leu Met Thr Lys Ser Asp Ile Lys Gly Gln His
115 120 125

Thr Glu Thr Leu Leu Ala Gly Ser Leu Ala Lys Ala Leu Cys Tyr Ile
130 135 140

His Arg Met Asn Lys Glu Val Lys Asp Asn Gln Glu Met Lys Ser Arg
145 150 155 160

Ile Leu Val Ile Lys Ala Ala Glu Asp Ser Ala Leu Gln Tyr Met Asn
165 170 175

Phe Met Asn Val Ile Phe Ala Ala Gln Lys Gln Asn Ile Leu Ile Asp
180 185 190

Ala Cys Val Leu Asp Ser Asp Ser Gly Leu Leu Gln Gln Ala Cys Asp
195 200 205

Ile Thr Gly Gly Leu Tyr Leu Lys Val Pro Gln Met Pro Ser Leu Leu
210 215 220

Gln Tyr Leu Leu Trp Val Phe Leu Pro Asp Gln Asp Gln Arg Ser Gln
225 230 235 240

Leu Ile Leu Pro Pro Pro Val His Val Asp Tyr Arg Ala Ala Cys Phe
245 250 255

Cys His Arg Asn Leu Ile Glu Ile Gly Tyr Val Cys Ser Val Cys Leu
260 265 270

Ser Ile Phe Cys Asn Phe Ser Pro Ile Cys Thr Thr Cys Glu Thr Ala
275 280 285

Phe Lys Ile Ser Gln Pro Pro Lys
290 295

<210> 28
<211> 202
<212> PRT
<213> Homo sapiens

<400> 28
Met Val Leu Gly Asn Ser His Leu Phe Met Asn Arg Ser Asn Lys Leu
1 5 10 15

Ala Val Ile Ala Ser His Ile Gln Glu Ser Arg Phe Leu Tyr Pro Gly
20 25 30

Lys Asn Gly Arg Leu Gly Asp Phe Phe Gly Asp Pro Gly Asn Pro Pro
35 40 45

Glu Phe Asn Pro Ser Gly Ser Lys Asp Gly Lys Tyr Glu Leu Leu Thr
50 55 60

Ser Ala Asn Glu Val Ile Val Glu Glu Ile Lys Asp Leu Met Thr Lys
65 70 75 80

Ser Asp Ile Lys Gly Gln His Thr Glu Thr Leu Leu Ala Gly Ser Leu
85 90 95

Ala Lys Ala Leu Cys Tyr Ile His Arg Met Asn Lys Glu Val Lys Asp
100 105 110

Asn Gln Glu Met Lys Ser Arg Ile Leu Val Ile Lys Ala Ala Glu Asp
115 120 125

Ser Ala Leu Gln Tyr Met Asn Phe Met Asn Val Ile Phe Ala Ala Gln
130 135 140

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

Leu Leu Gln Gln Ala Cys Asp Ile Thr Gly Gly Leu Tyr Leu Lys Val
165 170 175

Pro Gln Met Pro Ser Leu Leu Gln Tyr Leu Leu Trp Val Phe Leu Pro
180 185 190

Asp Gln Asp Gln Arg Ser Gln Pro Pro Lys
195 200

<210> 29
<211> 125
<212> PRT
<213> Homo sapiens

<400> 29
Met Val Ser Asp Glu Asp Glu Leu Asn Leu Leu Val Ile Val Val Asp
1 5 10 15

Ala Asn Pro Ile Trp Trp Gly Lys Gln Ala Leu Lys Glu Ser Gln Phe
20 25 30

Thr Leu Ser Lys Cys Ile Asp Ala Val Met Val Leu Gly Asn Ser His
35 40 45

Leu Phe Met Asn Arg Ser Asn Lys Leu Ala Val Ile Ala Ser His Ile
50 55 60

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Gln Glu Ser Arg Phe Leu Tyr Pro Gly Lys Asn Gly Arg Leu Gly Asp
65 70 75 80

Phe Phe Gly Asp Pro Gly Asn Pro Pro Glu Phe Asn Pro Ser Gly Ser
85 90 95

Lys Asp Gly Lys Tyr Glu Leu Leu Thr Ser Ala Asn Glu Val Ile Val
100 105 110

Glu Glu Ile Lys Asp Leu Met Thr Lys Ser Asn Asn Phe
115 120 125

<210> 30
<211> 84
<212> PRT
<213> Homo sapiens

<400> 30
Met Val Leu Gly Asn Ser His Leu Phe Met Asn Arg Ser Asn Lys Leu
1 5 10 15

Ala Val Ile Ala Ser His Ile Gln Glu Ser Arg Phe Leu Tyr Pro Gly
20 25 30

Lys Asn Gly Arg Leu Gly Asp Phe Phe Gly Asp Pro Gly Asn Pro Pro
35 40 45

Glu Phe Asn Pro Ser Gly Ser Lys Asp Gly Lys Tyr Glu Leu Leu Thr
50 55 60

Ser Ala Asn Glu Val Ile Val Glu Glu Ile Lys Asp Leu Met Thr Lys
65 70 75 80

Ser Asn Asn Phe

<210> 31
<211> 468
<212> PRT
<213> Homo sapiens

<400> 31
Met Arg Glu Arg Glu Val Met Glu Ser Thr Pro Ser Arg Gly Leu Asn
1 5 10 15

Arg Val His Leu Gln Cys Arg Asn Leu Gln Glu Phe Leu Gly Gly Leu
20 25 30

Ser Pro Gly Val Leu Asp Arg Leu Tyr Gly His Pro Ala Thr Cys Leu
35 40 45

Ala Val Phe Arg Glu Leu Pro Ser Leu Ala Lys Asn Trp Val Met Arg
50 55 60

Met Leu Phe Leu Glu Gln Pro Leu Pro Gln Ala Ala Val Ala Leu Trp
65 70 75 80

Val Lys Lys Glu Phe Ser Lys Ala Gln Glu Glu Ser Thr Gly Leu Leu
85 90 95

Ser Gly Leu Arg Ile Trp His Thr Gln Leu Leu Pro Gly Gly Leu Gln
100 105 110

Gly Leu Ile Leu Asn Pro Ile Phe Arg Gln Asn Leu Arg Ile Ala Leu
115 120 125

Leu Gly Gly Gly Lys Ala Trp Ser Asp Asp Thr Ser Gln Leu Gly Pro
130 135 140

Asp Lys His Ala Arg Asp Val Pro Ser Leu Asp Lys Tyr Ala Glu Glu
145 150 155 160

Arg Trp Glu Val Val Leu His Phe Met Val Gly Ser Pro Ser Ala Ala
165 170 175

Val Ser Gln Asp Leu Ala Gln Leu Leu Ser Gln Ala Gly Leu Met Lys
180 185 190

Ser Thr Glu Pro Gly Glu Pro Pro Cys Ile Thr Ser Ala Gly Phe Gln
195 200 205

Phe Leu Leu Leu Asp Thr Pro Ala Gln Leu Trp Tyr Phe Met Leu Gln
210 215 220

Tyr Leu Gln Thr Ala Gln Ser Arg Gly Met Asp Leu Val Glu Ile Leu
225 230 235 240

Ser Phe Leu Phe Gln Leu Ser Phe Ser Thr Leu Gly Lys Asp Tyr Ser
245 250 255

Val Glu Gly Met Ser Asp Ser Leu Leu Asn Phe Leu Gln His Leu Arg
260 265 270

Glu Phe Gly Leu Val Phe Gln Arg Lys Arg Lys Ser Arg Arg Tyr Tyr
275 280 285

Pro Thr Arg Leu Ala Ile Asn Leu Ser Ser Gly Val Ser Gly Ala Gly
290 295 300

Gly Thr Val His Gln Pro Gly Phe Ile Val Val Glu Thr Asn Tyr Arg
305 310 315 320

Leu Tyr Ala Tyr Thr Glu Ser Glu Leu Gln Ile Ala Leu Ile Ala Leu
325 330 335

Phe Ser Glu Met Leu Tyr Arg Phe Pro Asn Met Val Val Ala Gln Val

340 345 350

Thr Arg Glu Ser Val Gln Gln Ala Ile Ala Ser Gly Ile Thr Ala Gln
355 360 365

Gln Ile Ile His Phe Leu Arg Thr Arg Ala His Pro Val Met Leu Lys
370 375 380

Gln Thr Pro Val Leu Pro Pro Thr Ile Thr Asp Gln Ile Arg Leu Trp
385 390 395 400

Glu Leu Glu Arg Asp Arg Leu Arg Phe Thr Glu Gly Val Leu Tyr Asn
405 410 415

Gln Phe Leu Ser Gln Val Asp Phe Glu Leu Leu Leu Ala His Ala Arg
420 425 430

Glu Leu Gly Val Leu Val Phe Glu Asn Ser Ala Lys Arg Leu Met Val
435 440 445

Val Thr Pro Ala Gly His Ser Asp Val Lys Arg Phe Trp Lys Arg Gln
450 455 460

Lys His Ser Ser
465

<210> 32
<211> 22
<212> PRT
<213> Homo sapiens

<400> 32
Met Val Val Thr Pro Ala Gly His Ser Asp Val Lys Arg Phe Trp Lys
1 5 10 15

Arg Gln Lys His Ser Ser
20

<210> 33
<211> 87
<212> PRT
<213> Homo sapiens

<400> 33
Met Leu Lys Gln Thr Pro Val Leu Pro Pro Thr Ile Thr Asp Gln Ile
1 5 10 15

Arg Leu Trp Glu Leu Glu Arg Asp Arg Leu Arg Phe Thr Glu Gly Val
20 25 30

Leu Tyr Asn Gln Phe Leu Ser Gln Val Asp Phe Glu Leu Leu Leu Ala
35 40 45

His Ala Arg Glu Leu Gly Val Leu Val Phe Glu Asn Ser Ala Lys Arg
50 55 60

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Leu Met Val Val Thr Pro Ala Gly His Ser Asp Val Lys Arg Phe Trp
65 70 75 80

Lys Arg Gln Lys His Ser Ser
85

<210> 34
<211> 87
<212> PRT
<213> Homo sapiens

<400> 34
Met Leu Lys Gln Thr Pro Val Leu Pro Pro Thr Ile Thr Asp Gln Ile
1 5 10 15

Arg Leu Trp Glu Leu Glu Arg Asp Arg Leu Arg Phe Thr Glu Gly Val
20 25 30

Leu Tyr Asn Gln Phe Leu Ser Gln Val Asp Phe Glu Leu Leu Leu Ala
35 40 45

His Ala Arg Glu Leu Gly Val Leu Val Phe Glu Asn Ser Ala Lys Arg
50 55 60

Leu Met Val Val Thr Pro Ala Gly His Ser Asp Val Lys Arg Phe Trp
65 70 75 80

Lys Arg Gln Lys His Ser Ser
85

<210> 35
<211> 179
<212> PRT
<213> Homo sapiens

<400> 35
Met Glu Ser Thr Pro Ser Arg Gly Leu Asn Arg Val His Leu Gln Cys
1 5 10 15

Arg Asn Leu Gln Glu Phe Leu Gly Gly Leu Ser Pro Gly Val Leu Asp
20 25 30

Arg Leu Tyr Gly His Pro Ala Thr Cys Leu Ala Val Phe Arg Glu Phe
35 40 45

Pro Ser Leu Ala Lys Asn Trp Val Met Arg Met Leu Phe Leu Glu Gln
50 55 60

Pro Leu Pro Gln Ala Ala Val Ala Leu Trp Val Lys Lys Glu Phe Ser
65 70 75 80

Lys Ala Gln Glu Glu Ser Thr Gly Leu Leu Ser Gly Leu Arg Ile Trp
85 90 95

His Thr Gln Leu Leu Pro Gly Gly Leu Gln Gly Leu Ile Leu Asn Pro
100 105 110

Ile Phe Arg Gln Asn Leu Arg Ile Ala Pro Pro Ser Pro Thr Arg Ser
115 120 125

Gly Ser Gly Ser Trp Lys Gly Thr Asp Ser Gly Ser Leu Arg Val Ser
130 135 140

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

Thr Arg Gly Ser Trp Ala Cys Ser Cys Ser Arg Thr Arg Pro Ser Gly
165 170 175

Ser Trp Trp

<210> 36
<211> 281
<212> PRT
<213> Homo sapiens

<400> 36
Met Glu Ser Thr Pro Ser Arg Gly Leu Asn Arg Val His Leu Gln Cys
1 5 10 15

Arg Asn Leu Gln Glu Phe Leu Gly Gly Leu Ser Pro Gly Val Leu Asp
20 25 30

Arg Leu Tyr Gly His Pro Ala Thr Cys Leu Ala Val Phe Arg Glu Leu
35 40 45

Pro Ser Leu Ala Lys Asn Trp Val Met Arg Met Leu Phe Leu Glu Gln
50 55 60

Pro Leu Pro Gln Ala Ala Val Ala Leu Trp Val Lys Lys Glu Phe Ser
65 70 75 80

Lys Ala Gln Glu Glu Ser Thr Gly Leu Leu Ser Gly Leu Arg Ile Trp
85 90 95

His Thr Gln Leu Leu Pro Gly Gly Leu Gln Gly Leu Ile Leu Asn Pro
100 105 110

Ile Phe Arg Gln Asn Leu Arg Ile Ala Leu Leu Gly Gly Gly Lys Ala
115 120 125

Trp Ser Asp Asp Thr Ser Gln Leu Gly Pro Asp Lys His Ala Arg Asp
130 135 140

Val Pro Ser Leu Asp Lys Tyr Ala Glu Glu Arg Trp Glu Val Val Leu
145 150 155 160

His Phe Met Val Gly Ser Pro Ser Ala Ala Val Ser Gln Asp Leu Ala
165 170 175

Gln Leu Leu Ser Gln Ala Gly Leu Met Lys Ser Thr Glu Pro Gly Glu
180 185 190

Pro Pro Cys Ile Thr Ser Ala Gly Phe Gln Phe Leu Leu Leu Asp Thr
195 200 205

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

Gly Val Leu Tyr Asn Gln Phe Leu Ser Gln Val Asp Phe Glu Leu Leu
225 230 235 240

Leu Ala His Ala Arg Glu Leu Gly Val Leu Val Phe Glu Asn Ser Ala
245 250 255

Lys Arg Leu Met Val Val Thr Pro Ala Gly His Ser Asp Val Lys Arg
260 265 270

Phe Trp Lys Arg Gln Lys His Ser Ser
275 280

<210> 37
<211> 237
<212> PRT
<213> Homo sapiens

<400> 37
Met Glu Ser Thr Pro Ser Arg Gly Leu Asn Arg Val His Leu Gln Cys
1 5 10 15

Arg Asn Leu Gln Glu Phe Leu Gly Gly Leu Ser Pro Gly Val Leu Asp
20 25 30

Arg Leu Tyr Gly His Pro Ala Thr Cys Leu Ala Val Phe Arg Glu Leu
35 40 45

Pro Ser Leu Ala Lys Asn Trp Val Met Arg Met Leu Phe Leu Glu Gln
50 55 60

Pro Leu Pro Gln Ala Ala Val Ala Leu Trp Val Lys Lys Glu Phe Ser
65 70 75 80

Lys Ala Gln Glu Glu Ser Thr Gly Leu Leu Ser Gly Leu Arg Ile Trp
85 90 95

His Thr Gln Leu Leu Pro Gly Gly Leu Gln Gly Leu Ile Leu Asn Pro
100 105 110

Ile Phe Arg Gln Asn Leu Arg Ile Ala Leu Leu Gly Gly Gly Lys Ala

115 120 125

Trp Ser Asp Asp Thr Ser Gln Leu Gly Pro Asp Lys His Ala Arg Asp
130 135 140

Val Pro Ser Leu Asp Lys Tyr Ala Glu Glu Arg Trp Glu Val Val Leu
145 150 155 160

His Phe Met Val Gly Ser Pro Ser Ala Ala Val Ser Gln Asp Leu Ala
165 170 175

Gln Leu Leu Ser Gln Ala Gly Leu Met Lys Ser Thr Glu Pro Gly Glu
180 185 190

Pro Pro Cys Ile Thr Ser Ala Gly Phe Gln Phe Leu Leu Asp Thr
195 200 205

Pro Ala Gln Leu Trp Tyr Phe Met Leu Gln Tyr Leu Gln Thr Ala Arg
210 215 220

Ala Gln Arg Arg Gln Ala Leu Leu Glu Ala Ala Glu Thr
225 230 235

<210> 38
<211> 81
<212> PRT
<213> Homo sapiens

<400> 38
Met Glu Ser Thr Pro Ser Arg Gly Leu Asn Arg Val His Leu Gln Cys
1 5 10 15

Arg Asn Leu Gln Glu Phe Leu Gly Gly Leu Ser Pro Gly Val Leu Asp
20 25 30

Arg Leu Tyr Gly His Pro Ala Thr Cys Leu Ala Val Phe Arg Glu Leu
35 40 45

Pro Ser Leu Ala Lys Asn Trp Val Met Arg Met Leu Phe Leu Glu Gln
50 55 60

Pro Leu Pro Gln Ala Ala Val Ala Leu Trp Val Lys Lys Glu Phe Ser
65 70 75 80

Lys

<210> 39
<211> 46
<212> PRT
<213> Homo sapiens

<400> 39
Met Glu Ser Thr Pro Ser Arg Gly Leu Asn Arg Val His Leu Gln Cys
1 5 10 15

Arg Asn Leu Gln Glu Phe Leu Gly Gly Leu Ser Pro Gly Val Leu Asp
20 25 30

Arg Leu Tyr Gly His Pro Ala Thr Cys Leu Ala Val Phe Arg
35 40 45

<210> 40
<211> 81
<212> PRT
<213> Homo sapiens

<400> 40
Met Glu Ser Thr Pro Ser Arg Gly Leu Asn Arg Val His Leu Gln Cys
1 5 10 15

Arg Asn Leu Gln Glu Phe Leu Gly Gly Leu Ser Pro Gly Val Leu Asp
20 25 30

Arg Leu Tyr Gly His Pro Ala Thr Cys Leu Ala Val Phe Arg Glu Leu
35 40 45

Pro Ser Leu Ala Lys Asn Trp Val Met Arg Met Leu Phe Leu Glu Gln
50 55 60

Pro Leu Pro Gln Ala Ala Val Ala Leu Trp Val Lys Lys Glu Phe Ser
65 70 75 80

Lys

<210> 41
<211> 736
<212> PRT
<213> Homo sapiens

<400> 41
Met Arg Glu Leu Lys Arg Thr Leu Asp Ala Lys Gly His Gly Val Leu
1 5 10 15

Glu Met Pro Ser Gly Thr Gly Lys Thr Val Ser Leu Leu Ala Leu Ile
20 25 30

Met Ala Tyr Gln Arg Ala Tyr Pro Leu Glu Val Thr Lys Leu Ile Tyr
35 40 45

Cys Ser Arg Thr Val Pro Glu Ile Glu Lys Val Ile Glu Glu Leu Arg
50 55 60

Lys Leu Leu Asn Phe Tyr Glu Lys Gln Glu Gly Glu Lys Leu Pro Phe
65 70 75 80

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

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

Leu Thr Ala Ser Tyr Val Arg Ala Gln Tyr Gln His Asp Thr Ser Leu
115 120 125

Pro His Cys Arg Phe Tyr Glu Glu Phe Asp Ala His Gly Arg Glu Val
130 135 140

Pro Leu Pro Ala Gly Ile Tyr Asn Leu Asp Asp Leu Lys Ala Leu Gly
145 150 155 160

Arg Arg Gln Gly Trp Cys Pro Tyr Phe Leu Ala Arg Tyr Ser Ile Leu
165 170 175

His Ala Asn Val Val Val Tyr Ser Tyr His Tyr Leu Leu Asp Pro Lys
180 185 190

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

Phe Asp Glu Ala His Asn Ile Asp Asn Val Cys Ile Asp Ser Met Ser
210 215 220

Val Asn Leu Thr Arg Arg Thr Leu Asp Arg Cys Gln Gly Asn Leu Glu
225 230 235 240

Thr Leu Gln Lys Thr Val Leu Arg Ile Lys Glu Thr Asp Glu Gln Arg
245 250 255

Leu Arg Asp Glu Tyr Arg Arg Leu Val Glu Gly Leu Arg Glu Ala Ser
260 265 270

Ala Ala Arg Glu Thr Asp Ala His Leu Ala Asn Pro Val Leu Pro Asp
275 280 285

Glu Val Leu Gln Glu Ala Val Pro Gly Ser Ile Arg Thr Ala Glu His
290 295 300

Phe Leu Gly Phe Leu Arg Arg Leu Leu Glu Tyr Val Lys Trp Arg Leu
305 310 315 320

Arg Val Gln His Val Val Gln Glu Ser Pro Pro Ala Phe Leu Ser Gly
325 330 335

Leu Ala Gln Arg Val Cys Ile Gln Arg Lys Pro Leu Arg Phe Cys Ala
340 345 350

Glu Arg Leu Arg Ser Leu Leu His Thr Leu Glu Ile Thr Asp Leu Ala
355 360 365

Asp Phe Ser Pro Leu Thr Leu Leu Ala Asn Phe Ala Thr Leu Val Ser
370 375 380

Thr Tyr Ala Lys Gly Phe Thr Ile Ile Ile Glu Pro Phe Asp Asp Arg
385 390 395 400

Thr Pro Thr Ile Ala Asn Pro Ile Leu His Phe Ser Cys Met Asp Ala
405 410 415

Ser Leu Ala Ile Lys Pro Val Phe Glu Arg Phe Gln Ser Val Ile Ile
420 425 430

Thr Ser Gly Thr Leu Ser Pro Leu Asp Ile Tyr Pro Lys Ile Leu Asp
435 440 445

Phe His Pro Val Thr Met Ala Thr Phe Thr Met Thr Leu Ala Arg Val
450 455 460

Cys Leu Cys Pro Met Ile Ile Gly Arg Gly Asn Asp Gln Val Ala Ile
465 470 475 480

Ser Ser Lys Phe Glu Thr Arg Glu Asp Ile Ala Val Ile Arg Asn Tyr
485 490 495

Gly Asn Leu Leu Leu Glu Met Ser Ala Val Val Pro Asp Gly Ile Val
500 505 510

Ala Phe Phe Thr Ser Tyr Gln Tyr Met Glu Ser Thr Val Ala Ser Trp
515 520 525

Tyr Glu Gln Gly Ile Leu Glu Asn Ile Gln Arg Asn Lys Leu Leu Phe
530 535 540

Ile Glu Thr Gln Asp Gly Ala Glu Thr Ser Val Ala Leu Glu Lys Tyr
545 550 555 560

Gln Glu Ala Cys Glu Asn Gly Arg Gly Ala Ile Leu Leu Ser Val Ala
565 570 575

Arg Gly Lys Val Ser Glu Gly Ile Asp Phe Val His His Tyr Gly Arg
580 585 590

Ala Val Ile Met Phe Gly Val Pro Tyr Val Tyr Thr Gln Ser Arg Ile
595 600 605

Leu Lys Ala Arg Leu Glu Tyr Leu Arg Asp Gln Phe Gln Ile Arg Glu
610 615 620

Asn Asp Phe Leu Thr Phe Asp Ala Met Arg His Ala Ala Gln Cys Val
625 630 635 640

Gly Arg Ala Ile Arg Gly Lys Thr Asp Tyr Gly Leu Met Val Phe Ala

645 650 655

Asp Lys Arg Phe Ala Arg Gly Asp Lys Arg Gly Lys Leu Pro Arg Trp
660 665 670

Ile Gln Glu His Leu Thr Asp Ala Asn Leu Asn Leu Thr Val Asp Glu
675 680 685

Gly Val Gln Val Ala Lys Tyr Phe Leu Arg Gln Met Ala Gln Pro Phe
690 695 700

His Arg Glu Asp Gln Leu Gly Leu Ser Leu Leu Ser Leu Glu Gln Leu
705 710 715 720

Glu Ser Glu Glu Thr Leu Lys Arg Ile Glu Gln Ile Ala Gln Gln Leu
725 730 735

<210> 42
<211> 710
<212> PRT
<213> Homo sapiens

<400> 42
Met Arg Glu Leu Lys Arg Thr Leu Asp Ala Lys Ala Tyr Pro Leu Glu
1 5 10 15

Val Thr Lys Leu Ile Tyr Cys Ser Arg Thr Val Pro Glu Ile Glu Lys
20 25 30

Val Ile Glu Glu Leu Arg Lys Leu Leu Asn Phe Tyr Glu Lys Gln Glu
35 40 45

Gly Glu Lys Leu Pro Phe Leu Gly Leu Ala Leu Ser Ser Arg Lys Asn
50 55 60

Leu Cys Ile His Pro Glu Val Thr Pro Leu Arg Phe Gly Lys Asp Val
65 70 75 80

Asp Gly Lys Cys His Ser Leu Thr Ala Ser Tyr Val Arg Ala Gln Tyr
85 90 95

Gln His Asp Thr Ser Leu Pro His Cys Arg Phe Tyr Glu Glu Phe Asp
100 105 110

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

Asp Leu Lys Ala Leu Gly Arg Arg Gln Gly Trp Cys Pro Tyr Phe Leu
130 135 140

Ala Arg Tyr Ser Ile Leu His Ala Asn Val Val Val Tyr Ser Tyr His
145 150 155 160

Tyr Leu Leu Asp Pro Lys Ile Ala Asp Leu Val Ser Lys Glu Leu Ala
165 170 175

Arg Lys Ala Val Val Val Phe Asp Glu Ala His Asn Ile Asp Asn Val
180 185 190

Cys Ile Asp Ser Met Ser Val Asn Leu Thr Arg Arg Thr Leu Asp Arg
195 200 205

Cys Gln Gly Asn Leu Glu Thr Leu Gln Lys Thr Val Leu Arg Ile Lys
210 215 220

Glu Thr Asp Glu Gln Arg Leu Arg Asp Glu Tyr Arg Arg Leu Val Glu
225 230 235 240

Gly Leu Arg Glu Ala Ser Ala Ala Arg Glu Thr Asp Ala His Leu Ala
245 250 255

Asn Pro Val Leu Pro Asp Glu Val Leu Gln Glu Ala Val Pro Gly Ser
260 265 270

Ile Arg Thr Ala Glu His Phe Leu Gly Phe Leu Arg Arg Leu Leu Glu
275 280 285

Tyr Val Lys Trp Arg Leu Arg Val Gln His Val Val Gln Glu Ser Pro
290 295 300

Pro Ala Phe Leu Ser Gly Leu Ala Gln Arg Val Cys Ile Gln Arg Lys
305 310 315 320

Pro Leu Arg Phe Cys Ala Glu Arg Leu Arg Ser Leu Leu His Thr Leu
325 330 335

Glu Ile Thr Asp Leu Ala Asp Phe Ser Pro Leu Thr Leu Leu Ala Asn
340 345 350

Phe Ala Thr Leu Val Ser Thr Tyr Ala Lys Gly Phe Thr Ile Ile Ile
355 360 365

Glu Pro Phe Asp Asp Arg Thr Pro Thr Ile Ala Asn Pro Ile Leu His
370 375 380

Phe Ser Cys Met Asp Ala Ser Leu Ala Ile Lys Pro Val Phe Glu Arg
385 390 395 400

Phe Gln Ser Val Ile Ile Thr Ser Gly Thr Leu Ser Pro Leu Asp Ile
405 410 415

Tyr Pro Lys Ile Leu Asp Phe His Pro Val Thr Met Ala Thr Phe Thr
420 425 430

Met Thr Leu Ala Arg Val Cys Leu Cys Pro Met Ile Ile Gly Arg Gly

435 440 445

Asn Asp Gln Val Ala Ile Ser Ser Lys Phe Glu Thr Arg Glu Asp Ile
450 455 460

Ala Val Ile Arg Asn Tyr Gly Asn Leu Leu Leu Glu Met Ser Ala Val
465 470 475 480

Val Pro Asp Gly Ile Val Ala Phe Phe Thr Ser Tyr Gln Tyr Met Glu
485 490 495

Ser Thr Val Ala Ser Trp Tyr Glu Gln Gly Ile Leu Glu Asn Ile Gln
500 505 510

Arg Asn Lys Leu Leu Phe Ile Glu Thr Gln Asp Gly Ala Glu Thr Ser
515 520 525

Val Ala Leu Glu Lys Tyr Gln Glu Ala Cys Glu Asn Gly Arg Gly Ala
530 535 540

Ile Leu Leu Ser Val Ala Arg Gly Lys Val Ser Glu Gly Ile Asp Phe
545 550 555 560

Val His His Tyr Gly Arg Ala Val Ile Met Phe Gly Val Pro Tyr Val
565 570 575

Tyr Thr Gln Ser Arg Ile Leu Lys Ala Arg Leu Glu Tyr Leu Arg Asp
580 585 590

Gln Phe Gln Ile Arg Glu Asn Asp Phe Leu Thr Phe Asp Ala Met Arg
595 600 605

His Ala Ala Gln Cys Val Gly Arg Ala Ile Arg Gly Lys Thr Asp Tyr
610 615 620

Gly Leu Met Val Phe Ala Asp Lys Arg Phe Ala Arg Gly Asp Lys Arg
625 630 635 640

Gly Lys Leu Pro Arg Trp Ile Gln Glu His Leu Thr Asp Ala Asn Leu
645 650 655

Asn Leu Thr Val Asp Glu Gly Val Gln Val Ala Lys Tyr Phe Leu Arg
660 665 670

Gln Met Ala Gln Pro Phe His Arg Glu Asp Gln Leu Gly Leu Ser Leu
675 680 685

Leu Ser Leu Glu Gln Leu Glu Ser Glu Glu Thr Leu Lys Arg Ile Glu
690 695 700

Gln Ile Ala Gln Gln Leu
705 710

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<210> 43
<211> 736
<212> PRT
<213> Homo sapiens

<400> 43
Met Arg Glu Leu Lys Arg Thr Leu Asp Ala Lys Gly His Gly Val Leu
1 5 10 15

Glu Met Pro Ser Gly Thr Gly Lys Thr Val Ser Leu Leu Ala Leu Ile
20 25 30

Met Ala Tyr Gln Arg Ala Tyr Pro Leu Glu Val Thr Lys Leu Ile Tyr
35 40 45

Cys Ser Arg Thr Val Pro Glu Ile Glu Lys Val Ile Glu Glu Leu Arg
50 55 60

Lys Leu Leu Asn Phe Tyr Glu Lys Gln Glu Gly Glu Lys Leu Pro Phe
65 70 75 80

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

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

Leu Thr Ala Ser Tyr Val Arg Ala Gln Tyr Gln His Asp Thr Ser Leu
115 120 125

Pro His Cys Arg Phe Tyr Glu Glu Phe Asp Ala His Gly Arg Glu Val
130 135 140

Pro Leu Pro Ala Gly Ile Tyr Asn Leu Asp Asp Leu Lys Ala Leu Gly
145 150 155 160

Arg Arg Gln Gly Trp Cys Pro Tyr Phe Leu Ala Arg Tyr Ser Ile Leu
165 170 175

His Ala Asn Val Val Val Tyr Ser Tyr His Tyr Leu Leu Asp Pro Lys
180 185 190

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

Phe Asp Glu Ala His Asn Ile Asp Asn Val Cys Ile Asp Ser Met Ser
210 215 220

Val Asn Leu Thr Arg Arg Thr Leu Asp Arg Cys Gln Gly Asn Leu Glu
225 230 235 240

Thr Leu Gln Lys Thr Val Leu Arg Ile Lys Glu Thr Asp Glu Gln Arg

245 250 255

Leu Arg Asp Glu Tyr Arg Arg Leu Val Glu Gly Leu Arg Glu Ala Ser
260 265 270

Ala Ala Arg Glu Thr Asp Ala His Leu Ala Asn Pro Val Leu Pro Asp
275 280 285

Glu Val Leu Gln Glu Ala Val Pro Gly Ser Ile Arg Thr Ala Glu His
290 295 300

Phe Leu Gly Phe Leu Arg Arg Leu Leu Glu Tyr Val Lys Trp Arg Leu
305 310 315 320

Arg Val Gln His Val Val Gln Glu Ser Pro Pro Ala Phe Leu Ser Gly
325 330 335

Leu Ala Gln Arg Val Cys Ile Gln Arg Lys Pro Leu Arg Phe Cys Ala
340 345 350

Glu Arg Leu Arg Ser Leu Leu His Thr Leu Glu Ile Thr Asp Leu Ala
355 360 365

Asp Phe Ser Pro Leu Thr Leu Leu Ala Asn Phe Ala Thr Leu Val Ser
370 375 380

Thr Tyr Ala Lys Gly Phe Thr Ile Ile Ile Glu Pro Phe Asp Asp Arg
385 390 395 400

Thr Pro Thr Ile Ala Asn Pro Ile Leu His Phe Ser Cys Met Asp Ala
405 410 415

Ser Leu Ala Ile Lys Pro Val Phe Glu Arg Phe Gln Ser Val Ile Ile
420 425 430

Thr Ser Gly Thr Leu Ser Pro Leu Asp Ile Tyr Pro Lys Ile Leu Asp
435 440 445

Phe His Pro Val Thr Met Ala Thr Phe Thr Met Thr Leu Ala Arg Val
450 455 460

Cys Leu Cys Pro Met Ile Ile Gly Arg Gly Asn Asp Gln Val Ala Ile
465 470 475 480

Ser Ser Lys Phe Glu Thr Arg Glu Asp Ile Ala Val Ile Arg Asn Tyr
485 490 495

Gly Asn Leu Leu Leu Glu Met Ser Ala Val Val Pro Asp Gly Ile Val
500 505 510

Ala Phe Phe Thr Ser Tyr Gln Tyr Met Glu Ser Thr Val Ala Ser Trp
515 520 525

Tyr Glu Gln Gly Ile Leu Glu Asn Ile Gln Arg Asn Lys Leu Leu Phe
530 535 540

Ile Glu Thr Gln Asp Gly Ala Glu Thr Ser Val Ala Leu Glu Lys Tyr
545 550 555 560

Gln Glu Ala Cys Glu Asn Gly Arg Gly Ala Ile Leu Leu Ser Val Ala
565 570 575

Arg Gly Lys Val Ser Glu Gly Ile Asp Phe Val His His Tyr Gly Arg
580 585 590

Ala Val Ile Met Phe Gly Val Pro Tyr Val Tyr Thr Gln Ser Arg Ile
595 600 605

Leu Lys Ala Arg Leu Glu Tyr Leu Arg Asp Gln Phe Gln Ile Arg Glu
610 615 620

Asn Asp Phe Leu Thr Phe Asp Ala Met Arg His Ala Ala Gln Cys Val
625 630 635 640

Gly Arg Ala Ile Arg Gly Lys Thr Asp Tyr Gly Leu Met Val Phe Ala
645 650 655

Asp Lys Arg Phe Ala Arg Gly Asp Lys Arg Gly Lys Leu Pro Arg Trp
660 665 670

Ile Gln Glu His Leu Thr Asp Ala Asn Leu Asn Leu Thr Val Asp Glu
675 680 685

Gly Val Gln Val Ala Lys Tyr Phe Leu Arg Gln Met Ala Gln Pro Phe
690 695 700

His Arg Glu Asp Gln Leu Gly Leu Ser Leu Leu Ser Leu Glu Gln Leu
705 710 715 720

Glu Ser Glu Glu Thr Leu Lys Arg Ile Glu Gln Ile Ala Gln Gln Leu
725 730 735

<210> 44
<211> 193
<212> PRT
<213> Homo sapiens

<400> 44
Met Gln Ile Leu Gln Asn Phe Lys His Asn Pro Lys Ile Asn Thr Ile
1 5 10 15

Phe Ile Ser Lys Val Gly Asp Thr Ser Phe Asp Leu Pro Glu Ala Asn
20 25 30

Val Leu Ile Gln Ile Ser Ser His Gly Gly Ser Arg Arg Gln Glu Ala

35 40 45

Gln Arg Leu Gly Arg Val Leu Arg Ala Lys Lys Gly Met Val Ala Glu
50 55 60

Glu Tyr Asn Ala Phe Phe Tyr Ser Leu Val Ser Gln Asp Thr Gln Glu
65 70 75 80

Met Ala Tyr Ser Thr Lys Arg Gln Arg Phe Leu Val Asp Gln Gly Tyr
85 90 95

Ser Phe Lys Val Ile Thr Lys Leu Ala Gly Met Glu Glu Glu Asp Leu
100 105 110

Ala Phe Ser Thr Lys Glu Glu Gln Gln Leu Leu Gln Lys Val Leu
115 120 125

Ala Ala Thr Asp Leu Asp Ala Glu Glu Glu Val Val Ala Gly Glu Phe
130 135 140

Gly Ser Arg Ser Ser Gln Ala Ser Arg Arg Phe Gly Thr Met Ser Ser
145 150 155 160

Met Ser Gly Ala Asp Asp Thr Val Tyr Met Glu Tyr His Ser Ser Arg
165 170 175

Ser Lys Ala Pro Ser Lys His Val His Pro Leu Phe Lys Arg Phe Arg
180 185 190

Lys

<210> 45
<211> 278
<212> PRT
<213> Homo sapiens

<400> 45
Met Asp Asp Gln Gly Cys Pro Arg Cys Lys Thr Thr Lys Tyr Arg Asn
1 5 10 15

Pro Ser Leu Lys Leu Met Val Asn Val Cys Gly His Thr Leu Cys Glu
20 25 30

Ser Cys Val Asp Leu Leu Phe Val Arg Gly Ala Gly Asn Cys Pro Glu
35 40 45

Cys Gly Thr Pro Leu Arg Lys Ser Asn Phe Arg Val Gln Leu Phe Glu
50 55 60

Asp Pro Thr Val Asp Lys Glu Val Glu Ile Arg Lys Lys Val Leu Lys
65 70 75 80

```
Ile Tyr Asn Lys Arg Glu Glu Asp Phe Pro Ser Leu Arg Glu Tyr Asn
                85                  90                  95

Asp Phe Leu Glu Glu Val Glu Glu Ile Val Phe Asn Leu Thr Asn Asn
            100                 105                 110

Val Asp Leu Asp Asn Thr Lys Lys Lys Met Glu Ile Tyr Gln Lys Glu
        115                 120                 125

Asn Lys Asp Val Ile Gln Lys Asn Lys Leu Lys Leu Thr Arg Glu Gln
    130                 135                 140

Glu Glu Leu Glu Glu Ala Leu Glu Val Glu Arg Gln Glu Asn Glu Gln
145                 150                 155                 160

Arg Arg Leu Phe Ile Gln Lys Glu Glu Gln Leu Gln Gln Ile Leu Lys
                165                 170                 175

Arg Lys Asn Lys Gln Ala Phe Leu Asp Glu Leu Glu Ser Ser Asp Leu
            180                 185                 190

Pro Val Ala Leu Leu Leu Ala Gln His Lys Asp Arg Ser Thr Gln Leu
        195                 200                 205

Glu Met Gln Leu Glu Lys Pro Lys Pro Val Lys Pro Val Thr Phe Ser
    210                 215                 220

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

Leu Glu Glu Ala Leu Tyr Glu Tyr Gln Pro Leu Gln Ile Glu Thr Tyr
                245                 250                 255

Gly Pro His Val Pro Glu Leu Glu Met Leu Gly Arg Leu Gly Gly Phe
            260                 265                 270

Asp Thr Ile Ser Leu Ile
        275
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<210> 46
<211> 323
<212> PRT
<213> Homo sapiens

<400> 46

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Met Ala Leu Asp Val Lys Ser Arg Ala Lys Arg Tyr Glu Lys Leu Asp
1               5                   10                  15

Phe Leu Gly Glu Gly Gln Phe Ala Thr Val Tyr Lys Ala Arg Asp Lys
            20                  25                  30

Asn Thr Asn Gln Ile Val Ala Ile Lys Lys Ile Lys Leu Gly His Arg
        35                  40                  45
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Ser Glu Ala Lys Asp Gly Ile Asn Arg Thr Ala Leu Arg Glu Ile Lys
50 55 60

Leu Leu Gln Glu Leu Ser His Pro Asn Ile Ile Gly Val Ile Ile Lys
65 70 75 80

Asp Asn Ser Leu Val Leu Thr Pro Ser His Ile Lys Ala Tyr Met Leu
85 90 95

Met Thr Leu Gln Gly Leu Glu Tyr Leu His Gln His Trp Ile Leu His
100 105 110

Arg Asp Leu Lys Pro Asn Asn Leu Leu Leu Asp Glu Asn Gly Val Leu
115 120 125

Lys Leu Ala Asp Phe Gly Leu Ala Lys Ser Phe Gly Ser Pro Asn Arg
130 135 140

Ala Tyr Thr His Gln Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu
145 150 155 160

Leu Phe Gly Ala Arg Met Tyr Gly Val Gly Val Asp Met Trp Ala Val
165 170 175

Gly Cys Ile Leu Ala Glu Leu Leu Leu Arg Val Pro Phe Leu Pro Gly
180 185 190

Asp Ser Asp Leu Asp Gln Leu Thr Arg Ile Phe Glu Thr Leu Gly Thr
195 200 205

Pro Thr Glu Glu Gln Trp Pro Asp Met Cys Ser Leu Pro Asp Tyr Val
210 215 220

Thr Phe Lys Ser Phe Pro Gly Ile Pro Leu His His Ile Phe Ser Ala
225 230 235 240

Ala Gly Asp Asp Leu Leu Asp Leu Ile Gln Gly Leu Phe Leu Phe Asn
245 250 255

Pro Cys Ala Arg Ile Thr Ala Thr Gln Ala Leu Lys Met Lys Tyr Phe
260 265 270

Ser Asn Arg Pro Gly Pro Thr Pro Gly Cys Gln Leu Pro Arg Pro Asn
275 280 285

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

Lys Arg Lys Arg Thr Glu Ala Leu Glu Gln Gly Gly Leu Pro Lys Lys
305 310 315 320

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Leu Ile Phe

<210> 47
<211> 329
<212> PRT
<213> Homo sapiens

<400> 47

```
Met Tyr His Asn Ser Ser Gln Lys Arg His Trp Thr Phe Ser Ser Glu
1               5                  10                  15

Glu Gln Leu Ala Arg Leu Arg Ala Asp Ala Asn Arg Lys Phe Arg Cys
            20                  25                  30

Lys Ala Val Ala Asn Gly Lys Val Leu Pro Asn Asp Pro Val Phe Leu
        35                  40                  45

Glu Pro His Glu Glu Met Thr Leu Cys Lys Tyr Tyr Glu Lys Arg Leu
    50                  55                  60

Leu Glu Phe Cys Ser Val Phe Lys Pro Ala Met Pro Arg Ser Val Val
65                  70                  75                  80

Gly Thr Ala Cys Met Tyr Phe Lys Arg Phe Tyr Leu Asn Asn Ser Val
                85                  90                  95

Met Glu Tyr His Pro Arg Ile Ile Met Leu Thr Cys Ala Phe Leu Ala
            100                 105                 110

Cys Lys Val Asp Glu Phe Asn Val Ser Ser Pro Gln Phe Val Gly Asn
        115                 120                 125

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

Glu Tyr Glu Leu Leu Leu Ile Gln Gln Leu Asn Phe His Leu Ile Val
145                 150                 155                 160

His Asn Pro Tyr Arg Pro Phe Glu Gly Phe Leu Ile Asp Leu Lys Thr
                165                 170                 175

Arg Tyr Pro Ile Leu Glu Asn Pro Glu Ile Leu Arg Lys Thr Ala Asp
            180                 185                 190

Asp Phe Leu Asn Arg Ile Ala Leu Thr Asp Ala Tyr Leu Leu Tyr Thr
        195                 200                 205

Pro Ser Gln Ile Ala Leu Thr Ala Ile Leu Ser Ser Ala Ser Arg Ala
    210                 215                 220

Gly Ile Thr Met Glu Ser Tyr Leu Ser Glu Ser Leu Met Leu Lys Glu
225                 230                 235                 240
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Asn Arg Thr Cys Leu Ser Gln Leu Leu Asp Ile Met Lys Ser Met Arg
245 250 255

Asn Leu Val Lys Lys Tyr Glu Pro Pro Arg Ser Glu Glu Val Ala Val
260 265 270

Leu Lys Gln Lys Leu Glu Arg Cys His Ser Ala Glu Leu Ala Leu Asn
275 280 285

Val Ile Thr Lys Lys Arg Lys Gly Tyr Glu Asp Asp Asp Tyr Val Ser
290 295 300

Lys Lys Ser Lys His Glu Glu Val Cys Phe Thr Pro Lys Met Asn Ser
305 310 315 320

Lys Leu Phe Leu Leu Tyr Ile Leu Val
325

<210> 48
<211> 490
<212> PRT
<213> Homo sapiens

<400> 48
Met Ala Ala Leu Gly Pro Ser Ser Gln Asn Val Thr Glu Tyr Val Val
1 5 10 15

Arg Val Pro Lys Asn Thr Thr Lys Lys Tyr Asn Ile Met Ala Phe Asn
20 25 30

Ala Ala Asp Lys Val Asn Phe Ala Thr Trp Asn Gln Ala Arg Leu Glu
35 40 45

Arg Asp Leu Ser Asn Lys Lys Ile Tyr Gln Glu Glu Glu Met Pro Glu
50 55 60

Ser Gly Ala Gly Ser Glu Phe Asn Arg Lys Leu Arg Glu Glu Ala Arg
65 70 75 80

Arg Lys Phe Lys Gly Ile Lys Lys Gly Gly Val Thr Glu Asn Thr Ser
85 90 95

Tyr Tyr Ile Phe Thr Gln Cys Pro Asp Gly Ala Phe Glu Ala Phe Pro
100 105 110

Val His Asn Trp Tyr Asn Phe Thr Pro Leu Ala Arg His Arg Thr Leu
115 120 125

Thr Ala Glu Glu Ala Glu Glu Glu Trp Glu Arg Arg Asn Lys Val Leu
130 135 140

Asn His Phe Ser Ile Met Gln Gln Arg Arg Leu Lys Asp Gln Asp Gln
145 150 155 160

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Asp Glu Asp Glu Glu Glu Lys Glu Lys Arg Gly Arg Arg Lys Ala Ser
165 170 175

Glu Leu Arg Ile His Asp Leu Glu Asp Asp Leu Glu Met Ser Ser Asp
180 185 190

Ala Ser Asp Ala Ser Gly Glu Glu Gly Gly Arg Val Pro Lys Ala Lys
195 200 205

Lys Lys Ala Pro Leu Ala Lys Gly Gly Arg Lys Lys Lys Lys Lys Lys
210 215 220

Gly Ser Asp Asp Glu Ala Phe Glu Asp Ser Asp Asp Gly Asp Phe Glu
225 230 235 240

Gly Gln Glu Val Asp Tyr Met Ser Asp Gly Ser Ser Ser Ser Gln Glu
245 250 255

Glu Pro Glu Ser Lys Ala Lys Ala Pro Gln Gln Glu Glu Gly Pro Lys
260 265 270

Gly Val Asp Glu Gln Ser Asp Ser Ser Glu Glu Ser Glu Glu Glu Lys
275 280 285

Pro Pro Glu Glu Asp Lys Glu Glu Glu Glu Glu Lys Lys Ala Pro Thr
290 295 300

Pro Gln Glu Lys Lys Arg Arg Lys Asp Ser Ser Glu Glu Ser Asp Ser
305 310 315 320

Ser Glu Glu Ser Asp Ile Asp Ser Glu Ala Ser Ser Ala Leu Phe Met
325 330 335

Ala Lys Lys Lys Thr Pro Pro Lys Arg Glu Arg Lys Pro Ser Gly Gly
340 345 350

Ser Ser Arg Gly Asn Ser Arg Pro Gly Thr Pro Ser Ala Glu Gly Gly
355 360 365

Ser Thr Ser Ser Thr Leu Arg Ala Ala Ala Ser Lys Leu Glu Gln Gly
370 375 380

Lys Arg Val Ser Glu Met Pro Ala Ala Lys Arg Leu Arg Leu Asp Thr
385 390 395 400

Gly Pro Gln Ser Leu Ser Gly Lys Ser Thr Pro Gln Pro Pro Ser Gly
405 410 415

Lys Thr Thr Pro Asn Ser Gly Asp Val Gln Val Thr Glu Asp Ala Val
420 425 430

Arg Arg Tyr Leu Thr Arg Lys Pro Met Thr Thr Lys Asp Leu Leu Lys
435 440 445

Lys Phe Gln Thr Lys Lys Thr Gly Leu Ser Ser Glu Gln Thr Val Asn
450 455 460

Val Leu Ala Gln Ile Leu Lys Arg Leu Asn Pro Glu Arg Lys Met Ile
465 470 475 480

Asn Asp Lys Met His Phe Ser Leu Lys Glu
485 490

<210> 49
<211> 385
<212> PRT
<213> Homo sapiens

<400> 49
Met Ala Ala Leu Gly Pro Ser Ser Gln Asn Val Thr Glu Tyr Val Val
1 5 10 15

Arg Val Pro Lys Asn Thr Thr Lys Lys Tyr Asn Ile Met Ala Phe Asn
20 25 30

Ala Ala Asp Lys Val Asn Phe Ala Thr Trp Asn Gln Ala Arg Leu Glu
35 40 45

Arg Asp Leu Ser Asn Lys Lys Ile Tyr Gln Glu Glu Glu Lys Glu Lys
50 55 60

Arg Gly Arg Arg Lys Ala Ser Glu Leu Arg Ile His Asp Leu Glu Asp
65 70 75 80

Asp Leu Glu Met Ser Ser Asp Ala Ser Asp Ala Ser Gly Glu Glu Gly
85 90 95

Gly Arg Val Pro Lys Ala Lys Lys Lys Ala Pro Leu Ala Lys Gly Gly
100 105 110

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

Ser Asp Asp Gly Asp Phe Glu Gly Gln Glu Val Asp Tyr Met Ser Asp
130 135 140

Gly Ser Ser Ser Ser Gln Glu Glu Pro Glu Ser Lys Ala Lys Ala Pro
145 150 155 160

Gln Gln Glu Glu Gly Pro Lys Gly Val Asp Glu Gln Ser Asp Ser Ser
165 170 175

Glu Glu Ser Glu Glu Glu Lys Pro Pro Glu Glu Asp Lys Glu Glu Glu
180 185 190

Glu Glu Lys Lys Ala Pro Thr Pro Gln Glu Lys Lys Arg Arg Lys Asp
195 200 205

Ser Ser Glu Glu Ser Asp Ser Ser Glu Glu Ser Asp Ile Asp Ser Glu
210 215 220

Ala Ser Ser Ala Leu Phe Met Ala Lys Lys Lys Thr Pro Pro Lys Arg
225 230 235 240

Glu Arg Lys Pro Ser Gly Gly Ser Ser Arg Gly Asn Ser Arg Pro Gly
245 250 255

Thr Pro Ser Ala Glu Gly Gly Ser Thr Ser Ser Thr Leu Arg Ala Ala
260 265 270

Ala Ser Lys Leu Glu Gln Gly Lys Arg Val Ser Glu Met Pro Ala Ala
275 280 285

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

Thr Pro Gln Pro Pro Ser Gly Lys Thr Thr Pro Asn Ser Gly Asp Val
305 310 315 320

Gln Val Thr Glu Asp Ala Val Arg Arg Tyr Leu Thr Arg Lys Pro Met
325 330 335

Thr Thr Lys Asp Leu Leu Lys Lys Phe Gln Thr Lys Lys Thr Gly Leu
340 345 350

Ser Ser Glu Gln Thr Val Asn Val Leu Ala Gln Ile Leu Lys Arg Leu
355 360 365

Asn Pro Glu Arg Lys Met Ile Asn Asp Lys Met His Phe Ser Leu Lys
370 375 380

Glu
385

<210> 50
<211> 481
<212> PRT
<213> Homo sapiens

<400> 50
Met Ala Ala Leu Gly Pro Ser Ser Gln Asn Val Thr Glu Tyr Val Val
1 5 10 15

Arg Val Pro Lys Asn Thr Thr Lys Lys Tyr Asn Ile Met Ala Phe Asn
20 25 30

Ala Ala Asp Lys Val Asn Phe Ala Thr Trp Asn Gln Ala Arg Leu Glu

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        35                  40                  45

Arg Asp Leu Ser Asn Lys Lys Ile Tyr Gln Glu Glu Met Pro Glu
    50                  55                  60

Ser Gly Ala Gly Ser Glu Phe Asn Arg Lys Leu Arg Glu Glu Ala Arg
65                  70                  75                  80

Arg Lys Lys Tyr Gly Ile Val Leu Lys Glu Phe Arg Pro Glu Asp Gln
                85                  90                  95

Pro Trp Leu Leu Arg Val Asn Gly Lys Ser Gly Arg Lys Phe Lys Gly
            100                 105                 110

Ile Lys Lys Gly Gly Val Thr Glu Asn Thr Ser Tyr Tyr Ile Phe Thr
        115                 120                 125

Gln Cys Pro Asp Gly Ala Phe Glu Ala Phe Pro Val His Asn Trp Tyr
    130                 135                 140

Asn Phe Thr Pro Leu Ala Arg His Arg Thr Leu Thr Ala Glu Glu Ala
145                 150                 155                 160

Glu Glu Glu Trp Glu Arg Arg Asn Lys Val Leu Asn His Phe Ser Ile
                165                 170                 175

Met Gln Gln Arg Arg Leu Lys Asp Gln Asp Gln Asp Glu Asp Glu Glu
            180                 185                 190

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

Asp Leu Glu Asp Asp Leu Glu Met Ser Ser Asp Ala Ser Asp Ala Ser
    210                 215                 220

Gly Glu Glu Gly Gly Arg Val Pro Lys Ala Lys Lys Lys Ala Pro Leu
225                 230                 235                 240

Ala Lys Gly Gly Arg Lys Lys Lys Lys Lys Lys Gly Ser Asp Asp Glu
                245                 250                 255

Ala Phe Glu Asp Ser Asp Asp Gly Asp Phe Glu Gly Gln Glu Val Asp
            260                 265                 270

Tyr Met Ser Asp Gly Ser Ser Ser Ser Gln Glu Glu Pro Glu Ser Lys
        275                 280                 285

Ala Lys Ala Pro Gln Gln Glu Glu Gly Pro Lys Gly Val Asp Glu Gln
    290                 295                 300

Ser Asp Ser Ser Glu Glu Ser Glu Glu Glu Lys Pro Pro Glu Glu Asp
305                 310                 315                 320
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Lys Glu Glu Glu Glu Glu Lys Lys Ala Pro Thr Pro Gln Glu Lys Lys
325 330 335

Arg Arg Lys Asp Ser Ser Glu Glu Ser Asp Ser Ser Glu Glu Ser Asp
340 345 350

Ile Asp Ser Glu Ala Ser Ser Ala Phe Phe Met Ala Val Arg Pro Ser
355 360 365

Pro Val Ala Gly Glu Ala Trp Ala Ser Val Cys Arg Leu Thr His Leu
370 375 380

Pro Thr Leu Thr Ser Ala Glu Glu Glu Asp Ala Thr Gln Glu Arg Ala
385 390 395 400

Glu Ala Val Gly Arg Glu Leu Lys Gly Gln Gln Pro Pro Arg His Ala
405 410 415

Gln Arg Arg Gly Trp Gln His Leu Leu His Pro Ala Gly Gly Cys Gln
420 425 430

Gln Thr Arg Ala Arg Glu Ala Gly Glu Arg Asp Ala Cys Ser Gln Ala
435 440 445

Val Ala Ala Gly His Gly Thr Pro Glu Pro Val Trp Glu Val Asp Thr
450 455 460

Pro Ala Thr Ile Arg Gln Asp Asn Thr Gln Gln Arg Arg Arg Ala Gly
465 470 475 480

Asp

<210> 51
<211> 437
<212> PRT
<213> Homo sapiens

<400> 51
Met Ala Ala Leu Gly Pro Ser Ser Gln Asn Val Thr Glu Tyr Val Val
1 5 10 15

Arg Val Pro Lys Asn Thr Thr Lys Lys Tyr Asn Ile Met Ala Phe Asn
20 25 30

Ala Ala Asp Lys Val Asn Phe Ala Thr Trp Asn Gln Ala Arg Leu Glu
35 40 45

Arg Asp Leu Ser Asn Lys Lys Ile Tyr Gln Glu Glu Glu Met Pro Glu
50 55 60

Ser Gly Ala Gly Ser Glu Phe Asn Arg Lys Leu Arg Glu Glu Ala Arg

65 70 75 80

Arg Lys Lys Tyr Gly Ile Val Leu Lys Glu Phe Arg Pro Glu Asp Gln
85 90 95

Pro Trp Leu Leu Arg Val Asn Gly Lys Ser Gly Arg Lys Phe Lys Gly
100 105 110

Ile Lys Lys Gly Gly Val Thr Glu Asn Thr Ser Tyr Tyr Ile Phe Thr
115 120 125

Gln Cys Pro Asp Gly Ala Phe Glu Ala Phe Pro Val His Asn Trp Tyr
130 135 140

Asn Phe Thr Pro Leu Ala Arg His Arg Thr Leu Thr Ala Glu Glu Ala
145 150 155 160

Glu Glu Glu Trp Glu Arg Arg Asn Lys Val Leu Asn His Phe Ser Ile
165 170 175

Met Gln Gln Arg Arg Leu Lys Asp Gln Asp Gln Asp Glu Asp Glu Glu
180 185 190

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

Asp Leu Glu Asp Asp Leu Glu Met Ser Ser Asp Ala Ser Asp Ala Ser
210 215 220

Gly Glu Glu Gly Gly Arg Val Pro Lys Ala Lys Lys Lys Ala Pro Leu
225 230 235 240

Ala Lys Gly Gly Arg Lys Lys Lys Lys Lys Lys Gly Ser Asp Asp Glu
245 250 255

Ala Phe Glu Asp Ser Asp Asp Gly Asp Phe Glu Gly Gln Glu Val Asp
260 265 270

Tyr Met Ser Asp Gly Ser Ser Ser Ser Gln Glu Glu Pro Glu Ser Lys
275 280 285

Ala Lys Ala Pro Gln Gln Glu Glu Gly Pro Lys Gly Val Asp Glu Gln
290 295 300

Ser Asp Ser Ser Glu Glu Ser Glu Glu Glu Lys Pro Pro Glu Glu Asp
305 310 315 320

Lys Glu Glu Glu Glu Glu Lys Lys Ala Pro Thr Pro Gln Glu Lys Lys
325 330 335

Arg Arg Lys Asp Ser Ser Glu Glu Ser Asp Ser Ser Glu Glu Ser Asp
340 345 350

Ile Asp Ser Glu Ala Ser Ser Ala Leu Phe Met Ala Val Arg Pro Ser
355 360 365

Pro Val Ala Gly Glu Ala Trp Ala Ser Val Cys Arg Leu Thr His Leu
370 375 380

Pro Thr Leu Thr Ser Ala Glu Glu Glu Asp Ala Thr Gln Glu Arg Ala
385 390 395 400

Glu Ala Val Gly Arg Glu Leu Lys Gly Gln Gln Pro Pro Arg His Ala
405 410 415

Gln Arg Arg Gly Trp Gln His Leu Leu His Pro Ala Gly Gly Cys Gln
420 425 430

Gln Thr Arg Ala Arg
435

<210> 52
<211> 316
<212> PRT
<213> Homo sapiens

<400> 52
Met Ala Ala Leu Gly Pro Ser Ser Gln Asn Val Thr Glu Tyr Val Val
1 5 10 15

Arg Val Pro Lys Asn Thr Thr Lys Lys Tyr Asn Ile Met Ala Phe Asn
20 25 30

Ala Ala Asp Lys Val Asn Phe Ala Thr Trp Asn Gln Ala Arg Leu Glu
35 40 45

Arg Asp Leu Ser Asn Lys Lys Ile Tyr Gln Glu Glu Glu Met Pro Glu
50 55 60

Ser Gly Ala Gly Ser Glu Phe Asn Arg Lys Leu Arg Glu Glu Ala Arg
65 70 75 80

Arg Lys Lys Tyr Gly Ile Val Leu Lys Glu Phe Arg Pro Glu Asp Gln
85 90 95

Pro Trp Leu Leu Arg Val Asn Gly Lys Ser Gly Arg Lys Phe Lys Gly
100 105 110

Ile Lys Lys Gly Gly Val Thr Glu Asn Thr Ser Tyr Tyr Ile Phe Thr
115 120 125

Gln Cys Pro Asp Gly Ala Phe Glu Ala Phe Pro Val His Asn Trp Tyr
130 135 140

Asn Phe Thr Pro Leu Ala Arg His Arg Thr Leu Thr Ala Glu Glu Ala

145 150 155 160

Glu Glu Glu Trp Glu Arg Arg Asn Lys Val Leu Asn His Phe Ser Ile
165 170 175

Met Gln Gln Arg Arg Leu Lys Asp Gln Asp Gln Asp Glu Asp Glu Glu
180 185 190

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

Asp Leu Glu Asp Asp Leu Glu Met Ser Ser Asp Ala Ser Asp Ala Ser
210 215 220

Gly Glu Glu Gly Gly Arg Val Pro Lys Ala Lys Lys Lys Ala Pro Leu
225 230 235 240

Ala Lys Gly Gly Arg Lys Lys Lys Lys Lys Lys Gly Ser Asp Asp Glu
245 250 255

Ala Phe Glu Asp Ser Asp Asp Gly Asp Phe Glu Gly Gln Glu Val Asp
260 265 270

Tyr Met Ser Asp Gly Ser Ser Ser Ser Gln Glu Glu Pro Glu Ser Lys
275 280 285

Ala Lys Ala Pro Gln Gln Glu Glu Gly Pro Lys Gly Val Asp Glu Gln
290 295 300

Ser Asp Thr Asp Gln Gly Pro Val Leu Pro Thr Gly
305 310 315

<210> 53
<211> 161
<212> PRT
<213> Homo sapiens

<400> 53
Met Ala Ala Leu Gly Pro Ser Ser Gln Asn Val Thr Glu Tyr Val Val
1 5 10 15

Arg Val Pro Lys Asn Thr Thr Lys Lys Tyr Asn Ile Met Ala Phe Asn
20 25 30

Ala Ala Asp Lys Val Asn Phe Ala Thr Trp Asn Gln Ala Arg Leu Glu
35 40 45

Arg Asp Leu Ser Asn Lys Lys Ile Tyr Gln Glu Glu Glu Met Pro Glu
50 55 60

Ser Gly Ala Gly Ser Glu Phe Asn Arg Lys Leu Arg Glu Glu Ala Arg
65 70 75 80

Arg Lys Lys Tyr Gly Ile Val Leu Lys Glu Phe Arg Pro Glu Asp Gln
85 90 95

Pro Trp Leu Leu Arg Val Asn Gly Lys Ser Gly Arg Lys Phe Lys Gly
100 105 110

Ile Lys Lys Gly Gly Val Thr Glu Asn Thr Ser Tyr Tyr Ile Phe Thr
115 120 125

Gln Cys Pro Asp Gly Ala Phe Glu Ala Phe Pro Val His Asn Trp Tyr
130 135 140

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

Ser

<210> 54
<211> 478
<212> PRT
<213> Homo sapiens

<400> 54
Met Ala Ala Leu Gly Pro Ser Ser Gln Asn Val Thr Glu Tyr Val Val
1 5 10 15

Arg Val Pro Lys Asn Thr Thr Lys Lys Tyr Asn Ile Met Ala Phe Asn
20 25 30

Ala Ala Asp Lys Val Asn Phe Ala Thr Trp Asn Gln Ala Arg Leu Glu
35 40 45

Arg Asp Leu Ser Asn Lys Lys Ile Tyr Gln Glu Glu Glu Met Pro Glu
50 55 60

Ser Gly Ala Gly Ser Glu Phe Asn Arg Lys Leu Arg Glu Glu Ala Arg
65 70 75 80

Arg Lys Lys Tyr Gly Ile Val Leu Lys Glu Phe Arg Pro Glu Asp Gln
85 90 95

Pro Trp Leu Leu Arg Val Asn Gly Lys Ser Gly Arg Lys Phe Lys Gly
100 105 110

Ile Lys Lys Gly Gly Val Thr Glu Asn Thr Ser Tyr Tyr Ile Phe Thr
115 120 125

Gln Cys Pro Asp Gly Ala Phe Glu Ala Phe Pro Val His Asn Trp Tyr
130 135 140

Asn Phe Thr Pro Leu Ala Arg His Arg Thr Leu Thr Ala Glu Glu Ala
145 150 155 160

Glu Glu Glu Trp Glu Arg Arg Asn Lys Val Leu Asn His Phe Ser Ile
165 170 175

Met Gln Gln Arg Arg Leu Lys Asp Gln Asp Gln Asp Glu Asp Glu Glu
180 185 190

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

Asp Leu Glu Asp Asp Leu Glu Met Ser Ser Asp Ala Ser Asp Ala Ser
210 215 220

Gly Glu Glu Gly Gly Arg Val Pro Lys Ala Lys Lys Lys Ala Pro Leu
225 230 235 240

Ala Lys Gly Gly Arg Lys Lys Lys Lys Lys Lys Gly Ser Asp Asp Glu
245 250 255

Ala Phe Glu Asp Ser Asp Asp Gly Asp Phe Glu Gly Gln Glu Val Asp
260 265 270

Tyr Met Ser Asp Gly Ser Ser Ser Ser Gln Glu Glu Pro Glu Ser Lys
275 280 285

Ala Lys Ala Pro Gln Gln Glu Glu Gly Pro Lys Gly Val Asp Glu Gln
290 295 300

Ser Asp Ser Ser Glu Glu Ser Glu Glu Glu Lys Pro Pro Glu Glu Asp
305 310 315 320

Lys Glu Glu Glu Glu Glu Lys Lys Ala Pro Thr Pro Gln Glu Lys Lys
325 330 335

Arg Arg Lys Asp Ser Ser Glu Glu Ser Asp Ser Ser Glu Glu Ser Asp
340 345 350

Ile Asp Ser Glu Ala Ser Ser Ala Phe Phe Met Ala Val Arg Pro Ser
355 360 365

Pro Val Ala Gly Glu Ala Trp Ala Ser Val Cys Arg Leu Thr His Leu
370 375 380

Pro Thr Leu Thr Ser Ala Glu Glu Glu Asp Ala Thr Gln Glu Arg Ala
385 390 395 400

Glu Ala Val Gly Arg Glu Leu Lys Gly Gln Gln Pro Pro Arg His Ala
405 410 415

Gln Arg Arg Gly Trp Gln His Leu Leu His Pro Ala Gly Gly Cys Gln
420 425 430

Gln Thr Arg Ala Arg Glu Ala Gly Glu Arg Asp Ala Cys Ser Gln Ala
435 440 445

Val Ala Ala Gly His Gly Thr Pro Glu Pro Val Trp Glu Val Asp Thr
450 455 460

Pro Ala Thr Ile Arg Gln Asp Asn Thr Gln Gln Arg Val Ser
465 470 475

<210> 55
<211> 316
<212> PRT
<213> Homo sapiens

<400> 55
Met Ala Ala Leu Gly Pro Ser Ser Gln Asn Val Thr Glu Tyr Val Val
1 5 10 15

Arg Val Pro Lys Asn Thr Thr Lys Lys Tyr Asn Ile Met Ala Phe Asn
20 25 30

Ala Ala Asp Lys Val Asn Phe Ala Thr Trp Asn Gln Ala Arg Leu Glu
35 40 45

Arg Asp Leu Ser Asn Lys Lys Ile Tyr Gln Glu Glu Glu Met Pro Glu
50 55 60

Ser Gly Ala Gly Ser Glu Phe Asn Arg Lys Leu Arg Glu Glu Ala Arg
65 70 75 80

Arg Lys Lys Tyr Gly Ile Val Leu Lys Glu Phe Arg Pro Glu Asp Gln
85 90 95

Pro Trp Leu Leu Arg Val Asn Gly Lys Ser Gly Arg Lys Phe Lys Gly
100 105 110

Ile Lys Lys Gly Gly Val Thr Glu Asn Thr Ser Tyr Tyr Ile Phe Thr
115 120 125

Gln Cys Pro Asp Gly Ala Phe Glu Ala Phe Pro Val His Asn Trp Tyr
130 135 140

Asn Phe Thr Pro Leu Ala Arg His Arg Thr Leu Thr Ala Glu Glu Ala
145 150 155 160

Glu Glu Glu Trp Glu Arg Arg Asn Lys Val Leu Asn His Phe Ser Ile
165 170 175

Met Gln Gln Arg Arg Leu Lys Asp Gln Asp Gln Asp Glu Asp Glu Glu
180 185 190

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

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Asp Leu Glu Asp Asp Leu Glu Met Ser Ser Asp Ala Ser Asp Ala Ser
210 215 220

Gly Glu Glu Gly Gly Arg Val Pro Lys Ala Lys Lys Lys Ala Pro Leu
225 230 235 240

Ala Lys Gly Gly Arg Lys Lys Lys Lys Lys Lys Gly Ser Asp Asp Glu
245 250 255

Ala Phe Glu Asp Ser Asp Asp Gly Asp Phe Glu Gly Gln Glu Val Asp
260 265 270

Tyr Met Ser Asp Gly Ser Ser Ser Ser Gln Glu Glu Pro Glu Ser Lys
275 280 285

Gly Leu Cys Cys Pro Leu Gly Asn Phe Tyr Ser Ser Pro Phe His Phe
290 295 300

Pro Lys Ser Leu Phe Ser Cys Asp Leu Ser Thr Thr
305 310 315

<210> 56
<211> 359
<212> PRT
<213> Homo sapiens

<400> 56
Met Ala Ala Leu Gly Pro Ser Ser Gln Asn Val Thr Glu Tyr Val Val
1 5 10 15

Arg Val Pro Lys Asn Thr Thr Lys Lys Tyr Asn Ile Met Ala Phe Asn
20 25 30

Ala Ala Asp Lys Val Asn Phe Ala Thr Trp Asn Gln Ala Arg Leu Glu
35 40 45

Arg Asp Leu Ser Asn Lys Lys Ile Tyr Gln Glu Glu Glu Met Pro Glu
50 55 60

Ser Gly Ala Gly Ser Glu Phe Asn Arg Lys Leu Arg Glu Glu Ala Arg
65 70 75 80

Arg Lys Lys Tyr Gly Ile Val Leu Lys Glu Phe Arg Pro Glu Asp Gln
85 90 95

Pro Trp Leu Leu Arg Val Asn Gly Lys Ser Gly Arg Lys Phe Lys Gly
100 105 110

Ile Lys Lys Gly Gly Val Thr Glu Asn Thr Ser Tyr Tyr Ile Phe Thr
115 120 125

Gln Cys Pro Asp Gly Ala Phe Glu Ala Phe Pro Val His Asn Trp Tyr
130 135 140

Asn Phe Thr Pro Leu Ala Arg His Arg Thr Leu Thr Ala Glu Glu Ala
145 150 155 160

Glu Glu Glu Trp Glu Arg Arg Asn Lys Val Leu Asn His Phe Ser Ile
165 170 175

Met Gln Gln Arg Arg Leu Lys Asp Gln Asp Gln Asp Glu Asp Glu Glu
180 185 190

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

Asp Leu Glu Asp Asp Leu Glu Met Ser Ser Asp Ala Ser Asp Ala Ser
210 215 220

Gly Glu Glu Gly Gly Arg Val Pro Lys Ala Lys Lys Lys Ala Pro Leu
225 230 235 240

Ala Lys Gly Gly Arg Lys Lys Lys Lys Lys Lys Gly Ser Asp Asp Glu
245 250 255

Ala Phe Glu Asp Ser Asp Asp Gly Asp Phe Glu Gly Gln Glu Val Asp
260 265 270

Tyr Met Ser Asp Gly Ser Ser Ser Ser Gln Glu Glu Pro Glu Ser Lys
275 280 285

Ala Lys Ala Pro Gln Gln Glu Glu Gly Pro Lys Gly Val Asp Glu Gln
290 295 300

Ser Asp Ser Ser Glu Glu Ser Glu Glu Glu Lys Pro Pro Glu Lys Pro
305 310 315 320

Pro Pro Gly Ser Ala Ser Leu Thr Leu Thr Lys Gly Leu Cys Cys Pro
325 330 335

Leu Gly Asn Phe Tyr Ser Ser Pro Phe His Phe Pro Lys Ser Leu Phe
340 345 350

Ser Cys Asp Leu Ser Thr Thr
355

<210> 57
<211> 1430
<212> PRT
<213> Homo sapiens

<400> 57
Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr
1 5 10 15

Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly

20 25 30

Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
100 105 110

Ile Asn Glu Val Ala Glu Val Lys Asp Pro Trp Asn Leu Ser Asn Asp
115 120 125

Glu Tyr Tyr Tyr Pro Lys Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly
130 135 140

Asn Ile Ile Gln His Ser Ile Pro Ala Val Glu Leu Arg Gln Pro Phe
145 150 155 160

Phe Pro Thr His Met Gly Pro Ile Lys Leu Arg Gln Phe His Arg Pro
165 170 175

Pro Leu Lys Lys Tyr Ser Phe Gly Ala Leu Ser Gln Pro Gly Pro His
180 185 190

Ser Val Gln Pro Leu Leu Lys His Ile Lys Lys Lys Ala Lys Met Arg
195 200 205

Glu Gln Glu Arg Gln Ala Ser Gly Gly Gly Glu Met Phe Phe Met Arg
210 215 220

Thr Pro Gln Asp Leu Thr Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu
225 230 235 240

Tyr Ser Glu Glu Asn Gly Pro Leu Met Met Gln Val Gly Met Ala Thr
245 250 255

Lys Ile Lys Asn Tyr Tyr Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala
260 265 270

Pro Asp Cys Lys Tyr Gly Glu Thr Val Tyr Cys His Thr Ser Pro Phe
275 280 285

Leu Gly Ser Leu His Pro Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn
290 295 300

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Leu Phe Arg Ala Pro Ile Tyr Leu His Lys Met Pro Glu Thr Asp Phe
305                 310                 315                 320

Leu Ile Ile Arg Thr Arg Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp
                325                 330                 335

Ile Phe Val Val Gly Gln Gln Cys Pro Leu Phe Glu Val Pro Gly Pro
            340                 345                 350

Asn Ser Lys Arg Ala Asn Thr His Ile Arg Asp Phe Leu Gln Val Phe
        355                 360                 365

Ile Tyr Arg Leu Phe Trp Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg
    370                 375                 380

Met Glu Asp Ile Lys Lys Ala Phe Pro Ser His Ser Glu Ser Ser Ile
385                 390                 395                 400

Arg Lys Arg Leu Lys Leu Cys Ala Asp Phe Lys Arg Thr Gly Met Asp
                405                 410                 415

Ser Asn Trp Trp Val Leu Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu
            420                 425                 430

Glu Ile Arg Ala Met Val Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser
        435                 440                 445

Met Ile Ala Ala Glu Gln Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys
    450                 455                 460

Ser Phe Phe Ala Pro Glu Glu Glu Asn Glu Glu Asp Phe Gln Met Lys
465                 470                 475                 480

Ile Asp Asp Glu Val Arg Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe
                485                 490                 495

Ile Ala Ala Met Lys Gly Lys Cys Leu Leu Glu Val Thr Gly Val Ala
            500                 505                 510

Asp Pro Thr Gly Cys Gly Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn
        515                 520                 525

Lys Pro Thr Gln Gln Lys Asp Asp Lys Glu Pro Gln Pro Val Lys Lys
    530                 535                 540

Thr Val Thr Gly Thr Asp Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn
545                 550                 555                 560

Ala Lys Gln Leu Leu Arg Lys Phe Gly Val Pro Glu Glu Glu Ile Lys
                565                 570                 575
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Lys Leu Ser Arg Trp Glu Val Ile Asp Val Val Arg Thr Met Ser Thr
            580                 585                 590

Glu Gln Ala Arg Ser Gly Glu Gly Pro Met Ser Lys Phe Ala Arg Gly
        595                 600                 605

Ser Arg Phe Ser Val Ala Glu His Gln Glu Arg Tyr Lys Glu Glu Cys
    610                 615                 620

Gln Arg Ile Phe Asp Leu Gln Asn Lys Val Leu Ser Ser Thr Glu Val
625                 630                 635                 640

Leu Ser Thr Asp Thr Asp Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu
                645                 650                 655

Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys Lys Thr Ser
            660                 665                 670

Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu Leu Gln
        675                 680                 685

Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn Asn His Arg
    690                 695                 700

Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser Ser Ala Thr Gly
705                 710                 715                 720

Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp Glu Glu Gly Lys Glu
                725                 730                 735

Tyr Val Arg Cys Glu Thr Val Arg Lys Pro Ala Val Ile Asp Ala Tyr
            740                 745                 750

Val Arg Ile Arg Thr Thr Lys Asp Glu Glu Phe Ile Arg Lys Phe Ala
        755                 760                 765

Leu Phe Asp Glu Gln His Arg Glu Glu Met Arg Lys Glu Arg Arg Arg
    770                 775                 780

Ile Gln Glu Gln Leu Arg Arg Leu Lys Arg Asn Gln Glu Lys Glu Lys
785                 790                 795                 800

Leu Lys Gly Pro Pro Glu Lys Lys Pro Lys Lys Met Lys Glu Arg Pro
                805                 810                 815

Asp Leu Lys Leu Lys Cys Gly Ala Cys Gly Ala Ile Gly His Met Arg
            820                 825                 830

Thr Asn Lys Phe Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser
        835                 840                 845
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Asn Pro Val Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr
    850                 855                 860

Val Ile His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly Thr Lys
865                 870                 875                 880

Ile Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val Arg Arg
                885                 890                 895

Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro Lys Lys
            900                 905                 910

Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn Arg Pro
        915                 920                 925

His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val Thr Leu Ser
    930                 935                 940

Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg Asp Leu Pro Asn Thr
945                 950                 955                 960

Tyr Pro Phe His Thr Pro Val Asn Ala Lys Val Val Lys Asp Tyr Tyr
                965                 970                 975

Lys Ile Ile Thr Arg Pro Met Asp Leu Gln Thr Leu Arg Glu Asn Val
            980                 985                 990

Arg Lys Arg Leu Tyr Pro Ser Arg  Glu Glu Phe Arg Glu  His Leu Glu
        995                 1000                1005

Leu Ile  Val Lys Asn Ser Ala  Thr Tyr Asn Gly Pro  Lys His Ser
    1010                1015                1020

Leu Thr  Gln Ile Ser Gln Ser  Met Leu Asp Leu Cys  Asp Glu Lys
    1025                1030                1035

Leu Lys  Glu Lys Glu Asp Lys  Leu Ala Arg Leu Glu  Lys Ala Ile
    1040                1045                1050

Asn Pro  Leu Leu Asp Asp Asp  Asp Gln Val Ala Phe  Ser Phe Ile
    1055                1060                1065

Leu Asp  Asn Ile Val Thr Gln  Lys Met Met Ala Val  Pro Asp Ser
    1070                1075                1080

Trp Pro  Phe His His Pro Val  Asn Lys Lys Phe Val  Pro Asp Tyr
    1085                1090                1095

Tyr Lys  Val Ile Val Asn Pro  Met Asp Leu Glu Thr  Ile Arg Lys
    1100                1105                1110

Asn Ile  Ser Lys His Lys Tyr  Gln Ser Arg Glu Ser  Phe Leu Asp
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1115 1120 1125

Asp Val Asn Leu Ile Leu Ala Asn Ser Val Lys Tyr Asn Gly Pro
1130 1135 1140

Glu Ser Gln Tyr Thr Lys Thr Ala Gln Glu Ile Val Asn Val Cys
1145 1150 1155

Tyr Gln Thr Leu Thr Glu Tyr Asp Glu His Leu Thr Gln Leu Glu
1160 1165 1170

Lys Asp Ile Cys Thr Ala Lys Glu Ala Ala Leu Glu Glu Ala Glu
1175 1180 1185

Leu Glu Ser Leu Asp Pro Met Thr Pro Gly Pro Tyr Thr Pro Gln
1190 1195 1200

Pro Pro Asp Leu Tyr Asp Thr Asn Thr Ser Leu Ser Met Ser Arg
1205 1210 1215

Asp Ala Ser Val Phe Gln Asp Glu Ser Asn Met Ser Val Leu Asp
1220 1225 1230

Ile Pro Ser Ala Thr Pro Glu Lys Gln Val Thr Gln Glu Gly Glu
1235 1240 1245

Asp Gly Asp Gly Asp Leu Ala Asp Glu Glu Glu Gly Thr Val Gln
1250 1255 1260

Gln Pro Gln Ala Ser Val Leu Tyr Glu Asp Leu Leu Met Ser Glu
1265 1270 1275

Gly Glu Asp Asp Glu Glu Asp Ala Gly Ser Asp Glu Glu Gly Asp
1280 1285 1290

Asn Pro Phe Ser Ala Ile Gln Leu Ser Glu Ser Gly Ser Asp Ser
1295 1300 1305

Asp Val Gly Ser Gly Gly Ile Arg Pro Lys Gln Pro Arg Met Leu
1310 1315 1320

Gln Glu Asn Thr Arg Met Asp Met Glu Asn Glu Glu Ser Met Met
1325 1330 1335

Ser Tyr Glu Gly Asp Gly Gly Glu Ala Ser His Gly Leu Glu Asp
1340 1345 1350

Ser Asn Ile Ser Tyr Gly Ser Tyr Glu Glu Pro Asp Pro Lys Ser
1355 1360 1365

Asn Thr Gln Asp Thr Ser Phe Ser Ser Ile Gly Gly Tyr Glu Val
1370 1375 1380

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Ser Glu Glu Glu Glu Asp Glu Glu Glu Glu Glu Gln Arg Ser Gly
1385 1390 1395

Pro Ser Val Leu Ser Gln Val His Leu Ser Glu Asp Glu Glu Asp
1400 1405 1410

Ser Glu Asp Phe His Ser Ile Ala Gly Asp Ser Asp Leu Asp Ser
1415 1420 1425

Asp Glu
1430

<210> 58
<211> 1906
<212> PRT
<213> Homo sapiens

<400> 58
Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr
1 5 10 15

Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
20 25 30

Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
100 105 110

Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
115 120 125

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

Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
145 150 155 160

Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
165 170 175

Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met

180 185 190

Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
195 200 205

Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
210 215 220

Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
225 230 235 240

Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
245 250 255

Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
260 265 270

Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
275 280 285

Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
290 295 300

Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
305 310 315 320

Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
325 330 335

Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
340 345 350

Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
355 360 365

Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
370 375 380

Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
385 390 395 400

Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
405 410 415

Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
420 425 430

Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
435 440 445

Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
450 455 460

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Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
465                 470                 475                 480

Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu
                485                 490                 495

Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
            500                 505                 510

Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
        515                 520                 525

Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
    530                 535                 540

Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
545                 550                 555                 560

Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
                565                 570                 575

Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His Ser
            580                 585                 590

Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met Gly
        595                 600                 605

Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
    610                 615                 620

Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
625                 630                 635                 640

Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
                645                 650                 655

Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
            660                 665                 670

Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
        675                 680                 685

Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
    690                 695                 700

Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
705                 710                 715                 720

Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
                725                 730                 735
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Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
740 745 750

Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
755 760 765

Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln
770 775 780

Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
785 790 795 800

Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
805 810 815

Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
820 825 830

Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
835 840 845

Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
850 855 860

Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
865 870 875 880

Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
885 890 895

Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
900 905 910

Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
915 920 925

Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
930 935 940

Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
945 950 955 960

Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
965 970 975

Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
980 985 990

Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
995 1000 1005

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Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp
1010 1015 1020

Glu Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg
1025 1030 1035

Ser Gly Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe
1040 1045 1050

Ser Val Ala Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg
1055 1060 1065

Ile Phe Asp Leu Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu
1070 1075 1080

Ser Thr Asp Thr Asp Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu
1085 1090 1095

Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys Lys Thr
1100 1105 1110

Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu
1115 1120 1125

Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn
1130 1135 1140

Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser
1145 1150 1155

Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp
1160 1165 1170

Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro
1175 1180 1185

Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu
1190 1195 1200

Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu
1205 1210 1215

Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
1220 1225 1230

Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
1235 1240 1245

Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys
1250 1255 1260

Cys Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe

1265 1270 1275

Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val
1280 1285 1290

Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile
1295 1300 1305

His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile
1310 1315 1320

Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val Arg Arg
1325 1330 1335

Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro Lys
1340 1345 1350

Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn
1355 1360 1365

Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val
1370 1375 1380

Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg Asp
1385 1390 1395

Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala Lys Val
1400 1405 1410

Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met Asp Leu Gln
1415 1420 1425

Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser Arg Glu
1430 1435 1440

Glu Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn Ser Ala Thr
1445 1450 1455

Tyr Asn Gly Pro Lys His Ser Leu Thr Gln Ile Ser Gln Ser Met
1460 1465 1470

Leu Asp Leu Cys Asp Glu Lys Leu Lys Glu Lys Glu Asp Lys Leu
1475 1480 1485

Ala Arg Leu Glu Lys Ala Ile Asn Pro Leu Leu Asp Asp Asp Asp
1490 1495 1500

Gln Val Ala Phe Ser Phe Ile Leu Asp Asn Ile Val Thr Gln Lys
1505 1510 1515

Met Met Ala Val Pro Asp Ser Trp Pro Phe His His Pro Val Asn
1520 1525 1530

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Lys Lys Phe Val Pro Asp Tyr Tyr Lys Val Ile Val Asn Pro Met
1535 1540 1545

Asp Leu Glu Thr Ile Arg Lys Asn Ile Ser Lys His Lys Tyr Gln
1550 1555 1560

Ser Arg Glu Ser Phe Leu Asp Asp Val Asn Leu Ile Leu Ala Asn
1565 1570 1575

Ser Val Lys Tyr Asn Gly Pro Glu Ser Gln Tyr Thr Lys Thr Ala
1580 1585 1590

Gln Glu Ile Val Asn Val Cys Tyr Gln Thr Leu Thr Glu Tyr Asp
1595 1600 1605

Glu His Leu Thr Gln Leu Glu Lys Asp Ile Cys Thr Ala Lys Glu
1610 1615 1620

Ala Ala Leu Glu Glu Ala Glu Leu Glu Ser Leu Asp Pro Met Thr
1625 1630 1635

Pro Gly Pro Tyr Thr Pro Gln Pro Pro Asp Leu Tyr Asp Thr Asn
1640 1645 1650

Thr Ser Leu Ser Met Ser Arg Asp Ala Ser Val Phe Gln Asp Glu
1655 1660 1665

Ser Asn Met Ser Val Leu Asp Ile Pro Ser Ala Thr Pro Glu Lys
1670 1675 1680

Gln Val Thr Gln Met Arg Gln Gly Arg Gly Arg Leu Gly Glu Glu
1685 1690 1695

Asp Ser Asp Val Asp Ile Glu Gly Tyr Asp Asp Glu Glu Glu Asp
1700 1705 1710

Gly Lys Pro Lys Thr Pro Ala Pro Glu Gly Glu Asp Gly Asp Gly
1715 1720 1725

Asp Leu Ala Asp Glu Glu Glu Gly Thr Val Gln Gln Pro Gln Ala
1730 1735 1740

Ser Val Leu Tyr Glu Asp Leu Leu Met Ser Glu Gly Glu Asp Asp
1745 1750 1755

Glu Glu Asp Ala Gly Ser Asp Glu Glu Gly Asp Asn Pro Phe Ser
1760 1765 1770

Ala Ile Gln Leu Ser Glu Ser Gly Ser Asp Ser Asp Val Gly Ser
1775 1780 1785

Gly Gly Ile Arg Pro Lys Gln Pro Arg Met Leu Gln Glu Asn Thr
1790 1795 1800

Arg Met Asp Met Glu Asn Glu Glu Ser Met Met Ser Tyr Glu Gly
1805 1810 1815

Asp Gly Gly Glu Ala Ser His Gly Leu Glu Asp Ser Asn Ile Ser
1820 1825 1830

Tyr Gly Ser Tyr Glu Glu Pro Asp Pro Lys Ser Asn Thr Gln Asp
1835 1840 1845

Thr Ser Phe Ser Ser Ile Gly Gly Tyr Glu Val Ser Glu Glu Glu
1850 1855 1860

Glu Asp Glu Glu Glu Glu Glu Gln Arg Ser Gly Pro Ser Val Leu
1865 1870 1875

Ser Gln Val His Leu Ser Glu Asp Glu Glu Asp Ser Glu Asp Phe
1880 1885 1890

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1895 1900 1905

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Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Val Lys Asp Pro Trp Asn Leu
100 105 110

Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys Gln Gln Gly Leu Arg Gly Thr
115 120 125

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

Gln Pro Phe Phe Pro Thr His Met Gly Pro Ile Lys Leu Arg Gln Phe
145 150 155 160

His Arg Pro Pro Leu Lys Lys Tyr Ser Phe Gly Ala Leu Ser Gln Pro
165 170 175

Gly Pro His Ser Val Gln Pro Leu Leu Lys His Ile Lys Lys Lys Ala
180 185 190

Lys Met Arg Glu Gln Glu Arg Gln Ala Ser Gly Gly Gly Glu Met Phe
195 200 205

Phe Met Arg Thr Pro Gln Asp Leu Thr Gly Lys Asp Gly Asp Leu Ile
210 215 220

Leu Ala Glu Tyr Ser Glu Glu Asn Gly Pro Leu Met Met Gln Val Gly
225 230 235 240

Met Ala Thr Lys Ile Lys Asn Tyr Tyr Lys Arg Lys Pro Gly Lys Asp
245 250 255

Pro Gly Ala Pro Asp Cys Lys Tyr Gly Glu Thr Val Tyr Cys His Thr
260 265 270

Ser Pro Phe Leu Gly Ser Leu His Pro Gly Gln Leu Leu Gln Ala Phe
275 280 285

Glu Asn Asn Leu Phe Arg Ala Pro Ile Tyr Leu His Lys Met Pro Glu
290 295 300

Thr Asp Phe Leu Ile Ile Arg Thr Arg Gln Gly Tyr Tyr Ile Arg Glu
305 310 315 320

Leu Val Asp Ile Phe Val Val Gly Gln Gln Cys Pro Leu Phe Glu Val
325 330 335

Pro Gly Pro Asn Ser Lys Arg Ala Asn Thr His Ile Arg Asp Phe Leu
340 345 350

Gln Val Phe Ile Tyr Arg Leu Phe Trp Lys Ser Lys Asp Arg Pro Arg
355 360 365

Arg Ile Arg Met Glu Asp Ile Lys Lys Ala Phe Pro Ser His Ser Glu
370 375 380

Ser Ser Ile Arg Lys Arg Leu Lys Leu Cys Ala Asp Phe Lys Arg Thr
385 390 395 400

Gly Met Asp Ser Asn Trp Trp Val Leu Lys Ser Asp Phe Arg Leu Pro
405 410 415

Thr Glu Glu Glu Ile Arg Ala Met Val Ser Pro Glu Gln Cys Cys Ala
420 425 430

Tyr Tyr Ser Met Ile Ala Ala Glu Gln Arg Leu Lys Asp Ala Gly Tyr
435 440 445

Gly Glu Lys Ser Phe Phe Ala Pro Glu Glu Glu Asn Glu Glu Asp Phe
450 455 460

Gln Met Lys Ile Asp Asp Glu Val Arg Thr Ala Pro Trp Asn Thr Thr
465 470 475 480

Arg Ala Phe Ile Ala Ala Met Lys Gly Lys Cys Leu Leu Glu Val Thr
485 490 495

Gly Val Ala Asp Pro Thr Gly Cys Gly Glu Gly Phe Ser Tyr Val Lys
500 505 510

Ile Pro Asn Lys Pro Thr Gln Gln Lys Asp Asp Lys Glu Pro Gln Pro
515 520 525

Val Lys Lys Thr Val Thr Gly Thr Asp Ala Asp Leu Arg Arg Leu Ser
530 535 540

Leu Lys Asn Ala Lys Gln Leu Leu Arg Lys Phe Gly Val Pro Glu Glu
545 550 555 560

Glu Ile Lys Lys Leu Ser Arg Trp Glu Val Ile Asp Val Val Arg Thr
565 570 575

Met Ser Thr Glu Gln Ala Arg Ser Gly Glu Gly Pro Met Ser Lys Phe
580 585 590

Ala Arg Gly Ser Arg Phe Ser Val Ala Glu His Gln Glu Arg Tyr Lys
595 600 605

Glu Glu Cys Gln Arg Ile Phe Asp Leu Gln Asn Lys Val Leu Ser Ser
610 615 620

Thr Glu Val Leu Ser Thr Asp Thr Asp Ser Ser Ser Ala Glu Asp Ser
625 630 635 640

Asp Phe Glu Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys
645 650 655

Lys Thr Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys
660 665 670

Glu Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn
675 680 685

Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser Ser
690 695 700

Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp Glu Glu
705 710 715 720

Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro Ala Val Ile
725 730 735

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

Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu Glu Met Arg Lys Glu
755 760 765

Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg Leu Lys Arg Asn Gln Glu
770 775 780

Lys Glu Lys Leu Lys Gly Pro Pro Glu Lys Lys Pro Lys Lys Met Lys
785 790 795 800

Glu Arg Pro Asp Leu Lys Leu Lys Cys Gly Ala Cys Gly Ala Ile Gly
805 810 815

His Met Arg Thr Asn Lys Phe Cys Pro Leu Tyr Tyr Gln Thr Asn Ala
820 825 830

Pro Pro Ser Asn Pro Val Ala Met Thr Glu Glu Gln Glu Glu Glu Leu
835 840 845

Glu Lys Thr Val Ile His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu
850 855 860

Gly Thr Lys Ile Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu
865 870 875 880

Val Arg Arg Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro
885 890 895

Pro Lys Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu
900 905 910

Asn Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val
915 920 925

Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg Asp Leu
930 935 940

Pro Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala Lys Val Val Lys

945 950 955 960

Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met Asp Leu Gln Thr Leu Arg
965 970 975

Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser Arg Glu Glu Phe Arg Glu
980 985 990

His Leu Glu Leu Ile Val Lys Asn Ser Ala Thr Tyr Asn Gly Pro Lys
995 1000 1005

His Ser Leu Thr Gln Ile Ser Gln Ser Met Leu Asp Leu Cys Asp
1010 1015 1020

Glu Lys Leu Lys Glu Lys Glu Asp Lys Leu Ala Arg Leu Glu Lys
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Ala Ile Asn Pro Leu Leu Asp Asp Asp Asp Gln Val Ala Phe Ser
1040 1045 1050

Phe Ile Leu Asp Asn Ile Val Thr Gln Lys Met Met Ala Val Pro
1055 1060 1065

Asp Ser Trp Pro Phe His His Pro Val Asn Lys Lys Phe Val Pro
1070 1075 1080

Asp Tyr Tyr Lys Val Ile Val Asn Pro Met Asp Leu Glu Thr Ile
1085 1090 1095

Arg Lys Asn Ile Ser Lys His Lys Tyr Gln Ser Arg Glu Ser Phe
1100 1105 1110

Leu Asp Asp Val Asn Leu Ile Leu Ala Asn Ser Val Lys Tyr Asn
1115 1120 1125

Gly Pro Glu Ser Gln Tyr Thr Lys Thr Ala Gln Glu Ile Val Asn
1130 1135 1140

Val Cys Tyr Gln Thr Leu Thr Glu Tyr Asp Glu His Leu Thr Gln
1145 1150 1155

Leu Glu Lys Asp Ile Cys Thr Ala Lys Glu Ala Ala Leu Glu Glu
1160 1165 1170

Ala Glu Leu Glu Ser Leu Asp Pro Met Thr Pro Gly Pro Tyr Thr
1175 1180 1185

Pro Gln Pro Pro Asp Leu Tyr Asp Thr Asn Thr Ser Leu Ser Met
1190 1195 1200

Ser Arg Asp Ala Ser Val Phe Gln Asp Glu Ser Asn Met Ser Val
1205 1210 1215

Leu Asp Ile Pro Ser Ala Thr Pro Glu Lys Gln Val Thr Gln Glu
1220 1225 1230

Gly Glu Asp Gly Asp Gly Asp Leu Ala Asp Glu Glu Glu Gly Thr
1235 1240 1245

Val Gln Gln Pro Gln Ala Ser Val Leu Tyr Glu Asp Leu Leu Met
1250 1255 1260

Ser Glu Gly Glu Asp Asp Glu Glu Asp Ala Gly Ser Asp Glu Glu
1265 1270 1275

Gly Asp Asn Pro Phe Ser Ala Ile Gln Leu Ser Glu Ser Gly Ser
1280 1285 1290

Asp Ser Asp Val Gly Ser Gly Gly Ile Arg Pro Lys Gln Pro Arg
1295 1300 1305

Met Leu Gln Glu Asn Thr Arg Met Asp Met Glu Asn Glu Glu Ser
1310 1315 1320

Met Met Ser Tyr Glu Gly Asp Gly Gly Glu Ala Ser His Gly Leu
1325 1330 1335

Glu Asp Ser Asn Ile Ser Tyr Gly Ser Tyr Glu Glu Pro Asp Pro
1340 1345 1350

Lys Ser Asn Thr Gln Asp Thr Ser Phe Ser Ser Ile Gly Gly Tyr
1355 1360 1365

Glu Val Ser Glu Glu Glu Glu Asp Glu Glu Glu Glu Glu Glu Gln Arg
1370 1375 1380

Ser Gly Pro Ser Val Leu Ser Gln Val His Leu Ser Glu Asp Glu
1385 1390 1395

Glu Asp Ser Glu Asp Phe His Ser Ile Ala Gly Asp Ser Asp Leu
1400 1405 1410

Asp Ser Asp Glu
1415

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Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly

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Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
100 105 110

Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser Phe
115 120 125

Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu Lys
130 135 140

His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala Ser
145 150 155 160

Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr Gly
165 170 175

Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly Pro
180 185 190

Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr Lys
195 200 205

Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly Glu
210 215 220

Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro Gly
225 230 235 240

Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile Tyr
245 250 255

Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg Gln
260 265 270

Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln Gln
275 280 285

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

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His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp Lys
305 310 315 320

Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys Ala
325 330 335

Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu Cys
340 345 350

Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu Lys
355 360 365

Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val Ser
370 375 380

Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln Arg
385 390 395 400

Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu Glu
405 410 415

Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg Thr
420 425 430

Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly Lys
435 440 445

Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly Glu
450 455 460

Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys Asp
465 470 475 480

Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp Ala
485 490 495

Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg Lys
500 505 510

Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp Glu Val
515 520 525

Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg Ser Gly Glu
530 535 540

Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe Ser Val Ala Glu
545 550 555 560

His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg Ile Phe Asp Leu Gln
565 570 575

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Asn Lys Val Leu Ser Ser Thr Glu Val Leu Ser Thr Asp Thr Asp Ser
            580                 585                 590

Ser Ser Ala Glu Asp Ser Asp Phe Glu Glu Met Gly Lys Asn Ile Glu
        595                 600                 605

Asn Met Leu Gln Asn Lys Lys Thr Ser Ser Gln Leu Ser Arg Glu Arg
    610                 615                 620

Glu Glu Gln Glu Arg Lys Glu Leu Gln Arg Met Leu Leu Ala Ala Gly
625                 630                 635                 640

Ser Ala Ala Ser Gly Asn Asn His Arg Asp Asp Asp Thr Ala Ser Val
                645                 650                 655

Thr Ser Leu Asn Ser Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg
            660                 665                 670

Thr Phe Arg Asp Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val
        675                 680                 685

Arg Lys Pro Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys
    690                 695                 700

Asp Glu Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg
705                 710                 715                 720

Glu Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
                725                 730                 735

Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu Lys
            740                 745                 750

Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys Cys Gly
        755                 760                 765

Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe Cys Pro Leu
    770                 775                 780

Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val Ala Met Thr Glu
785                 790                 795                 800

Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile His Asn Asp Asn Glu
                805                 810                 815

Glu Leu Ile Lys Val Glu Gly Thr Lys Ile Val Leu Gly Lys Gln Leu
            820                 825                 830

Ile Glu Ser Ala Asp Glu Val Arg Arg Lys Ser Leu Val Leu Lys Phe
        835                 840                 845
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Pro Lys Gln Gln Leu Pro Pro Lys Lys Lys Arg Arg Val Gly Thr Thr
    850                 855                 860

Val His Cys Asp Tyr Leu Asn Arg Pro His Lys Ser Ile His Arg Arg
865                 870                 875                 880

Arg Thr Asp Pro Met Val Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile
                885                 890                 895

Asn Asp Met Arg Asp Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val
            900                 905                 910

Asn Ala Lys Val Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met
        915                 920                 925

Asp Leu Gln Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser
    930                 935                 940

Arg Glu Glu Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn Ser Ala
945                 950                 955                 960

Thr Tyr Asn Gly Pro Lys His Ser Leu Thr Gln Ile Ser Gln Ser Met
                965                 970                 975

Leu Asp Leu Cys Asp Glu Lys Leu Lys Glu Lys Glu Asp Lys Leu Ala
            980                 985                 990

Arg Leu Glu Lys Ala Ile Asn Pro  Leu Leu Asp Asp Asp  Asp Gln Val
        995                 1000                1005

Ala Phe  Ser Phe Ile Leu Asp  Asn Ile Val Thr Gln  Lys Met Met
    1010                1015                1020

Ala Val  Pro Asp Ser Trp Pro  Phe His His Pro Val  Asn Lys Lys
    1025                1030                1035

Phe Val  Pro Asp Tyr Tyr Lys  Val Ile Val Asn Pro  Met Asp Leu
    1040                1045                1050

Glu Thr  Ile Arg Lys Asn Ile  Ser Lys His Lys Tyr  Gln Ser Arg
    1055                1060                1065

Glu Ser  Phe Leu Asp Asp Val  Asn Leu Ile Leu Ala  Asn Ser Val
    1070                1075                1080

Lys Tyr  Asn Gly Pro Glu Ser  Gln Tyr Thr Lys Thr  Ala Gln Glu
    1085                1090                1095

Ile Val  Asn Val Cys Tyr Gln  Thr Leu Thr Glu Tyr  Asp Glu His
    1100                1105                1110

Leu Thr  Gln Leu Glu Lys Asp  Ile Cys Thr Ala Lys  Glu Ala Ala
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1115 1120 1125

Leu Glu Glu Ala Glu Leu Glu Ser Leu Asp Pro Met Thr Pro Gly
1130 1135 1140

Pro Tyr Thr Pro Gln Pro Pro Asp Leu Tyr Asp Thr Asn Thr Ser
1145 1150 1155

Leu Ser Met Ser Arg Asp Ala Ser Val Phe Gln Asp Glu Ser Asn
1160 1165 1170

Met Ser Val Leu Asp Ile Pro Ser Ala Thr Pro Glu Lys Gln Val
1175 1180 1185

Thr Gln Glu Gly Glu Asp Gly Asp Gly Asp Leu Ala Asp Glu Glu
1190 1195 1200

Glu Gly Thr Val Gln Gln Pro Gln Ala Ser Val Leu Tyr Glu Asp
1205 1210 1215

Leu Leu Met Ser Glu Gly Glu Asp Asp Glu Glu Asp Ala Gly Ser
1220 1225 1230

Asp Glu Glu Gly Asp Asn Pro Phe Ser Ala Ile Gln Leu Ser Glu
1235 1240 1245

Ser Gly Ser Asp Ser Asp Val Gly Ser Gly Gly Ile Arg Pro Lys
1250 1255 1260

Gln Pro Arg Met Leu Gln Glu Asn Thr Arg Met Asp Met Glu Asn
1265 1270 1275

Glu Glu Ser Met Met Ser Tyr Glu Gly Asp Gly Gly Glu Ala Ser
1280 1285 1290

His Gly Leu Glu Asp Ser Asn Ile Ser Tyr Gly Ser Tyr Glu Glu
1295 1300 1305

Pro Asp Pro Lys Ser Asn Thr Gln Asp Thr Ser Phe Ser Ser Ile
1310 1315 1320

Gly Gly Tyr Glu Val Ser Glu Glu Glu Glu Asp Glu Glu Glu Glu
1325 1330 1335

Glu Gln Arg Ser Gly Pro Ser Val Leu Ser Gln Val His Leu Ser
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Glu Asp Glu Glu Asp Ser Glu Asp Phe His Ser Ile Ala Gly Asp
1355 1360 1365

Ser Asp Leu Asp Ser Asp Glu
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Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser Phe Gly Ala
85 90 95

Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu Lys His Ile
100 105 110

Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala Ser Gly Gly
115 120 125

Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr Gly Lys Asp
130 135 140

Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly Pro Leu Met
145 150 155 160

Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr Lys Arg Lys
165 170 175

Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly Glu Thr Val
180 185 190

Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro Gly Gln Leu
195 200 205

Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile Tyr Leu His
210 215 220

Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg Gln Gly Tyr
225 230 235 240

Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln Gln Cys Pro

245 250 255

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

Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp Lys Ser Lys
275 280 285

Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys Ala Phe Pro
290 295 300

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

Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu Lys Ser Asp
325 330 335

Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val Ser Pro Glu
340 345 350

Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln Arg Leu Lys
355 360 365

Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu Glu Glu Asn
370 375 380

Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg Thr Ala Pro
385 390 395 400

Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly Lys Cys Leu
405 410 415

Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly Glu Gly Phe
420 425 430

Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys Asp Asp Lys
435 440 445

Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp Ala Asp Leu
450 455 460

Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg Lys Phe Gly
465 470 475 480

Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp Glu Val Ile Asp
485 490 495

Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg Ser Gly Glu Gly Pro
500 505 510

Met Ser Lys Phe Ala Arg Gly Ser Arg Phe Ser Val Ala Glu His Gln
515 520 525

Glu Arg Tyr Lys Glu Glu Cys Gln Arg Ile Phe Asp Leu Gln Asn Lys
530 535 540

Val Leu Ser Ser Thr Glu Val Leu Ser Thr Asp Thr Asp Ser Ser Ser
545 550 555 560

Ala Glu Asp Ser Asp Phe Glu Glu Met Gly Lys Asn Ile Glu Asn Met
565 570 575

Leu Gln Asn Lys Lys Thr Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu
580 585 590

Gln Glu Arg Lys Glu Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala
595 600 605

Ala Ser Gly Asn Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser
610 615 620

Leu Asn Ser Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe
625 630 635 640

Arg Asp Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys
645 650 655

Pro Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu
660 665 670

Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu Glu
675 680 685

Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg Leu Lys
690 695 700

Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu Lys Lys Pro
705 710 715 720

Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys Cys Gly Ala Cys
725 730 735

Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe Cys Pro Leu Tyr Tyr
740 745 750

Gln Thr Asn Ala Pro Pro Ser Asn Pro Val Ala Met Thr Glu Glu Gln
755 760 765

Glu Glu Glu Leu Glu Lys Thr Val Ile His Asn Asp Asn Glu Glu Leu
770 775 780

Ile Lys Val Glu Gly Thr Lys Ile Val Leu Gly Lys Gln Leu Ile Glu
785 790 795 800

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Ser Ala Asp Glu Val Arg Arg Lys Ser Leu Val Leu Lys Phe Pro Lys
805 810 815

Gln Gln Leu Pro Pro Lys Lys Lys Arg Arg Val Gly Thr Thr Val His
820 825 830

Cys Asp Tyr Leu Asn Arg Pro His Lys Ser Ile His Arg Arg Arg Thr
835 840 845

Asp Pro Met Val Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp
850 855 860

Met Arg Asp Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala
865 870 875 880

Lys Val Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met Asp Leu
885 890 895

Gln Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser Arg Glu
900 905 910

Glu Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn Ser Ala Thr Tyr
915 920 925

Asn Gly Pro Lys His Ser Leu Thr Gln Ile Ser Gln Ser Met Leu Asp
930 935 940

Leu Cys Asp Glu Lys Leu Lys Glu Lys Glu Asp Lys Leu Ala Arg Leu
945 950 955 960

Glu Lys Ala Ile Asn Pro Leu Leu Asp Asp Asp Asp Gln Val Ala Phe
965 970 975

Ser Phe Ile Leu Asp Asn Ile Val Thr Gln Lys Met Met Ala Val Pro
980 985 990

Asp Ser Trp Pro Phe His His Pro Val Asn Lys Lys Phe Val Pro Asp
995 1000 1005

Tyr Tyr Lys Val Ile Val Asn Pro Met Asp Leu Glu Thr Ile Arg
1010 1015 1020

Lys Asn Ile Ser Lys His Lys Tyr Gln Ser Arg Glu Ser Phe Leu
1025 1030 1035

Asp Asp Val Asn Leu Ile Leu Ala Asn Ser Val Lys Tyr Asn Gly
1040 1045 1050

Pro Glu Ser Gln Tyr Thr Lys Thr Ala Gln Glu Ile Val Asn Val
1055 1060 1065

Cys Tyr Gln Thr Leu Thr Glu Tyr Asp Glu His Leu Thr Gln Leu
1070 1075 1080

Glu Lys Asp Ile Cys Thr Ala Lys Glu Ala Ala Leu Glu Glu Ala
1085 1090 1095

Glu Leu Glu Ser Leu Asp Pro Met Thr Pro Gly Pro Tyr Thr Pro
1100 1105 1110

Gln Pro Pro Asp Leu Tyr Asp Thr Asn Thr Ser Leu Ser Met Ser
1115 1120 1125

Arg Asp Ala Ser Val Phe Gln Asp Glu Ser Asn Met Ser Val Leu
1130 1135 1140

Asp Ile Pro Ser Ala Thr Pro Glu Lys Gln Val Thr Gln Glu Gly
1145 1150 1155

Glu Asp Gly Asp Gly Asp Leu Ala Asp Glu Glu Glu Gly Thr Val
1160 1165 1170

Gln Gln Pro Gln Ala Ser Val Leu Tyr Glu Asp Leu Leu Met Ser
1175 1180 1185

Glu Gly Glu Asp Asp Glu Glu Asp Ala Gly Ser Asp Glu Glu Gly
1190 1195 1200

Asp Asn Pro Phe Ser Ala Ile Gln Leu Ser Glu Ser Gly Ser Asp
1205 1210 1215

Ser Asp Val Gly Ser Gly Gly Ile Arg Pro Lys Gln Pro Arg Met
1220 1225 1230

Leu Gln Glu Asn Thr Arg Met Asp Met Glu Asn Glu Glu Ser Met
1235 1240 1245

Met Ser Tyr Glu Gly Asp Gly Gly Glu Ala Ser His Gly Leu Glu
1250 1255 1260

Asp Ser Asn Ile Ser Tyr Gly Ser Tyr Glu Glu Pro Asp Pro Lys
1265 1270 1275

Ser Asn Thr Gln Asp Thr Ser Phe Ser Ser Ile Gly Gly Tyr Glu
1280 1285 1290

Val Ser Glu Glu Glu Glu Asp Glu Glu Glu Glu Glu Gln Arg Ser
1295 1300 1305

Gly Pro Ser Val Leu Ser Gln Val His Leu Ser Glu Asp Glu Glu
1310 1315 1320

Asp Ser Glu Asp Phe His Ser Ile Ala Gly Asp Ser Asp Leu Asp

1325 1330 1335

Ser Asp Glu
1340

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20 25 30

Ala Glu Tyr Ser Glu Glu Asn Gly Pro Leu Met Met Gln Val Gly Met
35 40 45

Ala Thr Lys Ile Lys Asn Tyr Tyr Lys Arg Lys Pro Gly Lys Asp Pro
50 55 60

Gly Ala Pro Asp Cys Lys Tyr Gly Glu Thr Val Tyr Cys His Thr Ser
65 70 75 80

Pro Phe Leu Gly Ser Leu His Pro Gly Gln Leu Leu Gln Ala Phe Glu
85 90 95

Asn Asn Leu Phe Arg Ala Pro Ile Tyr Leu His Lys Met Pro Glu Thr
100 105 110

Asp Phe Leu Ile Ile Arg Thr Arg Gln Gly Tyr Tyr Ile Arg Glu Leu
115 120 125

Val Asp Ile Phe Val Val Gly Gln Gln Cys Pro Leu Phe Glu Val Pro
130 135 140

Gly Pro Asn Ser Lys Arg Ala Asn Thr His Ile Arg Asp Phe Leu Gln
145 150 155 160

Val Phe Ile Tyr Arg Leu Phe Trp Lys Ser Lys Asp Arg Pro Arg Arg
165 170 175

Ile Arg Met Glu Asp Ile Lys Lys Ala Phe Pro Ser His Ser Glu Ser
180 185 190

Ser Ile Arg Lys Arg Leu Lys Leu Cys Ala Asp Phe Lys Arg Thr Gly
195 200 205

Met Asp Ser Asn Trp Trp Val Leu Lys Ser Asp Phe Arg Leu Pro Thr
210 215 220

```
Glu Glu Glu Ile Arg Ala Met Val Ser Pro Glu Gln Cys Cys Ala Tyr
225                 230                 235                 240

Tyr Ser Met Ile Ala Ala Glu Gln Arg Leu Lys Asp Ala Gly Tyr Gly
                245                 250                 255

Glu Lys Ser Phe Phe Ala Pro Glu Glu Glu Asn Glu Glu Asp Phe Gln
            260                 265                 270

Met Lys Ile Asp Asp Glu Val Arg Thr Ala Pro Trp Asn Thr Thr Arg
        275                 280                 285

Ala Phe Ile Ala Ala Met Lys Gly Lys Cys Leu Leu Glu Val Thr Gly
    290                 295                 300

Val Ala Asp Pro Thr Gly Cys Gly Glu Gly Phe Ser Tyr Val Lys Ile
305                 310                 315                 320

Pro Asn Lys Pro Thr Gln Gln Lys Asp Asp Lys Glu Pro Gln Pro Val
                325                 330                 335

Lys Lys Thr Val Thr Gly Thr Asp Ala Asp Leu Arg Arg Leu Ser Leu
            340                 345                 350

Lys Asn Ala Lys Gln Leu Leu Arg Lys Phe Gly Val Pro Glu Glu Glu
        355                 360                 365

Ile Lys Lys Leu Ser Arg Trp Glu Val Ile Asp Val Val Arg Thr Met
    370                 375                 380

Ser Thr Glu Gln Ala Arg Ser Gly Glu Gly Pro Met Ser Lys Phe Ala
385                 390                 395                 400

Arg Gly Ser Arg Phe Ser Val Ala Glu His Gln Glu Arg Tyr Lys Glu
                405                 410                 415

Glu Cys Gln Arg Ile Phe Asp Leu Gln Asn Lys Val Leu Ser Ser Thr
            420                 425                 430

Glu Val Leu Ser Thr Asp Thr Asp Ser Ser Ser Ala Glu Asp Ser Asp
        435                 440                 445

Phe Glu Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys Lys
    450                 455                 460

Thr Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu
465                 470                 475                 480

Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn Asn
                485                 490                 495

His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser Ser Ala
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500 505 510

Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp Glu Glu Gly
515 520 525

Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro Ala Val Ile Asp
530 535 540

Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu Glu Phe Ile Arg Lys
545 550 555 560

Phe Ala Leu Phe Asp Glu Gln His Arg Glu Glu Met Arg Lys Glu Arg
565 570 575

Arg Arg Ile Gln Glu Gln Leu Arg Arg Leu Lys Arg Asn Gln Glu Lys
580 585 590

Glu Lys Leu Lys Gly Pro Pro Glu Lys Lys Pro Lys Lys Met Lys Glu
595 600 605

Arg Pro Asp Leu Lys Leu Lys Cys Gly Ala Cys Gly Ala Ile Gly His
610 615 620

Met Arg Thr Asn Lys Phe Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro
625 630 635 640

Pro Ser Asn Pro Val Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu
645 650 655

Lys Thr Val Ile His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly
660 665 670

Thr Lys Ile Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val
675 680 685

Arg Arg Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro
690 695 700

Lys Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn
705 710 715 720

Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val Thr
725 730 735

Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg Asp Leu Pro
740 745 750

Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala Lys Val Val Lys Asp
755 760 765

Tyr Tyr Lys Ile Ile Thr Arg Pro Met Asp Leu Gln Thr Leu Arg Glu
770 775 780

```
Asn Val Arg Lys Arg Leu Tyr Pro Ser Arg Glu Glu Phe Arg Glu His
785                 790                 795                 800

Leu Glu Leu Ile Val Lys Asn Ser Ala Thr Tyr Asn Gly Pro Lys His
                805                 810                 815

Ser Leu Thr Gln Ile Ser Gln Ser Met Leu Asp Leu Cys Asp Glu Lys
            820                 825                 830

Leu Lys Glu Lys Glu Asp Lys Leu Ala Arg Leu Glu Lys Ala Ile Asn
        835                 840                 845

Pro Leu Leu Asp Asp Asp Asp Gln Val Ala Phe Ser Phe Ile Leu Asp
    850                 855                 860

Asn Ile Val Thr Gln Lys Met Met Ala Val Pro Asp Ser Trp Pro Phe
865                 870                 875                 880

His His Pro Val Asn Lys Lys Phe Val Pro Asp Tyr Tyr Lys Val Ile
                885                 890                 895

Val Asn Pro Met Asp Leu Glu Thr Ile Arg Lys Asn Ile Ser Lys His
            900                 905                 910

Lys Tyr Gln Ser Arg Glu Ser Phe Leu Asp Asp Val Asn Leu Ile Leu
        915                 920                 925

Ala Asn Ser Val Lys Tyr Asn Gly Pro Glu Ser Gln Tyr Thr Lys Thr
    930                 935                 940

Ala Gln Glu Ile Val Asn Val Cys Tyr Gln Thr Leu Thr Glu Tyr Asp
945                 950                 955                 960

Glu His Leu Thr Gln Leu Glu Lys Asp Ile Cys Thr Ala Lys Glu Ala
                965                 970                 975

Ala Leu Glu Glu Ala Glu Leu Glu Ser Leu Asp Pro Met Thr Pro Gly
            980                 985                 990

Pro Tyr Thr Pro Gln Pro Pro Asp  Leu Tyr Asp Thr Asn  Thr Ser Leu
        995                 1000                1005

Ser Met  Ser Arg Asp Ala Ser  Val Phe Gln Asp Glu  Ser Asn Met
    1010                1015                1020

Ser Val  Leu Asp Ile Pro Ser  Ala Thr Pro Glu Lys  Gln Val Thr
    1025                1030                1035

Gln Glu  Gly Glu Asp Gly Asp  Gly Asp Leu Ala Asp  Glu Glu Glu
    1040                1045                1050
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Gly Thr Val Gln Gln Pro Gln Ala Ser Val Leu Tyr Glu Asp Leu
1055 1060 1065

Leu Met Ser Glu Gly Glu Asp Asp Glu Glu Asp Ala Gly Ser Asp
1070 1075 1080

Glu Glu Gly Asp Asn Pro Phe Ser Ala Ile Gln Leu Ser Glu Ser
1085 1090 1095

Gly Ser Asp Ser Asp Val Gly Ser Gly Gly Ile Arg Pro Lys Gln
1100 1105 1110

Pro Arg Met Leu Gln Glu Asn Thr Arg Met Asp Met Glu Asn Glu
1115 1120 1125

Glu Ser Met Met Ser Tyr Glu Gly Asp Gly Gly Glu Ala Ser His
1130 1135 1140

Gly Leu Glu Asp Ser Asn Ile Ser Tyr Gly Ser Tyr Glu Glu Pro
1145 1150 1155

Asp Pro Lys Ser Asn Thr Gln Asp Thr Ser Phe Ser Ser Ile Gly
1160 1165 1170

Gly Tyr Glu Val Ser Glu Glu Glu Glu Asp Glu Glu Glu Glu Glu
1175 1180 1185

Gln Arg Ser Gly Pro Ser Val Leu Ser Gln Val His Leu Ser Glu
1190 1195 1200

Asp Glu Glu Asp Ser Glu Asp Phe His Ser Ile Ala Gly Asp Ser
1205 1210 1215

Asp Leu Asp Ser Asp Glu
1220

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Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr
1 5 10 15

Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
20 25 30

Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

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His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
100 105 110

Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser Phe
115 120 125

Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu Lys
130 135 140

His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala Ser
145 150 155 160

Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr Gly
165 170 175

Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly Pro
180 185 190

Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr Lys
195 200 205

Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly Glu
210 215 220

Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro Gly
225 230 235 240

Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile Tyr
245 250 255

Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg Gln
260 265 270

Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln Gln
275 280 285

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

His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp Lys
305 310 315 320

Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys Ala
325 330 335

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Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu Cys
            340                 345                 350

Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu Lys
        355                 360                 365

Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val Ser
    370                 375                 380

Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln Arg
385                 390                 395                 400

Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu Glu
                405                 410                 415

Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg Thr
            420                 425                 430

Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly Lys
        435                 440                 445

Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly Glu
    450                 455                 460

Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys Asp
465                 470                 475                 480

Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp Ala
                485                 490                 495

Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg Lys
            500                 505                 510

Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp Glu Val
        515                 520                 525

Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg Ser Gly Glu
    530                 535                 540

Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe Ser Val Ala Glu
545                 550                 555                 560

His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg Ile Phe Asp Leu Gln
                565                 570                 575

Asn Lys Val Leu Ser Ser Thr Glu Val Leu Ser Thr Asp Thr Asp Ser
            580                 585                 590

Ser Ser Ala Glu Asp Ser Asp Phe Glu Glu Met Gly Lys Asn Ile Glu
        595                 600                 605
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Asn Met Leu Gln Asn Lys Lys Thr Ser Ser Gln Leu Ser Arg Glu Arg
610 615 620

Glu Glu Gln Glu Arg Lys Glu Leu Gln Arg Met Leu Leu Ala Ala Gly
625 630 635 640

Ser Ala Ala Ser Gly Asn Asn His Arg Asp Asp Asp Thr Ala Ser Val
645 650 655

Thr Ser Leu Asn Ser Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg
660 665 670

Thr Phe Arg Asp Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val
675 680 685

Arg Lys Pro Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys
690 695 700

Asp Glu Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg
705 710 715 720

Glu Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
725 730 735

Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu Lys
740 745 750

Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys Cys Gly
755 760 765

Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe Cys Pro Leu
770 775 780

Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val Ala Met Thr Glu
785 790 795 800

Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile His Asn Asp Asn Glu
805 810 815

Glu Leu Ile Lys Val Glu Gly Thr Lys Ile Val Leu Gly Lys Gln Leu
820 825 830

Ile Glu Ser Ala Asp Glu Val Arg Arg Lys Ser Leu Val Leu Lys Phe
835 840 845

Pro Lys Gln Gln Leu Pro Pro Lys Lys Lys Arg Arg Val Gly Thr Thr
850 855 860

Val His Cys Asp Tyr Leu Asn Arg Pro His Lys Ser Ile His Arg Arg
865 870 875 880

Arg Thr Asp Pro Met Val Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile

885 890 895

Asn Asp Met Arg Asp Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val
900 905 910

Asn Ala Lys Val Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met
915 920 925

Asp Leu Gln Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser
930 935 940

Arg Glu Glu Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn Ser Ala
945 950 955 960

Thr Tyr Asn Gly Pro Lys His Ser Leu Thr Gln Ile Ser Gln Ser Met
965 970 975

Leu Asp Leu Cys Asp Glu Lys Leu Lys Glu Lys Glu Asp Lys Leu Ala
980 985 990

Arg Leu Glu Lys Ala Ile Asn Pro Leu Leu Asp Asp Asp Asp Gln Val
995 1000 1005

Ala Phe Ser Phe Ile Leu Asp Asn Ile Val Thr Gln Lys Met Met
1010 1015 1020

Ala Val Pro Asp Ser Trp Pro Phe His His Pro Val Asn Lys Lys
1025 1030 1035

Phe Val Pro Asp Tyr Tyr Lys Val Ile Val Asn Pro Met Asp Leu
1040 1045 1050

Glu Thr Ile Arg Lys Asn Ile Ser Lys His Lys Tyr Gln Ser Arg
1055 1060 1065

Glu Ser Phe Leu Asp Asp Val Asn Leu Ile Leu Ala Asn Ser Val
1070 1075 1080

Lys Tyr Asn Gly Pro Glu Ser Gln Tyr Thr Lys Thr Ala Gln Glu
1085 1090 1095

Ile Val Asn Val Cys Tyr Gln Thr Leu Thr Glu Tyr Asp Glu His
1100 1105 1110

Leu Thr Gln Leu Glu Lys Asp Ile Cys Thr Ala Lys Glu Ala Ala
1115 1120 1125

Leu Glu Glu Ala Glu Leu Glu Ser Leu Asp Pro Met Thr Pro Gly
1130 1135 1140

Pro Tyr Thr Pro Gln Pro Pro Asp Leu Tyr Asp Thr Asn Thr Ser
1145 1150 1155

Leu Ser Met Ser Arg Asp Ala Ser Val Phe Gln Asp Glu Ser Asn
1160 1165 1170

Met Ser Val Leu Asp Ile Pro Ser Ala Thr Pro Glu Lys Gln Val
1175 1180 1185

Thr Gln Glu Gly Glu Asp Gly Asp Gly Asp Leu Ala Asp Glu Glu
1190 1195 1200

Glu Gly Thr Val Gln Gln Pro Gln Ala Ser Val Leu Tyr Glu Asp
1205 1210 1215

Leu Leu Met Ser Glu Gly Glu Asp Asp Glu Glu Asp Ala Gly Ser
1220 1225 1230

Asp Glu Glu Gly Asp Asn Pro Phe Ser Ala Ile Gln Leu Ser Glu
1235 1240 1245

Ser Gly Ser Asp Ser Asp Val Gly Ser Gly Gly Ile Arg Pro Lys
1250 1255 1260

Gln Pro Arg Met Leu Gln Glu Asn Thr Arg Met Asp Met Glu Asn
1265 1270 1275

Glu Glu Ser Met Met Ser Tyr Glu Gly Asp Gly Gly Glu Ala Ser
1280 1285 1290

His Gly Leu Glu Asp Ser Asn Ile Ser Tyr Gly Ser Tyr Glu Glu
1295 1300 1305

Pro Asp Pro Lys Ser Asn Thr Gln Asp Thr Ser Phe Ser Ser Ile
1310 1315 1320

Gly Gly Tyr Glu Val Ser Glu Glu Glu Glu Asp Glu Glu Glu Glu
1325 1330 1335

Glu Gln Arg Ser Gly Pro Ser Val Leu Ser Gln Val His Leu Ser
1340 1345 1350

Glu Asp Glu Glu Asp Ser Glu Asp Phe His Ser Ile Ala Gly Asp
1355 1360 1365

Ser Asp Leu Asp Ser Asp Glu
1370 1375

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<212> PRT
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<400> 64
Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr

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Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
            20                  25                  30

Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
        35                  40                  45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
    50                  55                  60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65                  70                  75                  80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
                85                  90                  95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
            100                 105                 110

Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
        115                 120                 125

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

Asp Glu Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile
145                 150                 155                 160

Ile Trp Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg
                165                 170                 175

Ala Ser Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met
            180                 185                 190

Ala Tyr Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys
        195                 200                 205

Pro Trp Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly
    210                 215                 220

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

Leu Glu Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile
                245                 250                 255

Leu Glu Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser
            260                 265                 270

Lys Glu Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu
        275                 280                 285
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Gly Lys Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln
290 295 300

Pro Glu Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr
305 310 315 320

Pro Lys Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln
325 330 335

His Ser Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His
340 345 350

Met Gly Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys
355 360 365

Tyr Ser Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro
370 375 380

Leu Leu Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg
385 390 395 400

Gln Ala Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp
405 410 415

Leu Thr Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu
420 425 430

Asn Gly Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn
435 440 445

Tyr Tyr Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys
450 455 460

Tyr Gly Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu
465 470 475 480

His Pro Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala
485 490 495

Pro Ile Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg
500 505 510

Thr Arg Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val
515 520 525

Gly Gln Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg
530 535 540

Ala Asn Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu
545 550 555 560

Phe Trp Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile
565 570 575

Lys Lys Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu
580 585 590

Lys Leu Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp
595 600 605

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

Met Val Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala
625 630 635 640

Glu Gln Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala
645 650 655

Pro Glu Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu
660 665 670

Val Arg Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met
675 680 685

Lys Gly Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly
690 695 700

Cys Gly Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln
705 710 715 720

Gln Lys Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly
725 730 735

Thr Asp Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu
740 745 750

Leu Arg Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg
755 760 765

Trp Glu Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg
770 775 780

Ser Gly Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe Ser
785 790 795 800

Val Ala Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg Ile Phe
805 810 815

Asp Leu Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu Ser Thr Asp
820 825 830

```
Thr Asp Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu Glu Met Gly Lys
        835                 840                 845

Asn Ile Glu Asn Met Leu Gln Asn Lys Lys Thr Ser Ser Gln Leu Ser
    850                 855                 860

Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu Leu Gln Arg Met Leu Leu
865                 870                 875                 880

Ala Ala Gly Ser Ala Ala Ser Gly Asn Asn His Arg Asp Asp Asp Thr
                885                 890                 895

Ala Ser Val Thr Ser Leu Asn Ser Ser Ala Thr Gly Arg Cys Leu Lys
            900                 905                 910

Ile Tyr Arg Thr Phe Arg Asp Glu Glu Gly Lys Glu Tyr Val Arg Cys
        915                 920                 925

Glu Thr Val Arg Lys Pro Ala Val Ile Asp Ala Tyr Val Arg Ile Arg
    930                 935                 940

Thr Thr Lys Asp Glu Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu
945                 950                 955                 960

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

Leu Arg Arg Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro
            980                 985                 990

Pro Glu Lys Lys Pro Lys Lys Met  Lys Glu Arg Pro Asp  Leu Lys Leu
        995                 1000                1005

Lys Cys  Gly Ala Cys Gly Ala  Ile Gly His Met Arg  Thr Asn Lys
    1010                1015                1020

Phe Cys  Pro Leu Tyr Tyr Gln  Thr Asn Ala Pro Pro  Ser Asn Pro
    1025                1030                1035

Val Ala  Met Thr Glu Glu Gln  Glu Glu Glu Leu Glu  Lys Thr Val
    1040                1045                1050

Ile His  Asn Asp Asn Glu Glu  Leu Ile Lys Val Glu  Gly Thr Lys
    1055                1060                1065

Ile Val  Leu Gly Lys Gln Leu  Ile Glu Ser Ala Asp  Glu Val Arg
    1070                1075                1080

Arg Lys  Ser Leu Val Leu Lys  Phe Pro Lys Gln Gln  Leu Pro Pro
    1085                1090                1095

Lys Lys  Lys Arg Arg Val Gly  Thr Thr Val His Cys  Asp Tyr Leu
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1100 1105 1110

Asn Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met
1115 1120 1125

Val Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg
1130 1135 1140

Asp Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala Lys
1145 1150 1155

Val Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met Asp Leu
1160 1165 1170

Gln Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser Arg
1175 1180 1185

Glu Glu Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn Ser Ala
1190 1195 1200

Thr Tyr Asn Gly Pro Lys His Ser Leu Thr Gln Ile Ser Gln Ser
1205 1210 1215

Met Leu Asp Leu Cys Asp Glu Lys Leu Lys Glu Lys Glu Asp Lys
1220 1225 1230

Leu Ala Arg Leu Glu Lys Ala Ile Asn Pro Leu Leu Asp Asp Asp
1235 1240 1245

Asp Gln Val Ala Phe Ser Phe Ile Leu Asp Asn Ile Val Thr Gln
1250 1255 1260

Lys Met Met Ala Val Pro Asp Ser Trp Pro Phe His His Pro Val
1265 1270 1275

Asn Lys Lys Phe Val Pro Asp Tyr Tyr Lys Val Ile Val Asn Pro
1280 1285 1290

Met Asp Leu Glu Thr Ile Arg Lys Asn Ile Ser Lys His Lys Tyr
1295 1300 1305

Gln Ser Arg Glu Ser Phe Leu Asp Asp Val Asn Leu Ile Leu Ala
1310 1315 1320

Asn Ser Val Lys Tyr Asn Gly Pro Glu Ser Gln Tyr Thr Lys Thr
1325 1330 1335

Ala Gln Glu Ile Val Asn Val Cys Tyr Gln Thr Leu Thr Glu Tyr
1340 1345 1350

Asp Glu His Leu Thr Gln Leu Glu Lys Asp Ile Cys Thr Ala Lys
1355 1360 1365

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Glu Ala Ala Leu Glu Glu Ala Glu Leu Glu Ser Leu Asp Pro Met
1370 1375 1380

Thr Pro Gly Pro Tyr Thr Pro Gln Pro Pro Asp Leu Tyr Asp Thr
1385 1390 1395

Asn Thr Ser Leu Ser Met Ser Arg Asp Ala Ser Val Phe Gln Asp
1400 1405 1410

Glu Ser Asn Met Ser Val Leu Asp Ile Pro Ser Ala Thr Pro Glu
1415 1420 1425

Lys Gln Val Thr Gln Glu Gly Glu Asp Gly Asp Gly Asp Leu Ala
1430 1435 1440

Asp Glu Glu Glu Gly Thr Val Gln Gln Pro Gln Ala Ser Val Leu
1445 1450 1455

Tyr Glu Asp Leu Leu Met Ser Glu Gly Glu Asp Asp Glu Glu Asp
1460 1465 1470

Ala Gly Ser Asp Glu Glu Gly Asp Asn Pro Phe Ser Ala Ile Gln
1475 1480 1485

Leu Ser Glu Ser Gly Ser Asp Ser Asp Val Gly Ser Gly Gly Ile
1490 1495 1500

Arg Pro Lys Gln Pro Arg Met Leu Gln Glu Asn Thr Arg Met Asp
1505 1510 1515

Met Glu Asn Glu Glu Ser Met Met Ser Tyr Glu Gly Asp Gly Gly
1520 1525 1530

Glu Ala Ser His Gly Leu Glu Asp Ser Asn Ile Ser Tyr Gly Ser
1535 1540 1545

Tyr Glu Glu Pro Asp Pro Lys Ser Asn Thr Gln Asp Thr Ser Phe
1550 1555 1560

Ser Ser Ile Gly Gly Tyr Glu Val Ser Glu Glu Glu Glu Asp Glu
1565 1570 1575

Glu Glu Glu Glu Gln Arg Ser Gly Pro Ser Val Leu Ser Gln Val
1580 1585 1590

His Leu Ser Glu Asp Glu Glu Asp Ser Glu Asp Phe His Ser Ile
1595 1600 1605

Ala Gly Asp Ser Asp Leu Asp Ser Asp Glu
1610 1615

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Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr
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Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
20 25 30

Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Lys Leu
35 40 45

Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser Phe Gly Ala Leu
50 55 60

Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu Lys His Ile Lys
65 70 75 80

Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala Ser Gly Gly Gly
85 90 95

Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr Gly Lys Asp Gly
100 105 110

Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly Pro Leu Met Met
115 120 125

Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr Lys Arg Lys Pro
130 135 140

Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly Glu Thr Val Tyr
145 150 155 160

Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro Gly Gln Leu Leu
165 170 175

Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile Tyr Leu His Lys
180 185 190

Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg Gln Gly Tyr Tyr
195 200 205

Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln Gln Cys Pro Leu
210 215 220

Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn Thr His Ile Arg
225 230 235 240

Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp Lys Ser Lys Asp
245 250 255

Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys Ala Phe Pro Ser
260 265 270

His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu Cys Ala Asp Phe
275 280 285

Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu Lys Ser Asp Phe
290 295 300

Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val Ser Pro Glu Gln
305 310 315 320

Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln Arg Leu Lys Asp
325 330 335

Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu Glu Glu Asn Glu
340 345 350

Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg Thr Ala Pro Trp
355 360 365

Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly Lys Cys Leu Leu
370 375 380

Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly Glu Gly Phe Ser
385 390 395 400

Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys Asp Asp Lys Glu
405 410 415

Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp Ala Asp Leu Arg
420 425 430

Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg Lys Phe Gly Val
435 440 445

Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp Glu Val Ile Asp Val
450 455 460

Val Arg Thr Met Ser Thr Glu Gln Ala Arg Ser Gly Glu Gly Pro Met
465 470 475 480

Ser Lys Phe Ala Arg Gly Ser Arg Phe Ser Val Ala Glu His Gln Glu
485 490 495

Arg Tyr Lys Glu Glu Cys Gln Arg Ile Phe Asp Leu Gln Asn Lys Val
500 505 510

Leu Ser Ser Thr Glu Val Leu Ser Thr Asp Thr Asp Ser Ser Ser Ala
515 520 525

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Glu Asp Ser Asp Phe Glu Glu Met Gly Lys Asn Ile Glu Asn Met Leu
    530                 535                 540

Gln Asn Lys Lys Thr Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln
545                 550                 555                 560

Glu Arg Lys Glu Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala
                565                 570                 575

Ser Gly Asn Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu
            580                 585                 590

Asn Ser Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg
        595                 600                 605

Asp Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro
    610                 615                 620

Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu Glu
625                 630                 635                 640

Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu Glu Met
                645                 650                 655

Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg Leu Lys Arg
            660                 665                 670

Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu Lys Lys Pro Lys
        675                 680                 685

Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys Cys Gly Ala Cys Gly
    690                 695                 700

Ala Ile Gly His Met Arg Thr Asn Lys Phe Cys Pro Leu Tyr Tyr Gln
705                 710                 715                 720

Thr Asn Ala Pro Pro Ser Asn Pro Val Ala Met Thr Glu Glu Gln Glu
                725                 730                 735

Glu Glu Leu Glu Lys Thr Val Ile His Asn Asp Asn Glu Glu Leu Ile
            740                 745                 750

Lys Val Glu Gly Thr Lys Ile Val Leu Gly Lys Gln Leu Ile Glu Ser
        755                 760                 765

Ala Asp Glu Val Arg Arg Lys Ser Leu Val Leu Lys Phe Pro Lys Gln
    770                 775                 780

Gln Leu Pro Pro Lys Lys Lys Arg Arg Val Gly Thr Thr Val His Cys
785                 790                 795                 800
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Asp Tyr Leu Asn Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp
805 810 815

Pro Met Val Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met
820 825 830

Arg Asp Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala Lys
835 840 845

Val Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met Asp Leu Gln
850 855 860

Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser Arg Glu Glu
865 870 875 880

Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn Ser Ala Thr Tyr Asn
885 890 895

Gly Pro Lys His Ser Leu Thr Gln Ile Ser Gln Ser Met Leu Asp Leu
900 905 910

Cys Asp Glu Lys Leu Lys Glu Lys Glu Asp Lys Leu Ala Arg Leu Glu
915 920 925

Lys Ala Ile Asn Pro Leu Leu Asp Asp Asp Asp Gln Val Ala Phe Ser
930 935 940

Phe Ile Leu Asp Asn Ile Val Thr Gln Lys Met Met Ala Val Pro Asp
945 950 955 960

Ser Trp Pro Phe His His Pro Val Asn Lys Lys Phe Val Pro Asp Tyr
965 970 975

Tyr Lys Val Ile Val Asn Pro Met Asp Leu Glu Thr Ile Arg Lys Asn
980 985 990

Ile Ser Lys His Lys Tyr Gln Ser Arg Glu Ser Phe Leu Asp Asp Val
995 1000 1005

Asn Leu Ile Leu Ala Asn Ser Val Lys Tyr Asn Gly Pro Glu Ser
1010 1015 1020

Gln Tyr Thr Lys Thr Ala Gln Glu Ile Val Asn Val Cys Tyr Gln
1025 1030 1035

Thr Leu Thr Glu Tyr Asp Glu His Leu Thr Gln Leu Glu Lys Asp
1040 1045 1050

Ile Cys Thr Ala Lys Glu Ala Ala Leu Glu Glu Ala Glu Leu Glu
1055 1060 1065

Ser Leu Asp Pro Met Thr Pro Gly Pro Tyr Thr Pro Gln Pro Pro

1070 1075 1080

Asp Leu Tyr Asp Thr Asn Thr Ser Leu Ser Met Ser Arg Asp Ala
1085 1090 1095

Ser Val Phe Gln Asp Glu Ser Asn Met Ser Val Leu Asp Ile Pro
1100 1105 1110

Ser Ala Thr Pro Glu Lys Gln Val Thr Gln Glu Gly Glu Asp Gly
1115 1120 1125

Asp Gly Asp Leu Ala Asp Glu Glu Glu Gly Thr Val Gln Gln Pro
1130 1135 1140

Gln Ala Ser Val Leu Tyr Glu Asp Leu Leu Met Ser Glu Gly Glu
1145 1150 1155

Asp Asp Glu Glu Asp Ala Gly Ser Asp Glu Glu Gly Asp Asn Pro
1160 1165 1170

Phe Ser Ala Ile Gln Leu Ser Glu Ser Gly Ser Asp Ser Asp Val
1175 1180 1185

Gly Ser Gly Gly Ile Arg Pro Lys Gln Pro Arg Met Leu Gln Glu
1190 1195 1200

Asn Thr Arg Met Asp Met Glu Asn Glu Glu Ser Met Met Ser Tyr
1205 1210 1215

Glu Gly Asp Gly Gly Glu Ala Ser His Gly Leu Glu Asp Ser Asn
1220 1225 1230

Ile Ser Tyr Gly Ser Tyr Glu Glu Pro Asp Pro Lys Ser Asn Thr
1235 1240 1245

Gln Asp Thr Ser Phe Ser Ser Ile Gly Gly Tyr Glu Val Ser Glu
1250 1255 1260

Glu Glu Glu Asp Glu Glu Glu Glu Glu Gln Arg Ser Gly Pro Ser
1265 1270 1275

Val Leu Ser Gln Val His Leu Ser Glu Asp Glu Glu Asp Ser Glu
1280 1285 1290

Asp Phe His Ser Ile Ala Gly Asp Ser Asp Leu Asp Ser Asp Glu
1295 1300 1305

<210> 66
<211> 1392
<212> PRT
<213> Homo sapiens

<400> 66

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Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr
1               5                  10                  15

Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
            20                  25                  30

Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
        35                  40                  45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
    50                  55                  60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65                  70                  75                  80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
                85                  90                  95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
            100                 105                 110

Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
        115                 120                 125

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

Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
145                 150                 155                 160

Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
                165                 170                 175

Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
            180                 185                 190

Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
        195                 200                 205

Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
    210                 215                 220

Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
225                 230                 235                 240

Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
                245                 250                 255

Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
            260                 265                 270

Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
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275 280 285

Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
290 295 300

Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
305 310 315 320

Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
325 330 335

Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
340 345 350

Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
355 360 365

Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
370 375 380

Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
385 390 395 400

Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
405 410 415

Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
420 425 430

Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
435 440 445

Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
450 455 460

Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
465 470 475 480

Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu
485 490 495

Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
500 505 510

Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
515 520 525

Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
530 535 540

Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
545 550 555 560

Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
565 570 575

Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His Ser
580 585 590

Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met Gly
595 600 605

Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
610 615 620

Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
625 630 635 640

Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
645 650 655

Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
660 665 670

Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
675 680 685

Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
690 695 700

Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
705 710 715 720

Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
725 730 735

Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
740 745 750

Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
755 760 765

Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln
770 775 780

Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
785 790 795 800

Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
805 810 815

Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
820 825 830

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Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
        835                 840                 845

Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
    850                 855                 860

Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
865                 870                 875                 880

Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
                885                 890                 895

Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
            900                 905                 910

Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
        915                 920                 925

Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
    930                 935                 940

Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
945                 950                 955                 960

Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
                965                 970                 975

Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
            980                 985                 990

Ala Asp Leu Arg Arg Leu Ser Leu  Lys Asn Ala Lys Gln  Leu Leu Arg
        995                 1000                1005

Lys Phe  Gly Val Pro Glu Glu  Glu Ile Lys Lys Leu  Ser Arg Trp
    1010                1015                1020

Glu Val  Ile Asp Val Val Arg  Thr Met Ser Thr Glu  Gln Ala Arg
    1025                1030                1035

Ser Gly  Glu Gly Pro Met Ser  Lys Phe Ala Arg Gly  Ser Arg Phe
    1040                1045                1050

Ser Val  Ala Glu His Gln Glu  Arg Tyr Lys Glu Glu  Cys Gln Arg
    1055                1060                1065

Ile Phe  Asp Leu Gln Asn Lys  Val Leu Ser Ser Thr  Glu Val Leu
    1070                1075                1080

Ser Thr  Asp Thr Asp Ser Ser  Ser Ala Glu Asp Ser  Asp Phe Glu
    1085                1090                1095
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Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys Lys Thr
1100 1105 1110

Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu
1115 1120 1125

Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn
1130 1135 1140

Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser
1145 1150 1155

Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp
1160 1165 1170

Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro
1175 1180 1185

Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu
1190 1195 1200

Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu
1205 1210 1215

Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
1220 1225 1230

Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
1235 1240 1245

Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys
1250 1255 1260

Cys Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe
1265 1270 1275

Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val
1280 1285 1290

Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile
1295 1300 1305

His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile
1310 1315 1320

Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val Arg Arg
1325 1330 1335

Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro Lys
1340 1345 1350

Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn

1355 1360 1365

Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val
1370 1375 1380

Thr Leu Ser Ser Ile Leu Glu Pro Gly
1385 1390

<210> 67
<211> 1488
<212> PRT
<213> Homo sapiens

<400> 67
Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr
1 5 10 15

Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
20 25 30

Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
100 105 110

Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
115 120 125

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

Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
145 150 155 160

Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
165 170 175

Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
180 185 190

Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
195 200 205

Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
210 215 220

Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
225 230 235 240

Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
245 250 255

Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
260 265 270

Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
275 280 285

Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
290 295 300

Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
305 310 315 320

Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
325 330 335

Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
340 345 350

Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
355 360 365

Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
370 375 380

Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
385 390 395 400

Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
405 410 415

Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
420 425 430

Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
435 440 445

Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
450 455 460

Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
465 470 475 480

Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu

485 490 495

Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
500 505 510

Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
515 520 525

Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
530 535 540

Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
545 550 555 560

Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
565 570 575

Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His Ser
580 585 590

Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met Gly
595 600 605

Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
610 615 620

Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
625 630 635 640

Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
645 650 655

Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
660 665 670

Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
675 680 685

Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
690 695 700

Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
705 710 715 720

Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
725 730 735

Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
740 745 750

Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
755 760 765

Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln
770 775 780

Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
785 790 795 800

Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
805 810 815

Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
820 825 830

Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
835 840 845

Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
850 855 860

Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
865 870 875 880

Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
885 890 895

Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
900 905 910

Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
915 920 925

Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
930 935 940

Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
945 950 955 960

Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
965 970 975

Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
980 985 990

Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
995 1000 1005

Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp
1010 1015 1020

Glu Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg
1025 1030 1035

Ser Gly Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe
1040 1045 1050

Ser Val Ala Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg
1055 1060 1065

Ile Phe Asp Leu Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu
1070 1075 1080

Ser Thr Asp Thr Asp Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu
1085 1090 1095

Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys Lys Thr
1100 1105 1110

Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu
1115 1120 1125

Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn
1130 1135 1140

Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser
1145 1150 1155

Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp
1160 1165 1170

Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro
1175 1180 1185

Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu
1190 1195 1200

Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu
1205 1210 1215

Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
1220 1225 1230

Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
1235 1240 1245

Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys
1250 1255 1260

Cys Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe
1265 1270 1275

Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val
1280 1285 1290

Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile
1295 1300 1305

His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile
1310 1315 1320

Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val Arg Arg
1325 1330 1335

Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro Lys
1340 1345 1350

Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn
1355 1360 1365

Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val
1370 1375 1380

Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg Asp
1385 1390 1395

Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala Lys Val
1400 1405 1410

Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met Asp Leu Gln
1415 1420 1425

Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser Arg Glu
1430 1435 1440

Glu Phe Arg Glu His Leu Asp Asp Arg Trp Arg Pro Cys Leu Lys
1445 1450 1455

Lys Lys Lys Lys Glu Glu Glu Thr Trp Leu Ser Glu Tyr Ala Phe
1460 1465 1470

His Lys Pro Thr Arg Gly Cys Ser Leu Pro Thr Gln Ser Gln Phe
1475 1480 1485

<210> 68
<211> 1425
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<400> 68
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Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
20 25 30

Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
100 105 110

Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
115 120 125

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

Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
145 150 155 160

Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
165 170 175

Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
180 185 190

Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
195 200 205

Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
210 215 220

Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
225 230 235 240

Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
245 250 255

Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
260 265 270

Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
275 280 285

Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
290 295 300

Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
305 310 315 320

Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
325 330 335

Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
340 345 350

Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
355 360 365

Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
370 375 380

Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
385 390 395 400

Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
405 410 415

Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
420 425 430

Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
435 440 445

Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
450 455 460

Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
465 470 475 480

Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu
485 490 495

Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
500 505 510

Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
515 520 525

Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
530 535 540

Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
545 550 555 560

Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
565 570 575

Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His Ser
580 585 590

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

595 600 605

Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
610 615 620

Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
625 630 635 640

Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
645 650 655

Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
660 665 670

Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
675 680 685

Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
690 695 700

Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
705 710 715 720

Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
725 730 735

Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
740 745 750

Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
755 760 765

Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln
770 775 780

Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
785 790 795 800

Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
805 810 815

Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
820 825 830

Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
835 840 845

Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
850 855 860

Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
865 870 875 880

Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
885 890 895

Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
900 905 910

Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
915 920 925

Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
930 935 940

Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
945 950 955 960

Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
965 970 975

Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
980 985 990

Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
995 1000 1005

Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp
1010 1015 1020

Glu Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg
1025 1030 1035

Ser Gly Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe
1040 1045 1050

Ser Val Ala Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg
1055 1060 1065

Ile Phe Asp Leu Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu
1070 1075 1080

Ser Thr Asp Thr Asp Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu
1085 1090 1095

Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys Lys Thr
1100 1105 1110

Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu
1115 1120 1125

Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn
1130 1135 1140

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Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser
1145 1150 1155

Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp
1160 1165 1170

Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro
1175 1180 1185

Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu
1190 1195 1200

Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu
1205 1210 1215

Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
1220 1225 1230

Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
1235 1240 1245

Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys
1250 1255 1260

Cys Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe
1265 1270 1275

Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val
1280 1285 1290

Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile
1295 1300 1305

His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile
1310 1315 1320

Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val Arg Arg
1325 1330 1335

Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro Lys
1340 1345 1350

Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn
1355 1360 1365

Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val
1370 1375 1380

Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg Asp
1385 1390 1395

Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala Lys Val
1400 1405 1410

Val Lys Asp Tyr Tyr Lys Ile Ile Thr Gln Pro Gly
1415 1420 1425

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Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
100 105 110

Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
115 120 125

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

Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
145 150 155 160

Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
165 170 175

Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
180 185 190

Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
195 200 205

Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
210 215 220

Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
225 230 235 240

Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
245 250 255

Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
260 265 270

Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
275 280 285

Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
290 295 300

Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
305 310 315 320

Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
325 330 335

Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
340 345 350

Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
355 360 365

Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
370 375 380

Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
385 390 395 400

Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
405 410 415

Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
420 425 430

Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
435 440 445

Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
450 455 460

Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
465 470 475 480

Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu
485 490 495

Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
500 505 510

Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
515 520 525

Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
530 535 540

Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
545 550 555 560

Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
565 570 575

Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His Ser
580 585 590

Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met Gly
595 600 605

Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
610 615 620

Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
625 630 635 640

Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
645 650 655

Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
660 665 670

Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
675 680 685

Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
690 695 700

Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
705 710 715 720

Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
725 730 735

Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
740 745 750

Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
755 760 765

Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln

770 775 780

Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
785 790 795 800

Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
805 810 815

Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
820 825 830

Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
835 840 845

Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
850 855 860

Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
865 870 875 880

Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
885 890 895

Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
900 905 910

Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
915 920 925

Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
930 935 940

Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
945 950 955 960

Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
965 970 975

Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
980 985 990

Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
995 1000 1005

Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp
1010 1015 1020

Glu Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg
1025 1030 1035

Ser Gly Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe
1040 1045 1050

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Ser Val Ala Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg
1055 1060 1065

Ile Phe Asp Leu Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu
1070 1075 1080

Ser Thr Asp Thr Asp Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu
1085 1090 1095

Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys Lys Thr
1100 1105 1110

Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu
1115 1120 1125

Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn
1130 1135 1140

Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser
1145 1150 1155

Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp
1160 1165 1170

Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro
1175 1180 1185

Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu
1190 1195 1200

Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu
1205 1210 1215

Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
1220 1225 1230

Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
1235 1240 1245

Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys
1250 1255 1260

Cys Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe
1265 1270 1275

Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val
1280 1285 1290

Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile
1295 1300 1305

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His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile
1310 1315 1320

Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val Arg Arg
1325 1330 1335

Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro Lys
1340 1345 1350

Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn
1355 1360 1365

Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val
1370 1375 1380

Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Arg Trp Arg
1385 1390 1395

Pro Cys Leu Lys Lys Lys Lys Lys Glu Glu Glu Thr Trp Leu Ser
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Glu Tyr Ala Phe His Lys Pro Thr Arg Gly Cys Ser Leu Pro Thr
1415 1420 1425

Gln Ser Gln Phe
1430

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Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
100 105 110

Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
115 120 125

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

Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
145 150 155 160

Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
165 170 175

Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
180 185 190

Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
195 200 205

Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
210 215 220

Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
225 230 235 240

Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
245 250 255

Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
260 265 270

Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
275 280 285

Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
290 295 300

Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
305 310 315 320

Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
325 330 335

Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
340 345 350

Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
355 360 365

Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
370 375 380

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Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
385                 390                 395                 400

Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
                405                 410                 415

Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
            420                 425                 430

Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
        435                 440                 445

Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
    450                 455                 460

Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
465                 470                 475                 480

Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu
                485                 490                 495

Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
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Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
        515                 520                 525

Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
    530                 535                 540

Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
545                 550                 555                 560

Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
                565                 570                 575

Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His Ser
            580                 585                 590

Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met Gly
        595                 600                 605

Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
    610                 615                 620

Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
625                 630                 635                 640

Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
                645                 650                 655
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Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
660 665 670

Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
675 680 685

Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
690 695 700

Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
705 710 715 720

Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
725 730 735

Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
740 745 750

Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
755 760 765

Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln
770 775 780

Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
785 790 795 800

Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
805 810 815

Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
820 825 830

Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
835 840 845

Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
850 855 860

Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
865 870 875 880

Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
885 890 895

Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
900 905 910

Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
915 920 925

Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly

930 935 940

Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
945 950 955 960

Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
965 970 975

Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
980 985 990

Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
995 1000 1005

Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp
1010 1015 1020

Glu Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg
1025 1030 1035

Ser Gly Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe
1040 1045 1050

Ser Val Ala Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg
1055 1060 1065

Ile Phe Asp Leu Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu
1070 1075 1080

Ser Thr Asp Thr Asp Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu
1085 1090 1095

Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys Lys Thr
1100 1105 1110

Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu
1115 1120 1125

Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn
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Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser
1145 1150 1155

Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp
1160 1165 1170

Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro
1175 1180 1185

Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu
1190 1195 1200

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Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu
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Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
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Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
1235 1240 1245

Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys
1250 1255 1260

Cys Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe
1265 1270 1275

Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val
1280 1285 1290

Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile
1295 1300 1305

His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile
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Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val Arg Arg
1325 1330 1335

Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro Lys
1340 1345 1350

Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn
1355 1360 1365

Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val
1370 1375 1380

Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg Asp
1385 1390 1395

Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala Lys Val
1400 1405 1410

Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met Asp Leu Gln
1415 1420 1425

Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser Arg Glu
1430 1435 1440

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

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
100 105 110

Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
115 120 125

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

Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
145 150 155 160

Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
165 170 175

Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
180 185 190

Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
195 200 205

Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
210 215 220

Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
225 230 235 240

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Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
                245                 250                 255

Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
            260                 265                 270

Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
        275                 280                 285

Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
    290                 295                 300

Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
305                 310                 315                 320

Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
                325                 330                 335

Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
            340                 345                 350

Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
        355                 360                 365

Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
    370                 375                 380

Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
385                 390                 395                 400

Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
                405                 410                 415

Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
            420                 425                 430

Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
        435                 440                 445

Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
    450                 455                 460

Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
465                 470                 475                 480

Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu
                485                 490                 495

Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
            500                 505                 510
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Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
515 520 525

Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
530 535 540

Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
545 550 555 560

Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
565 570 575

Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His Ser
580 585 590

Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met Gly
595 600 605

Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
610 615 620

Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
625 630 635 640

Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
645 650 655

Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
660 665 670

Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
675 680 685

Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
690 695 700

Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
705 710 715 720

Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
725 730 735

Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
740 745 750

Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
755 760 765

Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln
770 775 780

Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
785 790 795 800

Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
805 810 815

Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
820 825 830

Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
835 840 845

Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
850 855 860

Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
865 870 875 880

Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
885 890 895

Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
900 905 910

Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
915 920 925

Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
930 935 940

Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
945 950 955 960

Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
965 970 975

Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
980 985 990

Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
995 1000 1005

Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp
1010 1015 1020

Glu Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg
1025 1030 1035

Ser Gly Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe
1040 1045 1050

Ser Val Ala Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg

1055 1060 1065

Ile Phe Asp Leu Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu
1070 1075 1080

Ser Thr Asp Thr Asp Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu
1085 1090 1095

Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys Lys Thr
1100 1105 1110

Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu
1115 1120 1125

Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn
1130 1135 1140

Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser
1145 1150 1155

Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp
1160 1165 1170

Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro
1175 1180 1185

Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu
1190 1195 1200

Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu
1205 1210 1215

Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
1220 1225 1230

Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
1235 1240 1245

Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys
1250 1255 1260

Cys Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe
1265 1270 1275

Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val
1280 1285 1290

Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile
1295 1300 1305

His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile
1310 1315 1320

Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val Arg Arg
1325 1330 1335

Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro Lys
1340 1345 1350

Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn
1355 1360 1365

Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val
1370 1375 1380

Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg Asp
1385 1390 1395

Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala Lys Val
1400 1405 1410

Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met Asp Leu Gln
1415 1420 1425

Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser Arg Glu
1430 1435 1440

Glu Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn Ser Ala Thr
1445 1450 1455

Tyr Asn Gly Lys Asn Gln Met Phe Arg Asp Cys Lys Gly His Cys
1460 1465 1470

Ser Asp Pro Tyr Ser Leu Leu Ala Leu Asn Ser Asp
1475 1480 1485

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<400> 72
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Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
20 25 30

Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu

65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
100 105 110

Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
115 120 125

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

Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
145 150 155 160

Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
165 170 175

Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
180 185 190

Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
195 200 205

Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
210 215 220

Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
225 230 235 240

Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
245 250 255

Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
260 265 270

Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
275 280 285

Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
290 295 300

Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
305 310 315 320

Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
325 330 335

Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
340 345 350

Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
355 360 365

Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
370 375 380

Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
385 390 395 400

Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
405 410 415

Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
420 425 430

Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
435 440 445

Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
450 455 460

Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
465 470 475 480

Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu
485 490 495

Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
500 505 510

Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
515 520 525

Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
530 535 540

Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
545 550 555 560

Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
565 570 575

Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His Ser
580 585 590

Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met Gly
595 600 605

Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
610 615 620

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Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
625                 630                 635                 640

Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
                645                 650                 655

Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
            660                 665                 670

Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
        675                 680                 685

Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
    690                 695                 700

Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
705                 710                 715                 720

Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
                725                 730                 735

Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
            740                 745                 750

Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
        755                 760                 765

Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln
    770                 775                 780

Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
785                 790                 795                 800

Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
                805                 810                 815

Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
            820                 825                 830

Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
        835                 840                 845

Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
    850                 855                 860

Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
865                 870                 875                 880

Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
                885                 890                 895
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Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
900 905 910

Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
915 920 925

Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
930 935 940

Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
945 950 955 960

Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
965 970 975

Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
980 985 990

Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
995 1000 1005

Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp
1010 1015 1020

Glu Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg
1025 1030 1035

Ser Gly Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe
1040 1045 1050

Ser Val Ala Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg
1055 1060 1065

Ile Phe Asp Leu Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu
1070 1075 1080

Ser Thr Asp Thr Asp Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu
1085 1090 1095

Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys Lys Thr
1100 1105 1110

Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu
1115 1120 1125

Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn
1130 1135 1140

Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser
1145 1150 1155

Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp

1160 1165 1170

Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro
1175 1180 1185

Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu
1190 1195 1200

Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu
1205 1210 1215

Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
1220 1225 1230

Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
1235 1240 1245

Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys
1250 1255 1260

Cys Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe
1265 1270 1275

Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val
1280 1285 1290

Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile
1295 1300 1305

His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile
1310 1315 1320

Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val Arg Arg
1325 1330 1335

Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro Lys
1340 1345 1350

Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn
1355 1360 1365

Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val
1370 1375 1380

Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg Asp
1385 1390 1395

Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala Lys Val
1400 1405 1410

Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met Asp Leu Gln
1415 1420 1425

Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser Arg Glu
1430 1435 1440

Glu Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn Ser Ala Thr
1445 1450 1455

Tyr Asn Gly Ile Gly Ile Arg Ile Lys His Thr Arg Ser Ile Glu
1460 1465 1470

Lys Gly His Ser His His His Leu Pro Arg Glu
1475 1480

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Met Gly Pro Gly Cys Asp Leu Leu Leu Arg Thr Ala Ala Thr Ile Thr
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Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
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Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
35 40 45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
50 55 60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65 70 75 80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
85 90 95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
100 105 110

Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
115 120 125

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

Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
145 150 155 160

Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
165 170 175

Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met

180 185 190

Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
195 200 205

Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
210 215 220

Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
225 230 235 240

Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
245 250 255

Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
260 265 270

Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
275 280 285

Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
290 295 300

Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
305 310 315 320

Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
325 330 335

Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
340 345 350

Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
355 360 365

Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
370 375 380

Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
385 390 395 400

Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
405 410 415

Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
420 425 430

Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
435 440 445

Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
450 455 460

Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
465 470 475 480

Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu
485 490 495

Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
500 505 510

Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
515 520 525

Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
530 535 540

Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
545 550 555 560

Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
565 570 575

Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His Ser
580 585 590

Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met Gly
595 600 605

Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
610 615 620

Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
625 630 635 640

Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
645 650 655

Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
660 665 670

Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
675 680 685

Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
690 695 700

Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
705 710 715 720

Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
725 730 735

Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
740 745 750

Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
755 760 765

Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln
770 775 780

Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
785 790 795 800

Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
805 810 815

Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
820 825 830

Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
835 840 845

Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
850 855 860

Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
865 870 875 880

Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
885 890 895

Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
900 905 910

Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
915 920 925

Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
930 935 940

Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
945 950 955 960

Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
965 970 975

Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
980 985 990

Ala Asp Leu Arg Arg Leu Ser Leu Lys Asn Ala Lys Gln Leu Leu Arg
995 1000 1005

Lys Phe Gly Val Pro Glu Glu Glu Ile Lys Lys Leu Ser Arg Trp
1010 1015 1020

Glu Val Ile Asp Val Val Arg Thr Met Ser Thr Glu Gln Ala Arg
1025 1030 1035

Ser Gly Glu Gly Pro Met Ser Lys Phe Ala Arg Gly Ser Arg Phe
1040 1045 1050

Ser Val Ala Glu His Gln Glu Arg Tyr Lys Glu Glu Cys Gln Arg
1055 1060 1065

Ile Phe Asp Leu Gln Asn Lys Val Leu Ser Ser Thr Glu Val Leu
1070 1075 1080

Ser Thr Asp Thr Asp Ser Ser Ser Ala Glu Asp Ser Asp Phe Glu
1085 1090 1095

Glu Met Gly Lys Asn Ile Glu Asn Met Leu Gln Asn Lys Lys Thr
1100 1105 1110

Ser Ser Gln Leu Ser Arg Glu Arg Glu Glu Gln Glu Arg Lys Glu
1115 1120 1125

Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn
1130 1135 1140

Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser
1145 1150 1155

Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp
1160 1165 1170

Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro
1175 1180 1185

Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu
1190 1195 1200

Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu
1205 1210 1215

Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
1220 1225 1230

Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
1235 1240 1245

Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys
1250 1255 1260

Cys Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe

1265 1270 1275

Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val
1280 1285 1290

Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile
1295 1300 1305

His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile
1310 1315 1320

Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val Arg Arg
1325 1330 1335

Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro Lys
1340 1345 1350

Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn
1355 1360 1365

Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val
1370 1375 1380

Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg Asp
1385 1390 1395

Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Ala Trp Met Thr Asp
1400 1405 1410

Gly Asp Pro Val Ser Lys Arg Lys Lys Lys Lys Lys Lys Arg Gly
1415 1420 1425

Phe Gln Ser Met Leu Ser Thr Ser Pro Leu Gly Val Ala Leu Cys
1430 1435 1440

Pro His Arg Ala Asn Ser Glu Trp Arg Gly Leu Pro Pro Arg Ser
1445 1450 1455

Leu Leu
1460

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<211> 1906
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Ala Ala Ala Ile Met Ser Asp Thr Asp Ser Asp Glu Asp Ser Ala Gly
20 25 30

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Gly Gly Pro Phe Ser Leu Ala Gly Phe Leu Phe Gly Asn Ile Asn Gly
        35                  40                  45

Ala Gly Gln Leu Glu Gly Glu Ser Val Leu Asp Asp Glu Cys Lys Lys
    50                  55                  60

His Leu Ala Gly Leu Gly Ala Leu Gly Leu Gly Ser Leu Ile Thr Glu
65                  70                  75                  80

Leu Thr Ala Asn Glu Glu Leu Thr Gly Thr Asp Gly Ala Leu Val Asn
                85                  90                  95

Asp Glu Gly Trp Val Arg Ser Thr Glu Asp Ala Val Asp Tyr Ser Asp
            100                 105                 110

Ile Asn Glu Val Ala Glu Asp Glu Ser Arg Arg Tyr Gln Gln Thr Met
        115                 120                 125

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

Asp Ala Asp Cys Glu Asp Ile Asp Cys Lys Leu Met Pro Pro Pro Pro
145                 150                 155                 160

Pro Pro Pro Gly Pro Met Lys Lys Asp Lys Asp Gln Asp Ser Ile Thr
                165                 170                 175

Gly Glu Lys Val Asp Phe Ser Ser Ser Ser Asp Ser Glu Ser Glu Met
            180                 185                 190

Gly Pro Gln Glu Ala Thr Gln Ala Glu Ser Glu Asp Gly Lys Leu Thr
        195                 200                 205

Leu Pro Leu Ala Gly Ile Met Gln His Asp Ala Thr Lys Leu Leu Pro
    210                 215                 220

Ser Val Thr Glu Leu Phe Pro Glu Phe Arg Pro Gly Lys Val Leu Arg
225                 230                 235                 240

Phe Leu Arg Leu Phe Gly Pro Gly Lys Asn Val Pro Ser Val Trp Arg
                245                 250                 255

Ser Ala Arg Arg Lys Arg Lys Lys Lys His Arg Glu Leu Ile Gln Glu
            260                 265                 270

Glu Gln Ile Gln Glu Val Glu Cys Ser Val Glu Ser Glu Val Ser Gln
        275                 280                 285

Lys Ser Leu Trp Asn Tyr Asp Tyr Ala Pro Pro Pro Pro Pro Glu Gln
    290                 295                 300

Cys Leu Ser Asp Asp Glu Ile Thr Met Met Ala Pro Val Glu Ser Lys
```

305 310 315 320

Phe Ser Gln Ser Thr Gly Asp Ile Asp Lys Val Thr Asp Thr Lys Pro
325 330 335

Arg Val Ala Glu Trp Arg Tyr Gly Pro Ala Arg Leu Trp Tyr Asp Met
340 345 350

Leu Gly Val Pro Glu Asp Gly Ser Gly Phe Asp Tyr Gly Phe Lys Leu
355 360 365

Arg Lys Thr Glu His Glu Pro Val Ile Lys Ser Arg Met Ile Glu Glu
370 375 380

Phe Arg Lys Leu Glu Glu Asn Asn Gly Thr Asp Leu Leu Ala Asp Glu
385 390 395 400

Asn Phe Leu Met Val Thr Gln Leu His Trp Glu Asp Asp Ile Ile Trp
405 410 415

Asp Gly Glu Asp Val Lys His Lys Gly Thr Lys Pro Gln Arg Ala Ser
420 425 430

Leu Ala Gly Trp Leu Pro Ser Ser Met Thr Arg Asn Ala Met Ala Tyr
435 440 445

Asn Val Gln Gln Gly Phe Ala Ala Thr Leu Asp Asp Asp Lys Pro Trp
450 455 460

Tyr Ser Ile Phe Pro Ile Asp Asn Glu Asp Leu Val Tyr Gly Arg Trp
465 470 475 480

Glu Asp Asn Ile Ile Trp Asp Ala Gln Ala Met Pro Arg Leu Leu Glu
485 490 495

Pro Pro Val Leu Thr Leu Asp Pro Asn Asp Glu Asn Leu Ile Leu Glu
500 505 510

Ile Pro Asp Glu Lys Glu Glu Ala Thr Ser Asn Ser Pro Ser Lys Glu
515 520 525

Ser Lys Lys Glu Ser Ser Leu Lys Lys Ser Arg Ile Leu Leu Gly Lys
530 535 540

Thr Gly Val Ile Lys Glu Glu Pro Gln Gln Asn Met Ser Gln Pro Glu
545 550 555 560

Val Lys Asp Pro Trp Asn Leu Ser Asn Asp Glu Tyr Tyr Tyr Pro Lys
565 570 575

Gln Gln Gly Leu Arg Gly Thr Phe Gly Gly Asn Ile Ile Gln His Ser
580 585 590

Ile Pro Ala Val Glu Leu Arg Gln Pro Phe Phe Pro Thr His Met Gly
595 600 605

Pro Ile Lys Leu Arg Gln Phe His Arg Pro Pro Leu Lys Lys Tyr Ser
610 615 620

Phe Gly Ala Leu Ser Gln Pro Gly Pro His Ser Val Gln Pro Leu Leu
625 630 635 640

Lys His Ile Lys Lys Lys Ala Lys Met Arg Glu Gln Glu Arg Gln Ala
645 650 655

Ser Gly Gly Gly Glu Met Phe Phe Met Arg Thr Pro Gln Asp Leu Thr
660 665 670

Gly Lys Asp Gly Asp Leu Ile Leu Ala Glu Tyr Ser Glu Glu Asn Gly
675 680 685

Pro Leu Met Met Gln Val Gly Met Ala Thr Lys Ile Lys Asn Tyr Tyr
690 695 700

Lys Arg Lys Pro Gly Lys Asp Pro Gly Ala Pro Asp Cys Lys Tyr Gly
705 710 715 720

Glu Thr Val Tyr Cys His Thr Ser Pro Phe Leu Gly Ser Leu His Pro
725 730 735

Gly Gln Leu Leu Gln Ala Phe Glu Asn Asn Leu Phe Arg Ala Pro Ile
740 745 750

Tyr Leu His Lys Met Pro Glu Thr Asp Phe Leu Ile Ile Arg Thr Arg
755 760 765

Gln Gly Tyr Tyr Ile Arg Glu Leu Val Asp Ile Phe Val Val Gly Gln
770 775 780

Gln Cys Pro Leu Phe Glu Val Pro Gly Pro Asn Ser Lys Arg Ala Asn
785 790 795 800

Thr His Ile Arg Asp Phe Leu Gln Val Phe Ile Tyr Arg Leu Phe Trp
805 810 815

Lys Ser Lys Asp Arg Pro Arg Arg Ile Arg Met Glu Asp Ile Lys Lys
820 825 830

Ala Phe Pro Ser His Ser Glu Ser Ser Ile Arg Lys Arg Leu Lys Leu
835 840 845

Cys Ala Asp Phe Lys Arg Thr Gly Met Asp Ser Asn Trp Trp Val Leu
850 855 860

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```
Lys Ser Asp Phe Arg Leu Pro Thr Glu Glu Glu Ile Arg Ala Met Val
865                 870                 875                 880

Ser Pro Glu Gln Cys Cys Ala Tyr Tyr Ser Met Ile Ala Ala Glu Gln
                885                 890                 895

Arg Leu Lys Asp Ala Gly Tyr Gly Glu Lys Ser Phe Phe Ala Pro Glu
            900                 905                 910

Glu Glu Asn Glu Glu Asp Phe Gln Met Lys Ile Asp Asp Glu Val Arg
        915                 920                 925

Thr Ala Pro Trp Asn Thr Thr Arg Ala Phe Ile Ala Ala Met Lys Gly
    930                 935                 940

Lys Cys Leu Leu Glu Val Thr Gly Val Ala Asp Pro Thr Gly Cys Gly
945                 950                 955                 960

Glu Gly Phe Ser Tyr Val Lys Ile Pro Asn Lys Pro Thr Gln Gln Lys
                965                 970                 975

Asp Asp Lys Glu Pro Gln Pro Val Lys Lys Thr Val Thr Gly Thr Asp
            980                 985                 990

Ala Asp Leu Arg Arg Leu Ser Leu  Lys Asn Ala Lys Gln  Leu Leu Arg
        995                 1000                1005

Lys Phe  Gly Val Pro Glu Glu  Glu Ile Lys Lys Leu  Ser Arg Trp
    1010                1015                1020

Glu Val  Ile Asp Val Val Arg  Thr Met Ser Thr Glu  Gln Ala Arg
    1025                1030                1035

Ser Gly  Glu Gly Pro Met Ser  Lys Phe Ala Arg Gly  Ser Arg Phe
    1040                1045                1050

Ser Val  Ala Glu His Gln Glu  Arg Tyr Lys Glu Glu  Cys Gln Arg
    1055                1060                1065

Ile Phe  Asp Leu Gln Asn Lys  Val Leu Ser Ser Thr  Glu Val Leu
    1070                1075                1080

Ser Thr  Asp Thr Asp Ser Ser  Ser Ala Glu Asp Ser  Asp Phe Glu
    1085                1090                1095

Glu Met  Gly Lys Asn Ile Glu  Asn Met Leu Gln Asn  Lys Lys Thr
    1100                1105                1110

Ser Ser  Gln Leu Ser Arg Glu  Arg Glu Glu Gln Glu  Arg Lys Glu
    1115                1120                1125
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Leu Gln Arg Met Leu Leu Ala Ala Gly Ser Ala Ala Ser Gly Asn
1130 1135 1140

Asn His Arg Asp Asp Asp Thr Ala Ser Val Thr Ser Leu Asn Ser
1145 1150 1155

Ser Ala Thr Gly Arg Cys Leu Lys Ile Tyr Arg Thr Phe Arg Asp
1160 1165 1170

Glu Glu Gly Lys Glu Tyr Val Arg Cys Glu Thr Val Arg Lys Pro
1175 1180 1185

Ala Val Ile Asp Ala Tyr Val Arg Ile Arg Thr Thr Lys Asp Glu
1190 1195 1200

Glu Phe Ile Arg Lys Phe Ala Leu Phe Asp Glu Gln His Arg Glu
1205 1210 1215

Glu Met Arg Lys Glu Arg Arg Arg Ile Gln Glu Gln Leu Arg Arg
1220 1225 1230

Leu Lys Arg Asn Gln Glu Lys Glu Lys Leu Lys Gly Pro Pro Glu
1235 1240 1245

Lys Lys Pro Lys Lys Met Lys Glu Arg Pro Asp Leu Lys Leu Lys
1250 1255 1260

Cys Gly Ala Cys Gly Ala Ile Gly His Met Arg Thr Asn Lys Phe
1265 1270 1275

Cys Pro Leu Tyr Tyr Gln Thr Asn Ala Pro Pro Ser Asn Pro Val
1280 1285 1290

Ala Met Thr Glu Glu Gln Glu Glu Glu Leu Glu Lys Thr Val Ile
1295 1300 1305

His Asn Asp Asn Glu Glu Leu Ile Lys Val Glu Gly Thr Lys Ile
1310 1315 1320

Val Leu Gly Lys Gln Leu Ile Glu Ser Ala Asp Glu Val Arg Arg
1325 1330 1335

Lys Ser Leu Val Leu Lys Phe Pro Lys Gln Gln Leu Pro Pro Lys
1340 1345 1350

Lys Lys Arg Arg Val Gly Thr Thr Val His Cys Asp Tyr Leu Asn
1355 1360 1365

Arg Pro His Lys Ser Ile His Arg Arg Arg Thr Asp Pro Met Val
1370 1375 1380

Thr Leu Ser Ser Ile Leu Glu Ser Ile Ile Asn Asp Met Arg Asp

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1385 1390 1395

Leu Pro Asn Thr Tyr Pro Phe His Thr Pro Val Asn Ala Lys Val
1400 1405 1410

Val Lys Asp Tyr Tyr Lys Ile Ile Thr Arg Pro Met Asp Leu Gln
1415 1420 1425

Thr Leu Arg Glu Asn Val Arg Lys Arg Leu Tyr Pro Ser Arg Glu
1430 1435 1440

Glu Phe Arg Glu His Leu Glu Leu Ile Val Lys Asn Ser Ala Thr
1445 1450 1455

Tyr Asn Gly Pro Lys His Ser Leu Thr Gln Ile Ser Gln Ser Met
1460 1465 1470

Leu Asp Leu Cys Asp Glu Lys Leu Lys Glu Lys Glu Asp Lys Leu
1475 1480 1485

Ala Arg Leu Glu Lys Ala Ile Asn Pro Leu Leu Asp Asp Asp Asp
1490 1495 1500

Gln Val Ala Phe Ser Phe Ile Leu Asp Asn Ile Val Thr Gln Lys
1505 1510 1515

Met Met Ala Val Pro Asp Ser Trp Pro Phe His His Pro Val Asn
1520 1525 1530

Lys Lys Phe Val Pro Asp Tyr Tyr Lys Val Ile Val Asn Pro Met
1535 1540 1545

Asp Leu Glu Thr Ile Arg Lys Asn Ile Ser Lys His Lys Tyr Gln
1550 1555 1560

Ser Arg Glu Ser Phe Leu Asp Asp Val Asn Leu Ile Leu Ala Asn
1565 1570 1575

Ser Val Lys Tyr Asn Gly Pro Glu Ser Gln Tyr Thr Lys Thr Ala
1580 1585 1590

Gln Glu Ile Val Asn Val Cys Tyr Gln Thr Leu Thr Glu Tyr Asp
1595 1600 1605

Glu His Leu Thr Gln Leu Glu Lys Asp Ile Cys Thr Ala Lys Glu
1610 1615 1620

Ala Ala Leu Glu Glu Ala Glu Leu Glu Ser Leu Asp Pro Met Thr
1625 1630 1635

Pro Gly Pro Tyr Thr Pro Gln Pro Pro Asp Leu Tyr Asp Thr Asn
1640 1645 1650

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Thr Ser Leu Ser Met Ser Arg Asp Ala Ser Val Phe Gln Asp Glu
1655 1660 1665

Ser Asn Met Ser Val Leu Asp Ile Pro Ser Ala Thr Pro Glu Lys
1670 1675 1680

Gln Val Thr Gln Met Arg Gln Gly Arg Gly Arg Leu Gly Glu Glu
1685 1690 1695

Asp Ser Asp Val Asp Ile Glu Gly Tyr Asp Asp Glu Glu Glu Asp
1700 1705 1710

Gly Lys Pro Lys Thr Pro Ala Pro Glu Gly Glu Asp Gly Asp Gly
1715 1720 1725

Asp Leu Ala Asp Glu Glu Glu Gly Thr Val Gln Gln Pro Gln Ala
1730 1735 1740

Ser Val Leu Tyr Glu Asp Leu Leu Met Ser Glu Gly Glu Asp Asp
1745 1750 1755

Glu Glu Asp Ala Gly Ser Asp Glu Glu Gly Asp Asn Pro Phe Ser
1760 1765 1770

Ala Ile Gln Leu Ser Glu Ser Gly Ser Asp Ser Asp Val Gly Ser
1775 1780 1785

Gly Gly Ile Arg Pro Lys Gln Pro Arg Met Leu Gln Glu Asn Thr
1790 1795 1800

Arg Met Asp Met Glu Asn Glu Glu Ser Met Met Ser Tyr Glu Gly
1805 1810 1815

Asp Gly Gly Glu Ala Ser His Gly Leu Glu Asp Ser Asn Ile Ser
1820 1825 1830

Tyr Gly Ser Tyr Glu Glu Pro Asp Pro Lys Ser Asn Thr Gln Asp
1835 1840 1845

Thr Ser Phe Ser Ser Ile Gly Gly Tyr Glu Val Ser Glu Glu Glu
1850 1855 1860

Glu Asp Glu Glu Glu Glu Glu Gln Arg Ser Gly Pro Ser Val Leu
1865 1870 1875

Ser Gln Val His Leu Ser Glu Asp Glu Glu Asp Ser Glu Asp Phe
1880 1885 1890

His Ser Ile Ala Gly Asp Ser Asp Leu Asp Ser Asp Glu
1895 1900 1905

<210> 75
<211> 1251
<212> PRT
<213> Homo sapiens

<400> 75

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Met Pro Leu Thr Gly Val Glu Pro Ala Arg Met Asn Arg Lys Lys Gly
1               5                  10                  15

Asp Lys Gly Phe Glu Ser Pro Arg Pro Tyr Lys Leu Thr His Gln Val
            20                  25                  30

Val Cys Ile Asn Asn Ile Asn Phe Gln Arg Lys Ser Val Val Gly Phe
        35                  40                  45

Val Glu Leu Thr Ile Phe Pro Thr Val Ala Asn Leu Asn Arg Ile Lys
    50                  55                  60

Leu Asn Ser Lys Gln Cys Arg Ile Tyr Arg Val Arg Ile Asn Asp Leu
65                  70                  75                  80

Glu Ala Ala Phe Ile Tyr Asn Asp Pro Thr Leu Glu Val Cys His Ser
                85                  90                  95

Glu Ser Lys Gln Arg Asn Leu Asn Tyr Phe Ser Asn Ala Tyr Ala Ala
            100                 105                 110

Ala Val Ser Ala Val Asp Pro Asp Ala Gly Asn Gly Glu Leu Cys Ile
        115                 120                 125

Lys Val Pro Ser Glu Leu Trp Lys His Val Asp Glu Leu Lys Val Leu
    130                 135                 140

Lys Ile His Ile Asn Phe Ser Leu Asp Gln Pro Lys Gly Gly Leu His
145                 150                 155                 160

Phe Val Val Pro Ser Val Glu Gly Ser Met Ala Glu Arg Gly Ala His
                165                 170                 175

Val Phe Ser Cys Gly Tyr Gln Asn Ser Thr Arg Phe Trp Phe Pro Cys
            180                 185                 190

Val Asp Ser Tyr Ser Glu Leu Cys Thr Trp Lys Leu Glu Phe Thr Val
        195                 200                 205

Asp Ala Ala Met Val Ala Val Ser Asn Gly Asp Leu Val Glu Thr Val
    210                 215                 220

Tyr Thr His Asp Met Arg Lys Lys Thr Phe His Tyr Met Leu Thr Ile
225                 230                 235                 240

Pro Thr Ala Ala Ser Asn Ile Ser Leu Ala Ile Gly Pro Phe Glu Ile
                245                 250                 255
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Leu Val Asp Pro Tyr Met His Glu Val Thr His Phe Cys Leu Pro Gln
260 265 270

Leu Leu Pro Leu Leu Lys His Thr Thr Ser Tyr Leu His Glu Val Phe
275 280 285

Glu Phe Tyr Glu Glu Ile Leu Thr Cys Arg Tyr Pro Tyr Ser Cys Phe
290 295 300

Lys Thr Val Phe Ile Asp Glu Ala Tyr Val Glu Val Ala Ala Tyr Ala
305 310 315 320

Ser Met Ser Ile Phe Ser Thr Asn Leu Leu His Ser Ala Met Ile Ile
325 330 335

Asp Glu Thr Pro Leu Thr Arg Arg Cys Leu Ala Gln Ser Leu Ala Gln
340 345 350

Gln Phe Phe Gly Cys Phe Ile Ser Arg Met Ser Trp Ser Asp Glu Trp
355 360 365

Val Leu Lys Gly Ile Ser Gly Tyr Ile Tyr Gly Leu Trp Met Lys Lys
370 375 380

Thr Phe Gly Val Asn Glu Tyr Arg His Trp Ile Lys Glu Glu Leu Asp
385 390 395 400

Lys Ile Val Ala Tyr Glu Leu Lys Thr Gly Gly Val Leu Leu His Pro
405 410 415

Ile Phe Gly Gly Gly Lys Glu Lys Asp Asn Pro Ala Ser His Leu His
420 425 430

Phe Ser Ile Lys His Pro His Thr Leu Ser Trp Glu Tyr Tyr Thr Met
435 440 445

Phe Gln Cys Lys Ala His Leu Val Met Arg Leu Ile Glu Asn Arg Ile
450 455 460

Ser Met Glu Phe Met Leu Gln Val Phe Asn Lys Leu Leu Ser Leu Ala
465 470 475 480

Ser Thr Ala Ser Ser Gln Lys Phe Gln Ser His Met Trp Ser Gln Met
485 490 495

Leu Val Ser Thr Ser Gly Phe Leu Lys Ser Ile Ser Asn Val Ser Gly
500 505 510

Lys Asp Ile Gln Pro Leu Ile Lys Gln Trp Val Asp Gln Ser Gly Val
515 520 525

Val Lys Phe Tyr Gly Ser Phe Ala Phe Asn Arg Lys Arg Asn Val Leu
530 535 540

Glu Leu Glu Ile Lys Gln Asp Tyr Thr Ser Pro Gly Thr Gln Lys Tyr
545 550 555 560

Val Gly Pro Leu Lys Val Thr Val Gln Glu Leu Asp Gly Ser Phe Asn
565 570 575

His Thr Leu Gln Ile Glu Glu Asn Ser Leu Lys His Asp Ile Pro Cys
580 585 590

His Ser Lys Ser Arg Arg Asn Lys Lys Lys Lys Ile Pro Leu Met Asn
595 600 605

Gly Glu Glu Val Asp Met Asp Leu Ser Ala Met Asp Ala Asp Ser Pro
610 615 620

Leu Leu Trp Ile Arg Ile Asp Pro Asp Met Ser Val Leu Arg Lys Val
625 630 635 640

Glu Phe Glu Gln Ala Asp Phe Met Trp Gln Tyr Gln Leu Arg Tyr Glu
645 650 655

Arg Asp Val Val Ala Gln Gln Glu Ser Ile Leu Ala Leu Glu Lys Phe
660 665 670

Pro Thr Pro Ala Ser Arg Leu Ala Leu Thr Asp Ile Leu Glu Gln Glu
675 680 685

Gln Cys Phe Tyr Arg Val Arg Met Ser Ala Cys Phe Cys Leu Ala Lys
690 695 700

Ile Ala Asn Ser Met Val Ser Thr Trp Thr Gly Pro Pro Ala Met Lys
705 710 715 720

Ser Leu Phe Thr Arg Met Phe Cys Cys Lys Ser Cys Pro Asn Ile Val
725 730 735

Lys Thr Asn Asn Phe Met Ser Phe Gln Ser Tyr Phe Leu Gln Lys Thr
740 745 750

Met Pro Val Ala Met Ala Leu Leu Arg Asp Val His Asn Leu Cys Pro
755 760 765

Lys Glu Val Leu Thr Phe Ile Leu Asp Leu Ile Lys Tyr Asn Asp Asn
770 775 780

Arg Lys Asn Lys Phe Ser Asp Asn Tyr Tyr Arg Ala Glu Met Ile Asp
785 790 795 800

Ala Leu Ala Asn Ser Val Thr Pro Ala Val Ser Val Asn Asn Glu Val
805 810 815

Arg Thr Leu Asp Asn Leu Asn Pro Asp Val Arg Leu Ile Leu Glu Glu
820 825 830

Ile Thr Arg Phe Leu Asn Met Glu Lys Leu Leu Pro Ser Tyr Arg His
835 840 845

Thr Ile Thr Val Ser Cys Leu Arg Ala Ile Arg Val Leu Gln Lys Asn
850 855 860

Gly His Val Pro Ser Asp Pro Ala Leu Phe Lys Ser Tyr Ala Glu Tyr
865 870 875 880

Gly His Phe Val Asp Ile Arg Ile Ala Ala Leu Glu Ala Val Val Asp
885 890 895

Tyr Thr Lys Val Asp Arg Ser Tyr Glu Glu Leu Gln Trp Leu Leu Asn
900 905 910

Met Ile Gln Asn Asp Pro Val Pro Tyr Val Arg His Lys Ile Leu Asn
915 920 925

Met Leu Thr Lys Asn Pro Pro Phe Thr Lys Asn Met Glu Ser Pro Leu
930 935 940

Cys Asn Glu Ala Leu Val Asp Gln Leu Trp Lys Leu Met Asn Ser Gly
945 950 955 960

Thr Ser His Asp Trp Arg Leu Arg Cys Gly Ala Val Asp Leu Tyr Phe
965 970 975

Thr Leu Phe Gly Leu Ser Arg Pro Ser Cys Leu Pro Leu Pro Glu Leu
980 985 990

Gly Leu Val Leu Asn Leu Lys Glu Lys Lys Ala Val Leu Asn Pro Thr
995 1000 1005

Ile Ile Pro Glu Ser Val Ala Gly Asn Gln Glu Ala Ala Asn Asn
1010 1015 1020

Pro Ser Ser His Pro Gln Leu Val Gly Phe Gln Asn Pro Glu Asp
1025 1030 1035

Asp His Leu Ala Lys Glu Ala Ser Cys Asn Ile Ser Ala His Gln
1040 1045 1050

Gln Gly Val Lys Arg Lys Ser Asp Thr Pro Leu Gly Ser Pro Leu
1055 1060 1065

Glu Pro Gly Gln Ile Leu Glu Lys Asn Glu Asp Ser Ser Lys Val

1070 1075 1080

Lys Leu Lys Ile Arg Phe Ser Ser Ser Gln Asp Glu Glu Glu Ile
1085 1090 1095

Asp Met Asp Thr Val His Asp Ser Gln Ala Phe Ile Ser His His
1100 1105 1110

Leu Asn Met Leu Glu Arg Pro Ser Thr Pro Gly Leu Ser Lys Tyr
1115 1120 1125

Arg Pro Ala Ser Ser Arg Ser Ala Leu Ile Pro Gln His Ser Ala
1130 1135 1140

Gly Cys Asp Ser Thr Pro Thr Thr Lys Pro Gln Trp Ser Leu Glu
1145 1150 1155

Leu Ala Arg Lys Gly Thr Gly Lys Glu Gln Ala Pro Leu Glu Met
1160 1165 1170

Ser Met His Pro Ala Ala Ser Ala Pro Leu Ser Val Phe Thr Lys
1175 1180 1185

Glu Ser Thr Ala Ser Lys His Ser Asp His His His His His His
1190 1195 1200

His Glu His Lys Lys Lys Lys Lys Lys His Lys His Lys His Lys
1205 1210 1215

His Lys His Lys His Asp Ser Lys Glu Lys Asp Lys Glu Pro Phe
1220 1225 1230

Thr Phe Ser Ser Pro Ala Ser Gly Arg Ser Ile Arg Ser Pro Ser
1235 1240 1245

Leu Ser Asp
1250

<210> 76
<211> 653
<212> PRT
<213> Homo sapiens

<400> 76
Met Ala Ala Gly Ser Asp Leu Leu Asp Glu Val Phe Phe Asn Ser Glu
1 5 10 15

Val Asp Glu Lys Val Gly Met Val Leu Val Arg Ser Glu Asn Gly Gln
20 25 30

Leu Leu Met Ile Pro Gln Gln Ala Leu Ala Gln Met Gln Ala Gln Ala
35 40 45

His Ala Gln Pro Gln Thr Thr Met Ala Pro Arg Pro Ala Thr Pro Thr
50 55 60

Ser Ala Pro Pro Val Gln Ile Ser Thr Val Gln Ala Pro Gly Thr Pro
65 70 75 80

Ile Ile Ala Arg Gln Val Thr Pro Thr Thr Ile Ile Lys Gln Val Ser
85 90 95

Gln Ala Gln Thr Thr Val Gln Pro Ser Ala Thr Leu Gln Arg Ser Pro
100 105 110

Gly Val Gln Pro Gln Leu Val Leu Gly Gly Ala Ala Gln Thr Ala Ser
115 120 125

Leu Gly Thr Ala Thr Ala Val Gln Thr Gly Thr Pro Gln Arg Thr Val
130 135 140

Pro Gly Ala Thr Thr Thr Ser Ser Ala Ala Thr Glu Thr Met Glu Asn
145 150 155 160

Val Lys Lys Cys Lys Asn Phe Leu Ser Thr Leu Ile Lys Leu Ala Ser
165 170 175

Ser Gly Lys Gln Ser Thr Glu Thr Ala Ala Asn Val Lys Glu Leu Val
180 185 190

Gln Asn Leu Leu Asp Gly Lys Ile Glu Ala Glu Asp Phe Thr Ser Arg
195 200 205

Leu Tyr Arg Glu Leu Asn Ser Ser Pro Gln Pro Tyr Leu Val Pro Phe
210 215 220

Leu Lys Arg Ser Leu Pro Ala Leu Arg Gln Leu Thr Pro Asp Ser Ala
225 230 235 240

Ala Phe Ile Gln Gln Ser Gln Gln Gln Pro Pro Pro Pro Thr Ser Gln
245 250 255

Ala Thr Thr Ala Leu Thr Ala Val Val Leu Ser Ser Ser Val Gln Arg
260 265 270

Thr Ala Gly Lys Thr Ala Ala Thr Val Thr Ser Ala Leu Gln Pro Pro
275 280 285

Val Leu Ser Leu Thr Gln Pro Thr Gln Val Gly Val Gly Lys Gln Gly
290 295 300

Gln Pro Thr Pro Leu Val Ile Gln Gln Pro Pro Lys Pro Gly Ala Leu
305 310 315 320

Ile Arg Pro Pro Gln Val Thr Leu Thr Gln Thr Pro Met Val Ala Leu

325 330 335

Arg Gln Pro His Asn Arg Ile Met Leu Thr Thr Pro Gln Gln Ile Gln
340 345 350

Leu Asn Pro Leu Gln Pro Val Pro Val Val Lys Pro Ala Val Leu Pro
355 360 365

Gly Thr Lys Ala Leu Ser Ala Val Ser Ala Gln Ala Ala Ala Ala Gln
370 375 380

Lys Asn Lys Leu Lys Glu Pro Gly Gly Gly Ser Phe Arg Asp Asp Asp
385 390 395 400

Asp Ile Asn Asp Val Ala Ser Met Ala Gly Val Asn Leu Ser Glu Glu
405 410 415

Ser Ala Arg Ile Leu Ala Thr Asn Ser Glu Leu Val Gly Thr Leu Thr
420 425 430

Arg Ser Cys Lys Asp Glu Thr Phe Leu Leu Gln Ala Pro Leu Gln Arg
435 440 445

Arg Ile Leu Glu Ile Gly Lys Lys His Gly Ile Thr Glu Leu His Pro
450 455 460

Asp Val Val Ser Tyr Val Ser His Ala Thr Gln Gln Arg Leu Gln Asn
465 470 475 480

Leu Val Glu Lys Ile Ser Glu Thr Ala Gln Gln Lys Asn Phe Ser Tyr
485 490 495

Lys Asp Asp Asp Arg Tyr Glu Gln Ala Ser Asp Val Arg Ala Gln Leu
500 505 510

Lys Phe Phe Glu Gln Leu Asp Gln Ile Glu Lys Gln Arg Lys Asp Glu
515 520 525

Gln Glu Arg Glu Ile Leu Met Arg Ala Ala Lys Ser Arg Ser Arg Gln
530 535 540

Glu Asp Pro Glu Gln Leu Arg Leu Lys Gln Lys Ala Lys Glu Met Gln
545 550 555 560

Gln Gln Glu Leu Ala Gln Met Arg Gln Arg Asp Ala Asn Leu Thr Ala
565 570 575

Leu Ala Ala Ile Gly Pro Arg Lys Lys Arg Lys Val Asp Cys Pro Gly
580 585 590

Pro Gly Ser Gly Ala Glu Gly Ser Gly Pro Gly Ser Val Val Pro Gly
595 600 605

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Ser Ser Gly Val Gly Thr Pro Arg Gln Phe Thr Arg Gln Arg Ile Thr
610 615 620

Arg Val Asn Leu Arg Asp Leu Ile Phe Cys Leu Glu Asn Glu Arg Glu
625 630 635 640

Thr Ser His Ser Leu Leu Leu Tyr Lys Ala Phe Leu Lys
645 650

<210> 77
<211> 85
<212> PRT
<213> Homo sapiens

<400> 77
Met Lys Arg Val Arg Thr Glu Gln Ile Gln Met Ala Val Ser Cys Tyr
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Leu Lys Arg Arg Gln Tyr Val Asp Ser Asp Gly Pro Leu Lys Gln Gly
20 25 30

Leu Arg Leu Ser Gln Thr Ala Glu Glu Met Ala Ala Asn Leu Thr Val
35 40 45

Gln Ser Glu Ser Gly Cys Ala Asn Ile Val Ser Ala Ala Pro Cys Gln
50 55 60

Ala Glu Pro Gln Gln Tyr Glu Val Gln Phe Gly Arg Leu Arg Asn Phe
65 70 75 80

Leu Thr Gly Cys Leu
85

<210> 78
<211> 499
<212> PRT
<213> Homo sapiens

<400> 78
Met Ser Glu Arg Glu Glu Arg Arg Phe Val Glu Ile Pro Arg Glu Ser
1 5 10 15

Val Arg Leu Met Ala Glu Ser Thr Gly Leu Glu Leu Ser Asp Glu Val
20 25 30

Ala Ala Leu Leu Ala Glu Asp Val Cys Tyr Arg Leu Arg Glu Ala Thr
35 40 45

Gln Asn Ser Ser Gln Phe Met Lys His Thr Lys Arg Arg Lys Leu Thr
50 55 60

Val Glu Asp Phe Asn Arg Ala Leu Arg Trp Ser Ser Val Glu Ala Val
65 70 75 80

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```
Cys Gly Tyr Gly Ser Gln Glu Ala Leu Pro Met Arg Pro Ala Arg Glu
                85                  90                  95

Gly Glu Leu Tyr Phe Pro Glu Asp Arg Glu Val Asn Leu Val Glu Leu
            100                 105                 110

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

Val His Val Ser Tyr Leu Asp Gly Lys Gly Asn Leu Ala Pro Gln Gly
    130                 135                 140

Ser Val Pro Ser Ala Val Ser Ser Leu Thr Asp Asp Leu Leu Lys Tyr
145                 150                 155                 160

Tyr His Gln Val Thr Arg Ala Val Leu Gly Asp Asp Pro Gln Leu Met
                165                 170                 175

Lys Val Ala Leu Gln Asp Leu Gln Thr Asn Ser Lys Ile Gly Ala Leu
            180                 185                 190

Leu Pro Tyr Phe Val Tyr Val Val Ser Gly Val Lys Ser Val Ser His
        195                 200                 205

Asp Leu Glu Gln Leu His Arg Leu Leu Gln Val Ala Arg Ser Leu Phe
    210                 215                 220

Arg Asn Pro His Leu Cys Leu Gly Pro Tyr Val Arg Cys Leu Val Gly
225                 230                 235                 240

Ser Val Leu Tyr Cys Val Leu Glu Pro Leu Ala Ala Ser Ile Asn Pro
                245                 250                 255

Leu Asn Asp His Trp Thr Leu Arg Asp Gly Ala Ala Leu Leu Leu Ser
            260                 265                 270

His Ile Phe Trp Thr His Gly Asp Leu Val Ser Gly Leu Tyr Gln His
        275                 280                 285

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

Cys Cys His Tyr Gly Ala Val Val Gly Leu His Ala Leu Gly Trp Lys
305                 310                 315                 320

Ala Val Glu Arg Val Leu Tyr Pro His Leu Ser Thr Tyr Trp Thr Asn
                325                 330                 335

Leu Gln Ala Val Leu Asp Asp Tyr Ser Val Ser Asn Ala Gln Val Lys
            340                 345                 350
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Ala Asp Gly His Lys Val Tyr Gly Ala Ile Leu Val Ala Val Glu Arg
355 360 365

Leu Leu Lys Met Lys Ala Gln Ala Ala Glu Pro Asn Arg Gly Gly Pro
370 375 380

Gly Gly Arg Gly Cys Arg Arg Leu Asp Asp Leu Pro Trp Asp Ser Leu
385 390 395 400

Leu Phe Gln Glu Ser Ser Ser Gly Gly Gly Ala Glu Pro Ser Phe Gly
405 410 415

Ser Gly Leu Pro Leu Pro Pro Gly Gly Ala Gly Pro Glu Asp Pro Ser
420 425 430

Leu Ser Val Thr Leu Ala Asp Ile Tyr Arg Glu Leu Tyr Ala Phe Phe
435 440 445

Gly Asp Ser Leu Ala Thr Arg Phe Gly Thr Gly Leu Ala Leu Arg Ala
450 455 460

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

Ala Leu Gly Leu Leu Ala Val Leu Ala Ala Leu Ser Gln Trp Pro Leu
485 490 495

Arg Ser Leu

<210> 79
<211> 316
<212> PRT
<213> Homo sapiens

<400> 79
Met Ser Glu Arg Glu Glu Arg Arg Phe Val Glu Ile Pro Arg Glu Ser
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Val Arg Leu Met Ala Glu Ser Thr Gly Leu Glu Leu Ser Asp Glu Val
20 25 30

Ala Ala Leu Leu Ala Glu Asp Val Cys Tyr Arg Leu Arg Glu Ala Thr
35 40 45

Gln Asn Ser Ser Gln Phe Met Lys His Thr Lys Arg Arg Lys Leu Thr
50 55 60

Val Glu Asp Phe Asn Arg Ala Leu Arg Trp Ser Ser Val Glu Ala Val
65 70 75 80

Cys Gly Tyr Gly Ser Gln Glu Ala Leu Pro Met Arg Pro Ala Arg Glu
85 90 95

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Gly Glu Leu Tyr Phe Pro Glu Asp Arg Glu Val Asn Leu Val Glu Leu
100 105 110

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

Val His Val Ser Tyr Leu Asp Gly Lys Gly Asn Leu Ala Pro Gln Gly
130 135 140

Ser Val Pro Ser Ala Val Ser Ser Leu Thr Asp Asp Leu Leu Lys Tyr
145 150 155 160

Tyr His Gln Val Thr Arg Ala Val Leu Gly Asp Asp Pro Gln Leu Met
165 170 175

Lys Val Ala Leu Gln Asp Leu Gln Thr Asn Ser Lys Ile Gly Ala Leu
180 185 190

Leu Pro Tyr Phe Val Tyr Val Val Ser Gly Val Lys Ser Val Ser His
195 200 205

Asp Leu Glu Gln Leu His Arg Leu Leu Gln Val Ala Arg Ser Leu Phe
210 215 220

Arg Asn Pro His Leu Cys Leu Gly Pro Tyr Val Arg Cys Leu Val Gly
225 230 235 240

Ser Val Leu Tyr Cys Val Leu Glu Pro Leu Ala Ala Ser Ile Asn Pro
245 250 255

Leu Asn Asp His Trp Thr Leu Arg Asp Gly Ala Ala Leu Leu Leu Ser
260 265 270

His Ile Phe Trp Thr His Gly Asp Leu Val Ser Gly Leu Tyr Gln His
275 280 285

Ile Leu Leu Ser Arg Pro Pro Val Gly Ala Leu Gly Leu Leu Ala Val
290 295 300

Leu Ala Ala Leu Ser Gln Trp Pro Leu Arg Ser Leu
305 310 315

<210> 80
<211> 302
<212> PRT
<213> Homo sapiens

<400> 80
Met Ser Glu Ser Gln Asp Glu Val Pro Asp Glu Val Glu Asn Gln Phe
1 5 10 15

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

Arg Ser Gln Ser Val Lys Met Lys Asp Lys Leu Lys Ile Asp Leu Leu
35 40 45

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

Ala Lys Leu Val Asp Leu Pro Cys Val Ile Glu Ser Leu Arg Thr Leu
65 70 75 80

Asp Lys Lys Thr Phe Tyr Lys Thr Ala Asp Ile Ser Gln Met Leu Val
85 90 95

Cys Thr Ala Asp Gly Asp Ile His Leu Ser Pro Glu Glu Pro Ala Ala
100 105 110

Ser Thr Asp Pro Asn Ile Val Arg Lys Lys Glu Arg Gly Arg Glu Glu
115 120 125

Lys Cys Val Trp Lys His Gly Ile Thr Pro Pro Leu Lys Asn Val Arg
130 135 140

Lys Lys Arg Phe Arg Lys Thr Gln Lys Lys Val Pro Asp Val Lys Glu
145 150 155 160

Met Glu Lys Ser Ser Phe Thr Glu Tyr Ile Glu Ser Pro Asp Val Glu
165 170 175

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

Arg Trp Glu Val Ile Ala Glu Asp Gly Thr Lys Glu Ile Glu Ser Gln
195 200 205

Gly Ser Ile Pro Gly Phe Leu Ile Ser Ser Gly Met Ser Ser His Lys
210 215 220

Gln Gly His Thr Ser Ser Val Met Glu Ile Gln Lys Gln Ile Glu Lys
225 230 235 240

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

Asp Leu Ile Met Lys Val Glu Asn Leu Thr Leu Lys Asn His Phe Gln
260 265 270

Ser Val Leu Glu Gln Leu Glu Leu Gln Glu Lys Gln Lys Asn Glu Lys
275 280 285

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

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<210> 81
<211> 96
<212> PRT
<213> Homo sapiens

<400> 81
Met Ser Glu Ser Gln Asp Glu Val Pro Asp Glu Val Glu Asn Gln Phe
1 5 10 15

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

Arg Ser Gln Ser Val Lys Met Lys Asp Lys Leu Lys Ile Asp Leu Leu
35 40 45

Pro His Phe Pro Thr Gly Thr Val Ala Ala Phe Ser Glu Glu Val Arg
50 55 60

Arg Ala Ile Gly Val Ala His Lys Pro Trp Ile His His Pro Asp Cys
65 70 75 80

Arg Leu Asp Glu Thr Val His Val Phe Val Pro Ser Val Ala Leu Cys
85 90 95

<210> 82
<211> 214
<212> PRT
<213> Homo sapiens

<400> 82
Met Ala Asp Ala Ala Ala Thr Ala Gly Ala Gly Gly Ser Gly Thr Arg
1 5 10 15

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

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

Gly Phe Glu Ser Ala Glu Lys Ala Ser Val Glu Thr Leu Thr Glu Met
50 55 60

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

Glu His Thr Ala Arg Thr Gln Pro Thr Leu Ser Asp Ile Val Val Thr
85 90 95

Leu Val Glu Met Gly Phe Asn Val Asp Thr Leu Pro Ala Tyr Ala Lys
100 105 110

Arg Ser Gln Arg Met Val Ile Thr Ala Pro Pro Val Thr Asn Gln Pro
115 120 125

Val Thr Pro Lys Ala Leu Thr Ala Gly Gln Asn Arg Pro His Pro Pro
130 135 140

His Ile Pro Ser His Phe Pro Glu Phe Pro Asp Pro His Thr Tyr Ile
145 150 155 160

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

Gln Gln Asn Pro Ser Leu Ser Gly Ser Arg Asn Gly Glu Glu Asn Ile
180 185 190

Ile Asp Asn Pro Tyr Leu Arg Pro Val Lys Lys Pro Lys Ile Arg Arg
195 200 205

Lys Lys Pro Asp Thr Phe
210

<210> 83
<211> 457
<212> PRT
<213> Homo sapiens

<400> 83
Met Ser Asp Ser Gly Ser Tyr Gly Gln Ser Gly Gly Glu Gln Gln Ser
1 5 10 15

Tyr Ser Thr Tyr Gly Asn Pro Gly Ser Gln Gly Tyr Gly Gln Ala Ser
20 25 30

Gln Ser Tyr Ser Gly Tyr Gly Gln Thr Thr Asp Ser Ser Tyr Gly Gln
35 40 45

Asn Tyr Ser Gly Tyr Ser Ser Tyr Gly Gln Ser Gln Ser Gly Tyr Ser
50 55 60

Gln Ser Tyr Gly Gly Tyr Glu Asn Gln Lys Gln Ser Ser Tyr Ser Gln
65 70 75 80

Gln Pro Tyr Asn Asn Gln Gly Gln Gln Gln Asn Met Glu Ser Ser Gly
85 90 95

Ser Gln Gly Gly Arg Ala Pro Ser Tyr Asp Gln Pro Asp Tyr Gly Gln
100 105 110

Gln Asp Ser Tyr Asp Gln Gln Ser Gly Tyr Asp Gln His Gln Gly Ser
115 120 125

Tyr Asp Glu Gln Ser Asn Tyr Asp Gln Gln His Asp Ser Tyr Ser Gln
130 135 140

Asn Gln Gln Ser Tyr His Ser Gln Arg Glu Asn Tyr Ser His His Thr
145 150 155 160

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Gln Asp Asp Arg Arg Asp Val Ser Arg Tyr Gly Glu Asp Asn Arg Gly
                165                 170                 175

Tyr Gly Gly Ser Gln Gly Gly Gly Arg Gly Arg Gly Gly Tyr Asp Lys
            180                 185                 190

Asp Gly Arg Gly Pro Met Thr Gly Ser Ser Gly Gly Asp Arg Gly Gly
        195                 200                 205

Phe Lys Asn Phe Gly Gly His Arg Asp Tyr Gly Pro Arg Thr Asp Ala
    210                 215                 220

Asp Ser Glu Ser Asp Asn Ser Asp Asn Asn Thr Ile Phe Val Gln Gly
225                 230                 235                 240

Leu Gly Glu Gly Val Ser Thr Asp Gln Val Gly Glu Phe Phe Lys Gln
                245                 250                 255

Ile Gly Ile Ile Lys Thr Asn Lys Lys Thr Gly Lys Pro Met Ile Asn
            260                 265                 270

Leu Tyr Thr Asp Lys Asp Thr Gly Lys Pro Lys Gly Glu Ala Thr Val
        275                 280                 285

Ser Phe Asp Asp Pro Pro Ser Ala Lys Ala Ala Ile Asp Trp Phe Asp
    290                 295                 300

Gly Lys Glu Phe His Gly Asn Ile Ile Lys Val Ser Phe Ala Thr Arg
305                 310                 315                 320

Arg Pro Glu Phe Met Arg Gly Gly Gly Ser Gly Gly Gly Arg Arg Gly
                325                 330                 335

Arg Gly Gly Tyr Arg Gly Arg Gly Gly Phe Gln Gly Arg Gly Gly Asp
            340                 345                 350

Pro Lys Ser Gly Asp Trp Val Cys Pro Asn Pro Ser Cys Gly Asn Met
        355                 360                 365

Asn Phe Ala Arg Arg Asn Ser Cys Asn Gln Cys Asn Glu Pro Arg Pro
    370                 375                 380

Glu Asp Ser Arg Pro Ser Gly Gly Glu Thr Thr Thr Glu Met Ile Ser
385                 390                 395                 400

Ala Thr Asp His Thr Asp Asp Cys Phe Glu Cys Ser Phe Val Ser Asp
                405                 410                 415

Met Ile His Ser Glu Ile Ala Arg Val Leu Pro Ala Ala Phe Leu Val
            420                 425                 430
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Ala Ser Ser Trp Val Val Lys Leu Ser Asp Ile Trp Ile Phe Ile Trp
435 440 445

Val Gly Gly Leu Gly Gln Phe Phe Phe
450 455

<210> 84
<211> 480
<212> PRT
<213> Homo sapiens

<400> 84
Met Ser Asp Ser Gly Ser Tyr Gly Gln Ser Gly Gly Glu Gln Gln Ser
1 5 10 15

Tyr Ser Thr Tyr Gly Asn Pro Gly Ser Gln Gly Tyr Gly Gln Ala Ser
20 25 30

Gln Ser Tyr Ser Gly Tyr Gly Gln Thr Thr Asp Ser Ser Tyr Gly Gln
35 40 45

Asn Tyr Ser Gly Tyr Ser Ser Tyr Gly Gln Ser Gln Ser Gly Tyr Ser
50 55 60

Gln Ser Tyr Gly Gly Tyr Glu Asn Gln Lys Gln Ser Ser Tyr Ser Gln
65 70 75 80

Gln Pro Tyr Asn Asn Gln Gly Gln Gln Gln Asn Met Glu Ser Ser Gly
85 90 95

Ser Gln Gly Gly Arg Ala Pro Ser Tyr Asp Gln Pro Asp Tyr Gly Gln
100 105 110

Gln Asp Ser Tyr Asp Gln Gln Ser Gly Tyr Asp Gln His Gln Gly Ser
115 120 125

Tyr Asp Glu Gln Ser Asn Tyr Asp Gln Gln His Asp Ser Tyr Ser Gln
130 135 140

Asn Gln Gln Ser Tyr His Ser Gln Arg Glu Asn Tyr Ser His His Thr
145 150 155 160

Gln Asp Asp Arg Arg Asp Val Ser Arg Tyr Gly Glu Asp Asn Arg Gly
165 170 175

Tyr Gly Gly Ser Gln Gly Gly Gly Arg Gly Arg Gly Gly Tyr Asp Lys
180 185 190

Asp Gly Arg Gly Pro Met Thr Gly Ser Ser Gly Gly Asp Arg Gly Gly
195 200 205

Phe Lys Asn Phe Gly Gly His Arg Asp Tyr Gly Pro Arg Thr Asp Ala
210 215 220

Asp Ser Glu Ser Asp Asn Ser Asp Asn Asn Thr Ile Phe Val Gln Gly
225 230 235 240

Leu Gly Glu Gly Val Ser Thr Asp Gln Val Gly Glu Phe Phe Lys Gln
245 250 255

Ile Gly Ile Ile Lys Thr Asn Lys Lys Thr Gly Lys Pro Met Ile Asn
260 265 270

Leu Tyr Thr Asp Lys Asp Thr Gly Lys Pro Lys Gly Glu Ala Thr Val
275 280 285

Ser Phe Asp Asp Pro Pro Ser Ala Lys Ala Ala Ile Asp Trp Phe Asp
290 295 300

Gly Lys Glu Phe His Gly Asn Ile Ile Lys Val Ser Phe Ala Thr Arg
305 310 315 320

Arg Pro Glu Phe Met Arg Gly Gly Gly Ser Gly Gly Gly Arg Arg Gly
325 330 335

Arg Gly Gly Tyr Arg Gly Arg Gly Gly Phe Gln Gly Arg Gly Gly Asp
340 345 350

Pro Lys Ser Gly Asp Trp Val Cys Pro Asn Pro Ser Cys Gly Asn Met
355 360 365

Asn Phe Ala Arg Arg Asn Ser Cys Asn Gln Cys Asn Glu Pro Arg Pro
370 375 380

Glu Asp Ser Arg Pro Ser Gly Gly Asp Phe Arg Gly Arg Gly Tyr Gly
385 390 395 400

Gly Glu Arg Gly Tyr Arg Gly Arg Gly Gly Arg Gly Gly Asp Arg Gly
405 410 415

Gly Tyr Gly Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly Asp Arg Ser
420 425 430

Ser Gly Gly Gly Tyr Ser Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly
435 440 445

Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Lys
450 455 460

Met Gly Gly Arg Asn Asp Tyr Arg Asn Asp Gln Arg Asn Arg Pro Tyr
465 470 475 480

<210> 85
<211> 532
<212> PRT
<213> Homo sapiens

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<400> 85

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Met Ser Asp Ser Gly Ser Tyr Gly Gln Ser Gly Gly Glu Gln Gln Ser
1               5                  10                  15

Tyr Ser Thr Tyr Gly Asn Pro Gly Ser Gln Gly Tyr Gly Gln Ala Ser
            20                  25                  30

Gln Ser Tyr Ser Gly Tyr Gly Gln Thr Thr Asp Ser Ser Tyr Gly Gln
        35                  40                  45

Asn Tyr Ser Gly Tyr Ser Ser Tyr Gly Gln Ser Gln Ser Gly Tyr Ser
    50                  55                  60

Gln Ser Tyr Gly Gly Tyr Glu Asn Gln Lys Gln Ser Ser Tyr Ser Gln
65                  70                  75                  80

Gln Pro Tyr Asn Asn Gln Gly Gln Gln Gln Asn Met Glu Ser Ser Gly
                85                  90                  95

Ser Gln Gly Gly Arg Ala Pro Ser Tyr Asp Gln Pro Asp Tyr Gly Gln
            100                 105                 110

Gln Asp Ser Tyr Asp Gln Gln Ser Gly Tyr Asp Gln His Gln Gly Ser
        115                 120                 125

Tyr Asp Glu Gln Ser Asn Tyr Asp Gln Gln His Asp Ser Tyr Ser Gln
    130                 135                 140

Asn Gln Gln Ser Tyr His Ser Gln Arg Glu Asn Tyr Ser His His Thr
145                 150                 155                 160

Gln Asp Asp Arg Arg Asp Val Ser Arg Tyr Gly Glu Asp Asn Arg Gly
                165                 170                 175

Tyr Gly Gly Ser Gln Gly Gly Gly Arg Gly Arg Gly Gly Tyr Asp Lys
            180                 185                 190

Asp Gly Arg Gly Pro Met Thr Gly Ser Ser Gly Gly Asp Arg Gly Gly
        195                 200                 205

Phe Lys Asn Phe Gly Gly His Arg Asp Tyr Gly Pro Arg Thr Asp Ala
    210                 215                 220

Asp Ser Glu Ser Asp Asn Ser Asp Asn Asn Thr Ile Phe Val Gln Gly
225                 230                 235                 240

Leu Gly Glu Gly Val Ser Thr Asp Gln Val Gly Glu Phe Phe Lys Gln
                245                 250                 255

Ile Gly Ile Ile Lys Thr Asn Lys Lys Thr Gly Lys Pro Met Ile Asn
            260                 265                 270
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Leu Tyr Thr Asp Lys Asp Thr Gly Lys Pro Lys Gly Glu Ala Thr Val
275 280 285

Ser Phe Asp Asp Pro Pro Ser Ala Lys Ala Ala Ile Asp Trp Phe Asp
290 295 300

Gly Lys Glu Phe His Gly Asn Ile Ile Lys Val Ser Phe Ala Thr Arg
305 310 315 320

Arg Pro Glu Phe Met Arg Gly Gly Gly Ser Gly Gly Gly Arg Arg Gly
325 330 335

Arg Gly Gly Tyr Arg Gly Arg Gly Gly Phe Gln Gly Arg Gly Gly Asp
340 345 350

Pro Lys Ser Gly Asp Trp Val Cys Pro Asn Pro Ser Cys Gly Asn Met
355 360 365

Asn Phe Ala Arg Arg Asn Ser Cys Asn Gln Cys Asn Glu Pro Arg Pro
370 375 380

Glu Asp Ser Arg Pro Ser Gly Gly Asp Phe Arg Gly Arg Gly Tyr Gly
385 390 395 400

Gly Glu Arg Gly Tyr Arg Gly Arg Gly Gly Arg Gly Gly Asp Arg Gly
405 410 415

Gly Tyr Gly Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly Asp Arg Ser
420 425 430

Ser Gly Gly Gly Tyr Ser Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly
435 440 445

Asp Arg Ser Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly
450 455 460

Gly Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Ser Gly
465 470 475 480

Tyr Gly Gly Asp Arg Ser Gly Gly Tyr Gly Gly Asp Arg Ser Gly Gly
485 490 495

Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly
500 505 510

Tyr Gly Gly Lys Met Gly Gly Arg Asn Asp Tyr Arg Asn Asp Gln Arg
515 520 525

Asn Arg Pro Tyr
530

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<210> 86
<211> 579
<212> PRT
<213> Homo sapiens

<400> 86

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Met Ser Asp Ser Gly Ser Tyr Gly Gln Ser Gly Gly Glu Gln Gln Ser
1               5                  10                  15

Tyr Ser Thr Tyr Gly Asn Pro Gly Ser Gln Gly Tyr Gly Gln Ala Ser
            20                  25                  30

Gln Ser Tyr Ser Gly Tyr Gly Gln Thr Thr Asp Ser Ser Tyr Gly Gln
        35                  40                  45

Asn Tyr Ser Gly Tyr Ser Ser Tyr Gly Gln Ser Gln Ser Gly Tyr Ser
    50                  55                  60

Gln Ser Tyr Gly Gly Tyr Glu Asn Gln Lys Gln Ser Ser Tyr Ser Gln
65                  70                  75                  80

Gln Pro Tyr Asn Asn Gln Gly Gln Gln Gln Asn Met Glu Ser Ser Gly
                85                  90                  95

Ser Gln Gly Gly Arg Ala Pro Ser Tyr Asp Gln Pro Asp Tyr Gly Gln
            100                 105                 110

Gln Asp Ser Tyr Asp Gln Gln Ser Gly Tyr Asp Gln His Gln Gly Ser
        115                 120                 125

Tyr Asp Glu Gln Ser Asn Tyr Asp Gln Gln His Asp Ser Tyr Ser Gln
    130                 135                 140

Asn Gln Gln Ser Tyr His Ser Gln Arg Glu Asn Tyr Ser His His Thr
145                 150                 155                 160

Gln Asp Asp Arg Arg Asp Val Ser Arg Tyr Gly Glu Asp Asn Arg Gly
                165                 170                 175

Tyr Asp Lys Asp Gly Arg Gly Pro Met Thr Gly Ser Ser Gly Gly Asp
            180                 185                 190

Arg Gly Gly Phe Lys Asn Phe Gly Gly His Arg Asp Tyr Gly Pro Arg
        195                 200                 205

Thr Asp Ala Asp Ser Glu Ser Asp Asn Ser Asp Asn Asn Thr Ile Phe
    210                 215                 220

Val Gln Gly Leu Gly Glu Gly Val Ser Thr Asp Gln Val Gly Glu Phe
225                 230                 235                 240

Phe Lys Gln Ile Gly Ile Ile Lys Thr Asn Lys Lys Thr Gly Lys Pro
                245                 250                 255
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Met Ile Asn Leu Tyr Thr Asp Lys Asp Thr Gly Lys Pro Lys Gly Glu
            260                 265                 270

Ala Thr Val Ser Phe Asp Asp Pro Pro Ser Ala Lys Ala Ala Ile Asp
        275                 280                 285

Trp Phe Asp Gly Lys Glu Phe His Gly Asn Ile Ile Lys Val Ser Phe
    290                 295                 300

Ala Thr Arg Arg Pro Glu Phe Met Arg Gly Gly Gly Ser Gly Gly Gly
305                 310                 315                 320

Arg Arg Gly Arg Gly Gly Tyr Arg Gly Arg Gly Gly Phe Gln Gly Arg
                325                 330                 335

Gly Gly Asp Pro Lys Ser Gly Asp Trp Val Cys Pro Asn Pro Ser Cys
            340                 345                 350

Gly Asn Met Asn Phe Ala Arg Arg Asn Ser Cys Asn Gln Cys Asn Glu
        355                 360                 365

Pro Arg Pro Glu Asp Ser Arg Pro Ser Gly Gly Asp Phe Arg Gly Arg
    370                 375                 380

Gly Tyr Gly Gly Glu Arg Gly Tyr Arg Gly Arg Gly Gly Arg Gly Gly
385                 390                 395                 400

Asp Arg Gly Gly Tyr Gly Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly
                405                 410                 415

Asp Arg Ser Ser Gly Gly Gly Tyr Ser Gly Asp Arg Ser Gly Gly Gly
            420                 425                 430

Tyr Gly Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly
        435                 440                 445

Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly
    450                 455                 460

Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly
465                 470                 475                 480

Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly
                485                 490                 495

Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp
            500                 505                 510

Arg Ser Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Ser Gly Tyr
        515                 520                 525
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Gly Gly Asp Arg Ser Gly Gly Tyr Gly Gly Asp Arg Ser Gly Gly Gly
530 535 540

Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr
545 550 555 560

Gly Gly Lys Met Gly Gly Arg Asn Asp Tyr Arg Asn Asp Gln Arg Asn
565 570 575

Arg Pro Tyr

<210> 87
<211> 1160
<212> PRT
<213> Homo sapiens

<400> 87
Met Lys Ala Gln Gly Glu Thr Glu Glu Ser Glu Lys Leu Ser Lys Met
1 5 10 15

Ser Ser Leu Leu Glu Arg Leu His Ala Lys Phe Asn Gln Asn Arg Pro
20 25 30

Trp Ser Glu Thr Ile Lys Leu Val Arg Gln Val Met Glu Lys Arg Val
35 40 45

Val Met Ser Ser Gly Gly His Gln His Leu Val Ser Cys Leu Glu Thr
50 55 60

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

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

Ser Gly Thr Glu Cys Tyr Ile Thr Ser Asp Met Phe Tyr Val Glu Val
100 105 110

Gln Leu Asp Pro Ala Gly Gln Leu Cys Asp Val Lys Val Ala His His
115 120 125

Gly Glu Asn Pro Val Ser Cys Pro Glu Leu Val Gln Gln Leu Arg Glu
130 135 140

Lys Asn Phe Asp Glu Phe Ser Lys His Leu Lys Gly Leu Val Asn Leu
145 150 155 160

Tyr Asn Leu Pro Gly Asp Asn Lys Leu Lys Thr Lys Met Tyr Leu Ala
165 170 175

Leu Gln Ser Leu Glu Gln Asp Leu Ser Lys Met Ala Ile Met Tyr Trp
180 185 190

Lys Ala Thr Asn Ala Gly Pro Leu Asp Lys Ile Pro His His Thr Pro
195 200 205

Pro Pro Val Ser Ser Met Ala Gly Asn Thr Lys Asn His Pro Met Leu
210 215 220

Met Asn Leu Leu Lys Asp Asn Pro Ala Gln Asp Phe Ser Thr Leu Tyr
225 230 235 240

Gly Ser Ser Pro Leu Glu Arg Gln Asn Ser Ser Ser Gly Ser Pro Arg
245 250 255

Met Glu Ile Cys Ser Gly Ser Asn Lys Thr Lys Lys Lys Lys Ser Ser
260 265 270

Arg Leu Pro Pro Glu Lys Pro Lys His Gln Thr Glu Asp Asp Phe Gln
275 280 285

Arg Glu Leu Phe Ser Met Asp Val Asp Ser Gln Asn Pro Ile Phe Asp
290 295 300

Val Asn Met Thr Ala Asp Thr Leu Asp Thr Pro His Ile Thr Pro Ala
305 310 315 320

Pro Ser Gln Cys Ser Thr Pro Pro Thr Thr Tyr Pro Gln Pro Val Pro
325 330 335

His Pro Gln Pro Ser Ile Gln Arg Met Val Arg Leu Ser Ser Ser Asp
340 345 350

Ser Ile Gly Pro Asp Val Thr Asp Ile Leu Ser Asp Ile Ala Glu Glu
355 360 365

Ala Ser Lys Leu Pro Ser Thr Ser Asp Asp Cys Pro Ala Ile Gly Thr
370 375 380

Pro Leu Arg Asp Ser Ser Ser Ser Gly His Ser Gln Ser Thr Leu Phe
385 390 395 400

Asp Ser Asp Val Phe Gln Thr Asn Asn Asn Glu Asn Pro Tyr Thr Asp
405 410 415

Pro Ala Asp Leu Ile Ala Asp Ala Ala Gly Ser Pro Ser Ser Asp Ser
420 425 430

Pro Thr Asn His Phe Phe His Asp Gly Val Asp Phe Asn Pro Asp Leu
435 440 445

Leu Asn Ser Gln Ser Gln Ser Gly Phe Gly Glu Glu Tyr Phe Asp Glu
450 455 460

Ser Ser Gln Ser Gly Asp Asn Asp Asp Phe Lys Gly Phe Ala Ser Gln
465 470 475 480

Ala Leu Asn Thr Leu Gly Val Pro Met Leu Gly Gly Asp Asn Gly Glu
485 490 495

Thr Lys Phe Lys Gly Asn Asn Gln Ala Asp Thr Val Asp Phe Ser Ile
500 505 510

Ile Ser Val Ala Gly Lys Ala Leu Ala Pro Ala Asp Leu Met Glu His
515 520 525

His Ser Gly Ser Gln Gly Pro Leu Leu Thr Thr Gly Asp Leu Gly Lys
530 535 540

Glu Lys Thr Gln Lys Arg Val Lys Glu Gly Asn Gly Thr Ser Asn Ser
545 550 555 560

Thr Leu Ser Gly Pro Gly Leu Asp Ser Lys Pro Gly Lys Arg Ser Arg
565 570 575

Thr Pro Ser Asn Asp Gly Lys Ser Lys Asp Lys Pro Pro Lys Arg Lys
580 585 590

Lys Ala Asp Thr Glu Gly Lys Ser Pro Ser His Ser Ser Ser Asn Arg
595 600 605

Pro Phe Thr Pro Pro Thr Ser Thr Gly Gly Ser Lys Ser Pro Gly Ser
610 615 620

Ala Gly Arg Ser Gln Thr Pro Pro Gly Val Ala Thr Pro Pro Ile Pro
625 630 635 640

Lys Ile Thr Ile Gln Ile Pro Lys Gly Thr Val Met Val Gly Lys Pro
645 650 655

Ser Ser His Ser Gln Tyr Thr Ser Ser Gly Ser Val Ser Ser Ser Gly
660 665 670

Ser Lys Ser His His Ser His Ser Ser Ser Ser Ser Ser Ser Ala Ser
675 680 685

Thr Ser Gly Lys Met Lys Ser Ser Lys Ser Glu Gly Ser Ser Ser Ser
690 695 700

Lys Leu Ser Ser Ser Met Tyr Ser Ser Gln Gly Ser Ser Gly Ser Ser
705 710 715 720

Gln Ser Lys Asn Ser Ser Gln Ser Gly Gly Lys Pro Gly Ser Ser Pro
725 730 735

Ile Thr Lys His Gly Leu Ser Ser Gly Ser Ser Ser Thr Lys Met Lys

740 745 750

Pro Gln Gly Lys Pro Ser Ser Leu Met Asn Pro Ser Leu Ser Lys Pro
755 760 765

Asn Ile Ser Pro Ser His Ser Arg Pro Pro Gly Gly Ser Asp Lys Leu
770 775 780

Ala Ser Pro Met Lys Pro Val Pro Gly Thr Pro Pro Ser Ser Lys Ala
785 790 795 800

Lys Ser Pro Ile Ser Ser Gly Ser Gly Gly Ser His Met Ser Gly Thr
805 810 815

Ser Ser Ser Ser Gly Met Lys Ser Ser Ser Gly Leu Gly Ser Ser Gly
820 825 830

Ser Leu Ser Gln Lys Thr Pro Pro Ser Ser Asn Ser Cys Thr Ala Ser
835 840 845

Ser Ser Ser Phe Ser Ser Ser Gly Ser Ser Met Ser Ser Ser Gln Asn
850 855 860

Gln His Gly Ser Ser Lys Gly Lys Ser Pro Ser Arg Asn Lys Lys Pro
865 870 875 880

Ser Leu Thr Ala Val Ile Asp Lys Leu Lys His Gly Val Val Thr Ser
885 890 895

Gly Pro Gly Gly Glu Asp Pro Leu Asp Gly Gln Met Gly Val Ser Thr
900 905 910

Asn Ser Ser Ser His Pro Met Ser Ser Lys His Asn Met Ser Gly Gly
915 920 925

Glu Phe Gln Gly Lys Arg Glu Lys Ser Asp Lys Asp Lys Ser Lys Val
930 935 940

Ser Thr Ser Gly Ser Ser Val Asp Ser Ser Lys Lys Thr Ser Glu Ser
945 950 955 960

Lys Asn Val Gly Ser Thr Gly Val Ala Lys Ile Ile Ile Ser Lys His
965 970 975

Asp Gly Gly Ser Pro Ser Ile Lys Ala Lys Val Thr Leu Gln Lys Pro
980 985 990

Gly Glu Ser Ser Gly Glu Gly Leu Arg Pro Gln Met Ala Ser Ser Lys
995 1000 1005

Asn Tyr Gly Ser Pro Leu Ile Ser Gly Ser Thr Pro Lys His Glu
1010 1015 1020

Arg Gly Ser Pro Ser His Ser Lys Ser Pro Ala Tyr Thr Pro Gln
1025 1030 1035

Asn Leu Asp Ser Glu Ser Glu Ser Gly Ser Ser Ile Ala Glu Lys
1040 1045 1050

Ser Tyr Gln Asn Ser Pro Ser Ser Asp Asp Gly Ile Arg Pro Leu
1055 1060 1065

Pro Glu Tyr Ser Thr Glu Lys His Lys Lys His Lys Lys Glu Lys
1070 1075 1080

Lys Lys Val Lys Asp Lys Asp Arg Asp Arg Asp Arg Asp Lys Asp
1085 1090 1095

Arg Asp Lys Lys Lys Ser His Ser Ile Lys Pro Glu Ser Trp Ser
1100 1105 1110

Lys Ser Pro Ile Ser Ser Asp Gln Ser Leu Ser Met Thr Ser Asn
1115 1120 1125

Thr Ile Leu Ser Ala Asp Arg Pro Ser Arg Leu Ser Pro Asp Phe
1130 1135 1140

Met Ile Gly Glu Glu Asp Asp Asp Leu Met Asp Val Ala Leu Ile
1145 1150 1155

Gly Asn
1160

<210> 88
<211> 78
<212> PRT
<213> Homo sapiens

<400> 88
Met Lys Ala Gln Gly Glu Thr Glu Glu Ser Glu Lys Leu Ser Lys Met
1 5 10 15

Ser Ser Leu Leu Glu Arg Leu His Ala Lys Phe Asn Gln Asn Arg Pro
20 25 30

Trp Ser Glu Thr Ile Lys Leu Val Arg Gln Val Met Glu Lys Arg Val
35 40 45

Val Met Ser Ser Gly Gly His Gln His Leu Val Ser Cys Leu Phe Asp
50 55 60

Gly Arg Gln His Gln Glu Pro Pro Asp Ala His Glu Pro Ser
65 70 75

<210> 89

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<211> 1270
<212> PRT
<213> Homo sapiens

<400> 89

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Met Lys Ala Gln Gly Glu Thr Glu Glu Ser Glu Lys Leu Ser Lys Met
1               5                  10                  15

Ser Ser Leu Leu Glu Arg Leu His Ala Lys Phe Asn Gln Asn Arg Pro
            20                  25                  30

Trp Ser Glu Thr Ile Lys Leu Val Arg Gln Val Met Glu Lys Arg Val
        35                  40                  45

Val Met Ser Ser Gly Gly His Gln His Leu Val Ser Cys Leu Glu Thr
    50                  55                  60

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

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

Ser Gly Thr Glu Cys Tyr Ile Thr Ser Asp Met Phe Tyr Val Glu Val
            100                 105                 110

Gln Leu Asp Pro Ala Gly Gln Leu Cys Asp Val Lys Val Ala His His
        115                 120                 125

Gly Glu Asn Pro Val Ser Cys Pro Glu Leu Val Gln Gln Leu Arg Glu
    130                 135                 140

Lys Asn Phe Asp Glu Phe Ser Lys His Leu Lys Gly Leu Val Asn Leu
145                 150                 155                 160

Tyr Asn Leu Pro Gly Asp Asn Lys Leu Lys Thr Lys Met Tyr Leu Ala
                165                 170                 175

Leu Gln Ser Leu Glu Gln Asp Leu Ser Lys Met Ala Ile Met Tyr Trp
            180                 185                 190

Lys Ala Thr Asn Ala Gly Pro Leu Asp Lys Ile Leu His Gly Ser Val
        195                 200                 205

Gly Tyr Leu Thr Pro Arg Ser Gly Gly His Leu Met Asn Leu Lys Tyr
    210                 215                 220

Tyr Val Ser Pro Ser Asp Leu Leu Asp Asp Lys Thr Ala Ser Pro Ile
225                 230                 235                 240

Ile Leu His Glu Asn Asn Val Ser Arg Ser Leu Gly Met Asn Ala Ser
                245                 250                 255
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Val Thr Ile Glu Gly Thr Ser Ala Val Tyr Lys Leu Pro Ile Ala Pro
260 265 270

Leu Ile Met Gly Ser His Pro Val Asp Asn Lys Trp Thr Pro Ser Phe
275 280 285

Ser Ser Ile Thr Ser Ala Asn Ser Val Asp Leu Pro Ala Cys Phe Phe
290 295 300

Leu Lys Phe Pro Gln Pro Ile Pro Val Ser Arg Ala Phe Val Gln Lys
305 310 315 320

Leu Gln Asn Cys Thr Gly Ile Pro Leu Phe Glu Thr Gln Pro Thr Tyr
325 330 335

Ala Pro Leu Tyr Glu Leu Ile Thr Gln Phe Glu Leu Ser Lys Asp Pro
340 345 350

Asp Pro Ile Pro Leu Asn His Asn Met Arg Phe Tyr Ala Ala Leu Pro
355 360 365

Gly Gln Gln His Cys Tyr Phe Leu Asn Lys Asp Ala Pro Leu Pro Asp
370 375 380

Gly Arg Ser Leu Gln Gly Thr Leu Val Ser Lys Ile Thr Phe Gln His
385 390 395 400

Pro Gly Arg Val Pro Leu Ile Leu Asn Leu Ile Arg His Gln Val Ala
405 410 415

Tyr Asn Thr Leu Ile Gly Ser Cys Val Lys Arg Thr Ile Leu Lys Glu
420 425 430

Asp Ser Pro Gly Leu Leu Gln Phe Glu Val Cys Pro Leu Ser Glu Ser
435 440 445

Arg Phe Ser Val Ser Phe Gln His Pro Val Asn Asp Ser Leu Val Cys
450 455 460

Val Val Met Asp Val Gln Asp Ser Thr His Val Ser Cys Lys Leu Tyr
465 470 475 480

Lys Gly Leu Ser Asp Ala Leu Ile Cys Thr Asp Asp Phe Ile Ala Lys
485 490 495

Val Val Gln Arg Cys Met Ser Ile Pro Val Thr Met Arg Ala Ile Arg
500 505 510

Arg Lys Ala Glu Thr Ile Gln Ala Asp Thr Pro Ala Leu Ser Leu Ile
515 520 525

Ala Glu Thr Val Glu Asp Met Val Lys Lys Asn Leu Pro Pro Ala Ser

530 535 540

Ser Pro Gly Tyr Gly Met Thr Thr Gly Asn Asn Pro Met Ser Gly Thr
545 550 555 560

Thr Thr Ser Thr Asn Thr Phe Pro Gly Gly Pro Ile Ala Thr Leu Phe
565 570 575

Asn Met Ser Met Ser Ile Lys Asp Arg His Glu Ser Val Gly His Gly
580 585 590

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

Gln Ile Thr Gly Asn Gly Gly Ser Thr Ile Gly Ser Ser Pro Thr Pro
610 615 620

Pro His His Thr Pro Pro Pro Val Ser Ser Met Ala Gly Asn Thr Lys
625 630 635 640

Asn His Pro Met Leu Met Asn Leu Leu Lys Asp Asn Pro Ala Gln Asp
645 650 655

Phe Ser Thr Leu Tyr Gly Ser Ser Pro Leu Glu Arg Gln Asn Ser Ser
660 665 670

Ser Gly Ser Pro Arg Met Glu Ile Cys Ser Gly Ser Asn Lys Thr Lys
675 680 685

Lys Lys Lys Ser Ser Arg Leu Pro Pro Glu Lys Pro Lys His Gln Thr
690 695 700

Glu Asp Asp Phe Gln Arg Glu Leu Phe Ser Met Asp Val Asp Ser Gln
705 710 715 720

Asn Pro Ile Phe Asp Val Asn Met Thr Ala Asp Thr Leu Asp Thr Pro
725 730 735

His Ile Thr Pro Ala Pro Ser Gln Cys Ser Thr Pro Pro Thr Thr Tyr
740 745 750

Pro Gln Pro Val Pro His Pro Gln Pro Ser Ile Gln Arg Met Val Arg
755 760 765

Leu Ser Ser Ser Asp Ser Ile Gly Pro Asp Val Thr Asp Ile Leu Ser
770 775 780

Asp Ile Ala Glu Glu Ala Ser Lys Leu Pro Ser Thr Ser Asp Asp Cys
785 790 795 800

Pro Ala Ile Gly Thr Pro Leu Arg Asp Ser Ser Ser Ser Gly His Ser
805 810 815

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Gln Ser Thr Leu Phe Asp Ser Asp Val Phe Gln Thr Asn Asn Asn Glu
820 825 830

Asn Pro Tyr Thr Asp Pro Ala Asp Leu Ile Ala Asp Ala Ala Gly Ser
835 840 845

Pro Ser Ser Asp Ser Pro Thr Asn His Phe Phe His Asp Gly Val Asp
850 855 860

Phe Asn Pro Asp Leu Leu Asn Ser Gln Ser Gln Ser Gly Phe Gly Glu
865 870 875 880

Glu Tyr Phe Asp Glu Ser Ser Gln Ser Gly Asp Asn Asp Asp Phe Lys
885 890 895

Gly Phe Ala Ser Gln Ala Leu Asn Thr Leu Gly Val Pro Met Leu Gly
900 905 910

Gly Asp Asn Gly Glu Thr Lys Phe Lys Gly Asn Asn Gln Ala Asp Thr
915 920 925

Val Asp Phe Ser Ile Ile Ser Val Ala Gly Lys Ala Leu Ala Pro Ala
930 935 940

Asp Leu Met Glu His His Ser Gly Ser Gln Gly Pro Leu Leu Thr Thr
945 950 955 960

Gly Asp Leu Gly Lys Glu Lys Thr Gln Lys Arg Val Lys Glu Gly Asn
965 970 975

Gly Thr Ser Asn Ser Thr Leu Ser Gly Pro Gly Leu Asp Ser Lys Pro
980 985 990

Gly Lys Arg Ser Arg Thr Pro Ser Asn Asp Gly Lys Ser Lys Asp Lys
995 1000 1005

Pro Pro Lys Arg Lys Lys Ala Asp Thr Glu Gly Lys Ser Pro Ser
1010 1015 1020

His Ser Ser Ser Asn Arg Pro Phe Thr Pro Pro Thr Ser Thr Gly
1025 1030 1035

Gly Ser Lys Ser Pro Gly Ser Ala Gly Arg Ser Gln Thr Pro Pro
1040 1045 1050

Gly Val Ala Thr Pro Pro Ile Pro Lys Ile Thr Ile Gln Ile Pro
1055 1060 1065

Lys Gly Thr Val Met Val Gly Lys Pro Ser Ser His Ser Gln Tyr
1070 1075 1080

Thr Ser Ser Gly Ser Val Ser Ser Ser Gly Ser Lys Ser His His
1085 1090 1095

Ser His Ser Ser Ser Ser Ser Ser Ser Ala Ser Thr Ser Gly Lys
1100 1105 1110

Met Lys Ser Ser Lys Ser Glu Gly Ser Ser Ser Ser Lys Leu Ser
1115 1120 1125

Ser Ser Met Tyr Ser Ser Gln Gly Ser Ser Gly Ser Ser Gln Ser
1130 1135 1140

Lys Asn Ser Ser Gln Asn Leu Asp Ser Glu Ser Glu Ser Gly Ser
1145 1150 1155

Ser Ile Ala Glu Lys Ser Tyr Gln Asn Ser Pro Ser Ser Asp Asp
1160 1165 1170

Gly Ile Arg Pro Leu Pro Glu Tyr Ser Thr Glu Lys His Lys Lys
1175 1180 1185

His Lys Lys Glu Lys Lys Lys Val Lys Asp Lys Asp Arg Asp Arg
1190 1195 1200

Asp Arg Asp Lys Asp Arg Asp Lys Lys Lys Ser His Ser Ile Lys
1205 1210 1215

Pro Glu Ser Trp Ser Lys Ser Pro Ile Ser Ser Asp Gln Ser Leu
1220 1225 1230

Ser Met Thr Ser Asn Thr Ile Leu Ser Ala Asp Arg Pro Ser Arg
1235 1240 1245

Leu Ser Pro Asp Phe Met Ile Gly Glu Glu Asp Asp Asp Leu Met
1250 1255 1260

Asp Val Ala Leu Ile Gly Asn
1265 1270

<210> 90
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<213> Homo sapiens

<400> 90
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20 25 30

Trp Ser Glu Thr Ile Lys Leu Val Arg Gln Val Met Glu Lys Arg Val
35 40 45

Val Met Ser Ser Gly Gly His Gln His Leu Val Ser Cys Leu Glu Thr
50 55 60

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

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

Ser Gly Thr Glu Cys Tyr Ile Thr Ser Asp Met Phe Tyr Val Glu Val
100 105 110

Gln Leu Asp Pro Ala Gly Gln Leu Cys Asp Val Lys Val Ala His His
115 120 125

Gly Glu Asn Pro Val Ser Cys Pro Glu Leu Val Gln Gln Leu Arg Glu
130 135 140

Lys Asn Phe Asp Glu Phe Ser Lys His Leu Lys Gly Leu Val Asn Leu
145 150 155 160

Tyr Asn Leu Pro Gly Asp Lys Lys Ala Thr Asn Ala Gly Pro Leu Asp
165 170 175

Lys Ile Leu His Gly Ser Val Gly Tyr Leu Thr Pro Arg Ser Gly Gly
180 185 190

His Leu Met Asn Leu Lys Tyr Tyr Val Ser Pro Ser Asp Leu Leu Asp
195 200 205

Asp Lys Thr Ala Ser Pro Ile Ile Leu His Glu Asn Asn Val Ser Arg
210 215 220

Ser Leu Gly Met Asn Ala Ser Val Thr Ile Glu Gly Thr Ser Ala Val
225 230 235 240

Tyr Lys Leu Pro Ile Ala Pro Leu Ile Met Gly Ser His Pro Val Asp
245 250 255

Asn Lys Trp Thr Pro Ser Phe Ser Ser Ile Thr Ser Ala Asn Ser Val
260 265 270

Asp Leu Pro Ala Cys Phe Phe Leu Lys Phe Pro Gln Pro Ile Pro Val
275 280 285

Ser Arg Ala Phe Val Gln Lys Leu Gln Asn Cys Thr Gly Ile Pro Leu
290 295 300

Phe Glu Thr Gln Pro Thr Tyr Ala Pro Leu Tyr Glu Leu Ile Thr Gln
305 310 315 320

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Phe Glu Leu Ser Lys Asp Pro Asp Pro Ile Pro Leu Asn His Asn Met
325 330 335

Arg Phe Tyr Ala Ala Leu Pro Gly Gln Gln His Cys Tyr Phe Leu Asn
340 345 350

Lys Asp Ala Pro Leu Pro Asp Gly Arg Ser Leu Gln Gly Thr Leu Val
355 360 365

Ser Lys Ile Thr Phe Gln His Pro Gly Arg Val Pro Leu Ile Leu Asn
370 375 380

Leu Ile Arg His Gln Val Ala Tyr Asn Thr Leu Ile Gly Ser Cys Val
385 390 395 400

Lys Arg Thr Ile Leu Lys Glu Asp Ser Pro Gly Leu Leu Gln Phe Glu
405 410 415

Val Cys Pro Leu Ser Glu Ser Arg Phe Ser Val Ser Phe Gln His Pro
420 425 430

Val Asn Asp Ser Leu Val Cys Val Val Met Asp Val Gln Asp Ser Thr
435 440 445

His Val Ser Cys Lys Leu Tyr Lys Gly Leu Ser Asp Ala Leu Ile Cys
450 455 460

Thr Asp Asp Phe Ile Ala Lys Val Val Gln Arg Cys Met Ser Ile Pro
465 470 475 480

Val Thr Met Arg Ala Ile Arg Arg Lys Ala Glu Thr Ile Gln Ala Asp
485 490 495

Thr Pro Ala Leu Ser Leu Ile Ala Glu Thr Val Glu Asp Met Val Lys
500 505 510

Lys Asn Leu Pro Pro Ala Ser Ser Pro Gly Tyr Gly Met Thr Thr Gly
515 520 525

Asn Asn Pro Met Ser Gly Thr Thr Thr Ser Thr Asn Thr Phe Pro Gly
530 535 540

Gly Pro Ile Ala Thr Leu Phe Asn Met Ser Met Ser Ile Lys Asp Arg
545 550 555 560

His Glu Ser Val Gly His Gly Glu Asp Phe Ser Lys Val Ser Gln Asn
565 570 575

Pro Ile Leu Thr Ser Leu Leu Gln Ile Thr Gly Asn Gly Gly Ser Thr
580 585 590

Ile Gly Ser Ser Pro Thr Pro Pro His His Thr Pro Pro Pro Val Ser
595 600 605

Ser Met Ala Gly Asn Thr Lys Asn His Pro Met Leu Met Asn Leu Leu
610 615 620

Lys Asp Asn Pro Ala Gln Asp Phe Ser Thr Leu Tyr Gly Ser Ser Pro
625 630 635 640

Leu Glu Arg Gln Asn Ser Ser Ser Gly Ser Pro Arg Met Glu Ile Cys
645 650 655

Ser Gly Ser Asn Lys Thr Lys Lys Lys Lys Ser Ser Arg Leu Pro Pro
660 665 670

Glu Lys Pro Lys His Gln Thr Glu Asp Asp Phe Gln Arg Glu Leu Phe
675 680 685

Ser Met Asp Val Asp Ser Gln Asn Pro Ile Phe Asp Val Asn Met Thr
690 695 700

Ala Asp Thr Leu Asp Thr Pro His Ile Thr Pro Ala Pro Ser Gln Cys
705 710 715 720

Ser Thr Pro Pro Thr Thr Tyr Pro Gln Pro Val Pro His Pro Gln Pro
725 730 735

Ser Ile Gln Arg Met Val Arg Leu Ser Ser Ser Asp Ser Ile Gly Pro
740 745 750

Asp Val Thr Asp Ile Leu Ser Asp Ile Ala Glu Glu Ala Ser Lys Leu
755 760 765

Pro Ser Thr Ser Asp Asp Cys Pro Ala Ile Gly Thr Pro Leu Arg Asp
770 775 780

Ser Ser Ser Ser Gly His Ser Gln Ser Thr Leu Phe Asp Ser Asp Val
785 790 795 800

Phe Gln Thr Asn Asn Asn Glu Asn Pro Tyr Thr Asp Pro Ala Asp Leu
805 810 815

Ile Ala Asp Ala Ala Gly Ser Pro Ser Ser Asp Ser Pro Thr Asn His
820 825 830

Phe Phe His Asp Gly Val Asp Phe Asn Pro Asp Leu Leu Asn Ser Gln
835 840 845

Ser Gln Ser Gly Phe Gly Glu Glu Tyr Phe Asp Glu Ser Ser Gln Ser
850 855 860

Gly Asp Asn Asp Asp Phe Lys Gly Phe Ala Ser Gln Ala Leu Asn Thr

865 870 875 880

Leu Gly Val Pro Met Leu Gly Gly Asp Asn Gly Glu Thr Lys Phe Lys
885 890 895

Gly Asn Asn Gln Ala Asp Thr Val Asp Phe Ser Ile Ile Ser Val Ala
900 905 910

Gly Lys Ala Leu Ala Pro Ala Asp Leu Met Glu His His Ser Gly Ser
915 920 925

Gln Gly Pro Leu Leu Thr Thr Gly Asp Leu Gly Lys Glu Lys Thr Gln
930 935 940

Lys Arg Val Lys Glu Gly Asn Gly Thr Ser Asn Ser Thr Leu Ser Gly
945 950 955 960

Pro Gly Leu Asp Ser Lys Pro Gly Lys Arg Ser Arg Thr Pro Ser Asn
965 970 975

Asp Gly Lys Ser Lys Asp Lys Pro Pro Lys Arg Lys Lys Ala Asp Thr
980 985 990

Glu Gly Lys Ser Pro Ser His Ser Ser Ser Asn Arg Pro Phe Thr Pro
995 1000 1005

Pro Thr Ser Thr Gly Gly Ser Lys Ser Pro Gly Ser Ala Gly Arg
1010 1015 1020

Ser Gln Thr Pro Pro Gly Val Ala Thr Pro Pro Ile Pro Lys Ile
1025 1030 1035

Thr Ile Gln Ile Pro Lys Gly Thr Val Met Val Gly Lys Pro Ser
1040 1045 1050

Ser His Ser Gln Tyr Thr Ser Ser Gly Ser Val Ser Ser Ser Gly
1055 1060 1065

Ser Lys Ser His His Ser His Ser Ser Ser Ser Ser Ser Ser Ala
1070 1075 1080

Ser Thr Ser Gly Lys Met Lys Ser Ser Lys Ser Glu Gly Ser Ser
1085 1090 1095

Ser Ser Lys Leu Ser Ser Ser Met Tyr Ser Ser Gln Gly Ser Ser
1100 1105 1110

Gly Ser Ser Gln Ser Lys Asn Ser Ser Gln Ser Gly Gly Lys Pro
1115 1120 1125

Gly Ser Ser Pro Ile Thr Lys His Gly Leu Ser Ser Gly Ser Ser
1130 1135 1140

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Ser Thr Lys Met Lys Pro Gln Gly Lys Pro Ser Ser Leu Met Asn
1145 1150 1155

Pro Ser Leu Ser Lys Pro Asn Ile Ser Pro Ser His Ser Arg Pro
1160 1165 1170

Pro Gly Gly Ser Asp Lys Leu Ala Ser Pro Met Lys Pro Val Pro
1175 1180 1185

Gly Thr Pro Pro Ser Ser Lys Ala Lys Ser Pro Ile Ser Ser Gly
1190 1195 1200

Ser Gly Gly Ser His Met Ser Gly Thr Ser Ser Ser Ser Gly Met
1205 1210 1215

Lys Ser Ser Ser Gly Leu Gly Ser Ser Gly Ser Leu Ser Gln Lys
1220 1225 1230

Thr Pro Pro Ser Ser Asn Ser Cys Thr Ala Ser Ser Ser Ser Phe
1235 1240 1245

Ser Ser Ser Gly Ser Ser Met Ser Ser Ser Gln Asn Gln His Gly
1250 1255 1260

Ser Ser Lys Gly Lys Ser Pro Ser Arg Asn Lys Lys Pro Ser Leu
1265 1270 1275

Thr Ala Val Ile Asp Lys Leu Lys His Gly Val Val Thr Ser Gly
1280 1285 1290

Pro Gly Gly Glu Asp Pro Leu Asp Gly Gln Met Gly Val Ser Thr
1295 1300 1305

Asn Ser Ser Ser His Pro Met Ser Ser Lys His Asn Met Ser Gly
1310 1315 1320

Gly Glu Phe Gln Gly Lys Arg Glu Lys Ser Asp Lys Asp Lys Ser
1325 1330 1335

Lys Val Ser Thr Ser Gly Ser Ser Val Asp Ser Ser Lys Lys Thr
1340 1345 1350

Ser Glu Ser Lys Asn Val Gly Ser Thr Gly Val Ala Lys Ile Ile
1355 1360 1365

Ile Ser Lys His Asp Gly Gly Ser Pro Ser Ile Lys Ala Lys Val
1370 1375 1380

Thr Leu Gln Lys Pro Gly Glu Ser Ser Gly Glu Gly Leu Arg Pro
1385 1390 1395

Gln Met Ala Ser Ser Lys Asn Tyr Gly Ser Pro Leu Ile Ser Gly
1400 1405 1410

Ser Thr Pro Lys His Glu Arg Gly Ser Pro Ser His Ser Lys Ser
1415 1420 1425

Pro Ala Tyr Thr Pro Gln Asn Leu Asp Ser Glu Ser Glu Ser Gly
1430 1435 1440

Ser Ser Ile Ala Glu Lys Ser Tyr Gln Asn Ser Pro Ser Ser Asp
1445 1450 1455

Asp Gly Ile Arg Pro Leu Pro Glu Tyr Ser Thr Glu Lys His Lys
1460 1465 1470

Lys His Lys Lys Glu Lys Lys Lys Val Lys Asp Lys Asp Arg Asp
1475 1480 1485

Arg Asp Arg Asp Lys Asp Arg Asp Lys Lys Lys Ser His Ser Ile
1490 1495 1500

Lys Pro Glu Ser Trp Ser Lys Ser Pro Ile Ser Ser Asp Gln Ser
1505 1510 1515

Leu Ser Met Thr Ser Asn Thr Ile Leu Ser Ala Asp Arg Pro Ser
1520 1525 1530

Arg Leu Ser Pro Asp Phe Met Ile Gly Glu Glu Asp Asp Asp Leu
1535 1540 1545

Met Asp Val Ala Leu Ile Gly Asn
1550 1555

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<400> 91
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Ser Ser Leu Leu Glu Arg Leu His Ala Lys Phe Asn Gln Asn Arg Pro
20 25 30

Trp Ser Glu Thr Ile Lys Leu Val Arg Gln Val Met Glu Lys Arg Val
35 40 45

Val Met Ser Ser Gly Gly His Gln His Leu Val Ser Cys Leu Glu Thr
50 55 60

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

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

Ser Gly Thr Glu Cys Tyr Ile Thr Ser Asp Met Phe Tyr Val Glu Val
100 105 110

Gln Leu Asp Pro Ala Gly Gln Leu Cys Asp Val Lys Val Ala His His
115 120 125

Gly Glu Asn Pro Val Ser Cys Pro Glu Leu Val Gln Gln Leu Ser Lys
130 135 140

Leu Lys Thr Lys Met Tyr Leu Ala Leu Gln Ser Leu Glu Gln Asp Leu
145 150 155 160

Ser Lys Met Ala Ile Met Tyr Trp Lys Ala Thr Asn Ala Gly Pro Leu
165 170 175

Asp Lys Ile Leu His Gly Ser Val Gly Tyr Leu Thr Pro Arg Ser Gly
180 185 190

Gly His Leu Met Asn Leu Lys Tyr Tyr Val Ser Pro Ser Asp Leu Leu
195 200 205

Asp Asp Lys Thr Ala Ser Pro Ile Ile Leu His Glu Asn Asn Val Ser
210 215 220

Arg Ser Leu Gly Met Asn Ala Ser Val Thr Ile Glu Gly Thr Ser Ala
225 230 235 240

Val Tyr Lys Leu Pro Ile Ala Pro Leu Ile Met Gly Ser His Pro Val
245 250 255

Asp Asn Lys Trp Thr Pro Ser Phe Ser Ser Ile Thr Ser Ala Asn Ser
260 265 270

Val Asp Leu Pro Ala Cys Phe Phe Leu Lys Phe Pro Gln Pro Ile Pro
275 280 285

Val Ser Arg Ala Phe Val Gln Lys Leu Gln Asn Cys Thr Gly Ile Pro
290 295 300

Leu Phe Glu Thr Gln Pro Thr Tyr Ala Pro Leu Tyr Glu Leu Ile Thr
305 310 315 320

Gln Phe Glu Leu Ser Lys Asp Pro Asp Pro Ile Pro Leu Asn His Asn
325 330 335

Met Arg Phe Tyr Ala Ala Leu Pro Gly Gln Gln His Cys Tyr Phe Leu
340 345 350

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Asn Lys Asp Ala Pro Leu Pro Asp Gly Arg Ser Leu Gln Gly Thr Leu
355 360 365

Val Ser Lys Ile Thr Phe Gln His Pro Gly Arg Val Pro Leu Ile Leu
370 375 380

Asn Leu Ile Arg His Gln Val Ala Tyr Asn Thr Leu Ile Gly Ser Cys
385 390 395 400

Val Lys Arg Thr Ile Leu Lys Glu Asp Ser Pro Gly Leu Leu Gln Phe
405 410 415

Glu Val Cys Pro Leu Ser Glu Ser Arg Phe Ser Val Ser Phe Gln His
420 425 430

Pro Val Asn Asp Ser Leu Val Cys Val Val Met Asp Val Gln Asp Ser
435 440 445

Thr His Val Ser Cys Lys Leu Tyr Lys Gly Leu Ser Asp Ala Leu Ile
450 455 460

Cys Thr Asp Asp Phe Ile Ala Lys Val Val Gln Arg Cys Met Ser Ile
465 470 475 480

Pro Val Thr Met Arg Ala Ile Arg Arg Lys Ala Glu Thr Ile Gln Ala
485 490 495

Asp Thr Pro Ala Leu Ser Leu Ile Ala Glu Thr Val Glu Asp Met Val
500 505 510

Lys Lys Asn Leu Pro Pro Ala Ser Ser Pro Gly Tyr Gly Met Thr Thr
515 520 525

Gly Asn Asn Pro Met Ser Gly Thr Thr Thr Ser Thr Asn Thr Phe Pro
530 535 540

Gly Gly Pro Ile Ala Thr Leu Phe Asn Met Ser Met Ser Ile Lys Asp
545 550 555 560

Arg His Glu Ser Val Gly His Gly Glu Asp Phe Ser Lys Val Ser Gln
565 570 575

Asn Pro Ile Leu Thr Ser Leu Leu Gln Ile Thr Gly Asn Gly Gly Ser
580 585 590

Thr Ile Gly Ser Ser Pro Thr Pro Pro His His Thr Pro Pro Pro Val
595 600 605

Ser Ser Met Ala Gly Asn Thr Lys Asn His Pro Met Leu Met Asn Leu
610 615 620

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Leu Lys Asp Asn Pro Ala Gln Asp Phe Ser Thr Leu Tyr Gly Ser Ser
625                 630                 635                 640

Pro Leu Glu Arg Gln Asn Ser Ser Ser Gly Ser Pro Arg Met Glu Ile
                645                 650                 655

Cys Ser Gly Ser Asn Lys Thr Lys Lys Lys Lys Ser Ser Arg Leu Pro
            660                 665                 670

Pro Glu Lys Pro Lys His Gln Thr Glu Asp Asp Phe Gln Arg Glu Leu
        675                 680                 685

Phe Ser Met Asp Val Asp Ser Gln Asn Pro Ile Phe Asp Val Asn Met
    690                 695                 700

Thr Ala Asp Thr Leu Asp Thr Pro His Ile Thr Pro Ala Pro Ser Gln
705                 710                 715                 720

Cys Ser Thr Pro Pro Thr Thr Tyr Pro Gln Pro Val Pro His Pro Gln
                725                 730                 735

Pro Ser Ile Gln Arg Met Val Arg Leu Ser Ser Ser Asp Ser Ile Gly
            740                 745                 750

Pro Asp Val Thr Asp Ile Leu Ser Asp Ile Ala Glu Glu Ala Ser Lys
        755                 760                 765

Leu Pro Ser Thr Ser Asp Asp Cys Pro Ala Ile Gly Thr Pro Leu Arg
    770                 775                 780

Asp Ser Ser Ser Ser Gly His Ser Gln Ser Thr Leu Phe Asp Ser Asp
785                 790                 795                 800

Val Phe Gln Thr Asn Asn Asn Glu Asn Pro Tyr Thr Asp Pro Ala Asp
                805                 810                 815

Leu Ile Ala Asp Ala Ala Gly Ser Pro Ser Ser Asp Ser Pro Thr Asn
            820                 825                 830

His Phe Phe His Asp Gly Val Asp Phe Asn Pro Asp Leu Leu Asn Ser
        835                 840                 845

Gln Ser Gln Ser Gly Phe Gly Glu Glu Tyr Phe Asp Glu Ser Ser Gln
    850                 855                 860

Ser Gly Asp Asn Asp Asp Phe Lys Gly Phe Ala Ser Gln Ala Leu Asn
865                 870                 875                 880

Thr Leu Gly Val Pro Met Leu Gly Gly Asp Asn Gly Glu Thr Lys Phe
                885                 890                 895

Lys Gly Asn Asn Gln Ala Asp Thr Val Asp Phe Ser Ile Ile Ser Val
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900 905 910

Ala Gly Lys Ala Leu Ala Pro Ala Asp Leu Met Glu His His Ser Gly
915 920 925

Ser Gln Gly Pro Leu Leu Thr Thr Gly Asp Leu Gly Lys Glu Lys Thr
930 935 940

Gln Lys Arg Val Lys Glu Gly Asn Gly Thr Ser Asn Ser Thr Leu Ser
945 950 955 960

Gly Pro Gly Leu Asp Ser Lys Pro Gly Lys Arg Ser Arg Thr Pro Ser
965 970 975

Asn Asp Gly Lys Ser Lys Asp Lys Pro Pro Lys Arg Lys Lys Ala Asp
980 985 990

Thr Glu Gly Lys Ser Pro Ser His Ser Ser Ser Asn Arg Pro Phe Thr
995 1000 1005

Pro Pro Thr Ser Thr Gly Gly Ser Lys Ser Pro Gly Ser Ala Gly
1010 1015 1020

Arg Ser Gln Thr Pro Pro Gly Val Ala Thr Pro Pro Ile Pro Lys
1025 1030 1035

Ile Thr Ile Gln Ile Pro Lys Gly Thr Val Met Val Gly Lys Pro
1040 1045 1050

Ser Ser His Ser Gln Tyr Thr Ser Ser Gly Ser Val Ser Ser Ser
1055 1060 1065

Gly Ser Lys Ser His His Ser His Ser Ser Ser Ser Ser Ser Ser Ser
1070 1075 1080

Ala Ser Thr Ser Gly Lys Met Lys Ser Ser Lys Ser Glu Gly Ser
1085 1090 1095

Ser Ser Ser Lys Leu Ser Ser Ser Met Tyr Ser Ser Gln Gly Ser
1100 1105 1110

Ser Gly Ser Ser Gln Ser Lys Asn Ser Ser Gln Ser Gly Gly Lys
1115 1120 1125

Pro Gly Ser Ser Pro Ile Thr Lys His Gly Leu Ser Ser Gly Ser
1130 1135 1140

Ser Ser Thr Lys Met Lys Pro Gln Gly Lys Pro Ser Ser Leu Met
1145 1150 1155

Asn Pro Ser Leu Ser Lys Pro Asn Ile Ser Pro Ser His Ser Arg
1160 1165 1170

Pro Pro Gly Gly Ser Asp Lys Leu Ala Ser Pro Met Lys Pro Val
1175 1180 1185

Pro Gly Thr Pro Pro Ser Ser Lys Ala Lys Ser Pro Ile Ser Ser
1190 1195 1200

Gly Ser Gly Gly Ser His Met Ser Gly Thr Ser Ser Ser Ser Gly
1205 1210 1215

Met Lys Ser Ser Ser Gly Leu Gly Ser Ser Gly Ser Leu Ser Gln
1220 1225 1230

Lys Thr Pro Pro Ser Ser Asn Ser Cys Thr Ala Ser Ser Ser Ser
1235 1240 1245

Phe Ser Ser Ser Gly Ser Ser Met Ser Ser Ser Gln Asn Gln His
1250 1255 1260

Gly Ser Ser Lys Gly Lys Ser Pro Ser Arg Asn Lys Lys Pro Ser
1265 1270 1275

Leu Thr Ala Val Ile Asp Lys Leu Lys His Gly Val Val Thr Ser
1280 1285 1290

Gly Pro Gly Gly Glu Asp Pro Leu Asp Gly Gln Met Gly Val Ser
1295 1300 1305

Thr Asn Ser Ser Met Ser His Pro Met Ser Ser Lys His Asn Met
1310 1315 1320

Ser Gly Gly Glu Phe Gln Gly Lys Arg Glu Lys Ser Asp Lys Asp
1325 1330 1335

Lys Ser Lys Val Ser Thr Ser Gly Ser Ser Val Asp Ser Ser Lys
1340 1345 1350

Lys Thr Ser Glu Ser Lys Asn Val Gly Ser Thr Gly Val Ala Lys
1355 1360 1365

Ile Ile Ile Ser Lys His Asp Gly Gly Ser Pro Ser Ile Lys Ala
1370 1375 1380

Lys Val Thr Leu Gln Lys Pro Gly Glu Ser Ser Gly Glu Gly Leu
1385 1390 1395

Arg Pro Gln Met Ala Ser Ser Lys Asn Tyr Gly Ser Pro Leu Ile
1400 1405 1410

Ser Gly Ser Thr Pro Lys His Glu Arg Gly Ser Pro Ser His Ser
1415 1420 1425

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Lys Ser Pro Ala Tyr Thr Pro Gln Asn Leu Asp Ser Glu Ser Glu
1430 1435 1440

Ser Gly Ser Ser Ile Ala Glu Lys Ser Tyr Gln Asn Ser Pro Ser
1445 1450 1455

Ser Asp Asp Gly Ile Arg Pro Leu Pro Glu Tyr Ser Thr Glu Lys
1460 1465 1470

His Lys Lys His Lys Lys Glu Lys Lys Lys Val Lys Asp Lys Asp
1475 1480 1485

Arg Asp Arg Asp Arg Asp Lys Asp Arg Asp Lys Lys Lys Ser His
1490 1495 1500

Ser Ile Lys Pro Glu Ser Trp Ser Lys Ser Pro Ile Ser Ser Asp
1505 1510 1515

Gln Ser Leu Ser Met Thr Ser Asn Thr Ile Leu Ser Ala Asp Arg
1520 1525 1530

Pro Ser Arg Leu Ser Pro Asp Phe Met Ile Gly Glu Glu Asp Asp
1535 1540 1545

Asp Leu Met Asp Val Ala Leu Ile Gly Asn
1550 1555

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<400> 92
Met Lys Ala Gln Gly Glu Thr Glu Glu Ser Glu Lys Leu Ser Lys Met
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Ser Ser Leu Leu Glu Arg Leu His Ala Lys Phe Asn Gln Asn Arg Pro
20 25 30

Trp Ser Glu Thr Ile Lys Leu Val Arg Gln Val Met Glu Lys Arg Val
35 40 45

Val Met Ser Ser Gly Gly His Gln His Leu Val Ser Cys Leu Glu Thr
50 55 60

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

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

Ser Gly Thr Glu Cys Tyr Ile Thr Ser Asp Met Phe Tyr Val Glu Val
100 105 110

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Gln Leu Asp Pro Ala Gly Gln Leu Cys Asp Val Lys Val Ala His His
115 120 125

Gly Glu Asn Pro Val Ser Cys Pro Glu Leu Val Gln Gln Leu Arg Glu
130 135 140

Lys Asn Phe Asp Glu Phe Ser Lys His Leu Lys Gly Leu Val Asn Leu
145 150 155 160

Tyr Asn Leu Pro Gly Asp Asn Lys Leu Lys Thr Lys Met Tyr Leu Ala
165 170 175

Leu Gln Ser Leu Glu Gln Asp Leu Ser Lys Met Ala Ile Met Tyr Trp
180 185 190

Lys Ala Thr Asn Ala Gly Pro Leu Asp Lys Ile Leu His Gly Ser Val
195 200 205

Gly Tyr Leu Thr Pro Arg Ser Gly Gly His Leu Met Asn Leu Lys Tyr
210 215 220

Tyr Val Ser Pro Ser Asp Leu Leu Asp Asp Lys Thr Ala Ser Pro Ile
225 230 235 240

Ile Leu His Glu Asn Asn Val Ser Arg Ser Leu Gly Met Asn Ala Ser
245 250 255

Val Thr Ile Glu Gly Thr Ser Ala Val Tyr Lys Leu Pro Ile Ala Pro
260 265 270

Leu Ile Met Gly Ser His Pro Val Asp Asn Lys Trp Thr Pro Ser Phe
275 280 285

Ser Ser Ile Thr Ser Ala Asn Ser Val Asp Leu Pro Ala Cys Phe Phe
290 295 300

Leu Lys Phe Pro Gln Pro Ile Pro Val Ser Arg Ala Phe Val Gln Lys
305 310 315 320

Leu Gln Asn Cys Thr Gly Ile Pro Leu Phe Glu Thr Gln Pro Thr Tyr
325 330 335

Ala Pro Leu Tyr Glu Leu Ile Thr Gln Phe Glu Leu Ser Lys Asp Pro
340 345 350

Asp Pro Ile Pro Leu Asn His Asn Met Arg Phe Tyr Ala Ala Leu Pro
355 360 365

Gly Gln Gln His Cys Tyr Phe Leu Asn Lys Asp Ala Pro Leu Pro Asp
370 375 380

Gly Arg Ser Leu Gln Gly Thr Leu Val Ser Lys Ile Thr Phe Gln His
385 390 395 400

Pro Gly Arg Val Pro Leu Ile Leu Asn Leu Ile Arg His Gln Val Ala
405 410 415

Tyr Asn Thr Leu Ile Gly Ser Cys Val Lys Arg Thr Ile Leu Lys Glu
420 425 430

Asp Ser Pro Gly Leu Leu Gln Phe Glu Val Cys Pro Leu Ser Glu Ser
435 440 445

Arg Phe Ser Val Ser Phe Gln His Pro Val Asn Asp Ser Leu Val Cys
450 455 460

Val Val Met Asp Val Gln Asp Ser Thr His Val Ser Cys Lys Leu Tyr
465 470 475 480

Lys Gly Leu Ser Asp Ala Leu Ile Cys Thr Asp Asp Phe Ile Ala Lys
485 490 495

Val Val Gln Arg Cys Met Ser Ile Pro Val Thr Met Arg Ala Ile Arg
500 505 510

Arg Lys Ala Glu Thr Ile Gln Ala Asp Thr Pro Ala Leu Ser Leu Ile
515 520 525

Ala Glu Thr Val Glu Asp Met Val Lys Lys Asn Leu Pro Pro Ala Ser
530 535 540

Ser Pro Gly Glu Arg Gly Val Tyr His Trp Leu Glu Ser Asp Pro Ser
545 550 555 560

Ser Ser His Ala Ala Thr Cys Leu Phe Asp Gly Arg Gln His Gln Glu
565 570 575

Pro Pro Asp Ala His Glu Pro Ser
580

<210> 93
<211> 1150
<212> PRT
<213> Homo sapiens

<400> 93
Met Lys Ala Gln Gly Glu Thr Glu Glu Ser Glu Lys Leu Ser Lys Met
1 5 10 15

Ser Ser Leu Leu Glu Arg Leu His Ala Lys Phe Asn Gln Asn Arg Pro
20 25 30

Trp Ser Glu Thr Ile Lys Leu Val Arg Gln Val Met Glu Lys Arg Val
35 40 45

Val Met Ser Ser Gly Gly His Gln His Leu Val Ser Cys Leu Glu Thr
50 55 60

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

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

Ser Gly Thr Glu Cys Tyr Ile Thr Ser Asp Met Phe Tyr Val Glu Val
100 105 110

Gln Leu Asp Pro Ala Gly Gln Leu Cys Asp Val Lys Val Ala His His
115 120 125

Gly Glu Asn Pro Val Ser Cys Pro Glu Leu Val Gln Gln Leu Arg Glu
130 135 140

Lys Asn Phe Asp Glu Phe Ser Lys His Leu Lys Gly Leu Val Asn Leu
145 150 155 160

Tyr Asn Leu Pro Gly Asp Asn Lys Leu Lys Thr Lys Met Tyr Leu Ala
165 170 175

Leu Gln Ser Leu Glu Gln Asp Leu Ser Lys Met Ala Ile Met Tyr Trp
180 185 190

Lys Ala Thr Asn Ala Gly Pro Leu Asp Lys Ile Leu His Gly Ser Val
195 200 205

Gly Tyr Leu Thr Pro Arg Ser Gly Gly His Leu Met Asn Leu Lys Tyr
210 215 220

Tyr Val Ser Pro Ser Asp Leu Leu Asp Asp Lys Thr Ala Ser Pro Ile
225 230 235 240

Ile Leu His Glu Asn Asn Val Ser Arg Ser Leu Gly Met Asn Ala Ser
245 250 255

Val Thr Ile Glu Gly Thr Ser Ala Val Tyr Lys Leu Pro Ile Ala Pro
260 265 270

Leu Ile Met Gly Ser His Pro Val Asp Asn Lys Trp Thr Pro Ser Phe
275 280 285

Ser Ser Ile Thr Ser Ala Asn Ser Val Asp Leu Pro Ala Cys Phe Phe
290 295 300

Leu Lys Phe Pro Gln Pro Ile Pro Val Ser Arg Ala Phe Val Gln Lys
305 310 315 320

Leu Gln Asn Cys Thr Gly Ile Pro Leu Phe Glu Thr Gln Pro Thr Tyr
325 330 335

Ala Pro Leu Tyr Glu Leu Ile Thr Gln Phe Glu Leu Ser Lys Asp Pro
340 345 350

Asp Pro Ile Pro Leu Asn His Asn Met Arg Phe Tyr Ala Ala Leu Pro
355 360 365

Gly Gln Gln His Cys Tyr Phe Leu Asn Lys Asp Ala Pro Leu Pro Asp
370 375 380

Gly Arg Ser Leu Gln Gly Thr Leu Val Ser Lys Ile Thr Phe Gln His
385 390 395 400

Pro Gly Arg Val Pro Leu Ile Leu Asn Leu Ile Arg His Gln Val Ala
405 410 415

Tyr Asn Thr Leu Ile Gly Ser Cys Val Lys Arg Thr Ile Leu Lys Glu
420 425 430

Asp Ser Pro Gly Leu Leu Gln Phe Glu Val Cys Pro Leu Ser Glu Ser
435 440 445

Arg Phe Ser Val Ser Phe Gln His Pro Val Asn Asp Ser Leu Val Cys
450 455 460

Val Val Met Asp Val Gln Asp Ser Thr His Val Ser Cys Lys Leu Tyr
465 470 475 480

Lys Gly Leu Ser Asp Ala Leu Ile Cys Thr Asp Asp Phe Ile Ala Lys
485 490 495

Val Val Gln Arg Cys Met Ser Ile Pro Val Thr Met Arg Ala Ile Arg
500 505 510

Arg Lys Ala Glu Thr Ile Gln Ala Asp Thr Pro Ala Leu Ser Leu Ile
515 520 525

Ala Glu Thr Val Glu Asp Met Val Lys Lys Asn Leu Pro Pro Ala Ser
530 535 540

Ser Pro Gly Tyr Gly Met Thr Thr Gly Asn Asn Pro Met Ser Gly Thr
545 550 555 560

Thr Thr Ser Thr Asn Thr Phe Pro Gly Gly Pro Ile Ala Thr Leu Phe
565 570 575

Asn Met Ser Met Ser Ile Lys Asp Arg His Glu Ser Val Gly His Gly
580 585 590

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

Gln Ile Thr Gly Asn Gly Gly Ser Thr Ile Gly Ser Ser Pro Thr Pro
610 615 620

Pro His His Thr Pro Pro Pro Val Ser Ser Met Ala Gly Asn Thr Lys
625 630 635 640

Asn His Pro Met Leu Met Asn Leu Leu Lys Asp Asn Pro Ala Gln Asp
645 650 655

Phe Ser Thr Leu Tyr Gly Ser Ser Pro Leu Glu Arg Gln Asn Ser Ser
660 665 670

Ser Gly Ser Pro Arg Met Glu Ile Cys Ser Gly Ser Asn Lys Thr Lys
675 680 685

Lys Lys Lys Ser Ser Arg Leu Pro Pro Glu Lys Pro Lys His Gln Thr
690 695 700

Glu Asp Asp Phe Gln Arg Glu Leu Phe Ser Met Asp Val Asp Ser Gln
705 710 715 720

Asn Pro Ile Phe Asp Val Asn Met Thr Ala Asp Thr Leu Asp Thr Pro
725 730 735

His Ile Thr Pro Ala Pro Ser Gln Cys Ser Thr Pro Pro Thr Thr Tyr
740 745 750

Pro Gln Pro Val Pro His Pro Gln Pro Ser Ile Gln Arg Met Val Arg
755 760 765

Leu Ser Ser Ser Asp Ser Ile Gly Pro Asp Val Thr Asp Ile Leu Ser
770 775 780

Asp Ile Ala Glu Glu Ala Ser Lys Leu Pro Ser Thr Ser Asp Asp Cys
785 790 795 800

Pro Ala Ile Gly Thr Pro Leu Arg Asp Ser Ser Ser Ser Gly His Ser
805 810 815

Gln Ser Thr Leu Phe Asp Ser Asp Val Phe Gln Thr Asn Asn Asn Glu
820 825 830

Asn Pro Tyr Thr Asp Pro Ala Asp Leu Ile Ala Asp Ala Ala Gly Ser
835 840 845

Pro Ser Ser Asp Ser Pro Thr Asn His Phe Phe His Asp Gly Val Asp
850 855 860

Phe Asn Pro Asp Leu Leu Asn Ser Gln Ser Gln Ser Gly Phe Gly Glu

865 870 875 880

Glu Tyr Phe Asp Glu Ser Ser Gln Ser Gly Asp Asn Asp Asp Phe Lys
885 890 895

Gly Phe Ala Ser Gln Ala Leu Asn Thr Leu Gly Val Pro Met Leu Gly
900 905 910

Gly Asp Asn Gly Glu Thr Lys Phe Lys Gly Asn Asn Gln Ala Asp Thr
915 920 925

Val Asp Phe Ser Ile Ile Ser Val Ala Gly Lys Ala Leu Ala Pro Ala
930 935 940

Asp Leu Met Glu His His Ser Gly Ser Gln Gly Pro Leu Leu Thr Thr
945 950 955 960

Gly Asp Leu Gly Lys Glu Lys Thr Gln Lys Arg Val Lys Glu Gly Asn
965 970 975

Gly Thr Ser Asn Ser Thr Leu Ser Gly Pro Gly Leu Asp Ser Lys Pro
980 985 990

Gly Lys Arg Ser Arg Thr Pro Ser Asn Asp Gly Lys Ser Lys Asp Lys
995 1000 1005

Pro Pro Lys Arg Lys Lys Ala Asp Thr Glu Gly Lys Ser Pro Ser
1010 1015 1020

His Ser Ser Ser Asn Arg Pro Phe Thr Pro Pro Thr Ser Thr Gly
1025 1030 1035

Gly Ser Lys Ser Pro Gly Ser Ala Gly Arg Ser Gln Thr Pro Pro
1040 1045 1050

Gly Val Ala Thr Pro Pro Ile Pro Lys Ile Thr Ile Gln Ile Pro
1055 1060 1065

Lys Gly Thr Val Met Val Gly Lys Pro Ser Ser His Ser Gln Tyr
1070 1075 1080

Thr Ser Ser Gly Ser Val Ser Ser Ser Gly Ser Lys Ser His His
1085 1090 1095

Ser His Ser Ser Ser Ser Ser Ser Ser Ala Ser Thr Ser Gly Lys
1100 1105 1110

Met Lys Ser Ser Lys Ser Glu Gly Ser Ser Ser Ser Lys Leu Ser
1115 1120 1125

Ser Ser Met Tyr Ser Ser Gln Gly Ser Ser Gly Ser Ser Gln Ser
1130 1135 1140

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Lys Asn Ser Ser Gln Thr Leu
1145 1150

<210> 94
<211> 270
<212> PRT
<213> Homo sapiens

<400> 94
Met Ala Ala Ser Ser Ser Gly Glu Lys Glu Lys Glu Arg Leu Gly Gly
1 5 10 15

Gly Leu Gly Val Ala Gly Gly Asn Ser Thr Arg Glu Arg Leu Leu Ser
20 25 30

Ala Leu Glu Asp Leu Glu Val Leu Ser Arg Glu Leu Ile Glu Met Leu
35 40 45

Ala Ile Ser Arg Asn Gln Lys Leu Leu Gln Ala Gly Glu Glu Asn Gln
50 55 60

Val Leu Glu Leu Leu Ile His Arg Asp Gly Glu Phe Gln Glu Leu Met
65 70 75 80

Lys Leu Ala Leu Asn Gln Gly Lys Ile His His Glu Met Gln Val Leu
85 90 95

Glu Lys Glu Val Glu Lys Arg Asp Ser Asp Ile Gln Gln Leu Gln Lys
100 105 110

Gln Leu Lys Glu Ala Glu Gln Ile Leu Ala Thr Ala Val Tyr Gln Ala
115 120 125

Lys Glu Lys Leu Lys Ser Ile Glu Lys Ala Arg Lys Gly Ala Ile Ser
130 135 140

Ser Glu Glu Ile Ile Lys Tyr Ala His Arg Ile Ser Ala Ser Asn Ala
145 150 155 160

Val Cys Ala Pro Leu Thr Trp Val Pro Gly Asp Pro Arg Arg Pro Tyr
165 170 175

Pro Thr Asp Leu Glu Met Arg Ser Gly Leu Leu Gly Gln Met Asn Asn
180 185 190

Pro Ser Thr Asn Gly Val Asn Gly His Leu Pro Gly Asp Ala Leu Ala
195 200 205

Ala Gly Arg Leu Pro Asp Val Leu Ala Pro Gln Tyr Pro Trp Gln Ser
210 215 220

Asn Asp Met Ser Met Asn Met Leu Pro Pro Asn His Ser Ser Asp Phe

225 230 235 240

Leu Leu Glu Pro Pro Gly His Asn Lys Glu Asn Glu Asp Asp Val Glu
245 250 255

Ile Met Ser Thr Asp Ser Ser Ser Ser Ser Ser Glu Ser Asp
260 265 270

<210> 95
<211> 257
<212> PRT
<213> Homo sapiens

<400> 95
Met Ala Ala Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val
1 5 10 15

Asp Ser Ser Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr
20 25 30

Phe Ser Glu Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu
35 40 45

Val Val Lys Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val
50 55 60

Gly Ile Glu Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile
65 70 75 80

Ile Arg Lys Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala
85 90 95

Asp Tyr Tyr Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly
100 105 110

Ser Val Ile Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser
115 120 125

Ala Phe Asp Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly
130 135 140

Tyr Trp Trp His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro
145 150 155 160

Lys Ala Lys Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg
165 170 175

Val Asp Ala Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe
180 185 190

Val Gln Leu Lys Pro Gly Glu Lys Pro Val Pro Val Asp Gln Thr Lys
195 200 205

Lys Glu Ala Glu Pro Ile Pro Glu Thr Val Lys Pro Glu Glu Lys Glu
210 215 220

Thr Thr Lys Asn Val Gln Gln Thr Val Ser Ala Lys Gly Pro Pro Glu
225 230 235 240

Lys Arg Met Arg Leu His Tyr Ile Ile Leu Ser Ile Lys Ile Asn Ser
245 250 255

Cys

<210> 96
<211> 97
<212> PRT
<213> Homo sapiens

<400> 96
Met Ala Ala Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val
1 5 10 15

Asp Ser Ser Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr
20 25 30

Phe Ser Glu Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu
35 40 45

Val Val Lys Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val
50 55 60

Gly Ile Glu Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile
65 70 75 80

Ile Arg Lys Gln Gln Arg Gln Ser Pro Ala Gln Gly Lys Met Cys Lys
85 90 95

Leu

<210> 97
<211> 238
<212> PRT
<213> Homo sapiens

<400> 97
Met Ala Ala Val Asp Ile Arg Asp Asn Leu Leu Gly Ile Ser Trp Val
1 5 10 15

Asp Ser Ser Trp Ile Pro Ile Leu Asn Ser Gly Ser Val Leu Asp Tyr
20 25 30

Phe Ser Glu Arg Ser Asn Pro Phe Tyr Asp Arg Thr Cys Asn Asn Glu
35 40 45

Val Val Lys Met Gln Arg Leu Thr Leu Glu His Leu Asn Gln Met Val

50 55 60

Gly Ile Glu Tyr Ile Leu Leu His Ala Gln Glu Pro Ile Leu Phe Ile
65 70 75 80

Ile Arg Lys Gln Gln Arg Gln Ser Pro Ala Gln Val Ile Pro Leu Ala
85 90 95

Asp Tyr Tyr Ile Ile Ala Gly Val Ile Tyr Gln Ala Pro Asp Leu Gly
100 105 110

Ser Val Ile Asn Ser Arg Val Leu Thr Ala Val His Gly Ile Gln Ser
115 120 125

Ala Phe Asp Glu Ala Met Ser Tyr Cys Arg Tyr His Pro Ser Lys Gly
130 135 140

Tyr Trp Trp His Phe Lys Asp His Glu Glu Gln Asp Lys Val Arg Pro
145 150 155 160

Lys Ala Lys Arg Lys Glu Glu Pro Ser Ser Ile Phe Gln Arg Gln Arg
165 170 175

Val Asp Ala Leu Leu Leu Asp Leu Arg Gln Lys Phe Pro Pro Lys Phe
180 185 190

Val Gln Leu Lys Pro Gly Glu Lys Pro Val Pro Val Asp His Leu Arg
195 200 205

Ser Glu Val Gln Asp Gln Pro Asp Gln Tyr Gly Glu Thr Pro Ser Leu
210 215 220

Leu Lys Ile Gln Lys Leu Ala Gly Arg Gly Gly Gly Arg Pro
225 230 235

<210> 98
<211> 69
<212> PRT
<213> Homo sapiens

<400> 98
Met Ala Glu Lys Phe Asp His Leu Glu Glu His Leu Glu Lys Phe Val
1 5 10 15

Glu Asn Ile Arg Gln Leu Gly Ile Ile Val Ser Asp Phe Gln Pro Ser
20 25 30

Ser Gln Ala Gly Leu Asn Gln Lys Leu Asn Phe Ile Val Thr Gly Leu
35 40 45

Gln Asp Ile Asp Lys Cys Arg Gln Gln Leu His Asp Ile Thr Val Pro
50 55 60

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Leu Glu Val Phe Glu
65

<210> 99
<211> 93
<212> PRT
<213> Homo sapiens

<400> 99
Met Ala Thr Tyr Ser Leu Ala Asn Glu Arg Leu Arg Ala Leu Glu Asp
1 5 10 15

Ile Glu Arg Glu Ile Gly Ala Ile Leu Gln Asn Ala Gly Thr Val Ile
20 25 30

Leu Glu Leu Ser Lys Glu Lys Thr Asn Glu Arg Leu Leu Asp Arg Gln
35 40 45

Ala Ala Ala Phe Thr Ala Ser Val Gln His Val Glu Ala Glu Leu Ser
50 55 60

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

Glu Arg Thr Pro Ala Leu Gly Gln Ser Leu Arg Leu Gly
85 90

<210> 100
<211> 2116
<212> PRT
<213> Homo sapiens

<400> 100
Met Lys Gln Ser Met Pro Ser Leu His Thr Lys Lys Ile Leu Phe Cys
1 5 10 15

Tyr Phe His Leu Thr Asn Ser Trp Cys Leu Arg Arg Tyr Gly Leu Gly
20 25 30

Lys Met Ala Ala Phe Gly Ile Leu Ser Tyr Glu His Arg Pro Leu Lys
35 40 45

Arg Pro Arg Pro Arg Leu Gly Pro Pro Asp Val Tyr Pro Gln Asp Pro
50 55 60

Lys Gln Lys Glu Asp Glu Leu Thr Ala Leu Asn Val Lys Gln Gly Phe
65 70 75 80

Asn Asn Gln Pro Ala Val Ser Gly Asp Glu His Gly Ser Ala Lys Asn
85 90 95

Val Ser Phe Asn Pro Ala Lys Ile Ser Ser Asn Phe Ser Ser Ile Ile
100 105 110

Ala Glu Lys Leu Arg Cys Asn Thr Leu Pro Asp Thr Gly Arg Arg Lys

115 120 125

Pro Gln Val Asn Gln Lys Asp Asn Phe Trp Leu Val Thr Ala Arg Ser
130 135 140

Gln Ser Ala Ile Asn Thr Trp Phe Thr Asp Leu Ala Gly Thr Lys Pro
145 150 155 160

Leu Thr Gln Leu Ala Lys Lys Val Pro Ile Phe Ser Lys Lys Glu Glu
165 170 175

Val Phe Gly Tyr Leu Ala Lys Tyr Thr Val Pro Val Met Arg Ala Ala
180 185 190

Trp Leu Ile Lys Met Thr Cys Ala Tyr Tyr Ala Ala Ile Ser Glu Thr
195 200 205

Lys Val Lys Lys Arg His Val Asp Pro Phe Met Glu Trp Thr Gln Ile
210 215 220

Ile Thr Lys Tyr Leu Trp Glu Gln Leu Gln Lys Met Ala Glu Tyr Tyr
225 230 235 240

Arg Pro Gly Pro Ala Gly Ser Gly Gly Cys Gly Ser Thr Ile Gly Pro
245 250 255

Leu Pro His Asp Val Glu Val Ala Ile Arg Gln Trp Asp Tyr Thr Glu
260 265 270

Lys Leu Ala Met Phe Met Phe Gln Asp Gly Met Leu Asp Arg His Glu
275 280 285

Phe Leu Thr Trp Val Leu Glu Cys Phe Glu Lys Ile Arg Pro Gly Glu
290 295 300

Asp Glu Leu Leu Lys Leu Leu Leu Pro Leu Leu Leu Arg Tyr Ser Gly
305 310 315 320

Glu Phe Val Gln Ser Ala Tyr Leu Ser Arg Arg Leu Ala Tyr Phe Cys
325 330 335

Thr Arg Arg Leu Ala Leu Gln Leu Asp Gly Val Ser Ser His Ser Ser
340 345 350

His Val Ile Ser Ala Gln Ser Thr Ser Thr Leu Pro Thr Thr Pro Ala
355 360 365

Pro Gln Pro Pro Thr Ser Ser Thr Pro Ser Thr Pro Phe Ser Asp Leu
370 375 380

Leu Met Cys Pro Gln His Arg Pro Leu Val Phe Gly Leu Ser Cys Ile
385 390 395 400

Leu Gln Thr Ile Leu Leu Cys Cys Pro Ser Ala Leu Val Trp His Tyr
405 410 415

Ser Leu Thr Asp Ser Arg Ile Lys Thr Gly Ser Pro Leu Asp His Leu
420 425 430

Pro Ile Ala Pro Ser Asn Leu Pro Met Pro Glu Gly Asn Ser Ala Phe
435 440 445

Thr Gln Gln Val Arg Ala Lys Leu Arg Glu Ile Glu Gln Gln Ile Lys
450 455 460

Glu Arg Gly Gln Ala Val Glu Val Arg Trp Ser Phe Asp Lys Cys Gln
465 470 475 480

Glu Ala Thr Ala Gly Phe Thr Ile Gly Arg Val Leu His Thr Leu Glu
485 490 495

Val Leu Asp Ser His Ser Phe Glu Arg Ser Asp Phe Ser Asn Ser Leu
500 505 510

Asp Ser Leu Cys Asn Arg Ile Phe Gly Leu Gly Pro Ser Lys Asp Gly
515 520 525

His Glu Ile Ser Ser Asp Asp Asp Ala Val Val Ser Leu Leu Cys Glu
530 535 540

Trp Ala Val Ser Cys Lys Arg Ser Gly Arg His Arg Ala Met Val Val
545 550 555 560

Ala Lys Leu Leu Glu Lys Arg Gln Ala Glu Ile Glu Ala Glu Arg Cys
565 570 575

Gly Glu Ser Glu Ala Ala Asp Glu Lys Gly Ser Ile Ala Ser Gly Ser
580 585 590

Leu Ser Ala Pro Ser Ala Pro Ile Phe Gln Asp Val Leu Leu Gln Phe
595 600 605

Leu Asp Thr Gln Ala Pro Met Leu Thr Asp Pro Arg Ser Glu Ser Glu
610 615 620

Arg Val Glu Phe Phe Asn Leu Val Leu Leu Phe Cys Glu Leu Ile Arg
625 630 635 640

His Asp Val Phe Ser His Asn Met Tyr Thr Cys Thr Leu Ile Ser Arg
645 650 655

Gly Asp Leu Ala Phe Gly Ala Pro Gly Pro Arg Pro Pro Ser Pro Phe
660 665 670

Asp Asp Pro Ala Asp Asp Pro Glu His Lys Glu Ala Glu Gly Ser Ser
675 680 685

Ser Ser Lys Leu Glu Asp Pro Gly Leu Ser Glu Ser Met Asp Ile Asp
690 695 700

Pro Ser Ser Ser Val Leu Phe Glu Asp Met Glu Lys Pro Asp Phe Ser
705 710 715 720

Leu Phe Ser Pro Thr Met Pro Cys Glu Gly Lys Gly Ser Pro Ser Pro
725 730 735

Glu Lys Pro Asp Val Glu Lys Glu Val Lys Pro Pro Pro Lys Glu Lys
740 745 750

Ile Glu Gly Thr Leu Gly Val Leu Tyr Asp Gln Pro Arg His Val Gln
755 760 765

Tyr Ala Thr His Phe Pro Ile Pro Gln Glu Glu Ser Cys Ser His Glu
770 775 780

Cys Asn Gln Arg Leu Val Val Leu Phe Gly Val Gly Lys Gln Arg Asp
785 790 795 800

Asp Ala Arg His Ala Ile Lys Lys Ile Thr Lys Asp Ile Leu Lys Val
805 810 815

Leu Asn Arg Lys Gly Thr Ala Glu Thr Asp Gln Leu Ala Pro Ile Val
820 825 830

Pro Leu Asn Pro Gly Asp Leu Thr Phe Leu Gly Gly Glu Asp Gly Gln
835 840 845

Lys Arg Arg Arg Asn Arg Pro Glu Ala Phe Pro Thr Ala Glu Asp Ile
850 855 860

Phe Ala Lys Phe Gln His Leu Ser His Tyr Asp Gln His Gln Val Thr
865 870 875 880

Ala Gln Val Ser Arg Asn Val Leu Glu Gln Ile Thr Ser Phe Ala Leu
885 890 895

Gly Met Ser Tyr His Leu Pro Leu Val Gln His Val Gln Phe Ile Phe
900 905 910

Asp Leu Met Glu Tyr Ser Leu Ser Ile Ser Gly Leu Ile Asp Phe Ala
915 920 925

Ile Gln Leu Leu Asn Glu Leu Ser Val Val Glu Ala Glu Leu Leu Leu
930 935 940

Lys Ser Ser Asp Leu Val Gly Ser Tyr Thr Thr Ser Leu Cys Leu Cys
945 950 955 960

Ile Val Ala Val Leu Arg His Tyr His Ala Cys Leu Ile Leu Asn Gln
965 970 975

Asp Gln Met Ala Gln Val Phe Glu Gly Leu Cys Gly Val Val Lys His
980 985 990

Gly Met Asn Arg Ser Asp Gly Ser Ser Ala Glu Arg Cys Ile Leu Ala
995 1000 1005

Tyr Leu Tyr Asp Leu Tyr Thr Ser Cys Ser His Leu Lys Asn Lys
1010 1015 1020

Phe Gly Glu Leu Phe Ser Asp Phe Cys Ser Lys Val Lys Asn Thr
1025 1030 1035

Ile Tyr Cys Asn Val Glu Pro Ser Glu Ser Asn Met Arg Trp Ala
1040 1045 1050

Pro Glu Phe Met Ile Asp Thr Leu Glu Asn Pro Ala Ala His Thr
1055 1060 1065

Phe Thr Tyr Thr Gly Leu Gly Lys Ser Leu Ser Glu Asn Pro Ala
1070 1075 1080

Asn Arg Tyr Ser Phe Val Cys Asn Ala Leu Met His Val Cys Val
1085 1090 1095

Gly His His Asp Pro Asp Arg Val Asn Asp Ile Ala Ile Leu Cys
1100 1105 1110

Ala Glu Leu Thr Gly Tyr Cys Lys Ser Leu Ser Ala Glu Trp Leu
1115 1120 1125

Gly Val Leu Lys Ala Leu Cys Cys Ser Ser Asn Asn Gly Thr Cys
1130 1135 1140

Gly Phe Asn Asp Leu Leu Cys Asn Val Asp Val Ser Asp Leu Ser
1145 1150 1155

Phe His Asp Ser Leu Ala Thr Phe Val Ala Ile Leu Ile Ala Arg
1160 1165 1170

Gln Cys Leu Leu Leu Glu Asp Leu Ile Arg Cys Ala Ala Ile Pro
1175 1180 1185

Ser Leu Leu Asn Ala Ala Cys Ser Glu Gln Asp Ser Glu Pro Gly
1190 1195 1200

Ala Arg Leu Thr Cys Arg Ile Leu Leu His Leu Phe Lys Thr Pro

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1205 1210 1215

Gln Leu Asn Pro Cys Gln Ser Asp Gly Asn Lys Pro Thr Val Gly
1220 1225 1230

Ile Arg Ser Ser Cys Asp Arg His Leu Leu Ala Ala Ser Gln Asn
1235 1240 1245

Arg Ile Val Asp Gly Ala Val Phe Ala Val Leu Lys Ala Val Phe
1250 1255 1260

Val Leu Gly Asp Ala Glu Leu Lys Gly Ser Gly Phe Thr Val Thr
1265 1270 1275

Gly Gly Thr Glu Glu Leu Pro Glu Glu Glu Gly Gly Gly Gly Ser
1280 1285 1290

Gly Gly Arg Arg Gln Gly Gly Arg Asn Ile Ser Val Glu Thr Ala
1295 1300 1305

Ser Leu Asp Val Tyr Ala Lys Tyr Val Leu Arg Ser Ile Cys Gln
1310 1315 1320

Gln Glu Trp Val Gly Glu Arg Cys Leu Lys Ser Leu Cys Glu Asp
1325 1330 1335

Ser Asn Asp Leu Gln Asp Pro Val Leu Ser Ser Ala Gln Ala Gln
1340 1345 1350

Arg Leu Met Gln Leu Ile Cys Tyr Pro His Arg Leu Leu Asp Asn
1355 1360 1365

Glu Asp Gly Glu Asn Pro Gln Arg Gln Arg Ile Lys Arg Ile Leu
1370 1375 1380

Gln Asn Leu Asp Gln Trp Thr Met Arg Gln Ser Ser Leu Glu Leu
1385 1390 1395

Gln Leu Met Ile Lys Gln Thr Pro Asn Asn Glu Met Asn Ser Leu
1400 1405 1410

Leu Glu Asn Ile Ala Lys Ala Thr Ile Glu Val Phe Gln Arg Ser
1415 1420 1425

Ala Glu Thr Gly Ser Ser Ser Gly Ser Thr Ala Ser Asn Met Pro
1430 1435 1440

Ser Ser Ser Lys Thr Lys Pro Val Leu Ser Ser Leu Glu Arg Ser
1445 1450 1455

Gly Val Trp Leu Val Ala Pro Leu Ile Ala Lys Leu Pro Thr Ser
1460 1465 1470

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Val Gln Gly His Val Leu Lys Ala Ala Gly Glu Glu Leu Glu Lys
1475 1480 1485

Gly Gln His Leu Gly Ser Ser Ser Arg Lys Glu Arg Asp Arg Gln
1490 1495 1500

Lys Gln Lys Ser Met Ser Leu Leu Ser Gln Gln Pro Phe Leu Ser
1505 1510 1515

Leu Val Leu Thr Cys Leu Lys Gly Gln Asp Glu Gln Arg Glu Gly
1520 1525 1530

Leu Leu Thr Ser Leu Tyr Ser Gln Val His Gln Ile Val Asn Asn
1535 1540 1545

Trp Arg Asp Asp Gln Tyr Leu Asp Asp Cys Lys Pro Lys Gln Leu
1550 1555 1560

Met His Glu Ala Leu Lys Leu Arg Leu Asn Leu Val Gly Gly Met
1565 1570 1575

Phe Asp Thr Val Gln Arg Ser Thr Gln Gln Thr Thr Glu Trp Ala
1580 1585 1590

Met Leu Leu Leu Glu Ile Ile Ile Ser Gly Thr Val Asp Met Gln
1595 1600 1605

Ser Asn Asn Glu Leu Phe Thr Thr Val Leu Asp Met Leu Ser Val
1610 1615 1620

Leu Ile Asn Gly Thr Leu Ala Ala Asp Met Ser Ser Ile Ser Gln
1625 1630 1635

Gly Ser Met Glu Glu Asn Lys Arg Ala Tyr Met Asn Leu Ala Lys
1640 1645 1650

Lys Leu Gln Lys Glu Leu Gly Glu Arg Gln Ser Asp Ser Leu Glu
1655 1660 1665

Lys Val Arg Gln Leu Leu Pro Leu Pro Lys Gln Thr Arg Asp Val
1670 1675 1680

Ile Thr Cys Glu Pro Gln Gly Ser Leu Ile Asp Thr Lys Gly Asn
1685 1690 1695

Lys Ile Ala Gly Phe Asp Ser Ile Phe Lys Lys Glu Gly Leu Gln
1700 1705 1710

Val Ser Thr Lys Gln Lys Ile Ser Pro Trp Asp Leu Phe Glu Gly
1715 1720 1725

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Leu Lys Pro Ser Ala Pro Leu Ser Trp Gly Trp Phe Gly Thr Val
1730 1735 1740

Arg Val Asp Arg Arg Val Ala Arg Gly Glu Glu Gln Gln Arg Leu
1745 1750 1755

Leu Leu Tyr His Thr His Leu Arg Pro Arg Pro Arg Ala Tyr Tyr
1760 1765 1770

Leu Glu Pro Leu Pro Leu Pro Pro Glu Asp Glu Glu Pro Pro Ala
1775 1780 1785

Pro Thr Leu Leu Glu Pro Glu Lys Lys Ala Pro Glu Pro Pro Lys
1790 1795 1800

Thr Asp Lys Pro Gly Ala Ala Pro Pro Ser Thr Glu Glu Arg Lys
1805 1810 1815

Lys Lys Ser Thr Lys Gly Lys Lys Arg Ser Gln Pro Ala Thr Lys
1820 1825 1830

Thr Glu Asp Tyr Gly Met Gly Pro Gly Arg Ser Gly Pro Tyr Gly
1835 1840 1845

Val Thr Val Pro Pro Asp Leu Leu His His Pro Asn Pro Gly Ser
1850 1855 1860

Ile Thr His Leu Asn Tyr Arg Gln Gly Ser Ile Gly Leu Tyr Thr
1865 1870 1875

Gln Asn Gln Pro Leu Pro Ala Gly Gly Pro Arg Val Asp Pro Tyr
1880 1885 1890

Arg Pro Val Arg Leu Pro Met Gln Lys Leu Pro Pro Ser Tyr Ser
1895 1900 1905

Ser Gln Pro Tyr Gln Ser Thr His Pro Ser Thr Asn Pro Thr Leu
1910 1915 1920

Val Asp Pro Thr Arg His Leu Gln Gln Arg Pro Ser Gly Tyr Val
1925 1930 1935

His Gln Gln Ala Pro Thr Tyr Gly His Gly Leu Thr Ser Thr Gln
1940 1945 1950

Arg Phe Ser His Gln Thr Leu Gln Gln Thr Pro Met Ile Ser Thr
1955 1960 1965

Met Thr Pro Met Ser Ala Gln Gly Val Gln Ala Gly Val Arg Ser
1970 1975 1980

Thr Ala Ile Leu Pro Glu Gln Gln Gln Gln Gln Gln Gln Gln
1985 1990 1995

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
2000 2005 2010

Gln Gln Tyr His Ile Arg Gln Gln Gln Gln Gln Ile Leu Arg
2015 2020 2025

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
2030 2035 2040

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Gln Gln Gln
2045 2050 2055

Gln Gln Gln Gln Ala Ala Pro Pro Gln Pro Gln Pro Gln Ser Gln
2060 2065 2070

Pro Gln Phe Gln Arg Gln Gly Leu Gln Gln Thr Gln Gln Gln Gln
2075 2080 2085

Gln Thr Ala Ala Leu Val Arg Gln Leu Gln Gln Gln Leu Ser Asn
2090 2095 2100

Thr Gln Pro Gln Pro Ser Thr Asn Ile Phe Gly Arg Tyr
2105 2110 2115

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Tyr Phe His Leu Thr Asn Ser Trp Cys Leu Arg Arg Tyr Gly Leu Gly
20 25 30

Lys Met Ala Ala Phe Gly Ile Leu Ser Tyr Glu His Arg Pro Leu Lys
35 40 45

Arg Pro Arg Pro Arg Leu Gly Pro Pro Asp Val Tyr Pro Gln Asp Pro
50 55 60

Lys Gln Lys Glu Asp Glu Leu Thr Ala Leu Asn Val Lys Gln Gly Phe
65 70 75 80

Asn Asn Gln Pro Ala Val Ser Gly Asp Glu His Gly Ser Ala Lys Asn
85 90 95

Val Ser Phe Asn Pro Ala Lys Ile Ser Ser Asn Phe Ser Ser Ile Ile
100 105 110

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Ala Glu Lys Leu Arg Cys Asn Thr Leu Pro Asp Thr Gly Arg Arg Lys
        115                 120                 125

Pro Gln Val Asn Gln Lys Asp Asn Phe Trp Leu Val Thr Ala Arg Ser
    130                 135                 140

Gln Ser Ala Ile Asn Thr Trp Phe Thr Asp Leu Ala Gly Thr Lys Pro
145                 150                 155                 160

Leu Thr Gln Leu Ala Lys Lys Val Pro Ile Phe Ser Lys Lys Glu Glu
                165                 170                 175

Val Phe Gly Tyr Leu Ala Lys Tyr Thr Val Pro Val Met Arg Ala Ala
            180                 185                 190

Trp Leu Ile Lys Met Thr Cys Ala Tyr Tyr Ala Ala Ile Ser Glu Thr
        195                 200                 205

Lys Val Lys Lys Arg His Val Asp Pro Phe Met Glu Trp Thr Gln Ile
    210                 215                 220

Ile Thr Lys Tyr Leu Trp Glu Gln Leu Gln Lys Met Ala Glu Tyr Tyr
225                 230                 235                 240

Arg Pro Gly Pro Ala Gly Ser Gly Gly Cys Gly Ser Thr Ile Gly Pro
                245                 250                 255

Leu Pro His Asp Val Glu Val Ala Ile Arg Gln Trp Asp Tyr Thr Glu
            260                 265                 270

Lys Leu Ala Met Phe Met Phe Gln Asp Gly Met Leu Asp Arg His Glu
        275                 280                 285

Phe Leu Thr Trp Val Leu Glu Cys Phe Glu Lys Ile Arg Pro Gly Glu
    290                 295                 300

Asp Glu Leu Leu Lys Leu Leu Leu Pro Leu Leu Leu Arg Tyr Ser Gly
305                 310                 315                 320

Glu Phe Val Gln Ser Ala Tyr Leu Ser Arg Arg Leu Ala Tyr Phe Cys
                325                 330                 335

Thr Arg Arg Leu Ala Leu Gln Leu Asp Gly Val Ser Ser His Ser Ser
            340                 345                 350

His Val Ile Ser Ala Gln Ser Thr Ser Thr Leu Pro Thr Thr Pro Ala
        355                 360                 365

Pro Gln Pro Pro Thr Ser Ser Thr Pro Ser Thr Pro Phe Ser Asp Leu
    370                 375                 380
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Leu Met Cys Pro Gln His Arg Pro Leu Val Phe Gly Leu Ser Cys Ile
385 390 395 400

Leu Gln Thr Ile Leu Leu Cys Cys Pro Ser Ala Leu Val Trp His Tyr
405 410 415

Ser Leu Thr Asp Ser Arg Ile Lys Thr Gly Ser Pro Leu Asp His Leu
420 425 430

Pro Ile Ala Pro Ser Asn Leu Pro Met Pro Glu Gly Asn Ser Ala Phe
435 440 445

Thr Gln Gln Val Arg Ala Lys Leu Arg Glu Ile Glu Gln Gln Ile Lys
450 455 460

Glu Arg Gly Gln Ala Val Glu Val Arg Trp Ser Phe Asp Lys Cys Gln
465 470 475 480

Glu Ala Thr Ala Gly Phe Thr Ile Gly Arg Val Leu His Thr Leu Glu
485 490 495

Val Leu Asp Ser His Ser Phe Glu Arg Ser Asp Phe Ser Asn Ser Leu
500 505 510

Asp Ser Leu Cys Asn Arg Ile Phe Gly Leu Gly Pro Ser Lys Asp Gly
515 520 525

His Glu Ile Ser Ser Asp Asp Asp Ala Val Val Ser Leu Leu Cys Glu
530 535 540

Trp Ala Val Ser Cys Lys Arg Ser Gly Arg His Arg Ala Met Val Val
545 550 555 560

Ala Lys Leu Leu Glu Lys Arg Gln Ala Glu Ile Glu Ala Glu Arg Cys
565 570 575

Gly Glu Ser Glu Ala Ala Asp Glu Lys Gly Ser Ile Ala Ser Gly Ser
580 585 590

Leu Ser Ala Pro Ser Ala Pro Ile Phe Gln Asp Val Leu Leu Gln Phe
595 600 605

Leu Asp Thr Gln Ala Pro Met Leu Thr Asp Pro Arg Ser Glu Ser Glu
610 615 620

Arg Val Glu Phe Phe Asn Leu Val Leu Leu Phe Cys Glu Leu Ile Arg
625 630 635 640

His Asp Val Phe Ser His Asn Met Tyr Thr Cys Thr Leu Ile Ser Arg
645 650 655

Gly Asp Leu Ala Phe Gly Ala Pro Gly Pro Arg Pro Pro Ser Pro Phe

660 665 670

Asp Asp Pro Ala Asp Asp Pro Glu His Lys Glu Ala Glu Gly Ser Ser
675 680 685

Ser Ser Lys Leu Glu Asp Pro Gly Leu Ser Glu Ser Met Asp Ile Asp
690 695 700

Pro Ser Ser Ser Val Leu Phe Glu Asp Met Glu Lys Pro Asp Phe Ser
705 710 715 720

Leu Phe Ser Pro Thr Met Pro Cys Glu Gly Lys Gly Ser Pro Ser Pro
725 730 735

Glu Lys Pro Asp Val Glu Lys Glu Val Lys Pro Pro Pro Lys Glu Lys
740 745 750

Ile Glu Gly Thr Leu Gly Val Leu Tyr Asp Gln Pro Arg His Val Gln
755 760 765

Tyr Ala Thr His Phe Pro Ile Pro Gln Glu Glu Ser Cys Ser His Glu
770 775 780

Cys Asn Gln Arg Leu Val Val Leu Phe Gly Val Gly Lys Gln Arg Asp
785 790 795 800

Asp Ala Arg His Ala Ile Lys Lys Ile Thr Lys Asp Ile Leu Lys Val
805 810 815

Leu Asn Arg Lys Gly Thr Ala Glu Thr Asp Gln Leu Ala Pro Ile Val
820 825 830

Pro Leu Asn Pro Gly Asp Leu Thr Phe Leu Gly Gly Glu Asp Gly Gln
835 840 845

Lys Arg Arg Arg Asn Arg Pro Glu Ala Phe Pro Thr Ala Glu Asp Ile
850 855 860

Phe Ala Lys Phe Gln His Leu Ser His Tyr Asp Gln His Gln Val Thr
865 870 875 880

Ala Gln Val Ser Arg Asn Val Leu Glu Gln Ile Thr Ser Phe Ala Leu
885 890 895

Gly Met Ser Tyr His Leu Pro Leu Val Gln His Val Gln Phe Ile Phe
900 905 910

Asp Leu Met Glu Tyr Ser Leu Ser Ile Ser Gly Leu Ile Asp Phe Ala
915 920 925

Ile Gln Leu Leu Asn Glu Leu Ser Val Val Glu Ala Glu Leu Leu Leu
930 935 940

Lys Ser Ser Asp Leu Val Gly Ser Tyr Thr Thr Ser Leu Cys Leu Cys
945 950 955 960

Ile Val Ala Val Leu Arg His Tyr His Ala Cys Leu Ile Leu Asn Gln
965 970 975

Asp Gln Met Ala Gln Val Phe Glu Gly Leu Cys Gly Val Val Lys His
980 985 990

Gly Met Asn Arg Ser Asp Gly Ser Ser Ala Glu Arg Cys Ile Leu Ala
995 1000 1005

Tyr Leu Tyr Asp Leu Tyr Thr Ser Cys Ser His Leu Lys Asn Lys
1010 1015 1020

Phe Gly Glu Leu Phe Ser Asp Phe Cys Ser Lys Val Lys Asn Thr
1025 1030 1035

Ile Tyr Cys Asn Val Glu Pro Ser Glu Ser Asn Met Arg Trp Ala
1040 1045 1050

Pro Glu Phe Met Ile Asp Thr Leu Glu Asn Pro Ala Ala His Thr
1055 1060 1065

Phe Thr Tyr Thr Gly Leu Gly Lys Ser Leu Ser Glu Asn Pro Ala
1070 1075 1080

Asn Arg Tyr Ser Phe Val Cys Asn Ala Leu Met His Val Cys Val
1085 1090 1095

Gly His His Asp Pro Asp Arg Val Asn Asp Ile Ala Ile Leu Cys
1100 1105 1110

Ala Glu Leu Thr Gly Tyr Cys Lys Ser Leu Ser Ala Glu Trp Leu
1115 1120 1125

Gly Val Leu Lys Ala Leu Cys Cys Ser Ser Asn Asn Gly Thr Cys
1130 1135 1140

Gly Phe Asn Asp Leu Leu Cys Asn Val Asp Val Ser Asp Leu Ser
1145 1150 1155

Phe His Asp Ser Leu Ala Thr Phe Val Ala Ile Leu Ile Ala Arg
1160 1165 1170

Gln Cys Leu Leu Leu Glu Asp Leu Ile Arg Cys Ala Ala Ile Pro
1175 1180 1185

Ser Leu Leu Asn Ala Ala Cys Ser Glu Gln Asp Ser Glu Pro Gly
1190 1195 1200

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Ala Arg Leu Thr Cys Arg Ile Leu Leu His Leu Phe Lys Thr Pro
1205 1210 1215

Gln Leu Asn Pro Cys Gln Ser Asp Gly Asn Lys Pro Thr Val Gly
1220 1225 1230

Ile Arg Ser Ser Cys Asp Arg His Leu Leu Ala Ala Ser Gln Asn
1235 1240 1245

Arg Ile Val Asp Gly Ala Val Phe Ala Val Leu Lys Ala Val Phe
1250 1255 1260

Val Leu Gly Asp Ala Glu Leu Lys Gly Ser Gly Phe Thr Val Thr
1265 1270 1275

Gly Gly Thr Glu Glu Leu Pro Glu Glu Glu Gly Gly Gly Gly Ser
1280 1285 1290

Gly Gly Arg Arg Gln Gly Gly Arg Asn Ile Ser Val Glu Thr Ala
1295 1300 1305

Ser Leu Asp Val Tyr Ala Lys Tyr Val Leu Arg Ser Ile Cys Gln
1310 1315 1320

Gln Glu Trp Val Gly Glu Arg Cys Leu Lys Ser Leu Cys Glu Asp
1325 1330 1335

Ser Asn Asp Leu Gln Asp Pro Val Leu Ser Ser Ala Gln Ala Gln
1340 1345 1350

Arg Leu Met Gln Leu Ile Cys Tyr Pro His Arg Leu Leu Asp Asn
1355 1360 1365

Glu Asp Gly Glu Asn Pro Gln Arg Gln Arg Ile Lys Arg Ile Leu
1370 1375 1380

Gln Asn Leu Asp Gln Trp Thr Met Arg Gln Ser Ser Leu Glu Leu
1385 1390 1395

Gln Leu Met Ile Lys Gln Thr Pro Asn Asn Glu Met Asn Ser Leu
1400 1405 1410

Leu Glu Asn Ile Ala Lys Ala Thr Ile Glu Val Phe Gln Arg Ser
1415 1420 1425

Ala Glu Thr Gly Ser Ser Ser Gly Ser Thr Ala Ser Asn Met Pro
1430 1435 1440

Ser Ser Ser Lys Thr Lys Pro Val Leu Ser Ser Leu Glu Arg Ser
1445 1450 1455

Gly Val Trp Leu Val Ala Pro Leu Ile Ala Lys Leu Pro Thr Ser
1460 1465 1470

Val Gln Gly His Val Leu Lys Ala Ala Gly Glu Glu Leu Glu Lys
1475 1480 1485

Gly Gln His Leu Gly Ser Ser Ser Arg Lys Glu Arg Asp Arg Gln
1490 1495 1500

Lys Gln Lys Ser Met Ser Leu Leu Ser Gln Gln Pro Phe Leu Ser
1505 1510 1515

Leu Val Leu Thr Cys Leu Lys Gly Gln Asp Glu Gln Arg Glu Gly
1520 1525 1530

Leu Leu Thr Ser Leu Tyr Ser Gln Val His Gln Ile Val Asn Asn
1535 1540 1545

Trp Arg Asp Asp Gln Tyr Leu Asp Asp Cys Lys Pro Lys Gln Leu
1550 1555 1560

Met His Glu Ala Leu Lys Leu Arg Leu Asn Leu Val Gly Gly Met
1565 1570 1575

Phe Asp Thr Val Gln Arg Ser Thr Gln Gln Thr Thr Glu Trp Ala
1580 1585 1590

Met Leu Leu Leu Glu Ile Ile Ile Ser Gly Thr Val Asp Met Gln
1595 1600 1605

Ser Asn Asn Glu Leu Phe Thr Thr Val Leu Asp Met Leu Ser Val
1610 1615 1620

Leu Ile Asn Gly Thr Leu Ala Ala Asp Met Ser Ser Ile Ser Gln
1625 1630 1635

Gly Ser Met Glu Glu Asn Lys Arg Ala Tyr Met Asn Leu Ala Lys
1640 1645 1650

Lys Leu Gln Lys Glu Leu Gly Glu Arg Gln Ser Asp Ser Leu Glu
1655 1660 1665

Lys Val Arg Gln Leu Leu Pro Leu Pro Lys Gln Thr Arg Asp Val
1670 1675 1680

Ile Thr Cys Glu Pro Gln Gly Ser Leu Ile Asp Thr Lys Gly Asn
1685 1690 1695

Lys Ile Ala Gly Phe Asp Ser Ile Phe Lys Lys Glu Gly Leu Gln
1700 1705 1710

Val Ser Thr Lys Gln Lys Ile Ser Pro Trp Asp Leu Phe Glu Gly

1715 1720 1725

Leu Lys Pro Ser Ala Pro Leu Ser Trp Gly Trp Phe Gly Thr Val
1730 1735 1740

Arg Val Asp Arg Arg Val Ala Arg Gly Glu Glu Gln Gln Arg Leu
1745 1750 1755

Leu Leu Tyr His Thr His Leu Arg Pro Arg Pro Arg Ala Tyr Tyr
1760 1765 1770

Leu Glu Pro Leu Pro Leu Pro Pro Glu Asp Glu Glu Pro Pro Ala
1775 1780 1785

Pro Thr Leu Leu Glu Pro Glu Lys Lys Ala Pro Glu Pro Pro Lys
1790 1795 1800

Thr Asp Lys Pro Gly Ala Ala Pro Pro Ser Thr Glu Glu Arg Lys
1805 1810 1815

Lys Lys Ser Thr Lys Gly Lys Lys Arg Ser Gln Pro Ala Thr Lys
1820 1825 1830

Thr Glu Asp Tyr Gly Met Gly Pro Gly Arg Ser Gly Pro Tyr Gly
1835 1840 1845

Val Thr Val Pro Pro Asp Leu Leu His His Pro Asn Pro Gly Ser
1850 1855 1860

Ile Thr His Leu Asn Tyr Arg Gln Gly Ser Ile Gly Leu Tyr Thr
1865 1870 1875

Gln Asn Gln Pro Leu Pro Ala Gly Gly Pro Arg Val Asp Pro Tyr
1880 1885 1890

Arg Pro Val Arg Leu Pro Met Gln Lys Leu Pro Thr Arg Pro Thr
1895 1900 1905

Tyr Pro Gly Val Leu Pro Thr Thr Met Thr Gly Val Met Gly Leu
1910 1915 1920

Glu Pro Ser Ser Tyr Lys Thr Ser Val Tyr Arg Gln Gln Gln Pro
1925 1930 1935

Ala Val Pro Gln Gly Gln Arg Leu Arg Gln Gln Leu Gln Ala Lys
1940 1945 1950

Ile Gln Ser Gln Gly Met Leu Gly Gln Ser Ser Val His Gln Met
1955 1960 1965

Thr Pro Ser Ser Ser Tyr Gly Leu Gln Thr Ser Gln Gly Tyr Thr
1970 1975 1980

Pro Tyr Val Ser His Val Gly Leu Gln Gln His Thr Gly Pro Ala
1985 1990 1995

Asp Pro Thr Arg His Leu Gln Gln Arg Pro Ser Gly Tyr Val His
2000 2005 2010

Gln Gln Ala Pro Thr Tyr Gly His Gly Leu Thr Ser Thr Gln Arg
2015 2020 2025

Phe Ser His Gln Thr Leu Gln Gln Thr Pro Met Ile Ser Thr Met
2030 2035 2040

Thr Pro Met Ser Ala Gln Gly Val Gln Ala Gly Val Arg Ser Thr
2045 2050 2055

Ala Ile Leu Pro Glu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
2060 2065 2070

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
2075 2080 2085

Gln Tyr His Ile Arg Gln Gln Gln Gln Gln Gln Ile Leu Arg Gln
2090 2095 2100

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
2105 2110 2115

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Gln Gln Gln Gln
2120 2125 2130

Gln Gln Gln Ala Ala Pro Pro Gln Pro Gln Pro Gln Ser Gln Pro
2135 2140 2145

Gln Phe Gln Arg Gln Gly Leu Gln Gln Thr Gln Gln Gln Gln Gln
2150 2155 2160

Thr Ala Ala Leu Val Arg Gln Leu Gln Gln Gln Leu Ser Asn Thr
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Gln Pro Gln Pro Ser Thr Asn Ile Phe Gly Arg Tyr
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Tyr Phe His Leu Thr Asn Ser Trp Cys Leu Arg Arg Tyr Gly Leu Gly

20 25 30

Lys Met Ala Ala Phe Gly Ile Leu Ser Tyr Glu His Arg Pro Leu Lys
35 40 45

Arg Pro Arg Pro Arg Leu Gly Pro Pro Asp Val Tyr Pro Gln Asp Pro
50 55 60

Lys Gln Lys Glu Asp Glu Leu Thr Ala Leu Asn Val Lys Gln Gly Phe
65 70 75 80

Asn Asn Gln Pro Ala Val Ser Gly Asp Glu His Gly Ser Ala Lys Asn
85 90 95

Val Ser Phe Asn Pro Ala Lys Ile Ser Ser Asn Phe Ser Ser Ile Ile
100 105 110

Ala Glu Lys Leu Arg Cys Asn Thr Leu Pro Asp Thr Gly Arg Arg Lys
115 120 125

Pro Gln Val Asn Gln Lys Asp Asn Phe Trp Leu Val Thr Ala Arg Ser
130 135 140

Gln Ser Ala Ile Asn Thr Trp Phe Thr Asp Leu Ala Gly Thr Lys Pro
145 150 155 160

Leu Thr Gln Leu Ala Lys Lys Val Pro Ile Phe Ser Lys Lys Glu Glu
165 170 175

Val Phe Gly Tyr Leu Ala Lys Tyr Thr Val Pro Val Met Arg Ala Ala
180 185 190

Trp Leu Ile Lys Met Thr Cys Ala Tyr Tyr Ala Ala Ile Ser Glu Thr
195 200 205

Lys Val Lys Lys Arg His Val Asp Pro Phe Met Glu Trp Thr Gln Ile
210 215 220

Ile Thr Lys Tyr Leu Trp Glu Gln Leu Gln Lys Met Ala Glu Tyr Tyr
225 230 235 240

Arg Pro Gly Pro Ala Gly Ser Gly Gly Cys Gly Ser Thr Ile Gly Pro
245 250 255

Leu Pro His Asp Val Glu Val Ala Ile Arg Gln Trp Asp Tyr Thr Glu
260 265 270

Lys Leu Ala Met Phe Met Phe Gln Asp Gly Met Leu Asp Arg His Glu
275 280 285

Phe Leu Thr Trp Val Leu Glu Cys Phe Glu Lys Ile Arg Pro Gly Glu
290 295 300

Asp Glu Leu Leu Lys Leu Leu Leu Pro Leu Leu Leu Arg Tyr Ser Gly
305 310 315 320

Glu Phe Val Gln Ser Ala Tyr Leu Ser Arg Arg Leu Ala Tyr Phe Cys
325 330 335

Thr Arg Arg Leu Ala Leu Gln Leu Asp Gly Val Ser Ser His Ser Ser
340 345 350

His Val Ile Ser Ala Gln Ser Thr Ser Thr Leu Pro Thr Thr Pro Ala
355 360 365

Pro Gln Pro Pro Thr Ser Ser Thr Pro Ser Thr Pro Phe Ser Asp Leu
370 375 380

Leu Met Cys Pro Gln His Arg Pro Leu Val Phe Gly Leu Ser Cys Ile
385 390 395 400

Leu Gln Thr Ile Leu Leu Cys Cys Pro Ser Ala Leu Val Trp His Tyr
405 410 415

Ser Leu Thr Asp Ser Arg Ile Lys Thr Gly Ser Pro Leu Asp His Leu
420 425 430

Pro Ile Ala Pro Ser Asn Leu Pro Met Pro Glu Gly Asn Ser Ala Phe
435 440 445

Thr Gln Gln Val Arg Ala Lys Leu Arg Glu Ile Glu Gln Gln Ile Lys
450 455 460

Glu Arg Gly Gln Ala Val Glu Val Arg Trp Ser Phe Asp Lys Cys Gln
465 470 475 480

Glu Ala Thr Ala Gly Phe Thr Ile Gly Arg Val Leu His Thr Leu Glu
485 490 495

Val Leu Asp Ser His Ser Phe Glu Arg Ser Asp Phe Ser Asn Ser Leu
500 505 510

Asp Ser Leu Cys Asn Arg Ile Phe Gly Leu Gly Pro Ser Lys Asp Gly
515 520 525

His Glu Ile Ser Ser Asp Asp Asp Ala Val Val Ser Leu Leu Cys Glu
530 535 540

Trp Ala Val Ser Cys Lys Arg Ser Gly Arg His Arg Ala Met Val Val
545 550 555 560

Ala Lys Leu Leu Glu Lys Arg Gln Ala Glu Ile Glu Ala Glu Arg Cys
565 570 575

Gly Glu Ser Glu Ala Ala Asp Glu Lys Gly Ser Ile Ala Ser Gly Ser
580 585 590

Leu Ser Ala Pro Ser Ala Pro Ile Phe Gln Asp Val Leu Leu Gln Phe
595 600 605

Leu Asp Thr Gln Ala Pro Met Leu Thr Asp Pro Arg Ser Glu Ser Glu
610 615 620

Arg Val Glu Phe Phe Asn Leu Val Leu Leu Phe Cys Glu Leu Ile Arg
625 630 635 640

His Asp Val Phe Ser His Asn Met Tyr Thr Cys Thr Leu Ile Ser Arg
645 650 655

Gly Asp Leu Ala Phe Gly Ala Pro Gly Pro Arg Pro Pro Ser Pro Phe
660 665 670

Asp Asp Pro Ala Asp Asp Pro Glu His Lys Glu Ala Glu Gly Ser Ser
675 680 685

Ser Ser Lys Leu Glu Asp Pro Gly Leu Ser Glu Ser Met Asp Ile Asp
690 695 700

Pro Ser Ser Ser Val Leu Phe Glu Asp Met Glu Lys Pro Asp Phe Ser
705 710 715 720

Leu Phe Ser Pro Thr Met Pro Cys Glu Gly Lys Gly Ser Pro Ser Pro
725 730 735

Glu Lys Pro Asp Val Glu Lys Glu Val Lys Pro Pro Pro Lys Glu Lys
740 745 750

Ile Glu Gly Thr Leu Gly Val Leu Tyr Asp Gln Pro Arg His Val Gln
755 760 765

Tyr Ala Thr His Phe Pro Ile Pro Gln Glu Glu Ser Cys Ser His Glu
770 775 780

Cys Asn Gln Arg Leu Val Val Leu Phe Gly Val Gly Lys Gln Arg Asp
785 790 795 800

Asp Ala Arg His Ala Ile Lys Lys Ile Thr Lys Asp Ile Leu Lys Val
805 810 815

Leu Asn Arg Lys Gly Thr Ala Glu Thr Asp Gln Leu Ala Pro Ile Val
820 825 830

Pro Leu Asn Pro Gly Asp Leu Thr Phe Leu Gly Gly Glu Asp Gly Gln
835 840 845

Lys Arg Arg Arg Asn Arg Pro Glu Ala Phe Pro Thr Ala Glu Asp Ile
850 855 860

Phe Ala Lys Phe Gln His Leu Ser His Tyr Asp Gln His Gln Val Thr
865 870 875 880

Ala Gln Val Ser Arg Asn Val Leu Glu Gln Ile Thr Ser Phe Ala Leu
885 890 895

Gly Met Ser Tyr His Leu Pro Leu Val Gln His Val Gln Phe Ile Phe
900 905 910

Asp Leu Met Glu Tyr Ser Leu Ser Ile Ser Gly Leu Ile Asp Phe Ala
915 920 925

Ile Gln Leu Leu Asn Glu Leu Ser Val Val Glu Ala Glu Leu Leu Leu
930 935 940

Lys Ser Ser Asp Leu Val Gly Ser Tyr Thr Thr Ser Leu Cys Leu Cys
945 950 955 960

Ile Val Ala Val Leu Arg His Tyr His Ala Cys Leu Ile Leu Asn Gln
965 970 975

Asp Gln Met Ala Gln Val Phe Glu Gly Leu Cys Gly Val Val Lys His
980 985 990

Gly Met Asn Arg Ser Asp Gly Ser Ser Ala Glu Arg Cys Ile Leu Ala
995 1000 1005

Tyr Leu Tyr Asp Leu Tyr Thr Ser Cys Ser His Leu Lys Asn Lys
1010 1015 1020

Phe Gly Glu Leu Phe Ser Asp Phe Cys Ser Lys Val Lys Asn Thr
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Ile Tyr Cys Asn Val Glu Pro Ser Glu Ser Asn Met Arg Trp Ala
1040 1045 1050

Pro Glu Phe Met Ile Asp Thr Leu Glu Asn Pro Ala Ala His Thr
1055 1060 1065

Phe Thr Tyr Thr Gly Leu Gly Lys Ser Leu Ser Glu Asn Pro Ala
1070 1075 1080

Asn Arg Tyr Ser Phe Val Cys Asn Ala Leu Met His Val Cys Val
1085 1090 1095

Gly His His Asp Pro Asp Arg Val Asn Asp Ile Ala Ile Leu Cys
1100 1105 1110

Ala Glu Leu Thr Gly Tyr Cys Lys Ser Leu Ser Ala Glu Trp Leu

1115 1120 1125

Gly Val Leu Lys Ala Leu Cys Cys Ser Ser Asn Asn Gly Thr Cys
1130 1135 1140

Gly Phe Asn Asp Leu Leu Cys Asn Val Asp Val Ser Asp Leu Ser
1145 1150 1155

Phe His Asp Ser Leu Ala Thr Phe Val Ala Ile Leu Ile Ala Arg
1160 1165 1170

Gln Cys Leu Leu Leu Glu Asp Leu Ile Arg Cys Ala Ala Ile Pro
1175 1180 1185

Ser Leu Leu Asn Ala Ala Cys Ser Glu Gln Asp Ser Glu Pro Gly
1190 1195 1200

Ala Arg Leu Thr Cys Arg Ile Leu Leu His Leu Phe Lys Thr Pro
1205 1210 1215

Gln Leu Asn Pro Cys Gln Ser Asp Gly Asn Lys Pro Thr Val Gly
1220 1225 1230

Ile Arg Ser Ser Cys Asp Arg His Leu Leu Ala Ala Ser Gln Asn
1235 1240 1245

Arg Ile Val Asp Gly Ala Val Phe Ala Val Leu Lys Ala Val Phe
1250 1255 1260

Val Leu Gly Asp Ala Glu Leu Lys Gly Ser Gly Phe Thr Val Thr
1265 1270 1275

Gly Gly Thr Glu Glu Leu Pro Glu Glu Glu Gly Gly Gly Gly Ser
1280 1285 1290

Gly Gly Arg Arg Gln Gly Gly Arg Asn Ile Ser Val Glu Thr Ala
1295 1300 1305

Ser Leu Asp Val Tyr Ala Lys Tyr Val Leu Arg Ser Ile Cys Gln
1310 1315 1320

Gln Glu Trp Val Gly Glu Arg Cys Leu Lys Ser Leu Cys Glu Asp
1325 1330 1335

Ser Asn Asp Leu Gln Asp Pro Val Leu Ser Ser Ala Gln Ala Gln
1340 1345 1350

Arg Leu Met Gln Leu Ile Cys Tyr Pro His Arg Leu Leu Asp Asn
1355 1360 1365

Glu Asp Gly Glu Asn Pro Gln Arg Gln Arg Ile Lys Arg Ile Leu
1370 1375 1380

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Gln Asn Leu Asp Gln Trp Thr Met Arg Gln Ser Ser Leu Glu Leu
1385 1390 1395

Gln Leu Met Ile Lys Gln Thr Pro Asn Asn Glu Met Asn Ser Leu
1400 1405 1410

Leu Glu Asn Ile Ala Lys Ala Thr Ile Glu Val Phe Gln Arg Ser
1415 1420 1425

Ala Glu Thr Gly Ser Ser Ser Gly Ser Thr Ala Ser Asn Met Pro
1430 1435 1440

Ser Ser Ser Lys Thr Lys Pro Val Leu Ser Ser Leu Glu Arg Ser
1445 1450 1455

Gly Val Trp Leu Val Ala Pro Leu Ile Ala Lys Leu Pro Thr Ser
1460 1465 1470

Val Gln Gly His Val Leu Lys Ala Ala Gly Glu Glu Leu Glu Lys
1475 1480 1485

Gly Gln His Leu Gly Ser Ser Ser Arg Lys Glu Arg Asp Arg Gln
1490 1495 1500

Lys Gln Lys Ser Met Ser Leu Leu Ser Gln Gln Pro Phe Leu Ser
1505 1510 1515

Leu Val Leu Thr Cys Leu Lys Gly Gln Asp Glu Gln Arg Glu Gly
1520 1525 1530

Leu Leu Thr Ser Leu Tyr Ser Gln Val His Gln Ile Val Asn Asn
1535 1540 1545

Trp Arg Asp Asp Gln Tyr Leu Asp Asp Cys Lys Pro Lys Gln Leu
1550 1555 1560

Met His Glu Ala Leu Lys Leu Arg Leu Asn Leu Val Gly Gly Met
1565 1570 1575

Phe Asp Thr Val Gln Arg Ser Thr Gln Gln Thr Thr Glu Trp Ala
1580 1585 1590

Met Leu Leu Leu Glu Ile Ile Ile Ser Gly Thr Val Asp Met Gln
1595 1600 1605

Ser Asn Asn Glu Leu Phe Thr Thr Val Leu Asp Met Leu Ser Val
1610 1615 1620

Leu Ile Asn Gly Thr Leu Ala Ala Asp Met Ser Ser Ile Ser Gln
1625 1630 1635

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Gly Ser Met Glu Glu Asn Lys Arg Ala Tyr Met Asn Leu Ala Lys
1640 1645 1650

Lys Leu Gln Lys Glu Leu Gly Glu Arg Gln Ser Asp Ser Leu Glu
1655 1660 1665

Lys Val Arg Gln Leu Leu Pro Leu Pro Lys Gln Thr Arg Asp Val
1670 1675 1680

Ile Thr Cys Glu Pro Gln Gly Ser Leu Ile Asp Thr Lys Gly Asn
1685 1690 1695

Lys Ile Ala Gly Phe Asp Ser Ile Phe Lys Lys Glu Gly Leu Gln
1700 1705 1710

Val Ser Thr Lys Gln Lys Ile Ser Pro Trp Asp Leu Phe Glu Gly
1715 1720 1725

Leu Lys Pro Ser Ala Pro Leu Ser Trp Gly Trp Phe Gly Thr Val
1730 1735 1740

Arg Val Asp Arg Arg Val Ala Arg Gly Glu Glu Gln Gln Arg Leu
1745 1750 1755

Leu Leu Tyr His Thr His Leu Arg Pro Arg Pro Arg Ala Tyr Tyr
1760 1765 1770

Leu Glu Pro Leu Pro Leu Pro Pro Glu Asp Glu Glu Pro Pro Ala
1775 1780 1785

Pro Thr Leu Leu Glu Pro Glu Lys Lys Ala Pro Glu Pro Pro Lys
1790 1795 1800

Thr Asp Lys Pro Gly Ala Ala Pro Pro Ser Thr Glu Glu Arg Lys
1805 1810 1815

Lys Lys Ser Thr Lys Gly Lys Lys Arg Ser Gln Pro Ala Thr Lys
1820 1825 1830

Thr Glu Asp Tyr Gly Met Gly Pro Gly Arg Ser Gly Pro Tyr Gly
1835 1840 1845

Val Thr Val Pro Pro Asp Leu Leu His His Pro Asn Pro Gly Ser
1850 1855 1860

Ile Thr His Leu Asn Tyr Arg Gln Gly Ser Ile Gly Leu Tyr Thr
1865 1870 1875

Gln Asn Gln Pro Leu Pro Ala Gly Gly Pro Arg Val Asp Pro Tyr
1880 1885 1890

Arg Pro Val Arg Leu Pro Met Gln Lys Leu Pro Thr Arg Pro Thr
1895 1900 1905

Tyr Pro Gly Val Leu Pro Thr Thr Met Thr Gly Val Met Gly Leu
1910 1915 1920

Glu Pro Ser Ser Tyr Lys Thr Ser Val Tyr Arg Gln Gln Gln Pro
1925 1930 1935

Ala Val Pro Gln Gly Gln Arg Leu Arg Gln Gln Leu Gln Ala Lys
1940 1945 1950

Ile Gln Ser Gln Gly Met Leu Gly Gln Ser Ser Val His Gln Met
1955 1960 1965

Thr Pro Ser Ser Ser Tyr Gly Leu Gln Thr Ser Gln Gly Tyr Thr
1970 1975 1980

Pro Tyr Val Ser His Val Gly Leu Gln Gln His Thr Gly Pro Ala
1985 1990 1995

Gly Thr Met Val Pro Pro Ser Tyr Ser Ser Gln Pro Tyr Gln Ser
2000 2005 2010

Thr His Pro Phe Leu Leu Ile Pro Asn Pro Ile Pro Gly Leu Ala
2015 2020 2025

Pro Val Val Val Gly Ala Leu Pro Ser Gly Ser Ile Phe Asn Lys
2030 2035 2040

Phe Leu Val Phe Leu Leu Met
2045 2050

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Tyr Phe His Leu Thr Asn Ser Trp Cys Leu Arg Arg Tyr Gly Leu Gly
20 25 30

Lys Met Ala Ala Phe Gly Ile Leu Ser Tyr Glu His Arg Pro Leu Lys
35 40 45

Arg Pro Arg Pro Arg Leu Gly Pro Pro Asp Val Tyr Pro Gln Asp Pro
50 55 60

Lys Gln Lys Glu Asp Glu Leu Thr Ala Leu Asn Val Lys Gln Gly Phe
65 70 75 80

```
Asn Asn Gln Pro Ala Val Ser Gly Asp Glu His Gly Ser Ala Lys Asn
                85                  90                  95

Val Ser Phe Asn Pro Ala Lys Ile Ser Ser Asn Phe Ser Ser Ile Ile
            100                 105                 110

Ala Glu Lys Leu Arg Cys Asn Thr Leu Pro Asp Thr Gly Arg Arg Lys
        115                 120                 125

Pro Gln Val Asn Gln Lys Asp Asn Phe Trp Leu Val Thr Ala Arg Ser
    130                 135                 140

Gln Ser Ala Ile Asn Thr Trp Phe Thr Asp Leu Ala Gly Thr Lys Pro
145                 150                 155                 160

Leu Thr Gln Leu Ala Lys Lys Val Pro Ile Phe Ser Lys Lys Glu Glu
                165                 170                 175

Val Phe Gly Tyr Leu Ala Lys Tyr Thr Val Pro Val Met Arg Ala Ala
            180                 185                 190

Trp Leu Ile Lys Met Thr Cys Ala Tyr Tyr Ala Ala Ile Ser Glu Thr
        195                 200                 205

Lys Val Lys Lys Arg His Val Asp Pro Phe Met Glu Trp Thr Gln Ile
    210                 215                 220

Ile Thr Lys Tyr Leu Trp Glu Gln Leu Gln Lys Met Ala Glu Tyr Tyr
225                 230                 235                 240

Arg Pro Gly Pro Ala Gly Ser Gly Gly Cys Gly Ser Thr Ile Gly Pro
                245                 250                 255

Leu Pro His Asp Val Glu Val Ala Ile Arg Gln Trp Asp Tyr Thr Glu
            260                 265                 270

Lys Leu Ala Met Phe Met Phe Gln Asp Gly Met Leu Asp Arg His Glu
        275                 280                 285

Phe Leu Thr Trp Val Leu Glu Cys Phe Glu Lys Ile Arg Pro Gly Glu
    290                 295                 300

Asp Glu Leu Leu Lys Leu Leu Leu Pro Leu Leu Leu Arg Tyr Ser Gly
305                 310                 315                 320

Glu Phe Val Gln Ser Ala Tyr Leu Ser Arg Arg Leu Ala Tyr Phe Cys
                325                 330                 335

Thr Arg Arg Leu Ala Leu Gln Leu Asp Gly Val Ser Ser His Ser Ser
            340                 345                 350
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His Val Ile Ser Ala Gln Ser Thr Ser Thr Leu Pro Thr Thr Pro Ala
355 360 365

Pro Gln Pro Pro Thr Ser Ser Thr Pro Ser Thr Pro Phe Ser Asp Leu
370 375 380

Leu Met Cys Pro Gln His Arg Pro Leu Val Phe Gly Leu Ser Cys Ile
385 390 395 400

Leu Gln Thr Ile Leu Leu Cys Cys Pro Ser Ala Leu Val Trp His Tyr
405 410 415

Ser Leu Thr Asp Ser Arg Ile Lys Thr Gly Ser Pro Leu Asp His Leu
420 425 430

Pro Ile Ala Pro Ser Asn Leu Pro Met Pro Glu Gly Asn Ser Ala Phe
435 440 445

Thr Gln Gln Val Arg Ala Lys Leu Arg Glu Ile Glu Gln Gln Ile Lys
450 455 460

Glu Arg Gly Gln Ala Val Glu Val Arg Trp Ser Phe Asp Lys Cys Gln
465 470 475 480

Glu Ala Thr Ala Gly Phe Thr Ile Gly Arg Val Leu His Thr Leu Glu
485 490 495

Val Leu Asp Ser His Ser Phe Glu Arg Ser Asp Phe Ser Asn Ser Leu
500 505 510

Asp Ser Leu Cys Asn Arg Ile Phe Gly Leu Gly Pro Ser Lys Asp Gly
515 520 525

His Glu Ile Ser Ser Asp Asp Asp Ala Val Val Ser Leu Leu Cys Glu
530 535 540

Trp Ala Val Ser Cys Lys Arg Ser Gly Arg His Arg Ala Met Val Val
545 550 555 560

Ala Lys Leu Leu Glu Lys Arg Gln Ala Glu Ile Glu Ala Glu Arg Cys
565 570 575

Gly Glu Ser Glu Ala Ala Asp Glu Lys Gly Ser Ile Ala Ser Gly Ser
580 585 590

Leu Ser Ala Pro Ser Ala Pro Ile Phe Gln Asp Val Leu Leu Gln Phe
595 600 605

Leu Asp Thr Gln Ala Pro Met Leu Thr Asp Pro Arg Ser Glu Ser Glu
610 615 620

Arg Val Glu Phe Phe Asn Leu Val Leu Leu Phe Cys Glu Leu Ile Arg

625 630 635 640

His Asp Val Phe Ser His Asn Met Tyr Thr Cys Thr Leu Ile Ser Arg
645 650 655

Gly Asp Leu Ala Phe Gly Ala Pro Gly Pro Arg Pro Pro Ser Pro Phe
660 665 670

Asp Asp Pro Ala Asp Asp Pro Glu His Lys Glu Ala Glu Gly Ser Ser
675 680 685

Ser Ser Lys Leu Glu Asp Pro Gly Leu Ser Glu Ser Met Asp Ile Asp
690 695 700

Pro Ser Ser Ser Val Leu Phe Glu Asp Met Glu Lys Pro Asp Phe Ser
705 710 715 720

Leu Phe Ser Pro Thr Met Pro Cys Glu Gly Lys Gly Ser Pro Ser Pro
725 730 735

Glu Lys Pro Asp Val Glu Lys Glu Val Lys Pro Pro Pro Lys Glu Lys
740 745 750

Ile Glu Gly Thr Leu Gly Val Leu Tyr Asp Gln Pro Arg His Val Gln
755 760 765

Tyr Ala Thr His Phe Pro Ile Pro Gln Glu Glu Ser Cys Ser His Glu
770 775 780

Cys Asn Gln Arg Leu Val Val Leu Phe Gly Val Gly Lys Gln Arg Asp
785 790 795 800

Asp Ala Arg His Ala Ile Lys Lys Ile Thr Lys Asp Ile Leu Lys Val
805 810 815

Leu Asn Arg Lys Gly Thr Ala Glu Thr Asp Gln Leu Ala Pro Ile Val
820 825 830

Pro Leu Asn Pro Gly Asp Leu Thr Phe Leu Gly Gly Glu Asp Gly Gln
835 840 845

Lys Arg Arg Arg Asn Arg Pro Glu Ala Phe Pro Thr Ala Glu Asp Ile
850 855 860

Phe Ala Lys Phe Gln His Leu Ser His Tyr Asp Gln His Gln Val Thr
865 870 875 880

Ala Gln Val Ser Arg Asn Val Leu Glu Gln Ile Thr Ser Phe Ala Leu
885 890 895

Gly Met Ser Tyr His Leu Pro Leu Val Gln His Val Gln Phe Ile Phe
900 905 910

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Asp Leu Met Glu Tyr Ser Leu Ser Ile Ser Gly Leu Ile Asp Phe Ala
915 920 925

Ile Gln Leu Leu Asn Glu Leu Ser Val Val Glu Ala Glu Leu Leu Leu
930 935 940

Lys Ser Ser Asp Leu Val Gly Ser Tyr Thr Thr Ser Leu Cys Leu Cys
945 950 955 960

Ile Val Ala Val Leu Arg His Tyr His Ala Cys Leu Ile Leu Asn Gln
965 970 975

Asp Gln Met Ala Gln Val Phe Glu Gly Leu Cys Gly Val Val Lys His
980 985 990

Gly Met Asn Arg Ser Asp Gly Ser Ser Ala Glu Arg Cys Ile Leu Ala
995 1000 1005

Tyr Leu Tyr Asp Leu Tyr Thr Ser Cys Ser His Leu Lys Asn Lys
1010 1015 1020

Phe Gly Glu Leu Phe Ser Asp Phe Cys Ser Lys Val Lys Asn Thr
1025 1030 1035

Ile Tyr Cys Asn Val Glu Pro Ser Glu Ser Asn Met Arg Trp Ala
1040 1045 1050

Pro Glu Phe Met Ile Asp Thr Leu Glu Asn Pro Ala Ala His Thr
1055 1060 1065

Phe Thr Tyr Thr Gly Leu Gly Lys Ser Leu Ser Glu Asn Pro Ala
1070 1075 1080

Asn Arg Tyr Ser Phe Val Cys Asn Ala Leu Met His Val Cys Val
1085 1090 1095

Gly His His Asp Pro Asp Arg Val Asn Asp Ile Ala Ile Leu Cys
1100 1105 1110

Ala Glu Leu Thr Gly Tyr Cys Lys Ser Leu Ser Ala Glu Trp Leu
1115 1120 1125

Gly Val Leu Lys Ala Leu Cys Cys Ser Ser Asn Asn Gly Thr Cys
1130 1135 1140

Gly Phe Asn Asp Leu Leu Cys Asn Val Asp Val Ser Asp Leu Ser
1145 1150 1155

Phe His Asp Ser Leu Ala Thr Phe Val Ala Ile Leu Ile Ala Arg
1160 1165 1170

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Gln Cys Leu Leu Leu Glu Asp Leu Ile Arg Cys Ala Ala Ile Pro
1175 1180 1185

Ser Leu Leu Asn Ala Ala Cys Ser Glu Gln Asp Ser Glu Pro Gly
1190 1195 1200

Ala Arg Leu Thr Cys Arg Ile Leu Leu His Leu Phe Lys Thr Pro
1205 1210 1215

Gln Leu Asn Pro Cys Gln Ser Asp Gly Asn Lys Pro Thr Val Gly
1220 1225 1230

Ile Arg Ser Ser Cys Asp Arg His Leu Leu Ala Ala Ser Gln Asn
1235 1240 1245

Arg Ile Val Asp Gly Ala Val Phe Ala Val Leu Lys Ala Val Phe
1250 1255 1260

Val Leu Gly Asp Ala Glu Leu Lys Gly Ser Gly Phe Thr Val Thr
1265 1270 1275

Gly Gly Thr Glu Glu Leu Pro Glu Glu Glu Gly Gly Gly Gly Ser
1280 1285 1290

Gly Gly Arg Arg Gln Gly Gly Arg Asn Ile Ser Val Glu Thr Ala
1295 1300 1305

Ser Leu Asp Val Tyr Ala Lys Tyr Val Leu Arg Ser Ile Cys Gln
1310 1315 1320

Gln Glu Trp Val Gly Glu Arg Cys Leu Lys Ser Leu Cys Glu Asp
1325 1330 1335

Ser Asn Asp Leu Gln Asp Pro Val Leu Ser Ser Ala Gln Ala Gln
1340 1345 1350

Arg Leu Met Gln Leu Ile Cys Tyr Pro His Arg Leu Leu Asp Asn
1355 1360 1365

Glu Asp Gly Glu Asn Pro Gln Arg Gln Arg Ile Lys Arg Ile Leu
1370 1375 1380

Gln Asn Leu Asp Pro Tyr Arg Pro Val Arg Leu Pro Met Gln Lys
1385 1390 1395

Leu Pro Thr Arg Pro Thr Tyr Pro Gly Val Leu Pro Thr Thr Met
1400 1405 1410

Thr Gly Val Met Gly Leu Glu Pro Ser Ser Tyr Lys Thr Ser Val
1415 1420 1425

Tyr Arg Gln Gln Gln Pro Ala Val Pro Gln Gly Gln Arg Leu Arg
1430 1435 1440

Gln Gln Leu Gln Gln Ser Gln Gly Met Leu Gly Gln Ser Ser Val
1445 1450 1455

His Gln Met Thr Pro Ser Ser Ser Tyr Gly Leu Gln Thr Ser Gln
1460 1465 1470

Gly Tyr Thr Pro Tyr Val Ser His Val Gly Leu Gln Gln His Thr
1475 1480 1485

Gly Pro Ala Gly Thr Met Val Pro Pro Ser Tyr Ser Ser Gln Pro
1490 1495 1500

Tyr Gln Ser Thr His Pro Ser Thr Asn Pro Thr Leu Val Asp Pro
1505 1510 1515

Thr Arg His Leu Gln Gln Arg Pro Ser Gly Tyr Val His Gln Gln
1520 1525 1530

Ala Pro Thr Tyr Gly His Gly Leu Thr Ser Thr Gln Arg Phe Ser
1535 1540 1545

His Gln Thr Leu Gln Gln Thr Pro Met Ile Ser Thr Met Thr Pro
1550 1555 1560

Met Ser Ala Gln Gly Val Gln Ala Gly Val Arg Ser Thr Ala Ile
1565 1570 1575

Leu Pro Glu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
1580 1585 1590

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Tyr
1595 1600 1605

His Ile Arg Gln Gln Gln Gln Gln Gln Ile Leu Arg Gln Gln Gln
1610 1615 1620

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
1625 1630 1635

Gln Gln Gln Gln Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln
1640 1645 1650

Gln Ala Ala Pro Pro Gln Pro Gln Pro Gln Ser Gln Pro Gln Phe
1655 1660 1665

Gln Arg Gln Gly Leu Gln Gln Thr Gln Gln Gln Gln Gln Thr Ala
1670 1675 1680

Ala Leu Val Arg Gln Leu Gln Gln Gln Leu Ser Asn Thr Gln Pro

1685 1690 1695

Gln Pro Ser Thr Asn Ile Phe Gly Arg Tyr
1700 1705

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<400> 104
Met Lys Gln Ser Met Pro Ser Leu His Thr Lys Lys Ile Leu Phe Cys
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Tyr Phe His Leu Thr Asn Ser Trp Cys Leu Arg Arg Tyr Gly Leu Gly
20 25 30

Lys Met Ala Ala Phe Gly Ile Leu Ser Tyr Glu His Arg Pro Leu Lys
35 40 45

Arg Pro Arg Pro Arg Leu Gly Pro Pro Asp Val Tyr Pro Gln Asp Pro
50 55 60

Lys Gln Lys Glu Asp Glu Leu Thr Ala Leu Asn Val Lys Gln Gly Phe
65 70 75 80

Asn Asn Gln Pro Ala Val Ser Gly Asp Glu His Gly Ser Ala Lys Asn
85 90 95

Val Ser Phe Asn Pro Ala Lys Ile Ser Ser Asn Phe Ser Ser Ile Ile
100 105 110

Ala Glu Lys Leu Arg Cys Asn Thr Leu Pro Asp Thr Gly Arg Arg Lys
115 120 125

Pro Gln Val Asn Gln Lys Asp Asn Phe Trp Leu Val Thr Ala Arg Ser
130 135 140

Gln Ser Ala Ile Asn Thr Trp Phe Thr Asp Leu Ala Gly Thr Lys Pro
145 150 155 160

Leu Thr Gln Leu Ala Lys Lys Val Pro Ile Phe Ser Lys Lys Glu Glu
165 170 175

Val Phe Gly Tyr Leu Ala Lys Tyr Thr Val Pro Val Met Arg Ala Ala
180 185 190

Trp Leu Ile Lys Met Thr Cys Ala Tyr Tyr Ala Ala Ile Ser Glu Thr
195 200 205

Lys Val Lys Lys Arg His Val Asp Pro Phe Met Glu Trp Thr Gln Ile
210 215 220

Ile Thr Lys Tyr Leu Trp Glu Gln Leu Gln Lys Met Ala Glu Tyr Tyr
225 230 235 240

Arg Pro Gly Pro Ala Gly Ser Gly Gly Cys Gly Ser Thr Ile Gly Pro
245 250 255

Leu Pro His Asp Val Glu Val Ala Ile Arg Gln Trp Asp Tyr Thr Glu
260 265 270

Lys Leu Ala Met Phe Met Phe Gln Asp Gly Met Leu Asp Arg His Glu
275 280 285

Phe Leu Thr Trp Val Leu Glu Cys Phe Glu Lys Ile Arg Pro Gly Glu
290 295 300

Asp Glu Leu Leu Lys Leu Leu Leu Pro Leu Leu Leu Arg Tyr Ser Gly
305 310 315 320

Glu Phe Val Gln Ser Ala Tyr Leu Ser Arg Arg Leu Ala Tyr Phe Cys
325 330 335

Thr Arg Arg Leu Ala Leu Gln Leu Asp Gly Val Ser Ser His Ser Ser
340 345 350

His Val Ile Ser Ala Gln Ser Thr Ser Thr Leu Pro Thr Thr Pro Ala
355 360 365

Pro Gln Pro Pro Thr Ser Ser Thr Pro Ser Thr Pro Phe Ser Asp Leu
370 375 380

Leu Met Cys Pro Gln His Arg Pro Leu Val Phe Gly Leu Ser Cys Ile
385 390 395 400

Leu Gln Thr Ile Leu Leu Cys Cys Pro Ser Ala Leu Val Trp His Tyr
405 410 415

Ser Leu Thr Asp Ser Arg Ile Lys Thr Gly Ser Pro Leu Asp His Leu
420 425 430

Pro Ile Ala Pro Ser Asn Leu Pro Met Pro Glu Gly Asn Ser Ala Phe
435 440 445

Thr Gln Gln Val Arg Ala Lys Leu Arg Glu Ile Glu Gln Gln Ile Lys
450 455 460

Glu Arg Gly Gln Ala Val Glu Val Arg Trp Ser Phe Asp Lys Cys Gln
465 470 475 480

Glu Ala Thr Ala Gly Phe Thr Ile Gly Arg Val Leu His Thr Leu Glu
485 490 495

Val Leu Asp Ser His Ser Phe Glu Arg Ser Asp Phe Ser Asn Ser Leu

500 505 510

Asp Ser Leu Cys Asn Arg Ile Phe Gly Leu Gly Pro Ser Lys Asp Gly
515 520 525

His Glu Ile Ser Ser Asp Asp Asp Ala Val Val Ser Leu Leu Cys Glu
530 535 540

Trp Ala Val Ser Cys Lys Arg Ser Gly Arg His Arg Ala Met Val Val
545 550 555 560

Ala Lys Leu Leu Glu Lys Arg Gln Ala Glu Ile Glu Ala Glu Arg Cys
565 570 575

Gly Glu Ser Glu Ala Ala Asp Glu Lys Gly Ser Ile Ala Ser Gly Ser
580 585 590

Leu Ser Ala Pro Ser Ala Pro Ile Phe Gln Asp Val Leu Leu Gln Phe
595 600 605

Leu Asp Thr Gln Ala Pro Met Leu Thr Asp Pro Arg Ser Glu Ser Glu
610 615 620

Arg Val Glu Phe Phe Asn Leu Val Leu Leu Phe Cys Glu Leu Ile Arg
625 630 635 640

His Asp Val Phe Ser His Asn Met Tyr Thr Cys Thr Leu Ile Ser Arg
645 650 655

Gly Asp Leu Ala Phe Gly Ala Pro Gly Pro Arg Pro Pro Ser Pro Phe
660 665 670

Asp Asp Pro Ala Asp Asp Pro Glu His Lys Glu Ala Glu Gly Ser Ser
675 680 685

Ser Ser Lys Leu Glu Asp Pro Gly Leu Ser Glu Ser Met Asp Ile Asp
690 695 700

Pro Ser Ser Ser Val Leu Phe Glu Asp Met Glu Lys Pro Asp Phe Ser
705 710 715 720

Leu Phe Ser Pro Thr Met Pro Cys Glu Gly Lys Gly Ser Pro Ser Pro
725 730 735

Glu Lys Pro Asp Val Glu Lys Glu Val Lys Pro Pro Pro Lys Glu Lys
740 745 750

Ile Glu Gly Thr Leu Gly Val Leu Tyr Asp Gln Pro Arg His Val Gln
755 760 765

Tyr Ala Thr His Phe Pro Ile Pro Gln Glu Glu Ser Cys Ser His Glu
770 775 780

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Cys Asn Gln Arg Leu Val Val Leu Phe Gly Val Gly Lys Gln Arg Asp
785 790 795 800

Asp Ala Arg His Ala Ile Lys Lys Ile Thr Lys Asp Ile Leu Lys Val
805 810 815

Leu Asn Arg Lys Gly Thr Ala Glu Thr Asp Gln Leu Ala Pro Ile Val
820 825 830

Pro Leu Asn Pro Gly Asp Leu Thr Phe Leu Gly Gly Glu Asp Gly Gln
835 840 845

Lys Arg Arg Arg Asn Arg Pro Glu Ala Phe Pro Thr Ala Glu Asp Ile
850 855 860

Phe Ala Lys Phe Gln His Leu Ser His Tyr Asp Gln His Gln Val Thr
865 870 875 880

Ala Gln Val Ser Arg Asn Val Leu Glu Gln Ile Thr Ser Phe Ala Leu
885 890 895

Gly Met Ser Tyr His Leu Pro Leu Val Gln His Val Gln Phe Ile Phe
900 905 910

Asp Leu Met Glu Tyr Ser Leu Ser Ile Ser Gly Leu Ile Asp Phe Ala
915 920 925

Ile Gln Leu Leu Asn Glu Leu Ser Val Val Glu Ala Glu Leu Leu Leu
930 935 940

Lys Ser Ser Asp Leu Val Gly Ser Tyr Thr Thr Ser Leu Cys Leu Cys
945 950 955 960

Ile Val Ala Val Leu Arg His Tyr His Ala Cys Leu Ile Leu Asn Gln
965 970 975

Asp Gln Met Ala Gln Val Phe Glu Gly Leu Cys Gly Val Val Lys His
980 985 990

Gly Met Asn Arg Ser Asp Gly Ser Ser Ala Glu Arg Cys Ile Leu Ala
995 1000 1005

Tyr Leu Tyr Asp Leu Tyr Thr Ser Cys Ser His Leu Lys Asn Lys
1010 1015 1020

Phe Gly Glu Leu Phe Ser Asp Phe Cys Ser Lys Val Lys Asn Thr
1025 1030 1035

Ile Tyr Cys Asn Val Glu Pro Ser Glu Ser Asn Met Arg Trp Ala
1040 1045 1050

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Pro Glu Phe Met Ile Asp Thr Leu Glu Asn Pro Ala Ala His Thr
1055 1060 1065

Phe Thr Tyr Thr Gly Leu Gly Lys Ser Leu Ser Glu Asn Pro Ala
1070 1075 1080

Asn Arg Tyr Ser Phe Val Cys Asn Ala Leu Met His Val Cys Val
1085 1090 1095

Gly His His Asp Pro Asp Arg Val Asn Asp Ile Ala Ile Leu Cys
1100 1105 1110

Ala Glu Leu Thr Gly Tyr Cys Lys Ser Leu Ser Ala Glu Trp Leu
1115 1120 1125

Gly Val Leu Lys Ala Leu Cys Cys Ser Ser Asn Asn Gly Thr Cys
1130 1135 1140

Gly Phe Asn Asp Leu Leu Cys Asn Val Asp Val Ser Asp Leu Ser
1145 1150 1155

Phe His Asp Ser Leu Ala Thr Phe Val Ala Ile Leu Ile Ala Arg
1160 1165 1170

Gln Cys Leu Leu Leu Glu Asp Leu Ile Arg Cys Ala Ala Ile Pro
1175 1180 1185

Ser Leu Leu Asn Ala Ala Cys Ser Glu Gln Asp Ser Glu Pro Gly
1190 1195 1200

Ala Arg Leu Thr Cys Arg Ile Leu Leu His Leu Phe Lys Thr Pro
1205 1210 1215

Gln Leu Asn Pro Cys Gln Ser Asp Gly Asn Lys Pro Thr Val Gly
1220 1225 1230

Ile Arg Ser Ser Cys Asp Arg His Leu Leu Ala Ala Ser Gln Asn
1235 1240 1245

Arg Ile Val Asp Gly Ala Val Phe Ala Val Leu Lys Ala Val Phe
1250 1255 1260

Val Leu Gly Asp Ala Glu Leu Lys Gly Ser Gly Phe Thr Val Thr
1265 1270 1275

Gly Gly Thr Glu Glu Leu Pro Glu Glu Glu Gly Gly Gly Gly Ser
1280 1285 1290

Gly Gly Arg Arg Gln Gly Gly Arg Asn Ile Ser Val Glu Thr Ala
1295 1300 1305

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Ser Leu Asp Val Tyr Ala Lys Tyr Val Leu Arg Ser Ile Cys Gln
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Gln Glu Trp Val Gly Glu Arg Cys Leu Lys Ser Leu Cys Glu Asp
1325 1330 1335

Ser Asn Asp Leu Gln Asp Pro Val Leu Ser Ser Ala Gln Ala Gln
1340 1345 1350

Arg Leu Met Gln Leu Ile Cys Tyr Pro His Arg Leu Leu Asp Asn
1355 1360 1365

Glu Asp Gly Glu Asn Pro Gln Arg Gln Arg Ile Lys Arg Ile Leu
1370 1375 1380

Gln Asn Leu Asp Gln Trp Thr Met Arg Gln Ser Ser Leu Glu Leu
1385 1390 1395

Gln Leu Met Ile Lys Gln Thr Pro Asn Asn Glu Met Asn Ser Leu
1400 1405 1410

Leu Glu Asn Ile Ala Lys Ala Thr Ile Glu Val Phe Gln Arg Ser
1415 1420 1425

Ala Glu Thr Gly Ser Ser Ser Gly Ser Thr Ala Ser Asn Met Pro
1430 1435 1440

Ser Ser Ser Lys Thr Lys Pro Val Leu Ser Ser Leu Glu Arg Ser
1445 1450 1455

Gly Val Trp Leu Val Ala Pro Leu Ile Ala Lys Leu Pro Thr Ser
1460 1465 1470

Val Gln Gly His Val Leu Lys Ala Ala Gly Glu Glu Leu Glu Lys
1475 1480 1485

Gly Gln His Leu Gly Ser Ser Ser Arg Lys Glu Arg Asp Arg Gln
1490 1495 1500

Lys Gln Lys Ser Met Ser Leu Leu Ser Gln Gln Pro Phe Leu Ser
1505 1510 1515

Leu Val Leu Thr Cys Leu Lys Gly Gln Asp Glu Gln Arg Glu Gly
1520 1525 1530

Leu Leu Thr Ser Leu Tyr Ser Gln Val His Gln Ile Val Asn Asn
1535 1540 1545

Trp Arg Asp Asp Gln Tyr Leu Asp Asp Cys Lys Pro Lys Gln Leu
1550 1555 1560

Met His Glu Ala Leu Lys Leu Arg Leu Asn Leu Val Gly Gly Met

1565 1570 1575

Phe Asp Thr Val Gln Arg Ser Thr Gln Gln Thr Thr Glu Trp Ala
1580 1585 1590

Met Leu Leu Leu Glu Ile Ile Ile Ser Gly Thr Val Asp Met Gln
1595 1600 1605

Ser Asn Asn Glu Leu Phe Thr Thr Val Leu Asp Met Leu Ser Val
1610 1615 1620

Leu Ile Asn Gly Thr Leu Ala Ala Asp Met Ser Ser Ile Ser Gln
1625 1630 1635

Gly Ser Met Glu Glu Asn Lys Arg Ala Tyr Met Asn Leu Ala Lys
1640 1645 1650

Lys Leu Gln Lys Glu Leu Gly Glu Arg Gln Ser Asp Ser Leu Glu
1655 1660 1665

Lys Val Arg Gln Leu Leu Pro Leu Pro Lys Gln Thr Arg Asp Val
1670 1675 1680

Ile Thr Cys Glu Pro Gln Gly Ser Leu Ile Asp Thr Lys Gly Asn
1685 1690 1695

Lys Ile Ala Gly Phe Asp Ser Ile Phe Lys Lys Glu Gly Leu Gln
1700 1705 1710

Val Ser Thr Lys Gln Lys Ile Ser Pro Trp Asp Leu Phe Glu Gly
1715 1720 1725

Leu Lys Pro Ser Ala Pro Leu Ser Trp Gly Trp Phe Gly Thr Val
1730 1735 1740

Arg Val Asp Arg Arg Val Ala Arg Gly Glu Glu Gln Gln Arg Leu
1745 1750 1755

Leu Leu Tyr His Thr His Leu Arg Pro Arg Pro Gln Ser Gln Pro
1760 1765 1770

Gln Phe Gln Arg Gln Gly Leu Gln Gln Thr Gln Gln Gln Gln Gln
1775 1780 1785

Thr Ala Ala Leu Val Arg Gln Leu Gln Gln Gln Leu Ser Asn Thr
1790 1795 1800

Gln Pro Gln Pro Ser Thr Asn Ile Phe Gly Arg Tyr
1805 1810 1815

<210> 105
<211> 2137

<212> PRT
<213> Homo sapiens

<400> 105

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Cys Asn Leu Phe Cys Leu Ala Asp Leu Thr Gly Ile Lys Trp Lys Lys
            20                  25                  30

Tyr Val Trp Gln Gly Pro Thr Ser Ala Pro Ile Leu Phe Pro Val Thr
        35                  40                  45

Glu Glu Asp Pro Ile Leu Ser Ser Phe Ser Arg Cys Leu Lys Ala Asp
    50                  55                  60

Val Leu Gly Val Trp Arg Arg Asp Gln Arg Pro Gly Arg Arg Glu Leu
65                  70                  75                  80

Trp Ile Phe Trp Trp Gly Glu Asp Pro Val Leu Leu Thr Leu Phe Thr
                85                  90                  95

Met Thr Tyr Gln Lys Lys Lys Met Glu Cys Gly Arg Met Asp Phe Pro
            100                 105                 110

Met Asn Ala Val Leu Cys Phe Ser Lys Ala Val His Asn Leu Leu Glu
        115                 120                 125

Arg Cys Leu Met Asn Arg Asn Phe Val Arg Ile Gly Lys Trp Phe Val
    130                 135                 140

Lys Pro Tyr Glu Lys Asp Glu Lys Pro Ile Asn Lys Ser Glu His Leu
145                 150                 155                 160

Ser Cys Ser Phe Thr Phe Phe Leu His Gly Asp Ser Asn Val Cys Thr
                165                 170                 175

Ser Val Glu Ile Asn Gln His Gln Pro Val Tyr Leu Leu Ser Glu Glu
            180                 185                 190

His Ile Thr Leu Ala Gln Gln Ser Asn Ser Pro Phe Gln Val Ile Leu
        195                 200                 205

Cys Pro Phe Gly Leu Asn Gly Thr Leu Thr Gly Gln Ala Phe Lys Met
    210                 215                 220

Ser Asp Ser Ala Thr Lys Lys Leu Ile Gly Glu Trp Lys Gln Phe Tyr
225                 230                 235                 240

Pro Ile Ser Cys Cys Leu Lys Glu Met Ser Glu Glu Lys Gln Glu Asp
                245                 250                 255

Met Asp Trp Glu Asp Asp Ser Leu Ala Ala Val Glu Val Leu Val Ala
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260 265 270

Gly Val Arg Met Ile Tyr Pro Ala Cys Phe Val Leu Val Pro Gln Ser
275 280 285

Asp Ile Pro Thr Pro Ser Pro Val Gly Ser Thr His Cys Ser Ser Ser
290 295 300

Cys Leu Gly Val His Gln Val Pro Ala Ser Thr Arg Asp Pro Ala Met
305 310 315 320

Ser Ser Val Thr Leu Thr Pro Pro Thr Ser Pro Glu Glu Val Gln Thr
325 330 335

Val Asp Pro Gln Ser Val Gln Lys Trp Val Lys Phe Ser Ser Val Ser
340 345 350

Asp Gly Phe Asn Ser Asp Ser Thr Ser His His Gly Gly Lys Ile Pro
355 360 365

Arg Lys Leu Ala Asn His Val Val Asp Arg Val Trp Gln Glu Cys Asn
370 375 380

Met Asn Arg Ala Gln Asn Lys His Lys Asn Leu Lys Ser Arg Asn Ala
385 390 395 400

Gly Gln Gln Gly Gln Ala Pro Ser Leu Gly Gln Gln Gln Gln Ile Leu
405 410 415

Pro Lys His Lys Thr Asn Glu Lys Gln Glu Lys Ser Glu Lys Pro Gln
420 425 430

Lys Arg Pro Leu Thr Pro Phe His His Arg Val Ser Val Ser Asp Asp
435 440 445

Val Gly Met Asp Ala Asp Ser Ala Ser Gln Arg Leu Val Ile Ser Ala
450 455 460

Pro Asp Ser Gln Val Arg Phe Ser Asn Ile Arg Thr Asn Asp Val Ala
465 470 475 480

Lys Thr Pro Gln Met His Gly Thr Glu Met Ala Asn Ser Pro Gln Pro
485 490 495

Pro Pro Leu Ser Pro His Pro Cys Asp Val Val Asp Glu Gly Val Thr
500 505 510

Lys Thr Pro Ser Thr Pro Gln Ser Gln His Phe Tyr Gln Met Pro Thr
515 520 525

Pro Asp Pro Leu Val Pro Ser Lys Pro Met Glu Asp Arg Ile Asp Ser
530 535 540

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

Val Tyr Val Gly Thr Ala Val Asn Leu Glu Glu Asp Glu Ala Asn Ile
565 570 575

Ala Trp Lys Tyr Tyr Lys Phe Pro Lys Lys Lys Asp Val Glu Phe Leu
580 585 590

Pro Pro Gln Leu Pro Ser Asp Lys Phe Lys Asp Asp Pro Val Gly Pro
595 600 605

Phe Gly Gln Glu Ser Val Thr Ser Val Thr Glu Leu Met Val Gln Cys
610 615 620

Lys Lys Pro Leu Lys Val Ser Asp Glu Leu Val Gln Gln Tyr Gln Ile
625 630 635 640

Lys Asn Gln Cys Leu Ser Ala Ile Ala Ser Asp Ala Glu Gln Glu Pro
645 650 655

Lys Ile Asp Pro Tyr Ala Phe Val Glu Gly Asp Glu Glu Phe Leu Phe
660 665 670

Pro Asp Lys Lys Asp Arg Gln Asn Ser Glu Arg Glu Ala Gly Lys Lys
675 680 685

His Lys Val Glu Asp Gly Thr Ser Ser Val Thr Val Leu Ser His Glu
690 695 700

Glu Asp Ala Met Ser Leu Phe Ser Pro Ser Ile Lys Gln Asp Ala Pro
705 710 715 720

Arg Pro Thr Ser His Ala Arg Pro Pro Ser Thr Ser Leu Ile Tyr Asp
725 730 735

Ser Asp Leu Ala Val Ser Tyr Thr Asp Leu Asp Asn Leu Phe Asn Ser
740 745 750

Asp Glu Asp Glu Leu Thr Pro Gly Ser Lys Arg Ser Ala Asn Gly Ser
755 760 765

Asp Asp Lys Ala Ser Cys Lys Glu Ser Lys Thr Gly Asn Leu Asp Pro
770 775 780

Leu Ser Cys Ile Ser Thr Ala Asp Leu His Lys Met Tyr Pro Thr Pro
785 790 795 800

Pro Ser Leu Glu Gln His Ile Met Gly Phe Ser Pro Met Asn Met Asn
805 810 815

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Asn Lys Glu Tyr Gly Ser Met Asp Thr Thr Pro Gly Gly Thr Val Leu
            820                 825                 830

Glu Gly Asn Ser Ser Ser Ile Gly Ala Gln Phe Lys Ile Glu Val Asp
        835                 840                 845

Glu Gly Phe Cys Ser Pro Lys Pro Ser Glu Ile Lys Asp Phe Ser Tyr
    850                 855                 860

Val Tyr Lys Pro Glu Asn Cys Gln Ile Leu Val Gly Cys Ser Met Phe
865                 870                 875                 880

Ala Pro Leu Lys Thr Leu Pro Ser Gln Tyr Leu Pro Leu Ile Lys Leu
                885                 890                 895

Pro Glu Glu Cys Ile Tyr Arg Gln Ser Trp Thr Val Gly Lys Leu Glu
            900                 905                 910

Leu Leu Ser Ser Gly Pro Ser Met Pro Phe Ile Lys Glu Gly Asp Gly
        915                 920                 925

Ser Asn Met Asp Gln Glu Tyr Gly Thr Ala Tyr Thr Pro Gln Thr His
    930                 935                 940

Thr Ser Cys Gly Met Pro Pro Ser Ser Ala Pro Pro Ser Asn Ser Gly
945                 950                 955                 960

Ala Gly Ile Leu Pro Ser Pro Ser Thr Pro Arg Phe Pro Thr Pro Arg
                965                 970                 975

Thr Pro Arg Thr Pro Arg Thr Pro Arg Gly Ala Gly Gly Pro Ala Ser
            980                 985                 990

Ala Gln Gly Ser Val Lys Tyr Glu  Asn Ser Asp Leu Tyr  Ser Pro Ala
        995                 1000                1005

Ser Thr  Pro Ser Thr Cys Arg  Pro Leu Asn Ser Val  Glu Pro Ala
    1010                1015                1020

Thr Val  Pro Ser Ile Pro Glu  Ala His Ser Leu Tyr  Val Asn Leu
    1025                1030                1035

Ile Leu  Ser Glu Ser Val Met  Asn Leu Phe Lys Asp  Cys Asn Ser
    1040                1045                1050

Asp Ser  Cys Cys Ile Cys Val  Cys Asn Met Asn Ile  Lys Gly Ala
    1055                1060                1065

Asp Val  Gly Val Tyr Ile Pro  Asp Pro Thr Gln Glu  Ala Gln Tyr
    1070                1075                1080
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Arg Cys Thr Cys Gly Phe Ser Ala Val Met Asn Arg Lys Phe Gly
1085 1090 1095

Asn Asn Ser Gly Leu Phe Leu Glu Asp Glu Leu Asp Ile Ile Gly
1100 1105 1110

Arg Asn Thr Asp Cys Gly Lys Glu Ala Glu Lys Arg Phe Glu Ala
1115 1120 1125

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

Ser Glu Lys Leu Ser Asp Asp Leu Ile Leu Leu Leu Gln Asp Gln
1145 1150 1155

Cys Thr Asn Leu Phe Ser Pro Phe Gly Ala Ala Asp Gln Asp Pro
1160 1165 1170

Phe Pro Lys Ser Gly Val Ile Ser Asn Trp Val Arg Val Glu Glu
1175 1180 1185

Arg Asp Cys Cys Asn Asp Cys Tyr Leu Ala Leu Glu His Gly Arg
1190 1195 1200

Gln Phe Met Asp Asn Met Ser Gly Gly Lys Val Asp Glu Ala Leu
1205 1210 1215

Val Lys Ser Ser Cys Leu His Pro Trp Ser Lys Arg Asn Asp Val
1220 1225 1230

Ser Met Gln Cys Ser Gln Asp Ile Leu Arg Met Leu Leu Ser Leu
1235 1240 1245

Gln Pro Val Leu Gln Asp Ala Ile Gln Lys Lys Arg Thr Val Arg
1250 1255 1260

Pro Trp Gly Val Gln Gly Pro Leu Thr Trp Gln Gln Phe His Lys
1265 1270 1275

Met Ala Gly Arg Gly Ser Tyr Gly Thr Asp Glu Ser Pro Glu Pro
1280 1285 1290

Leu Pro Ile Pro Thr Phe Leu Leu Gly Tyr Asp Tyr Asp Tyr Leu
1295 1300 1305

Val Leu Ser Pro Phe Ala Leu Pro Tyr Trp Glu Arg Leu Met Leu
1310 1315 1320

Glu Pro Tyr Gly Ser Gln Arg Asp Ile Ala Tyr Val Val Leu Cys
1325 1330 1335

Pro Glu Asn Glu Ala Leu Leu Asn Gly Ala Lys Ser Phe Phe Arg

1340 1345 1350

Asp Leu Thr Ala Ile Tyr Glu Ser Cys Arg Leu Gly Gln His Arg
1355 1360 1365

Pro Val Ser Arg Leu Leu Thr Asp Gly Ile Met Arg Val Gly Ser
1370 1375 1380

Thr Ala Ser Lys Lys Leu Ser Glu Lys Leu Val Ala Glu Trp Phe
1385 1390 1395

Ser Gln Ala Ala Asp Gly Asn Asn Glu Ala Phe Ser Lys Leu Lys
1400 1405 1410

Leu Tyr Ala Gln Val Cys Arg Tyr Asp Leu Gly Pro Tyr Leu Ala
1415 1420 1425

Ser Leu Pro Leu Asp Ser Ser Leu Leu Ser Gln Pro Asn Leu Val
1430 1435 1440

Ala Pro Thr Ser Gln Ser Leu Ile Thr Pro Pro Gln Met Thr Asn
1445 1450 1455

Thr Gly Asn Ala Asn Thr Pro Ser Ala Thr Leu Ala Ser Ala Ala
1460 1465 1470

Ser Ser Thr Met Thr Val Thr Ser Gly Val Ala Ile Ser Thr Ser
1475 1480 1485

Val Ala Thr Ala Asn Ser Thr Leu Thr Thr Ala Ser Thr Ser Ser
1490 1495 1500

Ser Ser Ser Ser Asn Leu Asn Ser Gly Val Ser Ser Asn Lys Leu
1505 1510 1515

Pro Ser Phe Pro Pro Phe Gly Ser Met Asn Ser Asn Ala Ala Gly
1520 1525 1530

Ser Met Ser Thr Gln Ala Asn Thr Val Gln Ser Gly Gln Leu Gly
1535 1540 1545

Gly Gln Gln Thr Ser Ala Leu Gln Thr Ala Gly Ile Ser Gly Glu
1550 1555 1560

Ser Ser Ser Leu Pro Thr Gln Pro His Pro Asp Val Ser Glu Ser
1565 1570 1575

Thr Met Asp Arg Asp Lys Val Gly Ile Pro Thr Asp Gly Asp Ser
1580 1585 1590

His Ala Val Thr Tyr Pro Pro Ala Ile Val Val Tyr Ile Ile Asp
1595 1600 1605

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Pro Phe Thr Tyr Glu Asn Thr Asp Glu Ser Thr Asn Ser Ser Ser
1610 1615 1620

Val Trp Thr Leu Gly Leu Leu Arg Cys Phe Leu Glu Met Val Gln
1625 1630 1635

Thr Leu Pro Pro His Ile Lys Ser Thr Val Ser Val Gln Ile Ile
1640 1645 1650

Pro Cys Gln Tyr Leu Leu Gln Pro Val Lys His Glu Asp Arg Glu
1655 1660 1665

Ile Tyr Pro Gln His Leu Lys Ser Leu Ala Phe Ser Ala Phe Thr
1670 1675 1680

Gln Cys Arg Arg Pro Leu Pro Thr Ser Thr Asn Val Lys Thr Leu
1685 1690 1695

Thr Gly Phe Gly Pro Gly Leu Ala Met Glu Thr Ala Leu Arg Ser
1700 1705 1710

Pro Asp Arg Pro Glu Cys Ile Arg Leu Tyr Ala Pro Pro Phe Ile
1715 1720 1725

Leu Ala Pro Val Lys Asp Lys Gln Thr Glu Leu Gly Glu Thr Phe
1730 1735 1740

Gly Glu Ala Gly Gln Lys Tyr Asn Val Leu Phe Val Gly Tyr Cys
1745 1750 1755

Leu Ser His Asp Gln Arg Trp Ile Leu Ala Ser Cys Thr Asp Leu
1760 1765 1770

Tyr Gly Glu Leu Leu Glu Thr Cys Ile Ile Asn Ile Asp Val Pro
1775 1780 1785

Asn Arg Ala Arg Arg Lys Lys Ser Ser Ala Arg Lys Phe Gly Leu
1790 1795 1800

Gln Lys Leu Trp Glu Trp Cys Leu Gly Leu Val Gln Met Ser Ser
1805 1810 1815

Leu Pro Trp Arg Val Val Ile Gly Arg Leu Gly Arg Ile Gly His
1820 1825 1830

Gly Glu Leu Lys Asp Trp Ser Cys Leu Leu Ser Arg Arg Asn Leu
1835 1840 1845

Gln Ser Leu Ser Lys Arg Leu Lys Asp Met Cys Arg Met Cys Gly
1850 1855 1860

Ile Ser Ala Ala Asp Ser Pro Ser Ile Leu Ser Ala Cys Leu Val
1865 1870 1875

Ala Met Glu Pro Gln Gly Ser Phe Val Ile Met Pro Asp Ser Val
1880 1885 1890

Ser Thr Gly Ser Val Phe Gly Arg Ser Thr Thr Leu Asn Met Gln
1895 1900 1905

Thr Ser Gln Leu Asn Thr Pro Gln Asp Thr Ser Cys Thr His Ile
1910 1915 1920

Leu Val Phe Pro Thr Ser Ala Ser Val Gln Val Ala Ser Ala Thr
1925 1930 1935

Tyr Thr Thr Glu Asn Leu Asp Leu Ala Phe Asn Pro Asn Asn Asp
1940 1945 1950

Gly Ala Asp Gly Met Gly Ile Phe Asp Leu Leu Asp Thr Gly Asp
1955 1960 1965

Asp Leu Asp Pro Asp Ile Ile Asn Ile Leu Pro Ala Ser Pro Thr
1970 1975 1980

Gly Ser Pro Val His Ser Pro Gly Ser His Tyr Pro His Gly Gly
1985 1990 1995

Asp Ala Gly Lys Gly Gln Ser Thr Asp Arg Leu Leu Ser Thr Glu
2000 2005 2010

Pro His Glu Glu Val Pro Asn Ile Leu Gln Gln Pro Leu Ala Leu
2015 2020 2025

Gly Tyr Phe Val Ser Thr Ala Lys Ala Gly Pro Leu Pro Asp Trp
2030 2035 2040

Phe Trp Ser Ala Cys Pro Gln Ala Gln Tyr Gln Cys Pro Leu Phe
2045 2050 2055

Leu Lys Ala Ser Leu His Leu His Val Pro Ser Val Gln Ser Asp
2060 2065 2070

Glu Leu Leu His Ser Lys His Ser His Pro Leu Asp Ser Asn Gln
2075 2080 2085

Thr Ser Asp Val Leu Arg Phe Val Leu Glu Gln Tyr Asn Ala Leu
2090 2095 2100

Ser Trp Leu Thr Cys Asp Pro Ala Thr Gln Asp Arg Arg Ser Cys
2105 2110 2115

Leu Pro Ile His Phe Val Val Leu Asn Gln Leu Tyr Asn Phe Ile
2120 2125 2130

Met Asn Met Leu
2135

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<213> Homo sapiens

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Cys Asn Leu Phe Cys Leu Ala Asp Leu Thr Gly Ile Lys Trp Lys Lys
20 25 30

Tyr Val Trp Gln Gly Pro Thr Ser Ala Pro Ile Leu Phe Pro Val Thr
35 40 45

Glu Glu Asp Pro Ile Leu Ser Ser Phe Ser Arg Cys Leu Lys Ala Asp
50 55 60

Val Leu Gly Val Trp Arg Arg Asp Gln Arg Pro Gly Arg Arg Glu Leu
65 70 75 80

Trp Ile Phe Trp Trp Gly Glu Asp Pro Val Leu Leu Thr Leu Phe Thr
85 90 95

Met Thr Tyr Gln Lys Lys Lys Met Glu Cys Gly Arg Met Asp Phe Pro
100 105 110

Met Asn Ala Val Leu Cys Phe Ser Lys Ala Val His Asn Leu Leu Glu
115 120 125

Arg Cys Leu Met Asn Arg Asn Phe Val Arg Ile Gly Lys Trp Phe Val
130 135 140

Lys Pro Tyr Glu Lys Asp Glu Lys Pro Ile Asn Lys Ser Glu His Leu
145 150 155 160

Ser Cys Ser Phe Thr Phe Phe Leu His Gly Asp Ser Asn Val Cys Thr
165 170 175

Ser Val Glu Ile Asn Gln His Gln Pro Val Tyr Leu Leu Ser Glu Glu
180 185 190

His Ile Thr Leu Ala Gln Gln Ser Asn Ser Pro Phe Gln Val Ile Leu
195 200 205

Cys Pro Phe Gly Leu Asn Gly Thr Leu Thr Gly Gln Ala Phe Lys Met
210 215 220

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Ser Asp Ser Ala Thr Lys Lys Leu Ile Gly Glu Trp Lys Gln Phe Tyr
225                 230                 235                 240

Pro Ile Ser Cys Cys Leu Lys Glu Met Ser Glu Glu Lys Gln Glu Asp
                245                 250                 255

Met Asp Trp Glu Asp Asp Ser Leu Ala Ala Val Glu Val Leu Val Ala
            260                 265                 270

Gly Val Arg Met Ile Tyr Pro Ala Cys Phe Val Leu Val Pro Gln Ser
        275                 280                 285

Asp Ile Pro Thr Pro Ser Pro Val Gly Ser Thr His Cys Ser Ser Ser
    290                 295                 300

Cys Leu Gly Val His Gln Val Pro Ala Ser Thr Arg Asp Pro Ala Met
305                 310                 315                 320

Ser Ser Val Thr Leu Thr Pro Pro Thr Ser Pro Glu Glu Val Gln Thr
                325                 330                 335

Val Asp Pro Gln Ser Val Gln Lys Trp Val Lys Phe Ser Ser Val Ser
            340                 345                 350

Asp Gly Phe Asn Ser Asp Ser Thr Ser His His Gly Gly Lys Ile Pro
        355                 360                 365

Arg Lys Leu Ala Asn His Val Val Asp Arg Val Trp Gln Glu Cys Asn
    370                 375                 380

Met Asn Arg Ala Gln Asn Lys Lys Lys Tyr Ser Ala Ser Ser Gly Gly
385                 390                 395                 400

Leu Cys Glu Glu Ala Thr Ala Ala Lys Val Ala Ser Trp Asp Phe Val
                405                 410                 415

Glu Ala Thr Gln Arg Thr Asn Cys Ser Cys Leu Arg Leu Met Val Gln
            420                 425                 430

Cys Lys Lys Pro Leu Lys Val Ser Asp Glu Leu Val Gln Gln Tyr Gln
        435                 440                 445

Ile Lys Asn Gln Cys Leu Ser Ala Ile Ala Ser Asp Ala Glu Gln Glu
    450                 455                 460

Pro Lys Ile Asp Pro Tyr Ala Phe Val Glu Gly Asp Glu Glu Phe Leu
465                 470                 475                 480

Phe Pro Asp Lys Lys Asp Arg Gln Asn Ser Glu Arg Glu Ala Gly Lys
                485                 490                 495
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Lys His Lys Val Glu Asp Gly Thr Ser Ser Val Thr Val Leu Ser His
500 505 510

Glu Glu Asp Ala Met Ser Leu Phe Ser Pro Ser Ile Lys Gln Asp Ala
515 520 525

Pro Arg Pro Thr Ser His Ala Arg Pro Pro Ser Thr Ser Leu Ile Tyr
530 535 540

Asp Ser Asp Leu Ala Val Ser Tyr Thr Asp Leu Asp Asn Leu Phe Asn
545 550 555 560

Ser Asp Glu Asp Glu Leu Thr Pro Gly Ser Lys Lys Ser Ala Asn Gly
565 570 575

Ser Asp Asp Lys Ala Ser Cys Lys Glu Ser Lys Thr Gly Asn Leu Asp
580 585 590

Pro Leu Ser Cys Ile Ser Thr Ala Asp Leu His Lys Met Tyr Pro Thr
595 600 605

Pro Pro Ser Leu Glu Gln His Ile Met Gly Phe Ser Pro Met Asn Met
610 615 620

Asn Asn Lys Glu Tyr Gly Ser Met Asp Thr Thr Pro Gly Gly Thr Val
625 630 635 640

Leu Glu Gly Asn Ser Ser Ser Ile Gly Ala Gln Phe Lys Ile Glu Val
645 650 655

Asp Glu Gly Phe Cys Ser Pro Lys Pro Ser Glu Ile Lys Asp Phe Ser
660 665 670

Tyr Val Tyr Lys Pro Glu Asn Cys Gln Ile Leu Val Gly Cys Ser Met
675 680 685

Phe Ala Pro Leu Lys Thr Leu Pro Ser Gln Tyr Leu Pro Leu Ile Lys
690 695 700

Leu Pro Glu Glu Cys Ile Tyr Arg Gln Ser Trp Thr Val Gly Lys Leu
705 710 715 720

Glu Leu Leu Ser Ser Gly Pro Ser Met Pro Phe Ile Lys Glu Gly Asp
725 730 735

Gly Ser Asn Met Asp Gln Glu Tyr Gly Thr Ala Tyr Thr Pro Gln Thr
740 745 750

His Thr Ser Cys Gly Met Pro Pro Ser Ser Ala Pro Pro Ser Asn Ser
755 760 765

Gly Ala Gly Ile Leu Pro Ser Pro Ser Thr Pro Arg Phe Pro Thr Pro

770 775 780

Arg Thr Pro Arg Thr Pro Arg Thr Pro Arg Gly Ala Gly Gly Pro Ala
785 790 795 800

Ser Ala Gln Gly Ser Val Lys Tyr Glu Asn Ser Asp Leu Tyr Ser Pro
805 810 815

Ala Ser Thr Pro Ser Thr Cys Arg Pro Leu Asn Ser Val Glu Pro Ala
820 825 830

Thr Val Pro Ser Ile Pro Glu Ala His Ser Leu Tyr Val Asn Leu Ile
835 840 845

Leu Ser Glu Ser Val Met Asn Leu Phe Lys Asp Cys Asn Ser Asp Ser
850 855 860

Cys Cys Ile Cys Val Cys Asn Met Asn Ile Lys Gly Ala Asp Val Gly
865 870 875 880

Val Tyr Ile Pro Asp Pro Thr Gln Glu Ala Gln Tyr Arg Cys Thr Cys
885 890 895

Gly Phe Ser Ala Val Met Asn Arg Lys Phe Gly Asn Asn Ser Gly Leu
900 905 910

Phe Leu Glu Asp Glu Leu Asp Ile Ile Gly Arg Asn Thr Asp Cys Gly
915 920 925

Lys Glu Ala Glu Lys Arg Phe Glu Ala Leu Arg Ala Thr Ser Ala Glu
930 935 940

His Val Asn Gly Gly Leu Lys Glu Ser Glu Lys Leu Ser Asp Asp Leu
945 950 955 960

Ile Leu Leu Leu Gln Asp Gln Cys Thr Asn Leu Phe Ser Pro Phe Gly
965 970 975

Ala Ala Asp Gln Asp Pro Phe Pro Lys Ser Gly Val Ile Ser Asn Trp
980 985 990

Val Arg Val Glu Glu Arg Asp Cys Cys Asn Asp Cys Tyr Leu Ala Leu
995 1000 1005

Glu His Gly Arg Gln Phe Met Asp Asn Met Ser Gly Gly Lys Val
1010 1015 1020

Asp Glu Ala Leu Val Lys Ser Ser Cys Leu His Pro Trp Ser Lys
1025 1030 1035

Arg Asn Asp Val Ser Met Gln Cys Ser Gln Asp Ile Leu Arg Met
1040 1045 1050

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Leu Leu Ser Leu Gln Pro Val Leu Gln Asp Ala Ile Gln Lys Lys
1055 1060 1065

Arg Thr Val Arg Pro Trp Gly Val Gln Gly Pro Leu Thr Trp Gln
1070 1075 1080

Gln Phe His Lys Met Ala Gly Arg Gly Ser Tyr Gly Thr Asp Glu
1085 1090 1095

Ser Pro Glu Pro Leu Pro Ile Pro Thr Phe Leu Leu Gly Tyr Asp
1100 1105 1110

Tyr Asp Tyr Leu Val Leu Ser Pro Phe Ala Leu Pro Tyr Trp Glu
1115 1120 1125

Arg Leu Met Leu Glu Pro Tyr Gly Ser Gln Arg Asp Ile Ala Tyr
1130 1135 1140

Val Val Leu Cys Pro Glu Asn Glu Ala Leu Leu Asn Gly Ala Lys
1145 1150 1155

Ser Phe Phe Arg Asp Leu Thr Ala Ile Tyr Glu Ser Cys Arg Leu
1160 1165 1170

Gly Gln His Arg Pro Val Ser Arg Leu Leu Thr Asp Gly Ile Met
1175 1180 1185

Arg Val Gly Ser Thr Ala Ser Lys Lys Leu Ser Glu Lys Leu Val
1190 1195 1200

Ala Glu Trp Phe Ser Gln Ala Ala Asp Gly Asn Asn Glu Ala Phe
1205 1210 1215

Ser Lys Leu Lys Leu Tyr Ala Gln Val Cys Arg Tyr Asp Leu Gly
1220 1225 1230

Pro Tyr Leu Ala Ser Leu Pro Leu Asp Ser Ser Leu Leu Ser Gln
1235 1240 1245

Pro Asn Leu Val Ala Pro Thr Ser Gln Ser Leu Ile Thr Pro Pro
1250 1255 1260

Gln Met Thr Asn Thr Gly Asn Ala Asn Thr Pro Ser Ala Thr Leu
1265 1270 1275

Ala Ser Ala Ala Ser Ser Thr Met Thr Val Thr Ser Gly Val Ala
1280 1285 1290

Ile Ser Thr Ser Val Ala Thr Ala Asn Ser Thr Leu Thr Thr Ala
1295 1300 1305

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Ser Thr Ser Ser Ser Ser Ser Ser Asn Leu Asn Ser Gly Val Ser
1310 1315 1320

Ser Asn Lys Leu Pro Ser Phe Pro Pro Phe Gly Ser Met Asn Ser
1325 1330 1335

Asn Ala Ala Gly Ser Met Ser Thr Gln Ala Asn Thr Val Gln Ser
1340 1345 1350

Gly Gln Leu Gly Gly Gln Gln Thr Ser Ala Leu Gln Thr Ala Gly
1355 1360 1365

Ile Ser Gly Glu Ser Ser Ser Leu Pro Thr Gln Pro His Pro Asp
1370 1375 1380

Val Ser Glu Ser Thr Met Asp Arg Asp Lys Val Gly Ile Pro Thr
1385 1390 1395

Asp Gly Asp Ser His Ala Val Thr Tyr Pro Pro Ala Ile Val Val
1400 1405 1410

Tyr Ile Ile Asp Pro Phe Thr Tyr Glu Asn Thr Asp Glu Ser Thr
1415 1420 1425

Asn Ser Ser Ser Val Trp Thr Leu Gly Leu Leu Arg Cys Phe Leu
1430 1435 1440

Glu Met Val Gln Thr Leu Pro Pro His Ile Lys Ser Thr Val Ser
1445 1450 1455

Val Gln Ile Ile Pro Cys Gln Tyr Leu Leu Gln Pro Val Lys His
1460 1465 1470

Glu Asp Arg Glu Ile Tyr Pro Gln His Leu Lys Ser Leu Ala Phe
1475 1480 1485

Ser Ala Phe Thr Gln Cys Arg Arg Pro Leu Pro Thr Ser Thr Asn
1490 1495 1500

Val Lys Thr Leu Thr Gly Phe Gly Pro Gly Leu Ala Met Glu Thr
1505 1510 1515

Ala Leu Arg Ser Pro Asp Arg Pro Glu Cys Ile Arg Leu Tyr Ala
1520 1525 1530

Pro Pro Phe Ile Leu Ala Pro Val Lys Asp Lys Gln Thr Glu Leu
1535 1540 1545

Gly Glu Thr Phe Gly Glu Ala Gly Gln Lys Tyr Asn Val Leu Phe
1550 1555 1560

Val Gly Tyr Cys Leu Ser His Asp Gln Arg Trp Ile Leu Ala Ser
1565 1570 1575

Cys Thr Asp Leu Tyr Gly Glu Leu Leu Glu Thr Cys Ile Ile Asn
1580 1585 1590

Ile Asp Val Pro Asn Arg Ala Arg Arg Lys Lys Ser Ser Ala Arg
1595 1600 1605

Lys Phe Gly Leu Gln Lys Leu Trp Glu Trp Cys Leu Gly Leu Val
1610 1615 1620

Gln Met Ser Ser Leu Pro Trp Arg Val Val Ile Gly Arg Leu Gly
1625 1630 1635

Arg Ile Gly His Gly Glu Leu Lys Asp Trp Ser Cys Leu Leu Ser
1640 1645 1650

Arg Arg Asn Leu Gln Ser Leu Ser Lys Arg Leu Lys Asp Met Cys
1655 1660 1665

Arg Met Cys Gly Ile Ser Ala Ala Asp Ser Pro Ser Ile Leu Ser
1670 1675 1680

Ala Cys Leu Val Ala Met Glu Pro Gln Gly Ser Phe Val Ile Met
1685 1690 1695

Pro Asp Ser Val Ser Thr Gly Ser Val Phe Gly Arg Ser Thr Thr
1700 1705 1710

Leu Asn Met Gln Thr Ser Gln Leu Asn Thr Pro Gln Asp Thr Ser
1715 1720 1725

Cys Thr His Ile Leu Val Phe Pro Thr Ser Ala Ser Val Gln Val
1730 1735 1740

Ala Ser Ala Thr Tyr Thr Thr Glu Asn Leu Asp Leu Ala Phe Asn
1745 1750 1755

Pro Asn Asn Asp Gly Ala Asp Gly Met Gly Ile Phe Asp Leu Leu
1760 1765 1770

Asp Thr Gly Asp Asp Leu Asp Pro Asp Ile Ile Asn Ile Leu Pro
1775 1780 1785

Ala Ser Pro Thr Gly Ser Pro Val His Ser Pro Gly Ser His Tyr
1790 1795 1800

Pro His Gly Gly Asp Ala Gly Lys Gly Gln Ser Thr Asp Arg Leu
1805 1810 1815

Leu Ser Thr Glu Pro His Glu Glu Val Pro Asn Ile Leu Gln Gln

1820 1825 1830

Pro Leu Ala Leu Gly Tyr Phe Val Ser Thr Ala Lys Ala Gly Pro
1835 1840 1845

Leu Pro Asp Trp Phe Trp Ser Ala Cys Pro Gln Ala Gln Tyr Gln
1850 1855 1860

Cys Pro Leu Phe Leu Lys Ala Ser Leu His Leu His Val Pro Ser
1865 1870 1875

Val Gln Ser Asp Glu Leu Leu His Ser Lys His Ser His Pro Leu
1880 1885 1890

Asp Ser Asn Gln Thr Ser Asp Val Leu Arg Phe Val Leu Glu Gln
1895 1900 1905

Tyr Asn Ala Leu Ser Trp Leu Thr Cys Asp Pro Ala Thr Gln Asp
1910 1915 1920

Arg Arg Ser Cys Leu Pro Ile His Phe Val Val Leu Asn Gln Leu
1925 1930 1935

Tyr Asn Phe Ile Met Asn Met Leu
1940 1945

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Pro Gly Ala Ala Val Ala Ala Ala Ala Ala Ala Ala Ala Ser Pro Gly
35 40 45

Tyr Arg Leu Ser Thr Leu Ile Glu Phe Leu Leu His Arg Ala Tyr Ser
50 55 60

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

Arg Lys Ile Glu Ile Val Gln Phe Ala Ser Arg Thr Arg Gln Leu Phe
85 90 95

Val Arg Leu Leu Ala Leu Val Lys Trp Ala Asn Asn Ala Gly Lys Val
100 105 110

Glu Lys Cys Ala Met Ile Ser Ser Phe Leu Asp Gln Gln Ala Ile Leu
115 120 125

Phe Val Asp Thr Ala Asp Arg Leu Ala Ser Leu Ala Arg Asp Ala Leu
130 135 140

Val His Ala Arg Leu Pro Ser Phe Ala Ile Pro Tyr Ala Ile Asp Val
145 150 155 160

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

Ile Ile Pro Pro Asp Pro Ile Thr Lys Ile Glu Lys Gln Ala Thr Leu
180 185 190

His Gln Leu Asn Gln Ile Leu Arg His Arg Leu Val Thr Thr Asp Leu
195 200 205

Pro Pro Gln Leu Ala Asn Leu Thr Val Ala Asn Gly Arg Val Lys Phe
210 215 220

Arg Val Glu Gly Glu Phe Glu Ala Thr Leu Thr Val Met Gly Asp Asp
225 230 235 240

Pro Asp Val Pro Trp Arg Leu Leu Lys Leu Glu Ile Leu Val Glu Asp
245 250 255

Lys Glu Thr Gly Asp Gly Arg Ala Leu Val His Ser Met Gln Ile Ser
260 265 270

Phe Ile His Gln Leu Val Gln Ser Arg Leu Phe Ala Asp Glu Lys Pro
275 280 285

Leu Gln Asp Met Tyr Asn Cys Leu His Ser Phe Cys Leu Ser Leu Gln
290 295 300

Leu Glu Val Leu His Ser Gln Thr Leu Met Leu Ile Arg Glu Arg Trp
305 310 315 320

Gly Asp Leu Val Gln Val Glu Arg Tyr His Ala Gly Lys Cys Leu Ser
325 330 335

Leu Ser Val Trp Asn Gln Gln Val Leu Gly Arg Lys Thr Gly Thr Ala
340 345 350

Ser Val His Lys Val Thr Ile Lys Ile Asp Glu Asn Asp Val Ser Lys
355 360 365

Pro Leu Gln Ile Phe His Asp Pro Pro Leu Pro Ala Ser Asp Ser Lys
370 375 380

Leu Val Glu Arg Ala Met Lys Ile Asp His Leu Ser Ile Glu Lys Leu

385 390 395 400

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

Lys Ala Ile Leu Arg Gly Phe Asn Ala Asn Glu Asn Ser Ser Ile Glu
420 425 430

Thr Ala Leu Pro Ala Leu Val Val Pro Ile Leu Glu Pro Cys Gly Asn
435 440 445

Ser Glu Cys Leu His Ile Phe Val Asp Leu His Ser Gly Met Phe Gln
450 455 460

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

Ser Val Asn Asp Asp Met Lys Arg Ile Ile Pro Trp Ile Gln Gln Leu
485 490 495

Lys Phe Trp Leu Gly Gln Gln Arg Cys Lys Gln Ser Ile Lys His Leu
500 505 510

Pro Thr Ile Ser Ser Glu Thr Leu Gln Leu Ser Asn Tyr Ser Thr His
515 520 525

Pro Ile Gly Asn Leu Ser Lys Asn Lys Leu Phe Ile Lys Leu Thr Arg
530 535 540

Leu Pro Gln Tyr Tyr Ile Val Val Glu Met Leu Glu Val Pro Asn Lys
545 550 555 560

Pro Thr Gln Leu Ser Tyr Lys Tyr Tyr Phe Met Ser Val Asn Ala Ala
565 570 575

Asp Arg Glu Asp Ser Pro Ala Met Ala Leu Leu Leu Gln Gln Phe Lys
580 585 590

Glu Asn Ile Gln Asp Leu Val Phe Arg Thr Lys Thr Gly Lys Gln Thr
595 600 605

Arg Thr Asn Ala Lys Arg Lys Leu Ser Asp Asp Pro Cys Pro Val Glu
610 615 620

Ser Lys Lys Thr Lys Arg Ala Gly Glu Met Cys Ala Phe Asn Lys Val
625 630 635 640

Leu Ala His Phe Val Ala Met Cys Asp Thr Asn Met Pro Phe Val Gly
645 650 655

Leu Arg Leu Glu Leu Ser Asn Leu Glu Ile Pro His Gln Gly Val Gln
660 665 670

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Val Glu Gly Asp Gly Phe Ser His Ala Ile Arg Leu Leu Lys Ile Pro
675 680 685

Pro Cys Lys Gly Ile Thr Glu Glu Thr Gln Lys Ala Leu Asp Arg Ser
690 695 700

Leu Leu Asp Cys Thr Phe Arg Leu Gln Gly Arg Asn Asn Arg Thr Trp
705 710 715 720

Val Ala Glu Leu Val Phe Ala Asn Cys Pro Leu Asn Gly Thr Ser Thr
725 730 735

Arg Glu Gln Gly Pro Ser Arg His Val Tyr Leu Thr Tyr Glu Asn Leu
740 745 750

Leu Ser Glu Pro Val Gly Gly Arg Lys Val Val Glu Met Phe Leu Asn
755 760 765

Asp Trp Asn Ser Ile Ala Arg Leu Tyr Glu Cys Val Leu Glu Phe Ala
770 775 780

Arg Ser Leu Pro Asp Ile Pro Ala His Leu Asn Ile Phe Ser Glu Val
785 790 795 800

Arg Val Tyr Asn Tyr Arg Lys Leu Ile Leu Cys Tyr Gly Thr Thr Lys
805 810 815

Gly Ser Ser Ile Ser Ile Gln Trp Asn Ser Ile His Gln Lys Phe His
820 825 830

Ile Ser Leu Gly Thr Val Gly Pro Asn Ser Gly Cys Ser Asn Cys His
835 840 845

Asn Thr Ile Leu His Gln Leu Gln Glu Met Phe Asn Lys Thr Pro Asn
850 855 860

Val Val Gln Leu Leu Gln Val Leu Phe Asp Thr Gln Ala Pro Leu Asn
865 870 875 880

Ala Ile Asn Lys Leu Pro Thr Val Pro Met Leu Gly Leu Thr Gln Arg
885 890 895

Thr Asn Thr Ala Tyr Gln Cys Phe Ser Ile Leu Pro Gln Ser Ser Thr
900 905 910

His Ile Arg Leu Ala Phe Arg Asn Met Tyr Cys Ile Asp Ile Tyr Cys
915 920 925

Arg Ser Arg Gly Val Val Ala Ile Arg Asp Gly Ala Tyr Ser Leu Phe
930 935 940

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Asp Asn Ser Lys Leu Val Glu Gly Phe Tyr Pro Ala Pro Gly Leu Lys
945                 950                 955                 960

Thr Phe Leu Asn Met Phe Val Asp Ser Asn Gln Asp Ala Arg Arg Arg
                965                 970                 975

Ser Val Asn Glu Asp Asp Asn Pro Pro Ser Pro Ile Gly Gly Asp Met
            980                 985                 990

Met Asp Ser Leu Ile Ser Gln Leu  Gln Pro Pro Pro Gln  Gln Gln Pro
        995                 1000                1005

Phe Pro  Lys Gln Pro Gly Thr  Ser Gly Ala Tyr Pro  Leu Thr Ser
    1010                1015                1020

Pro Pro  Thr Ser Tyr His Ser  Thr Val Asn Gln Ser  Pro Ser Met
    1025                1030                1035

Met His  Thr Gln Ser Pro Gly  Thr Leu Asp Pro Ser  Ser Pro Tyr
    1040                1045                1050

Thr Met  Val Ser Pro Ser Gly  Arg Ala Gly Asn Trp  Pro Gly Ser
    1055                1060                1065

Pro Gln  Val Ser Gly Pro Ser  Pro Ala Ala Arg Met  Pro Gly Met
    1070                1075                1080

Ser Pro  Ala Asn Pro Ser Leu  His Ser Pro Val Pro  Asp Ala Ser
    1085                1090                1095

His Ser  Pro Arg Ala Gly Thr  Ser Ser Gln Thr Met  Pro Thr Asn
    1100                1105                1110

Met Pro  Pro Pro Arg Lys Leu  Pro Gln Arg Ser Trp  Ala Ala Ser
    1115                1120                1125

Ile Pro  Thr Ile Leu Thr His  Ser Ala Leu Asn Ile  Leu Leu Leu
    1130                1135                1140

Pro Ser  Pro Thr Pro Gly Leu  Val Pro Gly Leu Ala  Gly Ser Tyr
    1145                1150                1155

Leu Cys  Ser Pro Leu Glu Arg  Phe Leu Gly Ser Val  Ile Met Arg
    1160                1165                1170

Arg His  Leu Gln Arg Ile Ile  Gln Gln Glu Thr Leu  Gln Leu Ile
    1175                1180                1185

Asn Ser  Asn Glu Pro Gly Val  Ile Met Phe Lys Thr  Asp Ala Leu
    1190                1195                1200
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Lys Cys Arg Val Ala Leu Ser Pro Lys Thr Asn Gln Thr Leu Gln
1205 1210 1215

Leu Lys Leu Thr Pro Glu Asn Ala Gly Gln Trp Lys Pro Asp Glu
1220 1225 1230

Leu Gln Val Leu Glu Lys Phe Phe Glu Thr Arg Val Ala Gly Pro
1235 1240 1245

Pro Phe Lys Ala Asn Thr Leu Ile Ala Phe Thr Lys Leu Leu Gly
1250 1255 1260

Ala Pro Thr His Ile Leu Arg Asp Cys Val His Ile Met Lys Leu
1265 1270 1275

Glu Leu Phe Pro Asp Gln Ala Thr Gln Leu Lys Trp Asn Val Gln
1280 1285 1290

Phe Cys Leu Thr Ile Pro Pro Ser Ala Pro Pro Ile Ala Pro Pro
1295 1300 1305

Gly Thr Pro Ala Val Val Leu Lys Ser Lys Met Leu Phe Phe Leu
1310 1315 1320

Gln Leu Thr Gln Lys Thr Ser Val Pro Pro Gln Glu Pro Val Ser
1325 1330 1335

Ile Ile Val Pro Ile Ile Tyr Asp Met Ala Ser Gly Thr Thr Gln
1340 1345 1350

Gln Ala Asp Ile Pro Arg Gln Gln Asn Ser Ser Val Ala Ala Pro
1355 1360 1365

Met Met Val Ser Asn Ile Leu Lys Arg Phe Ala Glu Met Asn Pro
1370 1375 1380

Pro Arg Gln Gly Glu Cys Thr Ile Phe Ala Ala Val Arg Asp Leu
1385 1390 1395

Met Ala Asn Leu Thr Leu Pro Pro Val Gly Arg Pro
1400 1405 1410

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<211> 1338
<212> PRT
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<400> 108
Met Ile Ser Ser Phe Leu Asp Gln Gln Ala Ile Leu Phe Val Asp Thr
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Ala Asp Arg Leu Ala Ser Leu Ala Arg Asp Ala Leu Val His Ala Arg
20 25 30

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

Ser Tyr Pro Arg Leu Pro Thr Cys Ile Arg Asp Lys Ile Ile Pro Pro
50 55 60

Asp Pro Ile Thr Lys Ile Glu Lys Gln Ala Thr Leu His Gln Leu Asn
65 70 75 80

Gln Ile Leu Arg His Arg Leu Val Thr Thr Asp Leu Pro Pro Gln Leu
85 90 95

Ala Asn Leu Thr Val Ala Asn Gly Arg Val Lys Phe Arg Val Glu Gly
100 105 110

Glu Phe Glu Ala Thr Leu Thr Val Met Gly Asp Asp Pro Asp Val Pro
115 120 125

Trp Arg Leu Leu Lys Leu Glu Ile Leu Val Glu Asp Lys Glu Thr Gly
130 135 140

Asp Gly Arg Ala Leu Val His Ser Met Gln Ile Ser Phe Ile His Gln
145 150 155 160

Leu Val Gln Ser Arg Leu Phe Ala Asp Glu Lys Pro Leu Gln Asp Met
165 170 175

Tyr Asn Cys Leu His Ser Phe Cys Leu Ser Leu Gln Leu Glu Val Leu
180 185 190

His Ser Gln Thr Leu Met Leu Ile Arg Glu Arg Trp Gly Asp Leu Val
195 200 205

Gln Val Glu Arg Tyr His Ala Gly Lys Cys Leu Ser Leu Ser Val Trp
210 215 220

Asn Gln Gln Val Leu Gly Arg Lys Thr Gly Thr Ala Ser Val His Lys
225 230 235 240

Val Thr Ile Lys Ile Asp Glu Asn Asp Val Ser Lys Pro Leu Gln Ile
245 250 255

Phe His Asp Pro Pro Leu Pro Ala Ser Asp Ser Lys Leu Val Glu Arg
260 265 270

Ala Met Lys Ile Asp His Leu Ser Ile Glu Lys Leu Leu Ile Asp Ser
275 280 285

Val His Ala Arg Ala His Gln Lys Leu Gln Glu Leu Lys Ala Ile Leu
290 295 300

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

Ala Leu Val Val Pro Ile Leu Glu Pro Cys Gly Asn Ser Glu Cys Leu
325 330 335

His Ile Phe Val Asp Leu His Ser Gly Met Phe Gln Leu Met Leu Tyr
340 345 350

Gly Leu Asp Gln Ala Thr Leu Asp Asp Met Glu Lys Ser Val Asn Asp
355 360 365

Asp Met Lys Arg Ile Ile Pro Trp Ile Gln Gln Leu Lys Phe Trp Leu
370 375 380

Gly Gln Gln Arg Cys Lys Gln Ser Ile Lys His Leu Pro Thr Ile Ser
385 390 395 400

Ser Glu Thr Leu Gln Leu Ser Asn Tyr Ser Thr His Pro Ile Gly Asn
405 410 415

Leu Ser Lys Asn Lys Leu Phe Ile Lys Leu Thr Arg Leu Pro Gln Tyr
420 425 430

Tyr Ile Val Val Glu Met Leu Glu Val Pro Asn Lys Pro Thr Gln Leu
435 440 445

Ser Tyr Lys Tyr Tyr Phe Met Ser Val Asn Ala Ala Asp Arg Glu Asp
450 455 460

Ser Pro Ala Met Ala Leu Leu Leu Gln Gln Phe Lys Glu Asn Ile Gln
465 470 475 480

Asp Leu Val Phe Arg Thr Lys Thr Gly Lys Gln Thr Arg Thr Asn Ala
485 490 495

Lys Arg Lys Leu Ser Asp Asp Pro Cys Pro Val Glu Ser Lys Lys Thr
500 505 510

Lys Arg Ala Gly Glu Met Cys Ala Phe Asn Lys Val Leu Ala His Phe
515 520 525

Val Ala Met Cys Asp Thr Asn Met Pro Phe Val Gly Leu Arg Leu Glu
530 535 540

Leu Ser Asn Leu Glu Ile Pro His Gln Gly Val Gln Val Glu Gly Asp
545 550 555 560

Gly Phe Ser His Ala Ile Arg Leu Leu Lys Ile Pro Pro Cys Lys Gly
565 570 575

Ile Thr Glu Glu Thr Gln Lys Ala Leu Asp Arg Ser Leu Leu Asp Cys

580 585 590

Thr Phe Arg Leu Gln Gly Arg Asn Asn Arg Thr Trp Val Ala Glu Leu
595 600 605

Val Phe Ala Asn Cys Pro Leu Asn Gly Thr Ser Thr Arg Glu Gln Gly
610 615 620

Pro Ser Arg His Val Tyr Leu Thr Tyr Glu Asn Leu Leu Ser Glu Pro
625 630 635 640

Val Gly Gly Arg Lys Val Val Glu Met Phe Leu Asn Asp Trp Asn Ser
645 650 655

Ile Ala Arg Leu Tyr Glu Cys Val Leu Glu Phe Ala Arg Ser Leu Pro
660 665 670

Asp Ile Pro Ala His Leu Asn Ile Phe Ser Glu Val Arg Val Tyr Asn
675 680 685

Tyr Arg Lys Leu Ile Leu Cys Tyr Gly Thr Thr Lys Gly Ser Ser Ile
690 695 700

Ser Ile Gln Trp Asn Ser Ile His Gln Lys Phe His Ile Ser Leu Gly
705 710 715 720

Thr Val Gly Pro Asn Ser Gly Cys Ser Asn Cys His Asn Thr Ile Leu
725 730 735

His Gln Leu Gln Glu Met Phe Asn Lys Thr Pro Asn Val Val Gln Leu
740 745 750

Leu Gln Val Leu Phe Asp Thr Gln Ala Pro Leu Asn Ala Ile Asn Lys
755 760 765

Leu Pro Thr Val Pro Met Leu Gly Leu Thr Gln Arg Thr Asn Thr Ala
770 775 780

Tyr Gln Cys Phe Ser Ile Leu Pro Gln Ser Ser Thr His Ile Arg Leu
785 790 795 800

Ala Phe Arg Asn Met Tyr Cys Ile Asp Ile Tyr Cys Arg Ser Arg Gly
805 810 815

Val Val Ala Ile Arg Asp Gly Ala Tyr Ser Leu Phe Asp Asn Ser Lys
820 825 830

Leu Val Glu Gly Phe Tyr Pro Ala Pro Gly Leu Lys Thr Phe Leu Asn
835 840 845

Met Phe Val Asp Ser Asn Gln Asp Ala Arg Arg Arg Ser Val Asn Glu
850 855 860

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Asp Asp Asn Pro Pro Ser Pro Ile Gly Gly Asp Met Met Asp Ser Leu
865 870 875 880

Ile Ser Gln Leu Gln Pro Pro Pro Gln Gln Gln Pro Phe Pro Lys Gln
885 890 895

Pro Gly Thr Ser Gly Ala Tyr Pro Leu Thr Ser Pro Pro Thr Ser Tyr
900 905 910

His Ser Thr Val Asn Gln Ser Pro Ser Met Met His Thr Gln Ser Pro
915 920 925

Gly Asn Leu His Ala Ala Ser Ser Pro Ser Gly Ala Leu Arg Ala Pro
930 935 940

Ser Pro Ala Ser Phe Val Pro Thr Pro Pro Pro Ser Ser His Gly Ile
945 950 955 960

Ser Ile Gly Pro Gly Ala Ser Phe Ala Ser Pro His Gly Thr Leu Asp
965 970 975

Pro Ser Ser Pro Tyr Thr Met Val Ser Pro Ser Gly Arg Ala Gly Asn
980 985 990

Trp Pro Gly Ser Pro Gln Val Ser Gly Pro Ser Pro Ala Ala Arg Met
995 1000 1005

Pro Gly Met Ser Pro Ala Asn Pro Ser Leu His Ser Pro Val Pro
1010 1015 1020

Asp Ala Ser His Ser Pro Arg Ala Gly Thr Ser Ser Gln Thr Met
1025 1030 1035

Pro Thr Asn Met Pro Pro Pro Arg Lys Leu Pro Gln Arg Ser Trp
1040 1045 1050

Ala Ala Ser Ile Pro Thr Ile Leu Thr His Ser Ala Leu Asn Ile
1055 1060 1065

Leu Leu Leu Pro Ser Pro Thr Pro Gly Leu Val Pro Gly Leu Ala
1070 1075 1080

Gly Ser Tyr Leu Cys Ser Pro Leu Glu Arg Phe Leu Gly Ser Val
1085 1090 1095

Ile Met Arg Arg His Leu Gln Arg Ile Ile Gln Gln Glu Thr Leu
1100 1105 1110

Gln Leu Ile Asn Ser Asn Glu Pro Gly Val Ile Met Phe Lys Thr
1115 1120 1125

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Asp Ala Leu Lys Cys Arg Val Ala Leu Ser Pro Lys Thr Asn Gln
1130 1135 1140

Thr Leu Gln Leu Lys Leu Thr Pro Glu Asn Ala Gly Gln Trp Lys
1145 1150 1155

Pro Asp Glu Leu Gln Val Leu Glu Lys Phe Phe Glu Thr Arg Val
1160 1165 1170

Ala Gly Pro Pro Phe Lys Ala Asn Thr Leu Ile Ala Phe Thr Lys
1175 1180 1185

Leu Leu Gly Ala Pro Thr His Ile Leu Arg Asp Cys Val His Ile
1190 1195 1200

Met Lys Leu Glu Leu Phe Pro Asp Gln Ala Thr Gln Leu Lys Trp
1205 1210 1215

Asn Val Gln Phe Cys Leu Thr Ile Pro Pro Ser Ala Pro Pro Ile
1220 1225 1230

Ala Pro Pro Gly Thr Pro Ala Val Val Leu Lys Ser Lys Met Leu
1235 1240 1245

Phe Phe Leu Gln Leu Thr Gln Lys Thr Ser Val Pro Pro Gln Glu
1250 1255 1260

Pro Val Ser Ile Ile Val Pro Ile Ile Tyr Asp Met Ala Ser Gly
1265 1270 1275

Thr Thr Gln Gln Ala Asp Ile Pro Arg Gln Gln Asn Ser Ser Val
1280 1285 1290

Ala Ala Pro Met Met Val Ser Asn Ile Leu Lys Arg Phe Ala Glu
1295 1300 1305

Met Asn Pro Pro Arg Gln Gly Glu Cys Thr Ile Phe Ala Ala Val
1310 1315 1320

Arg Asp Leu Met Ala Asn Leu Thr Leu Pro Pro Val Gly Arg Pro
1325 1330 1335

<210> 109
<211> 118
<212> PRT
<213> Homo sapiens

<400> 109
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Gly Gly Gly Gly Ser Gly Gly Pro Pro Ser Ala Pro Ala Pro Pro Pro
20 25 30

Pro Gly Ala Ala Val Ala Ala Ala Ala Ala Ala Ala Ala Ser Pro Gly
35 40 45

Tyr Arg Leu Ser Thr Leu Ile Glu Phe Leu Leu His Arg Ala Tyr Ser
50 55 60

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

Arg Lys Ile Glu Ile Val Gln Phe Ala Ser Arg Thr Arg Gln Leu Phe
85 90 95

Val Arg Leu Leu Ala Leu Val Lys Trp Ala Asn Asn Ala Gly Lys Val
100 105 110

Glu Lys Cys Ala Val Ser
115

<210> 110
<211> 1443
<212> PRT
<213> Homo sapiens

<400> 110
Met Ala Pro Val Gln Leu Glu Asn His Gln Leu Val Pro Pro Gly Gly
1 5 10 15

Gly Gly Gly Gly Ser Gly Gly Pro Pro Ser Ala Pro Ala Pro Pro Pro
20 25 30

Pro Gly Ala Ala Val Ala Ala Ala Ala Ala Ala Ala Ala Ser Pro Gly
35 40 45

Tyr Arg Leu Ser Thr Leu Ile Glu Phe Leu Leu His Arg Ala Tyr Ser
50 55 60

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

Arg Lys Ile Glu Ile Val Gln Phe Ala Ser Arg Thr Arg Gln Leu Phe
85 90 95

Val Arg Leu Leu Ala Leu Val Lys Trp Ala Asn Asn Ala Gly Lys Val
100 105 110

Glu Lys Cys Ala Met Ile Ser Ser Phe Leu Asp Gln Gln Ala Ile Leu
115 120 125

Phe Val Asp Thr Ala Asp Arg Leu Ala Ser Leu Ala Arg Asp Ala Leu
130 135 140

Val His Ala Arg Leu Pro Ser Phe Ala Ile Pro Tyr Ala Ile Asp Val

145 150 155 160

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

Ile Ile Pro Pro Asp Pro Ile Thr Lys Ile Glu Lys Gln Ala Thr Leu
180 185 190

His Gln Leu Asn Gln Ile Leu Arg His Arg Leu Val Thr Thr Asp Leu
195 200 205

Pro Pro Gln Leu Ala Asn Leu Thr Val Ala Asn Gly Arg Val Lys Phe
210 215 220

Arg Val Glu Gly Glu Phe Glu Ala Thr Leu Thr Val Met Gly Asp Asp
225 230 235 240

Pro Asp Val Pro Trp Arg Leu Leu Lys Leu Glu Ile Leu Val Glu Asp
245 250 255

Lys Glu Thr Gly Asp Gly Arg Ala Leu Val His Ser Met Gln Ile Ser
260 265 270

Phe Ile His Gln Leu Val Gln Ser Arg Leu Phe Ala Asp Glu Lys Pro
275 280 285

Leu Gln Asp Met Tyr Asn Cys Leu His Ser Phe Cys Leu Ser Leu Gln
290 295 300

Leu Glu Val Leu His Ser Gln Thr Leu Met Leu Ile Arg Glu Arg Trp
305 310 315 320

Gly Asp Leu Val Gln Val Glu Arg Tyr His Ala Gly Lys Cys Leu Ser
325 330 335

Leu Ser Val Trp Asn Gln Gln Val Leu Gly Arg Lys Thr Gly Thr Ala
340 345 350

Ser Val His Lys Val Thr Ile Lys Ile Asp Glu Asn Asp Val Ser Lys
355 360 365

Pro Leu Gln Ile Phe His Asp Pro Pro Leu Pro Ala Ser Asp Ser Lys
370 375 380

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

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

Lys Ala Ile Leu Arg Gly Phe Asn Ala Asn Glu Asn Ser Ser Ile Glu
420 425 430

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Thr Ala Leu Pro Ala Leu Val Val Pro Ile Leu Glu Pro Cys Gly Asn
435 440 445

Ser Glu Cys Leu His Ile Phe Val Asp Leu His Ser Gly Met Phe Gln
450 455 460

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

Ser Val Asn Asp Asp Met Lys Arg Ile Ile Pro Trp Ile Gln Gln Leu
485 490 495

Lys Phe Trp Leu Gly Gln Gln Arg Cys Lys Gln Ser Ile Lys His Leu
500 505 510

Pro Thr Ile Ser Ser Glu Thr Leu Gln Leu Ser Asn Tyr Ser Thr His
515 520 525

Pro Ile Gly Asn Leu Ser Lys Asn Lys Leu Phe Ile Lys Leu Thr Arg
530 535 540

Leu Pro Gln Tyr Tyr Ile Val Val Glu Met Leu Glu Val Pro Asn Lys
545 550 555 560

Pro Thr Gln Leu Ser Tyr Lys Tyr Tyr Phe Met Ser Val Asn Ala Ala
565 570 575

Asp Arg Glu Asp Ser Pro Ala Met Ala Leu Leu Leu Gln Gln Phe Lys
580 585 590

Glu Asn Ile Gln Asp Leu Val Phe Arg Thr Lys Thr Gly Lys Gln Thr
595 600 605

Arg Thr Asn Ala Lys Arg Lys Leu Ser Asp Asp Pro Cys Pro Val Glu
610 615 620

Ser Lys Lys Thr Lys Arg Ala Gly Glu Met Cys Ala Phe Asn Lys Val
625 630 635 640

Leu Ala His Phe Val Ala Met Cys Asp Thr Asn Met Pro Phe Val Gly
645 650 655

Leu Arg Leu Glu Leu Ser Asn Leu Glu Ile Pro His Gln Gly Val Gln
660 665 670

Val Glu Gly Asp Gly Phe Ser His Ala Ile Arg Leu Leu Lys Ile Pro
675 680 685

Pro Cys Lys Gly Ile Thr Glu Glu Thr Gln Lys Ala Leu Asp Arg Ser
690 695 700

Leu Leu Asp Cys Thr Phe Arg Leu Gln Gly Arg Asn Asn Arg Thr Trp
705 710 715 720

Val Ala Glu Leu Val Phe Ala Asn Cys Pro Leu Asn Gly Thr Ser Thr
725 730 735

Arg Glu Gln Gly Pro Ser Arg His Val Tyr Leu Thr Tyr Glu Asn Leu
740 745 750

Leu Ser Glu Pro Val Gly Gly Arg Lys Val Val Glu Met Phe Leu Asn
755 760 765

Asp Trp Asn Ser Ile Ala Arg Leu Tyr Glu Cys Val Leu Glu Phe Ala
770 775 780

Arg Ser Leu Pro Asp Ile Pro Ala His Leu Asn Ile Phe Ser Glu Val
785 790 795 800

Arg Val Tyr Asn Tyr Arg Lys Leu Ile Leu Cys Tyr Gly Thr Thr Lys
805 810 815

Gly Ser Ser Ile Ser Ile Gln Trp Asn Ser Ile His Gln Lys Phe His
820 825 830

Ile Ser Leu Gly Thr Val Gly Pro Asn Ser Gly Cys Ser Asn Cys His
835 840 845

Asn Thr Ile Leu His Gln Leu Gln Glu Met Phe Asn Lys Thr Pro Asn
850 855 860

Val Val Gln Leu Leu Gln Val Leu Phe Asp Thr Gln Ala Pro Leu Asn
865 870 875 880

Ala Ile Asn Lys Leu Pro Thr Val Pro Met Leu Gly Leu Thr Gln Arg
885 890 895

Thr Asn Thr Ala Tyr Gln Cys Phe Ser Ile Leu Pro Gln Ser Ser Thr
900 905 910

His Ile Arg Leu Ala Phe Arg Asn Met Tyr Cys Ile Asp Ile Tyr Cys
915 920 925

Arg Ser Arg Gly Val Val Ala Ile Arg Asp Gly Ala Tyr Ser Leu Phe
930 935 940

Asp Asn Ser Lys Leu Val Glu Gly Phe Tyr Pro Ala Pro Gly Leu Lys
945 950 955 960

Thr Phe Leu Asn Met Phe Val Asp Ser Asn Gln Asp Ala Arg Arg Arg
965 970 975

Ser Val Asn Glu Asp Asp Asn Pro Pro Ser Pro Ile Gly Gly Asp Met
980 985 990

Met Asp Ser Leu Ile Ser Gln Leu Gln Pro Pro Pro Gln Gln Gln Pro
995 1000 1005

Phe Pro Lys Gln Pro Gly Thr Ser Gly Ala Tyr Pro Leu Thr Ser
1010 1015 1020

Pro Pro Thr Ser Tyr His Ser Thr Val Asn Gln Ser Pro Ser Met
1025 1030 1035

Met His Thr Gln Ser Pro Gly Asn Leu His Ala Ala Ser Ser Pro
1040 1045 1050

Ser Gly Ala Leu Arg Ala Pro Ser Pro Ala Ser Phe Val Pro Thr
1055 1060 1065

Pro Pro Pro Ser Ser His Gly Ile Ser Ile Gly Pro Gly Ala Ser
1070 1075 1080

Phe Ala Ser Pro His Gly Thr Leu Asp Pro Ser Ser Pro Tyr Thr
1085 1090 1095

Met Val Ser Pro Ser Gly Arg Ala Gly Asn Trp Pro Gly Ser Pro
1100 1105 1110

Gln Val Ser Gly Pro Ser Pro Ala Ala Arg Met Pro Gly Met Ser
1115 1120 1125

Pro Ala Asn Pro Ser Leu His Ser Pro Val Pro Asp Ala Ser His
1130 1135 1140

Ser Pro Arg Ala Gly Thr Ser Ser Gln Thr Met Pro Thr Asn Met
1145 1150 1155

Pro Pro Pro Arg Lys Leu Pro Gln Arg Ser Trp Ala Ala Ser Ile
1160 1165 1170

Pro Thr Ile Leu Thr His Ser Ala Leu Asn Ile Leu Leu Leu Pro
1175 1180 1185

Ser Pro Thr Pro Gly Leu Val Pro Gly Leu Ala Gly Ser Tyr Leu
1190 1195 1200

Cys Ser Pro Leu Glu Arg Phe Leu Gly Ser Val Ile Met Arg Arg
1205 1210 1215

His Leu Gln Arg Ile Ile Gln Gln Glu Thr Leu Gln Leu Ile Asn
1220 1225 1230

Ser Asn Glu Pro Gly Val Ile Met Phe Lys Thr Asp Ala Leu Lys

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1235 1240 1245

Cys Arg Val Ala Leu Ser Pro Lys Thr Asn Gln Thr Leu Gln Leu
1250 1255 1260

Lys Leu Thr Pro Glu Asn Ala Gly Gln Trp Lys Pro Asp Glu Leu
1265 1270 1275

Gln Val Leu Glu Lys Phe Phe Glu Thr Arg Val Ala Gly Pro Pro
1280 1285 1290

Phe Lys Ala Asn Thr Leu Ile Ala Phe Thr Lys Leu Leu Gly Ala
1295 1300 1305

Pro Thr His Ile Leu Arg Asp Cys Val His Ile Met Lys Leu Glu
1310 1315 1320

Leu Phe Pro Asp Gln Ala Thr Gln Leu Lys Trp Asn Val Gln Phe
1325 1330 1335

Cys Leu Thr Ile Pro Pro Ser Ala Pro Pro Ile Ala Pro Pro Gly
1340 1345 1350

Thr Pro Ala Val Val Leu Lys Ser Lys Met Leu Phe Phe Leu Gln
1355 1360 1365

Leu Thr Gln Lys Thr Ser Val Pro Pro Gln Glu Pro Val Ser Ile
1370 1375 1380

Ile Val Pro Ile Ile Tyr Asp Met Ala Ser Gly Thr Thr Gln Gln
1385 1390 1395

Ala Asp Ile Pro Arg Gln Gln Asn Ser Ser Val Ala Ala Pro Met
1400 1405 1410

Met Val Ser Asn Ile Leu Lys Arg Phe Ala Glu Met Asn Pro Pro
1415 1420 1425

Arg Gln Gly Ser Ile Lys Gly Thr Gly Cys Pro Ser Asp Phe Leu
1430 1435 1440

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<212> PRT
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<400> 111
Met Arg Lys Ala Gly Val Ala His Ser Lys Ser Ser Lys Asp Met Glu
1 5 10 15

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

Val Ala Arg Leu Ile Ile His Phe Arg Asp Ile His Asn Lys Lys Ser
35 40 45

Gln Ala Ser Val Ser Asp Pro Met Asn Ala Leu Gln Ser Leu Thr Gly
50 55 60

Gly Pro Ala Ala Gly Ala Ala Gly Ile Gly Met Pro Pro Arg Gly Pro
65 70 75 80

Gly Gln Ser Leu Gly Gly Met Gly Ser Leu Gly Ala Met Gly Gln Pro
85 90 95

Met Ser Leu Ser Gly Gln Pro Pro Pro Gly Thr Ser Gly Met Ala Pro
100 105 110

His Ser Met Ala Val Val Ser Thr Ala Thr Pro Gln Thr Gln Leu Gln
115 120 125

Leu Gln Gln Val Ala Leu Gln Gln Gln Gln Gln Gln Gln Gln Phe Gln
130 135 140

Gln Gln Gln Gln Ala Ala Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln
145 150 155 160

Gln Gln Phe Gln Ala Gln Gln Ser Ala Met Gln Gln Gln Phe Gln Ala
165 170 175

Val Val Gln Gln Gln Gln Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln
180 185 190

His Leu Ile Lys Leu His His Gln Asn Gln Gln Gln Ile Gln Gln Gln
195 200 205

Gln Gln Gln Leu Gln Arg Ile Ala Gln Leu Gln Leu Gln Gln Gln Gln
210 215 220

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Leu Gln Ala
225 230 235 240

Gln Pro Pro Ile Gln Gln Pro Pro Met Gln Gln Pro Gln Pro Pro Pro
245 250 255

Ser Gln Ala Leu Pro Gln Gln Leu Gln Gln Met His His Thr Gln His
260 265 270

His Gln Pro Pro Pro Gln Pro Gln Gln Pro Pro Val Ala Gln Asn Gln
275 280 285

Pro Ser Gln Leu Pro Pro Gln Ser Gln Thr Gln Pro Leu Val Ser Gln
290 295 300

Ala Gln Ala Leu Pro Gly Gln Met Leu Tyr Thr Gln Pro Pro Leu Lys

305 310 315 320

Phe Val Arg Ala Pro Met Val Val Gln Gln Pro Pro Val Gln Pro Gln
325 330 335

Val Gln Gln Gln Gln Thr Ala Val Gln Thr Ala Gln Ala Ala Gln Met
340 345 350

Val Ala Pro Gly Val Gln Met Ile Thr Glu Ala Leu Ala Gln Gly Gly
355 360 365

Met His Ile Arg Ala Arg Phe Pro Pro Thr Thr Ala Val Ser Ala Ile
370 375 380

Pro Ser Ser Ser Ile Pro Leu Gly Arg Gln Pro Met Ala Gln Val Ser
385 390 395 400

Gln Ser Ser Leu Pro Met Leu Ser Ser Pro Ser Pro Gly Gln Gln Val
405 410 415

Gln Thr Pro Gln Ser Met Pro Pro Pro Pro Gln Pro Ser Pro Gln Pro
420 425 430

Gly Gln Pro Ser Ser Gln Pro Asn Ser Asn Val Ser Ser Gly Pro Ala
435 440 445

Pro Ser Pro Ser Ser Phe Leu Pro Ser Pro Ser Pro Gln Pro Ser Gln
450 455 460

Ser Pro Val Thr Ala Arg Thr Pro Gln Asn Phe Ser Val Pro Ser Pro
465 470 475 480

Gly Pro Leu Asn Thr Pro Val Asn Pro Ser Ser Val Met Ser Pro Ala
485 490 495

Gly Ser Ser Gln Ala Glu Glu Gln Gln Tyr Leu Asp Lys Leu Lys Gln
500 505 510

Leu Ser Lys Tyr Ile Glu Pro Leu Arg Arg Met Ile Asn Lys Ile Asp
515 520 525

Lys Asn Glu Asp Arg Lys Lys Asp Leu Ser Lys Met Lys Ser Leu Leu
530 535 540

Asp Ile Leu Thr Asp Pro Ser Lys Arg Cys Pro Leu Lys Thr Leu Gln
545 550 555 560

Lys Cys Glu Ile Ala Leu Glu Lys Leu Lys Asn Asp Met Ala Val Pro
565 570 575

Thr Pro Pro Pro Pro Pro Val Pro Pro Thr Lys Gln Gln Tyr Leu Cys
580 585 590

Gln Pro Leu Leu Asp Ala Val Leu Ala Asn Ile Arg Ser Pro Val Phe
595 600 605

Asn His Ser Leu Tyr Arg Thr Phe Val Pro Ala Met Thr Ala Ile His
610 615 620

Gly Pro Pro Ile Thr Ala Pro Val Val Cys Thr Arg Lys Arg Arg Leu
625 630 635 640

Glu Asp Asp Glu Arg Gln Ser Ile Pro Ser Val Leu Gln Gly Glu Val
645 650 655

Ala Arg Leu Asp Pro Lys Phe Leu Val Asn Leu Asp Pro Ser His Cys
660 665 670

Ser Asn Asn Gly Thr Val His Leu Ile Cys Lys Leu Asp Asp Lys Asp
675 680 685

Leu Pro Ser Val Pro Pro Leu Glu Leu Ser Val Pro Ala Asp Tyr Pro
690 695 700

Ala Gln Ser Pro Leu Trp Ile Asp Arg Gln Trp Gln Tyr Asp Ala Asn
705 710 715 720

Pro Phe Leu Gln Ser Val His Arg Cys Met Thr Ser Arg Leu Leu Gln
725 730 735

Leu Pro Asp Lys His Ser Val Thr Ala Leu Leu Asn Thr Trp Ala Gln
740 745 750

Ser Val His Gln Ala Cys Leu Ser Ala Ala
755 760

<210> 112
<211> 667
<212> PRT
<213> Homo sapiens

<400> 112
Met Asp Val Ser Gly Gln Glu Thr Asp Trp Arg Ser Thr Ala Phe Arg
1 5 10 15

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

Ala His Ser Lys Ser Ser Lys Asp Met Glu Ser His Val Phe Leu Lys
35 40 45

Ala Lys Thr Arg Asp Glu Tyr Leu Ser Leu Val Ala Arg Leu Ile Ile
50 55 60

His Phe Arg Asp Ile Pro Gln Leu Gln Leu Gln Gln Val Ala Leu Gln

65 70 75 80

Gln Gln Gln Gln Gln Gln Gln Phe Gln Gln Gln Gln Gln Ala Ala Leu
85 90 95

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Phe Gln Ala Gln Gln
100 105 110

Ser Ala Met Gln Gln Gln Phe Gln Ala Val Val Gln Gln Gln Gln Gln
115 120 125

Leu Gln Gln Gln Gln Gln Gln Gln Gln His Leu Ile Lys Leu His His
130 135 140

Gln Asn Gln Gln Gln Ile Gln Gln Gln Gln Gln Gln Leu Gln Arg Ile
145 150 155 160

Ala Gln Leu Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
165 170 175

Gln Gln Gln Gln Gln Ala Leu Gln Ala Gln Pro Pro Ile Gln Gln Pro
180 185 190

Pro Met Gln Gln Pro Gln Pro Pro Pro Ser Gln Ala Leu Pro Gln Gln
195 200 205

Leu Gln Gln Met His His Thr Gln His His Gln Pro Pro Pro Gln Pro
210 215 220

Gln Gln Pro Pro Val Ala Gln Asn Gln Pro Ser Gln Leu Pro Pro Gln
225 230 235 240

Ser Gln Thr Gln Pro Leu Val Ser Gln Ala Gln Ala Leu Pro Gly Gln
245 250 255

Met Leu Tyr Thr Gln Pro Pro Leu Lys Phe Val Arg Ala Pro Met Val
260 265 270

Val Gln Gln Pro Pro Val Gln Pro Gln Val Gln Gln Gln Gln Thr Ala
275 280 285

Val Gln Thr Ala Gln Ala Ala Gln Met Val Ala Pro Gly Val Gln Val
290 295 300

Ser Gln Ser Ser Leu Pro Met Leu Ser Ser Pro Ser Pro Gly Gln Gln
305 310 315 320

Val Gln Thr Pro Gln Ser Met Pro Pro Pro Pro Gln Pro Ser Pro Gln
325 330 335

Pro Gly Gln Pro Ser Ser Gln Pro Asn Ser Asn Val Ser Ser Gly Pro
340 345 350

Ala Pro Ser Pro Ser Ser Phe Leu Pro Ser Pro Ser Pro Gln Pro Ser
355 360 365

Gln Ser Pro Val Thr Ala Arg Thr Pro Gln Asn Phe Ser Val Pro Ser
370 375 380

Pro Gly Pro Leu Asn Thr Pro Val Asn Pro Ser Ser Val Met Ser Pro
385 390 395 400

Ala Gly Ser Ser Gln Ala Glu Glu Gln Gln Tyr Leu Asp Lys Leu Lys
405 410 415

Gln Leu Ser Lys Tyr Ile Glu Pro Leu Arg Arg Met Ile Asn Lys Ile
420 425 430

Asp Lys Asn Glu Asp Arg Lys Lys Asp Leu Ser Lys Met Lys Ser Leu
435 440 445

Leu Asp Ile Leu Thr Asp Pro Ser Lys Arg Cys Pro Leu Lys Thr Leu
450 455 460

Gln Lys Cys Glu Ile Ala Leu Glu Lys Leu Lys Asn Asp Met Ala Val
465 470 475 480

Pro Thr Pro Pro Pro Pro Pro Val Pro Pro Thr Lys Gln Gln Tyr Leu
485 490 495

Cys Gln Pro Leu Leu Asp Ala Val Leu Ala Asn Ile Arg Ser Pro Val
500 505 510

Phe Asn His Ser Leu Tyr Arg Thr Phe Val Pro Ala Met Thr Ala Ile
515 520 525

His Gly Pro Pro Ile Thr Ala Pro Val Val Cys Thr Arg Lys Arg Arg
530 535 540

Leu Glu Asp Asp Glu Arg Gln Ser Ile Pro Ser Val Leu Gln Gly Glu
545 550 555 560

Val Ala Arg Leu Asp Pro Lys Phe Leu Val Asn Leu Asp Pro Ser His
565 570 575

Cys Ser Asn Asn Gly Thr Val His Leu Ile Cys Lys Leu Asp Asp Lys
580 585 590

Asp Leu Pro Ser Val Pro Pro Leu Glu Leu Ser Val Pro Ala Asp Tyr
595 600 605

Pro Ala Gln Ser Pro Leu Trp Ile Asp Arg Gln Trp Gln Tyr Asp Ala
610 615 620

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Asn Pro Phe Leu Gln Ser Val His Arg Cys Met Thr Ser Arg Leu Leu
625 630 635 640

Gln Leu Pro Asp Lys His Ser Val Thr Ala Leu Leu Asn Thr Trp Ala
645 650 655

Gln Ser Val His Gln Ala Cys Leu Ser Ala Ala
660 665

<210> 113
<211> 792
<212> PRT
<213> Homo sapiens

<400> 113
Met Asp Val Ser Gly Gln Glu Thr Asp Trp Arg Ser Thr Ala Phe Arg
1 5 10 15

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

Ala His Ser Lys Ser Ser Lys Asp Met Glu Ser His Val Phe Leu Lys
35 40 45

Ala Lys Thr Arg Asp Glu Tyr Leu Ser Leu Val Ala Arg Leu Ile Ile
50 55 60

His Phe Arg Asp Ile His Asn Lys Lys Ser Gln Ala Ser Val Ser Asp
65 70 75 80

Pro Met Asn Ala Leu Gln Ser Leu Thr Gly Gly Pro Ala Ala Gly Ala
85 90 95

Ala Gly Ile Gly Met Pro Pro Arg Gly Pro Gly Gln Ser Leu Gly Gly
100 105 110

Met Gly Ser Leu Gly Ala Met Gly Gln Pro Met Ser Leu Ser Gly Gln
115 120 125

Pro Pro Pro Gly Thr Ser Gly Met Ala Pro His Ser Met Ala Val Val
130 135 140

Ser Thr Ala Thr Pro Gln Thr Gln Leu Gln Leu Gln Gln Val Ala Leu
145 150 155 160

Gln Gln Gln Gln Gln Gln Gln Gln Phe Gln Gln Gln Gln Gln Ala Ala
165 170 175

Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Phe Gln Ala Gln
180 185 190

Gln Ser Ala Met Gln Gln Gln Phe Gln Ala Val Val Gln Gln Gln Gln
195 200 205

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Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln His Leu Ile Lys Leu His
210 215 220

His Gln Asn Gln Gln Gln Ile Gln Gln Gln Gln Gln Gln Leu Gln Arg
225 230 235 240

Ile Ala Gln Leu Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
245 250 255

Gln Gln Gln Gln Gln Gln Ala Leu Gln Ala Gln Pro Pro Ile Gln Gln
260 265 270

Pro Pro Met Gln Gln Pro Gln Pro Pro Pro Ser Gln Ala Leu Pro Gln
275 280 285

Gln Leu Gln Gln Met His His Thr Gln His His Gln Pro Pro Pro Gln
290 295 300

Pro Gln Gln Pro Pro Val Ala Gln Asn Gln Pro Ser Gln Leu Pro Pro
305 310 315 320

Gln Ser Gln Thr Gln Pro Leu Val Ser Gln Ala Gln Ala Leu Pro Gly
325 330 335

Gln Met Leu Tyr Thr Gln Pro Pro Leu Lys Phe Val Arg Ala Pro Met
340 345 350

Val Val Gln Gln Pro Pro Val Gln Pro Gln Val Gln Gln Gln Gln Thr
355 360 365

Ala Val Gln Thr Ala Gln Ala Ala Gln Met Val Ala Pro Gly Val Gln
370 375 380

Met Ile Thr Glu Ala Leu Ala Gln Gly Gly Met His Ile Arg Ala Arg
385 390 395 400

Phe Pro Pro Thr Thr Ala Val Ser Ala Ile Pro Ser Ser Ser Ile Pro
405 410 415

Leu Gly Arg Gln Pro Met Ala Gln Val Ser Gln Ser Ser Leu Pro Met
420 425 430

Leu Ser Ser Pro Ser Pro Gly Gln Gln Val Gln Thr Pro Gln Ser Met
435 440 445

Pro Pro Pro Pro Gln Pro Ser Pro Gln Pro Gly Gln Pro Ser Ser Gln
450 455 460

Pro Asn Ser Asn Val Ser Ser Gly Pro Ala Pro Ser Pro Ser Ser Phe
465 470 475 480

Leu Pro Ser Pro Ser Pro Gln Pro Ser Gln Ser Pro Val Thr Ala Arg
485 490 495

Thr Pro Gln Asn Phe Ser Val Pro Ser Pro Gly Pro Leu Asn Thr Pro
500 505 510

Val Asn Pro Ser Ser Val Met Ser Pro Ala Gly Ser Ser Gln Ala Glu
515 520 525

Glu Gln Gln Tyr Leu Asp Lys Leu Lys Gln Leu Ser Lys Tyr Ile Glu
530 535 540

Pro Leu Arg Arg Met Ile Asn Lys Ile Asp Lys Asn Glu Asp Arg Lys
545 550 555 560

Lys Asp Leu Ser Lys Met Lys Ser Leu Leu Asp Ile Leu Thr Asp Pro
565 570 575

Ser Lys Arg Cys Pro Leu Lys Thr Leu Gln Lys Cys Glu Ile Ala Leu
580 585 590

Glu Lys Leu Lys Asn Asp Met Ala Val Pro Thr Pro Pro Pro Pro Pro
595 600 605

Val Pro Pro Thr Lys Gln Gln Tyr Leu Cys Gln Pro Leu Leu Asp Ala
610 615 620

Val Leu Ala Asn Ile Arg Ser Pro Val Phe Asn His Ser Leu Tyr Arg
625 630 635 640

Thr Phe Val Pro Ala Met Thr Ala Ile His Gly Pro Pro Ile Thr Ala
645 650 655

Pro Val Val Cys Thr Arg Lys Arg Arg Leu Glu Asp Asp Glu Arg Gln
660 665 670

Ser Ile Pro Ser Val Leu Gln Gly Glu Val Ala Arg Leu Asp Pro Lys
675 680 685

Phe Leu Val Asn Leu Asp Pro Ser His Cys Ser Asn Asn Gly Thr Val
690 695 700

His Leu Ile Cys Lys Leu Gly Glu Cys Pro Glu Gly Arg Asp Trp Cys
705 710 715 720

Gly Lys Ala Gly Pro Asp Arg Ser Pro Arg Thr Leu Pro Ser Lys Pro
725 730 735

Asp Gly Thr Ala Pro Arg Thr His Pro Val Phe Thr Pro Arg Gln Ala
740 745 750

Val Cys Ser Ile Leu Thr His Thr Gly Leu Gln Thr Ala Trp Pro Cys
755 760 765

Leu Ser Pro His Cys Gln Ser Pro His Thr Leu Thr Ser Pro Thr Gln
770 775 780

Met Trp Leu Cys Leu Pro Gly Pro
785 790

<210> 114
<211> 694
<212> PRT
<213> Homo sapiens

<400> 114
Met Asp Val Ser Gly Gln Glu Thr Asp Trp Arg Ser Thr Ala Phe Arg
1 5 10 15

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

Ala His Ser Lys Ser Ser Lys Asp Met Glu Ser His Val Phe Leu Lys
35 40 45

Ala Lys Thr Arg Asp Glu Tyr Leu Ser Leu Val Ala Arg Leu Ile Ile
50 55 60

His Phe Arg Asp Ile His Asn Lys Lys Ser Gln Ala Ser Val Ser Asp
65 70 75 80

Pro Met Asn Ala Leu Gln Ser Leu Thr Gly Gly Pro Ala Ala Gly Ala
85 90 95

Ala Gly Ile Gly Met Pro Pro Arg Gly Pro Gly Gln Ser Leu Gly Gly
100 105 110

Met Gly Ser Leu Gly Ala Met Gly Gln Pro Met Ser Leu Ser Gly Gln
115 120 125

Pro Pro Pro Gly Thr Ser Gly Met Ala Pro His Ser Met Ala Val Val
130 135 140

Ser Thr Ala Thr Pro Gln Thr Gln Leu Gln Leu Gln Gln Val Ala Leu
145 150 155 160

Gln Gln Gln Gln Gln Gln Gln Gln Phe Gln Gln Gln Gln Gln Ala Ala
165 170 175

Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Phe Gln Ala Gln
180 185 190

Gln Ser Ala Met Gln Gln Gln Phe Gln Ala Val Val Gln Gln Gln Gln
195 200 205

Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln His Leu Ile Lys Leu His
210 215 220

His Gln Asn Gln Gln Gln Ile Gln Gln Gln Gln Gln Gln Leu Gln Arg
225 230 235 240

Ile Ala Gln Leu Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
245 250 255

Gln Gln Gln Gln Gln Gln Ala Leu Gln Ala Gln Pro Pro Ile Gln Gln
260 265 270

Pro Pro Met Gln Gln Pro Gln Pro Pro Pro Ser Gln Ala Leu Pro Gln
275 280 285

Gln Leu Gln Gln Met His His Thr Gln His His Gln Pro Pro Pro Gln
290 295 300

Pro Gln Gln Pro Pro Val Ala Gln Asn Gln Pro Ser Gln Leu Pro Pro
305 310 315 320

Gln Ser Gln Thr Gln Pro Leu Val Ser Gln Ala Gln Ala Leu Pro Gly
325 330 335

Gln Met Leu Tyr Thr Gln Pro Pro Leu Lys Phe Val Arg Ala Pro Met
340 345 350

Val Val Gln Gln Pro Pro Val Gln Pro Gln Val Gln Gln Gln Gln Thr
355 360 365

Ala Val Gln Thr Ala Gln Ala Ala Gln Met Val Ala Pro Gly Val Gln
370 375 380

Met Ile Thr Glu Ala Leu Ala Gln Gly Gly Met His Ile Arg Ala Arg
385 390 395 400

Phe Pro Pro Thr Thr Ala Val Ser Ala Ile Pro Ser Ser Ser Ile Pro
405 410 415

Leu Gly Arg Gln Pro Met Ala Gln Val Ser Gln Ser Ser Leu Pro Met
420 425 430

Leu Ser Ser Pro Ser Pro Gly Gln Gln Val Gln Thr Pro Gln Ser Met
435 440 445

Pro Pro Pro Pro Gln Pro Ser Pro Gln Pro Gly Gln Pro Ser Ser Gln
450 455 460

Pro Asn Ser Asn Val Ser Ser Gly Pro Ala Pro Ser Pro Ser Ser Phe
465 470 475 480

Leu Pro Ser Pro Ser Pro Gln Pro Ser Gln Ser Pro Val Thr Ala Arg
485 490 495

Thr Pro Gln Asn Phe Ser Val Pro Ser Pro Gly Pro Leu Asn Thr Pro
500 505 510

Val Asn Pro Ser Ser Val Met Ser Pro Ala Gly Ser Ser Gln Ala Glu
515 520 525

Glu Gln Gln Tyr Leu Asp Lys Leu Lys Gln Leu Ser Lys Tyr Ile Glu
530 535 540

Pro Leu Arg Arg Met Ile Asn Lys Ile Asp Lys Asn Glu Asp Arg Lys
545 550 555 560

Lys Asp Leu Ser Lys Met Lys Ser Leu Leu Asp Ile Leu Thr Asp Pro
565 570 575

Ser Lys Arg Cys Pro Leu Lys Thr Leu Gln Lys Cys Glu Ile Ala Leu
580 585 590

Glu Lys Leu Lys Asn Asp Met Ala Val Pro Thr Pro Pro Pro Pro Pro
595 600 605

Val Pro Pro Thr Lys Gln Gln Tyr Leu Cys Gln Pro Leu Leu Asp Ala
610 615 620

Val Leu Ala Asn Ile Arg Ser Pro Val Phe Asn His Ser Leu Tyr Arg
625 630 635 640

Thr Phe Val Pro Ala Met Thr Ala Ile His Gly Pro Pro Ile Thr Tyr
645 650 655

Val Gln Leu Gly Trp Ala Leu Arg Arg Ala Ala Ser Pro Gly Pro Arg
660 665 670

Val Pro Gly Val Val Thr Met Pro Pro Pro Gln Gly Pro Ser Gly Val
675 680 685

His Pro Glu Ala Gln Ala
690

<210> 115
<211> 682
<212> PRT
<213> Homo sapiens

<400> 115
Met Asp Val Ser Gly Gln Glu Thr Asp Trp Arg Ser Thr Ala Phe Arg
1 5 10 15

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

```
Ala His Ser Lys Ser Ser Lys Asp Met Glu Ser His Val Phe Leu Lys
        35                  40                  45

Ala Lys Thr Arg Asp Glu Tyr Leu Ser Leu Val Ala Arg Leu Ile Ile
    50                  55                  60

His Phe Arg Asp Ile His Asn Lys Lys Ser Gln Ala Ser Val Ser Asp
65                  70                  75                  80

Pro Met Asn Ala Leu Gln Ser Leu Thr Gly Gly Pro Ala Ala Gly Ala
                85                  90                  95

Ala Gly Ile Gly Met Pro Pro Arg Gly Pro Gly Gln Ser Leu Gly Gly
            100                 105                 110

Met Gly Ser Leu Gly Ala Met Gly Gln Pro Met Ser Leu Ser Gly Gln
        115                 120                 125

Pro Pro Pro Gly Thr Ser Gly Met Ala Pro His Ser Met Ala Val Val
    130                 135                 140

Ser Thr Ala Thr Pro Gln Thr Gln Leu Gln Leu Gln Gln Val Ala Leu
145                 150                 155                 160

Gln Gln Gln Gln Gln Gln Gln Gln Phe Gln Gln Gln Gln Gln Ala Ala
                165                 170                 175

Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Phe Gln Ala Gln
            180                 185                 190

Gln Ser Ala Met Gln Gln Pro Gln Gln Pro Pro Val Ala Gln Asn Gln
        195                 200                 205

Pro Ser Gln Leu Pro Pro Gln Ser Gln Thr Gln Pro Leu Val Ser Gln
    210                 215                 220

Ala Gln Ala Leu Pro Gly Gln Met Leu Tyr Thr Gln Pro Pro Leu Lys
225                 230                 235                 240

Phe Val Arg Ala Pro Met Val Val Gln Gln Pro Pro Val Gln Pro Gln
                245                 250                 255

Val Gln Gln Gln Gln Thr Ala Val Gln Thr Ala Gln Ala Ala Gln Met
            260                 265                 270

Val Ala Pro Gly Val Gln Met Ile Thr Glu Ala Leu Ala Gln Gly Gly
        275                 280                 285

Met His Ile Arg Ala Arg Phe Pro Pro Thr Thr Ala Val Ser Ala Ile
    290                 295                 300
```

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Pro Ser Ser Ser Ile Pro Leu Gly Arg Gln Pro Met Ala Gln Val Ser
305                 310                 315                 320

Gln Ser Ser Leu Pro Met Leu Ser Ser Pro Ser Pro Gly Gln Gln Val
                325                 330                 335

Gln Thr Pro Gln Ser Met Pro Pro Pro Pro Gln Pro Ser Pro Gln Pro
            340                 345                 350

Gly Gln Pro Ser Ser Gln Pro Asn Ser Asn Val Ser Ser Gly Pro Ala
        355                 360                 365

Pro Ser Pro Ser Ser Phe Leu Pro Ser Pro Ser Pro Gln Pro Ser Gln
    370                 375                 380

Ser Pro Val Thr Ala Arg Thr Pro Gln Asn Phe Ser Val Pro Ser Pro
385                 390                 395                 400

Gly Pro Leu Asn Thr Pro Val Asn Pro Ser Ser Val Met Ser Pro Ala
                405                 410                 415

Gly Ser Ser Gln Ala Glu Glu Gln Gln Tyr Leu Asp Lys Leu Lys Gln
            420                 425                 430

Leu Ser Lys Tyr Ile Glu Pro Leu Arg Arg Met Ile Asn Lys Ile Asp
        435                 440                 445

Lys Asn Glu Asp Arg Lys Lys Asp Leu Ser Lys Met Lys Ser Leu Leu
    450                 455                 460

Asp Ile Leu Thr Asp Pro Ser Lys Arg Cys Pro Leu Lys Thr Leu Gln
465                 470                 475                 480

Lys Cys Glu Ile Ala Leu Glu Lys Leu Lys Asn Asp Met Ala Val Pro
                485                 490                 495

Thr Pro Pro Pro Pro Pro Val Pro Pro Thr Lys Gln Gln Tyr Leu Cys
            500                 505                 510

Gln Pro Leu Leu Asp Ala Val Leu Ala Asn Ile Arg Ser Pro Val Phe
        515                 520                 525

Asn His Ser Leu Tyr Arg Thr Phe Val Pro Ala Met Thr Ala Ile His
    530                 535                 540

Gly Pro Pro Ile Thr Ala Pro Val Val Cys Thr Arg Lys Arg Arg Leu
545                 550                 555                 560

Glu Asp Asp Glu Arg Gln Ser Ile Pro Ser Val Leu Gln Gly Glu Val
                565                 570                 575

Ala Arg Leu Asp Pro Lys Phe Leu Val Asn Leu Asp Pro Ser His Cys
```

580 585 590

Ser Asn Asn Gly Thr Val His Leu Ile Cys Lys Leu Asp Asp Lys Asp
595 600 605

Leu Pro Ser Val Pro Pro Leu Glu Leu Ser Val Pro Ala Asp Tyr Pro
610 615 620

Ala Gln Ser Pro Leu Trp Ile Asp Arg Gln Trp Gln Tyr Asp Ala Asn
625 630 635 640

Pro Phe Leu Gln Ser Val His Arg Cys Met Thr Ser Arg Leu Leu Gln
645 650 655

Leu Pro Asp Lys His Ser Val Thr Ala Leu Leu Asn Thr Trp Ala Gln
660 665 670

Ser Val His Gln Ala Cys Leu Ser Ala Ala
675 680

<210> 116
<211> 99
<212> PRT
<213> Homo sapiens

<400> 116
Met Cys Asp Leu Arg Arg Leu His Leu Gly Ala Cys Pro Thr Glu Glu
1 5 10 15

Cys Lys Ala Cys Thr Arg Cys Gly Cys Val Thr Met Leu Lys Ser Pro
20 25 30

Asn Arg Thr Thr Ala Val Lys Gln Trp Glu Gln Arg Trp Ile Lys Asn
35 40 45

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

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

His His Ser Pro Arg Thr Pro Arg Ser Leu Asp His Leu His Pro Glu
85 90 95

Asp Arg Pro

<210> 117
<211> 237
<212> PRT
<213> Homo sapiens

<400> 117
Met Cys Asp Leu Arg Arg Pro Ala Ala Gly Gly Met Met Asp Leu Ala
1 5 10 15

Tyr Val Cys Glu Trp Glu Lys Trp Ser Lys Ser Thr His Cys Pro Ser
20 25 30

Val Pro Leu Ala Cys Ala Trp Ser Cys Arg Asn Leu Ile Ala Phe Thr
35 40 45

Met Asp Leu Arg Ser Asp Asp Gln Asp Leu Thr Arg Met Ile His Ile
50 55 60

Leu Asp Thr Glu His Pro Trp Asp Leu His Ser Ile Pro Ser Glu His
65 70 75 80

His Glu Ala Ile Thr Cys Leu Glu Trp Asp Gln Ser Gly Ser Arg Leu
85 90 95

Leu Ser Ala Asp Ala Asp Gly Gln Ile Lys Cys Trp Ser Met Ala Asp
100 105 110

His Leu Ala Asn Ser Trp Glu Ser Ser Val Gly Ser Leu Val Glu Gly
115 120 125

Asp Pro Ile Val Ala Leu Ser Trp Leu His Asn Gly Val Lys Leu Ala
130 135 140

Leu His Leu Gly Ala Cys Pro Thr Glu Glu Cys Lys Ala Cys Thr Arg
145 150 155 160

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

Lys Gln Trp Glu Gln Arg Trp Ile Lys Asn Cys Leu Ala Val Glu Gly
180 185 190

Arg Gly Pro Asp Ala Cys Val Thr Ser Arg Ala Ser Glu Glu Ala Pro
195 200 205

Ala Phe Val Gln Leu Gly Pro Gln Ser Thr His His Ser Pro Arg Thr
210 215 220

Pro Arg Ser Leu Asp His Leu His Pro Glu Asp Arg Pro
225 230 235

<210> 118
<211> 368
<212> PRT
<213> Homo sapiens

<400> 118
Met Cys Asp Leu Arg Arg Pro Ala Ala Gly Gly Met Met Asp Leu Ala
1 5 10 15

Tyr Val Cys Glu Trp Glu Lys Trp Ser Lys Ser Thr His Cys Pro Ser

```
            20                  25                  30

Val Pro Leu Ala Cys Ala Trp Ser Cys Arg Asn Leu Ile Ala Ile Ser
        35                  40                  45

Ser Thr Leu Lys Ser Leu Leu Arg Pro His Phe Leu Asn Thr Pro Asp
    50                  55                  60

Lys Ser Pro Gly Asp Arg Leu Thr Glu Ile Cys Thr Lys Ile Thr Asp
65                  70                  75                  80

Val Asp Ile Asp Lys Val Met Ile Asn Leu Lys Thr Glu Glu Phe Val
                85                  90                  95

Leu Asp Met Asn Thr Leu Gln Ala Leu Gln Gln Leu Leu Gln Trp Val
            100                 105                 110

Gly Asp Phe Val Leu Tyr Leu Leu Ala Ser Leu Pro Asn Gln Gly Ser
        115                 120                 125

Leu Leu Arg Pro Gly His Ser Phe Leu Arg Asp Gly Thr Ser Leu Gly
    130                 135                 140

Met Leu Arg Glu Leu Met Val Val Ile Arg Ile Trp Gly Leu Leu Lys
145                 150                 155                 160

Pro Ser Cys Leu Pro Val Tyr Thr Ala Thr Ser Asp Thr Gln Asp Ser
                165                 170                 175

Met Ser Leu Leu Phe Arg Leu Leu Thr Lys Leu Trp Ile Cys Cys Arg
            180                 185                 190

Asp Glu Gly Pro Ala Ser Glu Pro Asp Glu Ala Leu Val Asp Glu Cys
        195                 200                 205

Cys Leu Leu Pro Ser Gln Leu Leu Ile Pro Ser Leu Asp Trp Leu Pro
    210                 215                 220

Ala Ser Asp Gly Leu Val Ser Arg Leu Gln Pro Lys Gln Pro Leu Arg
225                 230                 235                 240

Leu Gln Phe Gly Arg Ala Pro Thr Leu Pro Gly Ser Ala Ala Thr Leu
                245                 250                 255

Gln Leu Asp Gly Leu Ala Arg Ala Pro Gly Gln Pro Lys Ile Asp His
            260                 265                 270

Leu Arg Arg Leu His Leu Gly Ala Cys Pro Thr Glu Glu Cys Lys Ala
        275                 280                 285

Cys Thr Arg Cys Gly Cys Val Thr Met Leu Lys Ser Pro Asn Arg Thr
    290                 295                 300
```

Thr Ala Val Lys Gln Trp Glu Gln Arg Trp Ile Lys Asn Cys Leu Ala
305 310 315 320

Val Glu Gly Arg Gly Pro Asp Ala Cys Val Thr Ser Arg Ala Ser Glu
325 330 335

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

Pro Arg Thr Pro Arg Ser Leu Asp His Leu His Pro Glu Asp Arg Pro
355 360 365

<210> 119
<211> 638
<212> PRT
<213> Homo sapiens

<400> 119
Met Cys Asp Leu Arg Arg Pro Ala Ala Gly Gly Met Met Asp Leu Ala
1 5 10 15

Tyr Val Cys Glu Trp Glu Lys Trp Ser Lys Ser Thr His Cys Pro Ser
20 25 30

Val Pro Leu Ala Cys Ala Trp Ser Cys Arg Asn Leu Ile Ala Phe Thr
35 40 45

Met Asp Leu Arg Ser Asp Asp Gln Asp Leu Thr Arg Met Ile His Ile
50 55 60

Leu Asp Thr Glu His Pro Trp Asp Leu His Ser Ile Pro Ser Glu His
65 70 75 80

His Glu Ala Ile Thr Cys Leu Glu Trp Asp Gln Ser Gly Ser Arg Leu
85 90 95

Leu Ser Ala Asp Ala Asp Gly Gln Ile Lys Cys Trp Ser Met Ala Asp
100 105 110

His Leu Ala Asn Ser Trp Glu Ser Ser Val Gly Ser Leu Val Glu Gly
115 120 125

Asp Pro Ile Val Ala Leu Ser Trp Leu His Asn Gly Val Lys Leu Ala
130 135 140

Leu Ala Phe His Asp Gly Ser Val His Ile Val His Arg Leu Ser Leu
145 150 155 160

Gln Thr Met Ala Val Phe Tyr Ser Ser Ala Ala Pro Arg Pro Val Asp
165 170 175

Glu Pro Ala Met Lys Arg Pro Arg Thr Ala Gly Pro Ala Val His Leu

```
            180                 185                 190

Lys Ala Met Gln Leu Ser Trp Thr Ser Leu Ala Leu Val Gly Ile Asp
        195                 200                 205

Ser His Gly Lys Leu Ser Val Leu Arg Leu Ser Pro Ser Met Gly His
    210                 215                 220

Pro Leu Glu Val Gly Leu Ala Leu Arg His Leu Leu Phe Leu Leu Glu
225                 230                 235                 240

Tyr Cys Met Val Thr Gly Tyr Asp Trp Trp Asp Ile Leu Leu His Val
                245                 250                 255

Gln Pro Ser Met Val Gln Ser Leu Val Glu Lys Leu His Glu Glu Tyr
            260                 265                 270

Thr Arg Gln Thr Ala Ala Leu Gln Gln Val Leu Ser Thr Arg Ile Leu
        275                 280                 285

Ala Met Lys Ala Ser Leu Cys Lys Leu Ser Pro Cys Thr Val Thr Arg
    290                 295                 300

Val Cys Asp Tyr His Thr Lys Leu Phe Leu Ile Ala Ile Ser Ser Thr
305                 310                 315                 320

Leu Lys Ser Leu Leu Arg Pro His Phe Leu Asn Thr Pro Asp Lys Ser
                325                 330                 335

Pro Gly Asp Arg Leu Thr Glu Ile Cys Thr Lys Ile Thr Asp Val Asp
            340                 345                 350

Ile Asp Lys Val Met Ile Asn Leu Lys Thr Glu Glu Phe Val Leu Asp
        355                 360                 365

Met Asn Thr Leu Gln Ala Leu Gln Gln Leu Leu Gln Trp Val Gly Asp
    370                 375                 380

Phe Val Leu Tyr Leu Leu Ala Ser Leu Pro Asn Gln Gly Ser Leu Leu
385                 390                 395                 400

Arg Pro Gly His Ser Phe Leu Arg Asp Gly Thr Ser Leu Gly Met Leu
                405                 410                 415

Arg Glu Leu Met Val Val Ile Arg Ile Trp Gly Leu Leu Lys Pro Ser
            420                 425                 430

Cys Leu Pro Val Tyr Thr Ala Thr Ser Asp Thr Gln Asp Ser Met Ser
        435                 440                 445

Leu Leu Phe Arg Leu Leu Thr Lys Leu Trp Ile Cys Cys Arg Asp Glu
    450                 455                 460
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Gly Pro Ala Ser Glu Pro Asp Glu Ala Leu Val Asp Glu Cys Cys Leu
465 470 475 480

Leu Pro Ser Gln Leu Leu Ile Pro Ser Leu Asp Trp Leu Pro Ala Ser
485 490 495

Asp Gly Leu Val Ser Arg Leu Gln Pro Lys Gln Pro Leu Arg Leu Gln
500 505 510

Phe Gly Arg Ala Pro Thr Leu Pro Gly Ser Ala Ala Thr Leu Gln Leu
515 520 525

Asp Gly Leu Ala Arg Ala Pro Gly Gln Pro Lys Ile Asp His Leu Arg
530 535 540

Arg Leu His Leu Gly Ala Cys Pro Thr Glu Glu Cys Lys Ala Cys Thr
545 550 555 560

Arg Cys Gly Cys Val Thr Met Leu Lys Ser Pro Asn Arg Thr Thr Ala
565 570 575

Val Lys Gln Trp Glu Gln Arg Trp Ile Lys Asn Cys Leu Ala Val Glu
580 585 590

Gly Arg Gly Pro Asp Ala Cys Val Thr Ser Arg Ala Ser Glu Glu Ala
595 600 605

Pro Ala Phe Val Gln Leu Gly Pro Gln Ser Thr His His Ser Pro Arg
610 615 620

Thr Pro Arg Ser Leu Asp His Leu His Pro Glu Asp Arg Pro
625 630 635

<210> 120
<211> 282
<212> PRT
<213> Homo sapiens

<400> 120
Met Ile Asn Leu Lys Thr Glu Glu Phe Val Leu Asp Met Asn Thr Leu
1 5 10 15

Gln Ala Leu Gln Gln Leu Leu Gln Trp Val Gly Asp Phe Val Leu Tyr
20 25 30

Leu Leu Ala Ser Leu Pro Asn Gln Gly Ser Leu Leu Arg Pro Gly His
35 40 45

Ser Phe Leu Arg Asp Gly Thr Ser Leu Gly Met Leu Arg Glu Leu Met
50 55 60

Val Val Ile Arg Ile Trp Gly Leu Leu Lys Pro Ser Cys Leu Pro Val

65 70 75 80

Tyr Thr Ala Thr Ser Asp Thr Gln Asp Ser Met Ser Leu Leu Phe Arg
85 90 95

Leu Leu Thr Lys Leu Trp Ile Cys Cys Arg Asp Glu Gly Pro Ala Ser
100 105 110

Glu Pro Asp Glu Ala Leu Val Asp Glu Cys Cys Leu Leu Pro Ser Gln
115 120 125

Leu Leu Ile Pro Ser Leu Asp Trp Leu Pro Ala Ser Asp Gly Leu Val
130 135 140

Ser Arg Leu Gln Pro Lys Gln Pro Leu Arg Leu Gln Phe Gly Arg Ala
145 150 155 160

Pro Thr Leu Pro Gly Ser Ala Ala Thr Leu Gln Leu Asp Gly Leu Ala
165 170 175

Arg Ala Pro Gly Gln Pro Lys Ile Asp His Leu Arg Arg Leu His Leu
180 185 190

Gly Ala Cys Pro Thr Glu Glu Cys Lys Ala Cys Thr Arg Cys Gly Cys
195 200 205

Val Thr Met Leu Lys Ser Pro Asn Arg Thr Thr Ala Val Lys Gln Trp
210 215 220

Glu Gln Arg Trp Ile Lys Asn Cys Leu Ala Val Glu Gly Arg Gly Pro
225 230 235 240

Asp Ala Cys Val Thr Ser Arg Ala Ser Glu Glu Ala Pro Ala Phe Val
245 250 255

Gln Leu Gly Pro Gln Ser Thr His His Ser Pro Arg Thr Pro Arg Ser
260 265 270

Leu Asp His Leu His Pro Glu Asp Arg Pro
275 280

<210> 121
<211> 147
<212> PRT
<213> Homo sapiens

<400> 121
Met Cys Asp Leu Arg Arg Pro Ala Ala Gly Gly Met Met Asp Leu Ala
1 5 10 15

Tyr Val Cys Glu Trp Glu Lys Trp Ser Lys Ser Thr His Cys Pro Ser
20 25 30

Val Pro Leu Ala Cys Ala Trp Ser Cys Arg Asn Leu Ile Ala Phe Thr
35 40 45

Met Asp Leu Arg Ser Asp Asp Gln Asp Leu Thr Arg Met Ile His Ile
50 55 60

Leu Asp Thr Glu His Pro Trp Asp Leu His Ser Ile Pro Ser Glu His
65 70 75 80

His Glu Ala Ile Thr Cys Leu Glu Trp Asp Gln Ser Gly Ser Arg Leu
85 90 95

Leu Ser Ala Asp Ala Asp Gly Gln Ile Lys Cys Trp Ser Met Ala Asp
100 105 110

His Pro Ala Ala Ala Arg Ala Thr Ala Arg Pro Gly Leu Ser Ser Ala
115 120 125

Arg Leu Thr Ser Ala Arg Pro Ala Gly Leu Leu Lys Ala Val Gly Arg
130 135 140

Thr Pro Ala
145

<210> 122
<211> 408
<212> PRT
<213> Homo sapiens

<400> 122
Met Cys Asp Leu Arg Arg Pro Ala Ala Gly Gly Met Met Asp Leu Ala
1 5 10 15

Tyr Asp Trp Trp Asp Ile Leu Leu His Val Gln Pro Ser Met Val Gln
20 25 30

Ser Leu Val Glu Lys Leu His Glu Glu Tyr Thr Arg Gln Thr Ala Ala
35 40 45

Leu Gln Gln Val Leu Ser Thr Arg Ile Leu Ala Met Lys Ala Ser Leu
50 55 60

Cys Lys Leu Ser Pro Cys Thr Val Thr Arg Val Cys Asp Tyr His Thr
65 70 75 80

Lys Leu Phe Leu Ile Ala Ile Ser Ser Thr Leu Lys Ser Leu Leu Arg
85 90 95

Pro His Phe Leu Asn Thr Pro Asp Lys Ser Pro Gly Asp Arg Leu Thr
100 105 110

Glu Ile Cys Thr Lys Ile Thr Asp Val Asp Ile Asp Lys Val Met Ile
115 120 125

Asn Leu Lys Thr Glu Glu Phe Val Leu Asp Met Asn Thr Leu Gln Ala
130 135 140

Leu Gln Gln Leu Leu Gln Trp Val Gly Asp Phe Val Leu Tyr Leu Leu
145 150 155 160

Ala Ser Leu Pro Asn Gln Gly Ser Leu Leu Arg Pro Gly His Ser Phe
165 170 175

Leu Arg Asp Gly Thr Ser Leu Gly Met Leu Arg Glu Leu Met Val Val
180 185 190

Ile Arg Ile Trp Gly Leu Leu Lys Pro Ser Cys Leu Pro Val Tyr Thr
195 200 205

Ala Thr Ser Asp Thr Gln Asp Ser Met Ser Leu Leu Phe Arg Leu Leu
210 215 220

Thr Lys Leu Trp Ile Cys Cys Arg Asp Glu Gly Pro Ala Ser Glu Pro
225 230 235 240

Asp Glu Ala Leu Val Asp Glu Cys Cys Leu Leu Pro Ser Gln Leu Leu
245 250 255

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

Leu Gln Pro Lys Gln Pro Leu Arg Leu Gln Phe Gly Arg Ala Pro Thr
275 280 285

Leu Pro Gly Ser Ala Ala Thr Leu Gln Leu Asp Gly Leu Ala Arg Ala
290 295 300

Pro Gly Gln Pro Lys Ile Asp His Leu Arg Arg Leu His Leu Gly Ala
305 310 315 320

Cys Pro Thr Glu Glu Cys Lys Ala Cys Thr Arg Cys Gly Cys Val Thr
325 330 335

Met Leu Lys Ser Pro Asn Arg Thr Thr Ala Val Lys Gln Trp Glu Gln
340 345 350

Arg Trp Ile Lys Asn Cys Leu Ala Val Glu Gly Arg Gly Pro Asp Ala
355 360 365

Cys Val Thr Ser Arg Ala Ser Glu Glu Ala Pro Ala Phe Val Gln Leu
370 375 380

Gly Pro Gln Ser Thr His His Ser Pro Arg Thr Pro Arg Ser Leu Asp
385 390 395 400

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His Leu His Pro Glu Asp Arg Pro
405

<210> 123
<211> 365
<212> PRT
<213> Homo sapiens

<400> 123
Met Cys Asp Leu Arg Arg Pro Ala Ala Gly Gly Met Met Asp Leu Ala
1 5 10 15

Tyr Val Cys Glu Trp Glu Lys Trp Ser Lys Ser Thr His Cys Pro Ser
20 25 30

Val Pro Leu Ala Cys Ala Trp Ser Cys Arg Asn Leu Ile Ala Phe Thr
35 40 45

Met Asp Leu Leu Arg Pro His Phe Leu Asn Thr Pro Asp Lys Ser Pro
50 55 60

Gly Asp Arg Leu Thr Glu Ile Cys Thr Lys Ile Thr Asp Val Asp Ile
65 70 75 80

Asp Lys Val Met Ile Asn Leu Lys Thr Glu Glu Phe Val Leu Asp Met
85 90 95

Asn Thr Leu Gln Ala Leu Gln Gln Leu Leu Gln Trp Val Gly Asp Phe
100 105 110

Val Leu Tyr Leu Leu Ala Ser Leu Pro Asn Gln Gly Ser Leu Leu Arg
115 120 125

Pro Gly His Ser Phe Leu Arg Asp Gly Thr Ser Leu Gly Met Leu Arg
130 135 140

Glu Leu Met Val Val Ile Arg Ile Trp Gly Leu Leu Lys Pro Ser Cys
145 150 155 160

Leu Pro Val Tyr Thr Ala Thr Ser Asp Thr Gln Asp Ser Met Ser Leu
165 170 175

Leu Phe Arg Leu Leu Thr Lys Leu Trp Ile Cys Cys Arg Asp Glu Gly
180 185 190

Pro Ala Ser Glu Pro Asp Glu Ala Leu Val Asp Glu Cys Cys Leu Leu
195 200 205

Pro Ser Gln Leu Leu Ile Pro Ser Leu Asp Trp Leu Pro Ala Ser Asp
210 215 220

Gly Leu Val Ser Arg Leu Gln Pro Lys Gln Pro Leu Arg Leu Gln Phe
225 230 235 240

Gly Arg Ala Pro Thr Leu Pro Gly Ser Ala Ala Thr Leu Gln Leu Asp
245 250 255

Gly Leu Ala Arg Ala Pro Gly Gln Pro Lys Ile Asp His Leu Arg Arg
260 265 270

Leu His Leu Gly Ala Cys Pro Thr Glu Glu Cys Lys Ala Cys Thr Arg
275 280 285

Cys Gly Cys Val Thr Met Leu Lys Ser Pro Asn Arg Thr Thr Ala Val
290 295 300

Lys Gln Trp Glu Gln Arg Trp Ile Lys Asn Cys Leu Ala Val Glu Gly
305 310 315 320

Arg Gly Pro Asp Ala Cys Val Thr Ser Arg Ala Ser Glu Glu Ala Pro
325 330 335

Ala Phe Val Gln Leu Gly Pro Gln Ser Thr His His Ser Pro Arg Thr
340 345 350

Pro Arg Ser Leu Asp His Leu His Pro Glu Asp Arg Pro
355 360 365

<210> 124
<211> 497
<212> PRT
<213> Homo sapiens

<400> 124
Met Cys Asp Leu Arg Arg Pro Ala Ala Gly Gly Met Met Asp Leu Ala
1 5 10 15

Tyr Val Cys Glu Trp Glu Lys Trp Ser Lys Ser Thr His Cys Pro Ser
20 25 30

Val Pro Leu Ala Cys Ala Trp Ser Cys Arg Asn Leu Ile Ala Phe Thr
35 40 45

Met Asp Leu Arg Ser Asp Asp Gln Asp Leu Thr Arg Met Ile His Ile
50 55 60

Leu Asp Thr Glu His Pro Trp Asp Leu His Ser Ile Pro Ser Pro Ser
65 70 75 80

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

Leu Leu Glu Tyr Cys Met Val Thr Gly Tyr Asp Trp Trp Asp Ile Leu
100 105 110

Leu His Val Gln Pro Ser Met Val Gln Ser Leu Val Glu Lys Leu His
115 120 125

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Glu Glu Tyr Thr Arg Gln Thr Ala Ala Leu Gln Gln Val Leu Ser Thr
130 135 140

Arg Ile Leu Ala Met Lys Ala Ser Leu Cys Lys Leu Ser Pro Cys Thr
145 150 155 160

Val Thr Arg Val Cys Asp Tyr His Thr Lys Leu Phe Leu Ile Ala Ile
165 170 175

Ser Ser Thr Leu Lys Ser Leu Leu Arg Pro His Phe Leu Asn Thr Pro
180 185 190

Asp Lys Ser Pro Gly Asp Arg Leu Thr Glu Ile Cys Thr Lys Ile Thr
195 200 205

Asp Val Asp Ile Asp Lys Val Met Ile Asn Leu Lys Thr Glu Glu Phe
210 215 220

Val Leu Asp Met Asn Thr Leu Gln Ala Leu Gln Gln Leu Leu Gln Trp
225 230 235 240

Val Gly Asp Phe Val Leu Tyr Leu Leu Ala Ser Leu Pro Asn Gln Gly
245 250 255

Ser Leu Leu Arg Pro Gly His Ser Phe Leu Arg Asp Gly Thr Ser Leu
260 265 270

Gly Met Leu Arg Glu Leu Met Val Val Ile Arg Ile Trp Gly Leu Leu
275 280 285

Lys Pro Ser Cys Leu Pro Val Tyr Thr Ala Thr Ser Asp Thr Gln Asp
290 295 300

Ser Met Ser Leu Leu Phe Arg Leu Leu Thr Lys Leu Trp Ile Cys Cys
305 310 315 320

Arg Asp Glu Gly Pro Ala Ser Glu Pro Asp Glu Ala Leu Val Asp Glu
325 330 335

Cys Cys Leu Leu Pro Ser Gln Leu Leu Ile Pro Ser Leu Asp Trp Leu
340 345 350

Pro Ala Ser Asp Gly Leu Val Ser Arg Leu Gln Pro Lys Gln Pro Leu
355 360 365

Arg Leu Gln Phe Gly Arg Ala Pro Thr Leu Pro Gly Ser Ala Ala Thr
370 375 380

Leu Gln Leu Asp Gly Leu Ala Arg Ala Pro Gly Gln Pro Lys Ile Asp
385 390 395 400

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His Leu Arg Arg Leu His Leu Gly Ala Cys Pro Thr Glu Glu Cys Lys
405 410 415

Ala Cys Thr Arg Cys Gly Cys Val Thr Met Leu Lys Ser Pro Asn Arg
420 425 430

Thr Thr Ala Val Lys Gln Trp Glu Gln Arg Trp Ile Lys Asn Cys Leu
435 440 445

Ala Val Glu Gly Arg Gly Pro Asp Ala Cys Val Thr Ser Arg Ala Ser
450 455 460

Glu Glu Ala Pro Ala Phe Val Gln Leu Gly Pro Gln Ser Thr His His
465 470 475 480

Ser Pro Arg Thr Pro Arg Ser Leu Asp His Leu His Pro Glu Asp Arg
485 490 495

Pro

<210> 125
<211> 808
<212> PRT
<213> Homo sapiens

<400> 125
Met Cys Asp Leu Arg Arg Pro Ala Ala Gly Gly Met Met Asp Leu Ala
1 5 10 15

Tyr Val Cys Glu Trp Glu Lys Trp Ser Lys Ser Thr His Cys Pro Ser
20 25 30

Val Pro Leu Ala Cys Ala Trp Ser Cys Arg Asn Leu Ile Ala Phe Thr
35 40 45

Met Asp Leu Arg Ser Asp Asp Gln Asp Leu Thr Arg Met Ile His Ile
50 55 60

Leu Asp Thr Glu His Pro Trp Asp Leu His Ser Ile Pro Ser Glu His
65 70 75 80

His Glu Ala Ile Thr Cys Leu Glu Trp Asp Gln Ser Gly Ser Arg Leu
85 90 95

Leu Ser Ala Asp Ala Asp Gly Gln Ile Lys Cys Trp Ser Met Ala Asp
100 105 110

His Leu Ala Asn Ser Trp Glu Ser Ser Val Gly Ser Leu Val Glu Gly
115 120 125

Asp Pro Ile Val Ala Leu Ser Trp Leu His Asn Gly Val Lys Leu Ala
130 135 140

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

Arg Val Lys Phe Ser Pro Ser Leu Thr Leu Phe Gly Gly Lys Pro Met
165 170 175

Glu Gly Trp Ile Ala Val Thr Val Ser Gly Leu Val Thr Val Ser Leu
180 185 190

Leu Lys Pro Ser Gly Gln Val Leu Thr Ser Thr Glu Ser Leu Cys Arg
195 200 205

Leu Arg Gly Arg Val Ala Leu Ala Asp Ile Ala Phe Thr Gly Gly Gly
210 215 220

Asn Ile Val Val Ala Thr Ala Asp Gly Ser Ser Ala Ser Pro Val Gln
225 230 235 240

Phe Tyr Lys Val Cys Val Ser Val Val Ser Glu Lys Cys Arg Ile Asp
245 250 255

Thr Glu Ile Leu Pro Ser Leu Phe Met Arg Cys Thr Thr Asp Leu Asn
260 265 270

Arg Lys Asp Lys Phe Pro Ala Ile Thr His Leu Lys Phe Leu Ala Arg
275 280 285

Asp Met Ser Glu Gln Val Leu Leu Cys Ala Ser Ser Gln Thr Ser Ser
290 295 300

Ile Val Glu Cys Trp Ser Leu Arg Lys Glu Gly Leu Pro Val Asn Asn
305 310 315 320

Ile Phe Gln Gln Ile Ser Pro Val Val Gly Asp Lys Gln Pro Thr Ile
325 330 335

Leu Lys Trp Arg Ile Leu Ser Ala Thr Asn Asp Leu Asp Arg Val Ser
340 345 350

Ala Val Ala Leu Pro Lys Leu Pro Ile Ser Leu Thr Asn Thr Asp Leu
355 360 365

Lys Val Ala Ser Asp Thr Gln Phe Tyr Pro Gly Leu Gly Leu Ala Leu
370 375 380

Ala Phe His Asp Gly Ser Val His Ile Val His Arg Leu Ser Leu Gln
385 390 395 400

Thr Met Ala Val Phe Tyr Ser Ser Ala Ala Pro Arg Pro Val Asp Glu
405 410 415

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Pro Ala Met Lys Arg Pro Arg Thr Ala Gly Pro Ala Val His Leu Lys
420 425 430

Ala Met Gln Leu Ser Trp Thr Ser Leu Ala Leu Val Gly Ile Asp Ser
435 440 445

His Gly Lys Val Leu Ser Thr Arg Ile Leu Ala Met Lys Ala Ser Leu
450 455 460

Cys Lys Leu Ser Pro Cys Thr Val Thr Arg Val Cys Asp Tyr His Thr
465 470 475 480

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

Pro His Phe Leu Asn Thr Pro Asp Lys Ser Pro Gly Asp Arg Leu Thr
500 505 510

Glu Ile Cys Thr Lys Ile Thr Asp Val Asp Ile Asp Lys Val Met Ile
515 520 525

Asn Leu Lys Thr Glu Glu Phe Val Leu Asp Met Asn Thr Leu Gln Ala
530 535 540

Leu Gln Gln Leu Leu Gln Trp Val Gly Asp Phe Val Leu Tyr Leu Leu
545 550 555 560

Ala Ser Leu Pro Asn Gln Gly Ser Leu Leu Arg Pro Gly His Ser Phe
565 570 575

Leu Arg Asp Gly Thr Ser Leu Gly Met Leu Arg Glu Leu Met Val Val
580 585 590

Ile Arg Ile Trp Gly Leu Leu Lys Pro Ser Cys Leu Pro Val Tyr Thr
595 600 605

Ala Thr Ser Asp Thr Gln Asp Ser Met Ser Leu Leu Phe Arg Leu Leu
610 615 620

Thr Lys Leu Trp Ile Cys Cys Arg Asp Glu Gly Pro Ala Ser Glu Pro
625 630 635 640

Asp Glu Ala Leu Val Asp Glu Cys Cys Leu Leu Pro Ser Gln Leu Leu
645 650 655

Ile Pro Ser Leu Asp Trp Leu Pro Ala Ser Asp Gly Leu Val Ser Arg
660 665 670

Leu Gln Pro Lys Gln Pro Leu Arg Leu Gln Phe Gly Arg Ala Pro Thr
675 680 685

Leu Pro Gly Ser Ala Ala Thr Leu Gln Leu Asp Gly Leu Ala Arg Ala
690 695 700

Pro Gly Gln Pro Lys Ile Asp His Leu Arg Arg Leu His Leu Gly Ala
705 710 715 720

Cys Pro Thr Glu Glu Cys Lys Ala Cys Thr Arg Cys Gly Cys Val Thr
725 730 735

Met Leu Lys Ser Pro Asn Arg Thr Thr Ala Val Lys Gln Trp Glu Gln
740 745 750

Arg Trp Ile Lys Asn Cys Leu Ala Val Glu Gly Arg Gly Pro Asp Ala
755 760 765

Cys Val Thr Ser Arg Ala Ser Glu Glu Ala Pro Ala Phe Val Gln Leu
770 775 780

Gly Pro Gln Ser Thr His His Ser Pro Arg Thr Pro Arg Ser Leu Asp
785 790 795 800

His Leu His Pro Glu Asp Arg Pro
805

<210> 126
<211> 465
<212> PRT
<213> Homo sapiens

<400> 126
Met Cys Asp Leu Arg Arg Pro Ala Ala Gly Gly Met Met Asp Leu Ala
1 5 10 15

Tyr Val Cys Glu Trp Glu Lys Trp Ser Lys Ser Thr His Cys Pro Ser
20 25 30

Val Pro Leu Ala Cys Ala Trp Ser Cys Arg Asn Leu Ile Ala Phe Thr
35 40 45

Met Asp Leu Arg Ser Asp Asp Gln Asp Leu Thr Arg Met Ile His Ile
50 55 60

Leu Asp Thr Glu His Pro Trp Asp Leu His Ser Ile Pro Ser Glu His
65 70 75 80

His Glu Ala Ile Thr Cys Leu Glu Trp Asp Gln Ser Gly Ser Arg Leu
85 90 95

Leu Ser Ala Asp Ala Asp Gly Gln Ile Lys Cys Trp Ser Met Ala Asp
100 105 110

His Leu Ala Asn Ser Trp Glu Ser Ser Val Gly Ser Leu Val Glu Gly
115 120 125

```
Asp Pro Ile Val Ala Leu Ser Trp Leu His Asn Gly Val Lys Leu Ala
    130                 135                 140

Leu His Val Glu Lys Ser Leu Leu Arg Pro His Phe Leu Asn Thr Pro
145                 150                 155                 160

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

Asp Val Asp Ile Asp Lys Val Met Ile Asn Leu Lys Thr Glu Glu Phe
            180                 185                 190

Val Leu Asp Met Asn Thr Leu Gln Ala Leu Gln Gln Leu Leu Gln Trp
        195                 200                 205

Val Gly Asp Phe Val Leu Tyr Leu Leu Ala Ser Leu Pro Asn Gln Gly
    210                 215                 220

Ser Leu Leu Arg Pro Gly His Ser Phe Leu Arg Asp Gly Thr Ser Leu
225                 230                 235                 240

Gly Met Leu Arg Glu Leu Met Val Val Ile Arg Ile Trp Gly Leu Leu
                245                 250                 255

Lys Pro Ser Cys Leu Pro Val Tyr Thr Ala Thr Ser Asp Thr Gln Asp
            260                 265                 270

Ser Met Ser Leu Leu Phe Arg Leu Leu Thr Lys Leu Trp Ile Cys Cys
        275                 280                 285

Arg Asp Glu Gly Pro Ala Ser Glu Pro Asp Glu Ala Leu Val Asp Glu
    290                 295                 300

Cys Cys Leu Leu Pro Ser Gln Leu Leu Ile Pro Ser Leu Asp Trp Leu
305                 310                 315                 320

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

Arg Leu Gln Phe Gly Arg Ala Pro Thr Leu Pro Gly Ser Ala Ala Thr
            340                 345                 350

Leu Gln Leu Asp Gly Leu Ala Arg Ala Pro Gly Gln Pro Lys Ile Asp
        355                 360                 365

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

Ala Cys Thr Arg Cys Gly Cys Val Thr Met Leu Lys Ser Pro Asn Arg
385                 390                 395                 400
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Thr Thr Ala Val Lys Gln Trp Glu Gln Arg Trp Ile Lys Asn Cys Leu
405 410 415

Ala Val Glu Gly Arg Gly Pro Asp Ala Cys Val Thr Ser Arg Ala Ser
420 425 430

Glu Glu Ala Pro Ala Phe Val Gln Leu Gly Pro Gln Ser Thr His His
435 440 445

Ser Pro Arg Thr Pro Arg Ser Leu Asp His Leu His Pro Glu Asp Arg
450 455 460

Pro
465

<210> 127
<211> 349
<212> PRT
<213> Homo sapiens

<400> 127
Met Lys Ala Ser Leu Cys Lys Leu Ser Pro Cys Thr Val Thr Arg Val
1 5 10 15

Cys Asp Tyr His Thr Lys Leu Phe Leu Ile Ala Ile Ser Ser Thr Leu
20 25 30

Lys Ser Leu Leu Arg Pro His Phe Leu Asn Thr Pro Asp Lys Ser Pro
35 40 45

Gly Asp Arg Leu Thr Glu Ile Cys Thr Lys Ile Thr Asp Val Asp Ile
50 55 60

Asp Lys Val Met Ile Asn Leu Lys Thr Glu Glu Phe Val Leu Asp Met
65 70 75 80

Asn Thr Leu Gln Ala Leu Gln Gln Leu Leu Gln Trp Val Gly Asp Phe
85 90 95

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

Pro Gly His Ser Phe Leu Arg Asp Gly Thr Ser Leu Gly Met Leu Arg
115 120 125

Glu Leu Met Val Val Ile Arg Ile Trp Gly Leu Leu Lys Pro Ser Cys
130 135 140

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

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

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Pro Ala Ser Glu Pro Asp Glu Ala Leu Val Asp Glu Cys Cys Leu Leu
180 185 190

Pro Ser Gln Leu Leu Ile Pro Ser Leu Asp Trp Leu Pro Ala Ser Asp
195 200 205

Gly Leu Val Ser Arg Leu Gln Pro Lys Gln Pro Leu Arg Leu Gln Phe
210 215 220

Gly Arg Ala Pro Thr Leu Pro Gly Ser Ala Ala Thr Leu Gln Leu Asp
225 230 235 240

Gly Leu Ala Arg Ala Pro Gly Gln Pro Lys Ile Asp His Leu Arg Arg
245 250 255

Leu His Leu Gly Ala Cys Pro Thr Glu Glu Cys Lys Ala Cys Thr Arg
260 265 270

Cys Gly Cys Val Thr Met Leu Lys Ser Pro Asn Arg Thr Thr Ala Val
275 280 285

Lys Gln Trp Glu Gln Arg Trp Ile Lys Asn Cys Leu Ala Val Glu Gly
290 295 300

Arg Gly Pro Asp Ala Cys Val Thr Ser Arg Ala Ser Glu Glu Ala Pro
305 310 315 320

Ala Phe Val Gln Leu Gly Pro Gln Ser Thr His His Ser Pro Arg Thr
325 330 335

Pro Arg Ser Leu Asp His Leu His Pro Glu Asp Arg Pro
340 345

<210> 128
<211> 508
<212> PRT
<213> Homo sapiens

<400> 128
Met Cys Asp Leu Arg Arg Pro Ala Ala Gly Gly Met Met Ala Leu Ala
1 5 10 15

Phe His Asp Gly Ser Val His Ile Val His Arg Leu Ser Leu Gln Thr
20 25 30

Met Ala Val Phe Tyr Ser Ser Ala Ala Pro Arg Pro Val Asp Glu Pro
35 40 45

Ala Met Lys Arg Pro Arg Thr Ala Gly Pro Ala Val His Leu Lys Ala
50 55 60

Met Gln Leu Ser Trp Thr Ser Leu Ala Leu Val Gly Ile Asp Ser His
65 70 75 80

```
Gly Lys Leu Ser Val Leu Arg Leu Ser Pro Ser Met Gly His Pro Leu
                85                  90                  95

Glu Val Gly Leu Ala Leu Arg His Leu Leu Phe Leu Leu Glu Tyr Cys
            100                 105                 110

Met Val Thr Gly Tyr Asp Trp Trp Asp Ile Leu Leu His Val Gln Pro
        115                 120                 125

Ser Met Val Gln Ser Leu Val Glu Lys Leu His Glu Glu Tyr Thr Arg
    130                 135                 140

Gln Thr Ala Ala Leu Gln Gln Val Leu Ser Thr Arg Ile Leu Ala Met
145                 150                 155                 160

Lys Ala Ser Leu Cys Lys Leu Ser Pro Cys Thr Val Thr Arg Val Cys
                165                 170                 175

Asp Tyr His Thr Lys Leu Phe Leu Ile Ala Ile Ser Ser Thr Leu Lys
            180                 185                 190

Ser Leu Leu Arg Pro His Phe Leu Asn Thr Pro Asp Lys Ser Pro Gly
        195                 200                 205

Asp Arg Leu Thr Glu Ile Cys Thr Lys Ile Thr Asp Val Asp Ile Asp
    210                 215                 220

Lys Val Met Ile Asn Leu Lys Thr Glu Glu Phe Val Leu Asp Met Asn
225                 230                 235                 240

Thr Leu Gln Ala Leu Gln Gln Leu Leu Gln Trp Val Gly Asp Phe Val
                245                 250                 255

Leu Tyr Leu Leu Ala Ser Leu Pro Asn Gln Gly Ser Leu Leu Arg Pro
            260                 265                 270

Gly His Ser Phe Leu Arg Asp Gly Thr Ser Leu Gly Met Leu Arg Glu
        275                 280                 285

Leu Met Val Val Ile Arg Ile Trp Gly Leu Leu Lys Pro Ser Cys Leu
    290                 295                 300

Pro Val Tyr Thr Ala Thr Ser Asp Thr Gln Asp Ser Met Ser Leu Leu
305                 310                 315                 320

Phe Arg Leu Leu Thr Lys Leu Trp Ile Cys Cys Arg Asp Glu Gly Pro
                325                 330                 335

Ala Ser Glu Pro Asp Glu Ala Leu Val Asp Glu Cys Cys Leu Leu Pro
            340                 345                 350
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Ser Gln Leu Leu Ile Pro Ser Leu Asp Trp Leu Pro Ala Ser Asp Gly
355 360 365

Leu Val Ser Arg Leu Gln Pro Lys Gln Pro Leu Arg Leu Gln Phe Gly
370 375 380

Arg Ala Pro Thr Leu Pro Gly Ser Ala Ala Thr Leu Gln Leu Asp Gly
385 390 395 400

Leu Ala Arg Ala Pro Gly Gln Pro Lys Ile Asp His Leu Arg Arg Leu
405 410 415

His Leu Gly Ala Cys Pro Thr Glu Glu Cys Lys Ala Cys Thr Arg Cys
420 425 430

Gly Cys Val Thr Met Leu Lys Ser Pro Asn Arg Thr Thr Ala Val Lys
435 440 445

Gln Trp Glu Gln Arg Trp Ile Lys Asn Cys Leu Ala Val Glu Gly Arg
450 455 460

Gly Pro Asp Ala Cys Val Thr Ser Arg Ala Ser Glu Glu Ala Pro Ala
465 470 475 480

Phe Val Gln Leu Gly Pro Gln Ser Thr His His Ser Pro Arg Thr Pro
485 490 495

Arg Ser Leu Asp His Leu His Pro Glu Asp Arg Pro
500 505

<210> 129
<211> 505
<212> PRT
<213> Homo sapiens

<400> 129
Met Ser Gly Val Arg Ala Val Arg Ile Ser Ile Glu Ser Ala Cys Glu
1 5 10 15

Lys Gln Val His Glu Val Gly Leu Asp Gly Thr Glu Thr Tyr Leu Pro
20 25 30

Pro Leu Ser Met Ser Gln Asn Leu Ala Arg Leu Ala Gln Arg Ile Asp
35 40 45

Phe Ser Gln Gly Ser Gly Ser Glu Glu Glu Glu Ala Ala Gly Thr Glu
50 55 60

Gly Asp Ala Gln Glu Trp Pro Gly Ala Gly Ser Ser Ala Asp Gln Asp
65 70 75 80

Asp Glu Glu Gly Val Val Lys Phe Gln Pro Ser Leu Trp Pro Trp Asp
85 90 95

Ser Val Arg Asn Asn Leu Arg Ser Ala Leu Thr Glu Met Cys Val Leu
100 105 110

Tyr Asp Val Leu Ser Ile Val Arg Asp Lys Lys Phe Met Thr Leu Asp
115 120 125

Pro Val Ser Gln Asp Ala Leu Pro Pro Lys Gln Asn Pro Gln Thr Leu
130 135 140

Gln Leu Ile Ser Lys Lys Lys Ser Leu Ala Gly Ala Ala Gln Ile Leu
145 150 155 160

Leu Lys Gly Ala Glu Arg Leu Thr Lys Ser Val Thr Glu Asn Gln Glu
165 170 175

Asn Lys Leu Gln Arg Asp Phe Asn Ser Glu Leu Leu Arg Leu Arg Gln
180 185 190

His Trp Lys Leu Arg Lys Val Gly Asp Lys Ile Leu Gly Asp Leu Ser
195 200 205

Tyr Arg Ser Ala Gly Ser Leu Phe Pro His His Gly Thr Phe Glu Val
210 215 220

Ile Lys Asn Thr Asp Leu Asp Leu Asp Lys Lys Ile Pro Glu Asp Tyr
225 230 235 240

Cys Pro Leu Asp Val Gln Ile Pro Ser Asp Leu Glu Gly Ser Ala Tyr
245 250 255

Ile Lys Val Ser Ile Gln Lys Gln Ala Pro Asp Ile Gly Asp Leu Gly
260 265 270

Thr Val Asn Leu Phe Lys Arg Pro Leu Pro Lys Ser Lys Pro Gly Ser
275 280 285

Pro His Trp Gln Thr Lys Leu Glu Ala Ala Gln Asn Val Leu Leu Cys
290 295 300

Lys Glu Ile Phe Ala Gln Leu Ser Arg Glu Ala Val Gln Ile Lys Ser
305 310 315 320

Gln Val Pro His Ile Val Val Lys Asn Gln Ile Ile Ser Gln Pro Phe
325 330 335

Pro Ser Leu Gln Leu Ser Ile Ser Leu Cys His Ser Ser Asn Asp Lys
340 345 350

Lys Ser Gln Lys Phe Ala Thr Glu Lys Gln Cys Pro Glu Asp His Leu
355 360 365

Tyr Val Leu Glu His Asn Leu His Leu Leu Ile Arg Glu Phe Val Met
370 375 380

Asp Leu Lys Val Ala Ala Arg Leu Trp Phe Ser Phe Leu Val Thr Asn
385 390 395 400

Val Lys Thr Phe Gln Lys Val Met Phe Tyr Lys Ile Thr Asn Gly Val
405 410 415

Ile Phe Val Gly His Ser Lys Lys Phe Ser Gly Ile Lys Trp Lys Val
420 425 430

Glu Ile Leu Phe Ile Lys Trp Ser Cys Leu Cys Leu His Leu Ala Leu
435 440 445

Val Tyr Tyr Asp Phe Phe Gln Met Phe Pro Lys Glu Val Ser Arg Asn
450 455 460

Phe Asp Leu Lys Cys Leu Gln Ile Asn Tyr Lys His Lys Glu Glu Ile
465 470 475 480

Thr Ser Lys Arg Val Leu Phe Leu Lys Ile Ile Ile Arg Lys Cys Leu
485 490 495

Phe Ser Thr Phe Lys Leu Phe Thr Leu
500 505

<210> 130
<211> 177
<212> PRT
<213> Homo sapiens

<400> 130
Met Arg Glu Leu Pro Gly Ser Thr Glu Leu Thr Gly Ser Thr Asn Leu
1 5 10 15

Ile Thr His Tyr Asn Leu Glu Gln Ala Tyr Asn Lys Phe Cys Gly Lys
20 25 30

Lys Val Lys Glu Lys Leu Ser Asn Phe Leu Pro Asp Leu Pro Gly Met
35 40 45

Ile Asp Leu Pro Gly Ser His Asp Asn Ser Ser Leu Arg Ser Leu Ile
50 55 60

Glu Lys Pro Pro Ile Leu Ser Ser Ser Phe Asn Pro Ile Thr Gly Thr
65 70 75 80

Met Leu Ala Gly Phe Arg Leu His Thr Gly Pro Leu Pro Glu Gln Cys
85 90 95

Arg Leu Met His Ile Gln Pro Pro Lys Lys Lys Asn Lys His Lys His
100 105 110

Lys Gln Ser Arg Thr Gln Asp Pro Val Pro Pro Glu Thr Pro Ser Asp
115 120 125

Ser Asp His Lys Lys Lys Lys Lys Lys Lys Glu Glu Asp Pro Glu Arg
130 135 140

Lys Arg Lys Lys Lys Glu Lys Lys Lys Lys Lys Asn Arg His Ser Pro
145 150 155 160

Asp His Pro Gly Met Gly Ser Ser Gln Ala Ser Ser Ser Ser Ser Leu
165 170 175

Arg

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

<400> 131
Met Glu Asn Phe Thr Ala Leu Phe Gly Ala Gln Ala Asp Pro Pro Pro
1 5 10 15

Pro Pro Thr Ala Leu Gly Phe Gly Pro Gly Lys Pro Pro Pro Pro Pro
20 25 30

Pro Pro Pro Ala Gly Gly Gly Pro Gly Thr Ala Pro Pro Pro Thr Ala
35 40 45

Ala Thr Ala Pro Pro Gly Ala Asp Lys Ser Gly Ala Gly Cys Gly Pro
50 55 60

Phe Tyr Leu Met Arg Glu Leu Pro Gly Ser Thr Glu Leu Thr Gly Ser
65 70 75 80

Thr Asn Leu Ile Thr His Tyr Asn Leu Glu Gln Ala Tyr Asn Lys Phe
85 90 95

Cys Gly Lys Lys Val Lys Glu Lys Leu Ser Asn Phe Leu Pro Asp Leu
100 105 110

Pro Gly Met Ile Asp Leu Pro Gly Ser His Asp Asn Ser Ser Leu Arg
115 120 125

Ser Leu Ile Glu Lys Pro Pro Ile Leu Ser Ser Ser Phe Asn Pro Ile
130 135 140

Thr Gly Thr Met Leu Ala Gly Phe Arg Leu His Thr Gly Pro Leu Pro
145 150 155 160

Glu Gln Cys Arg Leu Met His Ile Gln Pro Pro Lys Lys Lys Asn Lys

165 170 175

His Lys His Lys Gln Ser Arg Thr Gln Asp Pro Val Pro Pro Gly Lys
180 185 190

Lys Gln Phe Tyr Ser Lys Gln Lys Lys Lys Lys Lys Lys Asn Leu
195 200 205

Thr Phe
210

<210> 132
<211> 190
<212> PRT
<213> Homo sapiens

<400> 132
Met Glu Asn Phe Thr Ala Leu Phe Gly Ala Gln Ala Asp Pro Pro Pro
1 5 10 15

Pro Pro Thr Ala Leu Gly Phe Gly Pro Gly Lys Pro Pro Pro Pro Pro
20 25 30

Pro Pro Pro Ala Gly Gly Gly Pro Gly Thr Ala Pro Pro Pro Thr Ala
35 40 45

Ala Thr Ala Pro Pro Gly Ala Asp Lys Ser Gly Ala Gly Cys Gly Pro
50 55 60

Phe Tyr Leu Met Arg Glu Leu Pro Gly Ser Thr Glu Leu Thr Gly Ser
65 70 75 80

Thr Asn Leu Ile Thr His Tyr Asn Leu Glu Gln Ala Tyr Asn Lys Phe
85 90 95

Cys Gly Lys Lys Val Lys Glu Lys Leu Ser Asn Phe Leu Pro Asp Leu
100 105 110

Pro Gly Met Ile Asp Leu Pro Gly Ser His Asp Asn Ser Ser Leu Arg
115 120 125

Ser Leu Ile Glu Lys Pro Pro Ile Leu Ser Ser Ser Phe Asn Pro Ile
130 135 140

Thr Gly Thr Met Leu Ala Gly Phe Arg Leu His Thr Gly Pro Val Ser
145 150 155 160

Pro Val Gly Gly Arg Arg Gln Met Gly Arg Pro Lys His Gly Asp Gly
165 170 175

Phe Ser Leu Gln Val Cys Ser Phe Ile Met Glu Gln Asn Gly
180 185 190

<210> 133
<211> 204
<212> PRT
<213> Homo sapiens

<400> 133
Met Pro Val Ala Glu Gly Lys Ser Val Gln Gln Thr Val Glu Leu Leu
1 5 10 15

Thr Arg Lys Leu Glu Met Leu Gly Ala Glu Lys Gln Gly Thr Phe Cys
20 25 30

Val Asp Cys Glu Thr Tyr His Thr Ala Ala Ser Thr Leu Gly Ser Gln
35 40 45

Gly Gln Thr Gly Lys Leu Met Tyr Val Met His Asn Ser Glu Tyr Pro
50 55 60

Leu Ser Cys Phe Ala Leu Phe Glu Asn Gly Pro Cys Leu Ile Ala Asp
65 70 75 80

Thr Asn Phe Asp Val Leu Met Val Lys Leu Lys Gly Phe Phe Gln Ser
85 90 95

Ala Lys Ala Ser Lys Ile Glu Thr Arg Gly Thr Arg Tyr Gln Tyr Cys
100 105 110

Asp Phe Leu Val Lys Val Gly Thr Val Thr Met Gly Pro Ser Ala Arg
115 120 125

Gly Ile Ser Val Glu Val Glu Tyr Gly Pro Cys Val Val Ala Ser Asp
130 135 140

Cys Trp Ser Leu Leu Leu Glu Phe Leu Gln Ser Phe Leu Gly Ser His
145 150 155 160

Thr Pro Gly Ala Pro Ala Val Phe Gly Asn Arg His Asp Ala Val Tyr
165 170 175

Gly Pro Ala Asp Thr Met Val Gln Tyr Met Glu Leu Phe Asn Lys Ile
180 185 190

Arg Lys Gln Gln Gln Val Pro Val Ala Gly Ile Arg
195 200

<210> 134
<211> 145
<212> PRT
<213> Homo sapiens

<400> 134
Met Gly Val Thr Cys Val Ser Gln Met Pro Val Ala Glu Gly Lys Ser
1 5 10 15

Val Gln Gln Thr Val Glu Leu Leu Thr Arg Lys Leu Glu Met Leu Gly

20 25 30

Ala Glu Lys Gln Gly Thr Phe Cys Val Asp Cys Glu Thr Tyr His Thr
35 40 45

Ala Ala Ser Thr Leu Gly Ser Gln Gly Gln Thr Gly Lys Leu Met Tyr
50 55 60

Val Met His Asn Ser Glu Tyr Pro Leu Ser Cys Phe Ala Leu Phe Glu
65 70 75 80

Asn Gly Pro Cys Leu Ile Ala Asp Thr Asn Phe Asp Val Leu Met Val
85 90 95

Lys Leu Lys Gly Phe Phe Gln Ser Ala Lys Ala Ser Lys Ile Glu Thr
100 105 110

Arg Gly Thr Arg Tyr Gln Tyr Cys Asp Phe Leu Val Lys Val Gly Thr
115 120 125

Val Thr Met Gly Pro Ser Ala Arg Gly Ile Ser Val Glu Val Arg Pro
130 135 140

Trp
145

<210> 135
<211> 159
<212> PRT
<213> Homo sapiens

<400> 135
Met Ala Asp Arg Leu Thr Gln Leu Gln Asp Ala Val Asn Ser Leu Ala
1 5 10 15

Asp Gln Phe Cys Asn Ala Ile Gly Val Leu Gln Gln Cys Gly Pro Pro
20 25 30

Ala Ser Phe Asn Asn Ile Gln Thr Ala Ile Asn Lys Asp Gln Pro Ala
35 40 45

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

Thr Ala Lys Asp Ile Asp Val Leu Ile Asp Ser Leu Pro Ser Glu Glu
65 70 75 80

Ser Thr Ala Ala Leu Gln Ala Ala Ser Leu Tyr Lys Leu Glu Glu Glu
85 90 95

Asn His Glu Ala Ala Thr Cys Leu Glu Asp Val Val Tyr Arg Gly Asp
100 105 110

Met Leu Leu Glu Lys Ile Gln Ser Ala Leu Ala Asp Ile Ala Gln Ser
115 120 125

Gln Leu Lys Thr Arg Ser Gly Glu Val Ser Val Thr Gln Ala Glu Val
130 135 140

Gln Phe Cys Asp His Gly Ser Leu Gln Leu His Pro Gly Phe Arg
145 150 155

<210> 136
<211> 53
<212> PRT
<213> Homo sapiens

<400> 136
Met Ala Gln Gln Arg Ala Leu Pro Gln Ser Lys Glu Thr Leu Leu Gln
1 5 10 15

Ser Tyr Asn Lys Arg Leu Lys Asp Asp Ile Lys Ser Ile Met Asp Asn
20 25 30

Phe Thr Glu Ile Ile Lys Thr Ala Lys Val Gly Val Gly Trp Pro Thr
35 40 45

Lys Gly Ser Arg Val
50

<210> 137
<211> 976
<212> PRT
<213> Homo sapiens

<400> 137
Met Lys Val Val Asn Leu Lys Gln Ala Ile Leu Gln Ala Trp Lys Glu
1 5 10 15

Arg Trp Ser Asp Tyr Gln Trp Ala Ile Asn Met Lys Lys Phe Phe Pro
20 25 30

Lys Gly Ala Thr Trp Asp Ile Leu Asn Leu Ala Asp Ala Leu Leu Glu
35 40 45

Gln Ala Met Ile Gly Pro Ser Pro Asn Pro Leu Ile Leu Ser Tyr Leu
50 55 60

Lys Tyr Ala Ile Ser Ser Gln Phe Asp Asp Phe Ser Arg Asp Leu Cys
65 70 75 80

Val Gln Ala Leu Leu Asp Ile Met Asp Met Phe Cys Asp Arg Leu Ser
85 90 95

Cys His Gly Lys Ala Glu Glu Cys Ile Gly Leu Cys Arg Ala Leu Leu
100 105 110

Ser Ala Leu His Trp Leu Leu Arg Cys Thr Ala Ala Ser Ala Glu Arg

115 120 125

Leu Arg Glu Gly Leu Glu Ala Gly Thr Pro Ala Ala Gly Glu Lys Gln
130 135 140

Leu Ala Met Cys Leu Gln Arg Leu Glu Lys Thr Leu Ser Ser Thr Lys
145 150 155 160

Asn Arg Ala Leu Leu His Ile Ala Lys Leu Glu Glu Ala Ser Ser Trp
165 170 175

Thr Ala Ile Glu His Ser Leu Leu Lys Leu Gly Glu Ile Leu Ala Asn
180 185 190

Leu Ser Asn Pro Gln Leu Arg Ser Gln Ala Glu Gln Cys Gly Thr Leu
195 200 205

Ile Arg Ser Ile Pro Thr Met Leu Ser Val His Ala Glu Gln Met His
210 215 220

Lys Thr Gly Phe Pro Thr Val His Ala Val Ile Leu Leu Glu Gly Thr
225 230 235 240

Met Asn Leu Thr Gly Glu Thr Gln Ser Leu Val Glu Gln Leu Thr Met
245 250 255

Val Lys Arg Met Gln His Ile Pro Thr Pro Leu Phe Val Leu Glu Ile
260 265 270

Trp Lys Ala Cys Phe Val Gly Leu Ile Glu Ser Pro Glu Gly Thr Glu
275 280 285

Glu Leu Lys Trp Thr Ala Phe Thr Phe Leu Lys Ile Pro Gln Val Leu
290 295 300

Val Lys Leu Lys Lys Tyr Ser His Gly Asp Lys Asp Phe Thr Glu Asp
305 310 315 320

Val Asn Cys Ala Phe Glu Phe Leu Leu Lys Leu Thr Pro Leu Leu Asp
325 330 335

Lys Ala Asp Gln Arg Cys Asn Cys Asp Cys Thr Asn Phe Leu Leu Gln
340 345 350

Glu Cys Gly Lys Gln Gly Leu Leu Ser Glu Ala Ser Val Asn Asn Leu
355 360 365

Met Ala Lys Arg Lys Ala Asp Arg Glu His Ala Pro Gln Gln Lys Ser
370 375 380

Gly Glu Asn Ala Asn Ile Gln Pro Asn Ile Gln Leu Ile Leu Arg Ala
385 390 395 400

Glu Pro Thr Val Thr Asn Ile Leu Lys Thr Met Asp Ala Asp His Ser
405 410 415

Lys Ser Pro Glu Gly Leu Leu Gly Val Leu Gly His Met Leu Ser Gly
420 425 430

Lys Ser Leu Asp Leu Leu Leu Ala Ala Ala Ala Ala Thr Gly Lys Leu
435 440 445

Lys Ser Phe Ala Arg Lys Phe Ile Asn Leu Asn Glu Phe Thr Thr Tyr
450 455 460

Gly Ser Glu Glu Ser Thr Lys Pro Ala Ser Val Arg Ala Leu Leu Phe
465 470 475 480

Asp Ile Ser Phe Leu Met Leu Cys His Val Ala Gln Thr Tyr Gly Ser
485 490 495

Glu Val Ile Leu Ser Glu Ser Arg Thr Gly Ala Glu Val Pro Phe Phe
500 505 510

Glu Thr Trp Met Gln Thr Cys Met Pro Glu Glu Gly Lys Ile Leu Asn
515 520 525

Pro Asp His Pro Cys Phe Arg Pro Asp Ser Thr Lys Val Glu Ser Leu
530 535 540

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

Trp His Glu Ala Cys Leu Ser Ile Ser Ala Ala Ile Leu Glu Ile Leu
565 570 575

Asn Ala Trp Glu Asn Gly Val Leu Ala Phe Glu Ser Ile Gln Lys Ile
580 585 590

Thr Asp Asn Ile Lys Gly Lys Val Cys Ser Leu Ala Val Cys Ala Val
595 600 605

Ala Trp Leu Val Ala His Val Arg Met Leu Gly Leu Asp Glu Arg Glu
610 615 620

Lys Ser Leu Gln Met Ile Arg Gln Leu Ala Gly Pro Leu Phe Ser Glu
625 630 635 640

Asn Thr Leu Gln Phe Tyr Asn Glu Arg Val Val Ile Met Asn Ser Ile
645 650 655

Leu Glu Arg Met Cys Ala Asp Val Leu Gln Gln Thr Ala Thr Gln Ile
660 665 670

Lys Phe Pro Ser Thr Gly Val Asp Thr Met Pro Tyr Trp Asn Leu Leu
675 680 685

Pro Pro Lys Arg Pro Ile Lys Glu Val Leu Thr Asp Ile Phe Ala Lys
690 695 700

Val Leu Glu Lys Gly Trp Val Asp Ser Arg Ser Ile His Ile Phe Asp
705 710 715 720

Thr Leu Leu His Met Gly Gly Val Tyr Trp Phe Cys Asn Asn Leu Ile
725 730 735

Lys Glu Leu Leu Lys Glu Thr Arg Lys Glu His Thr Leu Arg Ala Val
740 745 750

Glu Leu Leu Tyr Ser Ile Phe Cys Leu Asp Met Gln Gln Val Thr Leu
755 760 765

Val Leu Leu Gly His Ile Leu Pro Gly Leu Leu Thr Asp Ser Ser Lys
770 775 780

Trp His Ser Leu Met Asp Pro Pro Gly Thr Ala Leu Ala Lys Leu Ala
785 790 795 800

Val Trp Cys Ala Leu Ser Ser Tyr Ser Ser His Lys Gly Gln Ala Ser
805 810 815

Thr Arg Gln Lys Lys Arg His Arg Glu Asp Ile Glu Asp Tyr Ile Ser
820 825 830

Leu Phe Pro Leu Asp Asp Val Gln Pro Ser Lys Leu Met Arg Leu Leu
835 840 845

Ser Ser Asn Glu Asp Asp Ala Asn Ile Leu Ser Ser Pro Thr Asp Arg
850 855 860

Ser Met Ser Ser Ser Leu Ser Ala Ser Gln Leu His Thr Val Asn Met
865 870 875 880

Arg Asp Pro Leu Asn Arg Val Leu Ala Asn Leu Phe Leu Leu Ile Ser
885 890 895

Ser Ile Leu Gly Ser Arg Thr Ala Gly Pro His Thr Gln Phe Val Gln
900 905 910

Trp Phe Met Glu Glu Cys Val Asp Cys Leu Glu Gln Gly Gly Arg Gly
915 920 925

Ser Val Leu Gln Phe Met Pro Phe Thr Thr Val Ser Glu Leu Val Lys
930 935 940

Val Ser Ala Met Ser Ser Pro Lys Val Val Leu Ala Ile Thr Asp Leu
945 950 955 960

Ser Leu Pro Leu Gly Arg Gln Val Ala Ala Lys Ala Ile Ala Ala Leu
965 970 975

<210> 138
<211> 995
<212> PRT
<213> Homo sapiens

<400> 138
Met Lys Val Val Asn Leu Lys Gln Ala Ile Leu Gln Ala Trp Lys Glu
1 5 10 15

Arg Trp Ser Asp Tyr Gln Trp Ala Ile Asn Met Lys Lys Phe Phe Pro
20 25 30

Lys Gly Ala Thr Trp Asp Ile Leu Asn Leu Ala Asp Ala Leu Leu Glu
35 40 45

Gln Ala Met Ile Gly Pro Ser Pro Asn Pro Leu Ile Leu Ser Tyr Leu
50 55 60

Lys Tyr Ala Ile Ser Ser Gln Phe Asp Asp Phe Ser Arg Asp Leu Cys
65 70 75 80

Val Gln Ala Leu Leu Asp Ile Met Asp Met Phe Cys Asp Arg Leu Ser
85 90 95

Cys His Gly Lys Ala Glu Glu Cys Ile Gly Leu Cys Arg Ala Leu Leu
100 105 110

Ser Ala Leu His Trp Leu Leu Arg Cys Thr Ala Ala Ser Ala Glu Arg
115 120 125

Leu Arg Glu Gly Leu Glu Ala Gly Thr Pro Ala Ala Gly Glu Lys Gln
130 135 140

Leu Ala Met Cys Leu Gln Arg Leu Glu Lys Thr Leu Ser Ser Thr Lys
145 150 155 160

Asn Arg Ala Leu Leu His Ile Ala Lys Leu Glu Glu Ala Ser Leu His
165 170 175

Thr Ser Gln Gly Leu Gly Gln Gly Gly Thr Arg Ala Asn Gln Pro Thr
180 185 190

Ala Ser Trp Thr Ala Ile Glu His Ser Leu Leu Lys Leu Gly Glu Ile
195 200 205

Leu Ala Asn Leu Ser Asn Pro Gln Leu Arg Ser Gln Ala Glu Gln Cys
210 215 220

```
Gly Thr Leu Ile Arg Ser Ile Pro Thr Met Leu Ser Val His Ala Glu
225                 230                 235                 240

Gln Met His Lys Thr Gly Phe Pro Thr Val His Ala Val Ile Leu Leu
                245                 250                 255

Glu Gly Thr Met Asn Leu Thr Gly Glu Thr Gln Ser Leu Val Glu Gln
            260                 265                 270

Leu Thr Met Val Lys Arg Met Gln His Ile Pro Thr Pro Leu Phe Val
        275                 280                 285

Leu Glu Ile Trp Lys Ala Cys Phe Val Gly Leu Ile Glu Ser Pro Glu
    290                 295                 300

Gly Thr Glu Glu Leu Lys Trp Thr Ala Phe Thr Phe Leu Lys Ile Pro
305                 310                 315                 320

Gln Val Leu Val Lys Leu Lys Lys Tyr Ser His Gly Asp Lys Asp Phe
                325                 330                 335

Thr Glu Asp Val Asn Cys Ala Phe Glu Phe Leu Leu Lys Leu Thr Pro
            340                 345                 350

Leu Leu Asp Lys Ala Asp Gln Arg Cys Asn Cys Asp Cys Thr Asn Phe
        355                 360                 365

Leu Leu Gln Glu Cys Gly Lys Gln Gly Leu Leu Ser Glu Ala Ser Val
    370                 375                 380

Asn Asn Leu Met Ala Lys Arg Lys Ala Asp Arg Glu His Ala Pro Gln
385                 390                 395                 400

Gln Lys Ser Gly Glu Asn Ala Asn Ile Gln Pro Asn Ile Gln Leu Ile
                405                 410                 415

Leu Arg Ala Glu Pro Thr Val Thr Asn Ile Leu Lys Thr Met Asp Ala
            420                 425                 430

Asp His Ser Lys Ser Pro Glu Gly Leu Leu Gly Val Leu Gly His Met
        435                 440                 445

Leu Ser Gly Lys Ser Leu Asp Leu Leu Leu Ala Ala Ala Ala Ala Thr
    450                 455                 460

Gly Lys Leu Lys Ser Phe Ala Arg Lys Phe Ile Asn Leu Asn Glu Phe
465                 470                 475                 480

Thr Thr Tyr Gly Ser Glu Glu Ser Thr Lys Pro Ala Ser Val Arg Ala
                485                 490                 495
```

Leu Leu Phe Asp Ile Ser Phe Leu Met Leu Cys His Val Ala Gln Thr
500 505 510

Tyr Gly Ser Glu Val Ile Leu Ser Glu Ser Arg Thr Gly Ala Glu Val
515 520 525

Pro Phe Phe Glu Thr Trp Met Gln Thr Cys Met Pro Glu Glu Gly Lys
530 535 540

Ile Leu Asn Pro Asp His Pro Cys Phe Arg Pro Asp Ser Thr Lys Val
545 550 555 560

Glu Ser Leu Val Ala Leu Leu Asn Asn Ser Ser Glu Met Lys Leu Val
565 570 575

Gln Met Lys Trp His Glu Ala Cys Leu Ser Ile Ser Ala Ala Ile Leu
580 585 590

Glu Ile Leu Asn Ala Trp Glu Asn Gly Val Leu Ala Phe Glu Ser Ile
595 600 605

Gln Lys Ile Thr Asp Asn Ile Lys Gly Lys Val Cys Ser Leu Ala Val
610 615 620

Cys Ala Val Ala Trp Leu Val Ala His Val Arg Met Leu Gly Leu Asp
625 630 635 640

Glu Arg Glu Lys Ser Leu Gln Met Ile Arg Gln Leu Ala Gly Pro Leu
645 650 655

Phe Ser Glu Asn Thr Leu Gln Phe Tyr Asn Glu Arg Val Val Ile Met
660 665 670

Asn Ser Ile Leu Glu Arg Met Cys Ala Asp Val Leu Gln Gln Thr Ala
675 680 685

Thr Gln Ile Lys Phe Pro Ser Thr Gly Val Asp Thr Met Pro Tyr Trp
690 695 700

Asn Leu Leu Pro Pro Lys Arg Pro Ile Lys Glu Val Leu Thr Asp Ile
705 710 715 720

Phe Ala Lys Val Leu Glu Lys Gly Trp Val Asp Ser Arg Ser Ile His
725 730 735

Ile Phe Asp Thr Leu Leu His Met Gly Gly Val Tyr Trp Phe Cys Asn
740 745 750

Asn Leu Ile Lys Glu Leu Leu Lys Glu Thr Arg Lys Glu His Thr Leu
755 760 765

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

770 775 780

Val Thr Leu Val Leu Leu Gly His Ile Leu Pro Gly Leu Leu Thr Asp
785 790 795 800

Ser Ser Lys Trp His Ser Leu Met Asp Pro Pro Gly Thr Ala Leu Ala
805 810 815

Lys Leu Ala Val Trp Cys Ala Leu Ser Ser Tyr Ser Ser His Lys Gly
820 825 830

Gln Ala Ser Thr Arg Gln Lys Lys Arg His Arg Glu Asp Ile Glu Asp
835 840 845

Tyr Ile Ser Leu Phe Pro Leu Asp Asp Val Gln Pro Ser Lys Leu Met
850 855 860

Arg Leu Leu Ser Ser Asn Glu Asp Asp Ala Asn Ile Leu Ser Ser Pro
865 870 875 880

Thr Asp Arg Ser Met Ser Ser Ser Leu Ser Ala Ser Gln Leu His Thr
885 890 895

Val Asn Met Arg Asp Pro Leu Asn Arg Val Leu Ala Asn Leu Phe Leu
900 905 910

Leu Ile Ser Ser Ile Leu Gly Ser Arg Thr Ala Gly Pro His Thr Gln
915 920 925

Phe Val Gln Trp Phe Met Glu Glu Cys Val Asp Cys Leu Glu Gln Gly
930 935 940

Gly Arg Gly Ser Val Leu Gln Phe Met Pro Phe Thr Thr Val Ser Glu
945 950 955 960

Leu Val Lys Val Ser Ala Met Ser Ser Pro Lys Val Val Leu Ala Ile
965 970 975

Thr Asp Leu Ser Leu Pro Leu Gly Arg Gln Val Ala Ala Lys Ala Ile
980 985 990

Ala Ala Leu
995

<210> 139
<211> 1032
<212> PRT
<213> Homo sapiens

<400> 139
Met Lys Val Val Asn Leu Lys Gln Ala Ile Leu Gln Ala Trp Lys Glu
1 5 10 15

```
Arg Trp Ser Asp Tyr Gln Trp Ala Ile Asn Met Lys Lys Phe Phe Pro
            20                  25                  30

Lys Gly Ala Thr Trp Asp Ile Leu Asn Leu Ala Asp Ala Leu Leu Glu
        35                  40                  45

Gln Ala Met Ile Gly Pro Ser Pro Asn Pro Leu Ile Leu Ser Tyr Leu
    50                  55                  60

Lys Tyr Ala Ile Ser Ser Gln Met Val Ser Tyr Ser Ser Val Leu Thr
65                  70                  75                  80

Ala Ile Ser Lys Phe Asp Asp Phe Ser Arg Asp Leu Cys Val Gln Ala
                85                  90                  95

Leu Leu Asp Ile Met Asp Met Phe Cys Asp Arg Leu Ser Cys His Gly
            100                 105                 110

Lys Ala Glu Glu Cys Ile Gly Leu Cys Arg Ala Leu Leu Ser Ala Leu
        115                 120                 125

His Trp Leu Leu Arg Cys Thr Ala Ala Ser Ala Glu Arg Leu Arg Glu
    130                 135                 140

Gly Leu Glu Ala Gly Thr Pro Ala Ala Gly Glu Lys Gln Leu Ala Met
145                 150                 155                 160

Cys Leu Gln Arg Leu Glu Lys Thr Leu Ser Ser Thr Lys Asn Arg Ala
                165                 170                 175

Leu Leu His Ile Ala Lys Leu Glu Glu Ala Ser Ser Trp Thr Ala Ile
            180                 185                 190

Glu His Ser Leu Leu Lys Leu Gly Glu Ile Leu Ala Asn Leu Ser Asn
        195                 200                 205

Pro Gln Leu Arg Ser Gln Ala Glu Gln Cys Gly Thr Leu Ile Arg Ser
    210                 215                 220

Ile Pro Thr Met Leu Ser Val His Ala Glu Gln Met His Lys Thr Gly
225                 230                 235                 240

Phe Pro Thr Val His Ala Val Ile Leu Leu Glu Gly Thr Met Asn Leu
                245                 250                 255

Thr Gly Glu Thr Gln Ser Leu Val Glu Gln Leu Thr Met Val Lys Arg
            260                 265                 270

Met Gln His Ile Pro Thr Pro Leu Phe Val Leu Glu Ile Trp Lys Ala
        275                 280                 285

Cys Phe Val Gly Leu Ile Glu Ser Pro Glu Gly Thr Glu Glu Leu Lys
```

290 295 300

Trp Thr Ala Phe Thr Phe Leu Lys Ile Pro Gln Val Leu Val Lys Leu
305 310 315 320

Lys Lys Tyr Ser His Gly Asp Lys Asp Phe Thr Glu Asp Val Asn Cys
325 330 335

Ala Phe Glu Phe Leu Leu Lys Leu Thr Pro Leu Leu Asp Lys Ala Asp
340 345 350

Gln Arg Cys Asn Cys Asp Cys Thr Asn Phe Leu Leu Gln Glu Cys Gly
355 360 365

Lys Gln Gly Leu Leu Ser Glu Ala Ser Val Asn Asn Leu Met Ala Lys
370 375 380

Arg Lys Ala Asp Arg Glu His Ala Pro Gln Gln Lys Ser Gly Glu Asn
385 390 395 400

Ala Asn Ile Gln Pro Asn Ile Gln Leu Ile Leu Arg Ala Glu Pro Thr
405 410 415

Val Thr Asn Ile Leu Lys Thr Met Asp Ala Asp His Ser Lys Ser Pro
420 425 430

Glu Gly Leu Leu Gly Val Leu Gly His Met Leu Ser Gly Lys Ser Leu
435 440 445

Asp Leu Leu Leu Ala Ala Ala Ala Ala Thr Gly Lys Leu Lys Ser Phe
450 455 460

Ala Arg Lys Phe Ile Asn Leu Asn Glu Phe Thr Thr Tyr Gly Ser Glu
465 470 475 480

Glu Ser Thr Lys Pro Ala Ser Val Arg Ala Leu Leu Phe Asp Ile Ser
485 490 495

Phe Leu Met Leu Cys His Val Ala Gln Thr Tyr Gly Ser Glu Val Ile
500 505 510

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

Met Gln Thr Cys Met Pro Glu Glu Gly Lys Ile Leu Asn Pro Asp His
530 535 540

Pro Cys Phe Arg Pro Asp Ser Thr Lys Val Glu Ser Leu Val Ala Leu
545 550 555 560

Leu Asn Asn Ser Ser Glu Met Lys Leu Val Gln Met Lys Trp His Glu
565 570 575

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Ala Cys Leu Ser Ile Ser Ala Ala Ile Leu Glu Ile Leu Asn Ala Trp
580 585 590

Glu Asn Gly Val Leu Ala Phe Glu Ser Ile Gln Lys Ile Thr Asp Asn
595 600 605

Ile Lys Gly Lys Val Cys Ser Leu Ala Val Cys Ala Val Ala Trp Leu
610 615 620

Val Ala His Val Arg Met Leu Gly Leu Asp Glu Arg Glu Lys Ser Leu
625 630 635 640

Gln Met Ile Arg Gln Leu Ala Gly Pro Leu Phe Ser Glu Asn Thr Leu
645 650 655

Gln Phe Tyr Asn Glu Arg Val Val Ile Met Asn Ser Ile Leu Glu Arg
660 665 670

Met Cys Ala Asp Val Leu Gln Gln Thr Ala Thr Gln Ile Lys Phe Pro
675 680 685

Ser Thr Gly Val Asp Thr Met Pro Tyr Trp Asn Leu Leu Pro Pro Lys
690 695 700

Arg Pro Ile Lys Glu Val Leu Thr Asp Ile Phe Ala Lys Val Leu Glu
705 710 715 720

Lys Gly Trp Val Asp Ser Arg Ser Ile His Ile Phe Asp Thr Leu Leu
725 730 735

His Met Gly Gly Val Tyr Trp Phe Cys Asn Asn Leu Ile Lys Glu Leu
740 745 750

Leu Lys Glu Thr Arg Lys Glu His Thr Leu Arg Ala Val Glu Leu Leu
755 760 765

Tyr Ser Ile Phe Cys Leu Asp Met Gln Gln Val Thr Leu Val Leu Leu
770 775 780

Gly His Ile Leu Pro Gly Leu Leu Thr Asp Ser Ser Lys Trp His Ser
785 790 795 800

Leu Met Asp Pro Pro Gly Thr Ala Leu Ala Lys Leu Ala Val Trp Cys
805 810 815

Ala Leu Ser Ser Tyr Ser Ser His Lys Gly Gln Ala Ser Thr Arg Gln
820 825 830

Lys Lys Arg His Arg Glu Asp Ile Glu Asp Tyr Ile Ser Leu Phe Pro
835 840 845

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Leu Asp Asp Val Gln Pro Ser Lys Leu Met Arg Leu Leu Ser Ser Asn
850 855 860

Glu Asp Asp Ala Asn Ile Leu Ser Ser Pro Arg Ser Ser Leu Gly Ser
865 870 875 880

Pro Cys Thr Ser Tyr Leu Arg Trp Val Lys Val Gly Leu Gly His Pro
885 890 895

Arg Gly Ala Pro Leu Leu His Ser Ala Gly Cys Phe Pro Ala Leu His
900 905 910

Leu Leu Arg Pro Thr Ala Asp Arg Ser Met Ser Ser Ser Leu Ser Ala
915 920 925

Ser Gln Leu His Thr Val Asn Met Arg Asp Pro Leu Asn Arg Val Leu
930 935 940

Ala Asn Leu Phe Leu Leu Ile Ser Ser Ile Leu Gly Ser Arg Thr Ala
945 950 955 960

Gly Pro His Thr Gln Phe Val Gln Trp Phe Met Glu Glu Cys Val Asp
965 970 975

Cys Leu Glu Gln Gly Gly Arg Gly Ser Val Leu Gln Phe Met Pro Phe
980 985 990

Thr Thr Val Ser Glu Leu Val Lys Val Ser Ala Met Ser Ser Pro Lys
995 1000 1005

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

Val Ala Ala Lys Ala Ile Ala Ala Leu
1025 1030

<210> 140
<211> 486
<212> PRT
<213> Homo sapiens

<400> 140
Met Lys Val Val Asn Leu Lys Gln Ala Ile Leu Gln Ala Trp Lys Glu
1 5 10 15

Arg Trp Ser Asp Tyr Gln Trp Ala Ile Asn Met Lys Lys Phe Phe Pro
20 25 30

Lys Gly Ala Thr Trp Asp Ile Leu Asn Leu Ala Asp Ala Leu Leu Glu
35 40 45

Gln Ala Met Ile Gly Pro Ser Pro Asn Pro Leu Ile Leu Ser Tyr Leu
50 55 60

Lys Tyr Ala Ile Ser Ser Gln Met Val Ser Tyr Ser Ser Val Leu Thr
65 70 75 80

Ala Ile Leu Glu Ile Leu Asn Ala Trp Glu Asn Gly Val Leu Ala Phe
85 90 95

Glu Ser Ile Gln Lys Ile Thr Asp Asn Ile Lys Gly Lys Val Cys Ser
100 105 110

Leu Ala Val Cys Ala Val Ala Trp Leu Val Ala His Val Arg Met Leu
115 120 125

Gly Leu Asp Glu Arg Glu Lys Ser Leu Gln Met Ile Arg Gln Leu Ala
130 135 140

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

Val Ile Met Asn Ser Ile Leu Glu Arg Met Cys Ala Asp Val Leu Gln
165 170 175

Gln Thr Ala Thr Gln Ile Lys Phe Pro Ser Thr Gly Val Asp Thr Met
180 185 190

Pro Tyr Trp Asn Leu Leu Pro Pro Lys Arg Pro Ile Lys Glu Val Leu
195 200 205

Thr Asp Ile Phe Ala Lys Val Leu Glu Lys Gly Trp Val Asp Ser Arg
210 215 220

Ser Ile His Ile Phe Asp Thr Leu Leu His Met Gly Gly Val Tyr Trp
225 230 235 240

Phe Cys Asn Asn Leu Ile Lys Glu Leu Leu Lys Glu Thr Arg Lys Glu
245 250 255

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

Met Gln Gln Val Thr Leu Val Leu Leu Gly His Ile Leu Pro Gly Leu
275 280 285

Leu Thr Asp Ser Ser Lys Trp His Ser Leu Met Asp Pro Pro Gly Thr
290 295 300

Ala Leu Ala Lys Leu Ala Val Trp Cys Ala Leu Ser Ser Tyr Ser Ser
305 310 315 320

His Lys Gly Gln Ala Ser Thr Arg Gln Lys Lys Arg His Arg Glu Asp
325 330 335

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```
Ile Glu Asp Tyr Ile Ser Leu Phe Pro Leu Asp Asp Val Gln Pro Ser
            340                 345                 350

Lys Leu Met Arg Leu Leu Ser Ser Asn Glu Asp Asp Ala Asn Ile Leu
        355                 360                 365

Ser Ser Pro Thr Asp Arg Ser Met Ser Ser Ser Leu Ser Ala Ser Gln
    370                 375                 380

Leu His Thr Val Asn Met Arg Asp Pro Leu Asn Arg Val Leu Ala Asn
385                 390                 395                 400

Leu Phe Leu Leu Ile Ser Ser Ile Leu Gly Ser Arg Thr Ala Gly Pro
                405                 410                 415

His Thr Gln Phe Val Gln Trp Phe Met Glu Glu Cys Val Asp Cys Leu
            420                 425                 430

Glu Gln Gly Gly Arg Gly Ser Val Leu Gln Phe Met Pro Phe Thr Thr
        435                 440                 445

Val Ser Glu Leu Val Lys Val Ser Ala Met Ser Ser Pro Lys Val Val
    450                 455                 460

Leu Ala Ile Thr Asp Leu Ser Leu Pro Leu Gly Arg Gln Val Ala Ala
465                 470                 475                 480

Lys Ala Ile Ala Ala Leu
                485
```

<210> 141
<211> 713
<212> PRT
<213> Homo sapiens

<400> 141

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Met Lys Val Val Asn Leu Lys Gln Ala Ile Leu Gln Ala Trp Lys Glu
1               5                   10                  15

Arg Trp Ser Asp Tyr Gln Trp Ala Ile Asn Met Lys Lys Phe Phe Pro
            20                  25                  30

Lys Gly Ala Thr Trp Asp Ile Leu Asn Leu Ala Asp Ala Leu Leu Glu
        35                  40                  45

Gln Ala Met Ile Gly Pro Ser Pro Asn Pro Leu Ile Leu Ser Tyr Leu
    50                  55                  60

Lys Tyr Ala Ile Ser Ser Gln Met Val Ser Tyr Ser Ser Val Leu Thr
65                  70                  75                  80

Ala Ile Ser Lys Phe Asp Asp Phe Ser Arg Asp Leu Cys Val Gln Ala
                85                  90                  95
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Leu Leu Asp Ile Met Asp Met Phe Cys Asp Arg Leu Ser Cys His Gly
100 105 110

Lys Ala Glu Glu Cys Ile Gly Leu Cys Arg Ala Leu Leu Ser Ala Leu
115 120 125

His Trp Leu Leu Arg Cys Thr Ala Ala Ser Ala Glu Arg Leu Arg Glu
130 135 140

Gly Leu Glu Ala Gly Thr Pro Ala Ala Gly Glu Lys Gln Leu Ala Met
145 150 155 160

Cys Leu Gln Arg Leu Glu Lys Thr Leu Ser Ser Thr Lys Asn Arg Ala
165 170 175

Leu Leu His Ile Ala Thr Gly Lys Leu Lys Ser Phe Ala Arg Lys Phe
180 185 190

Ile Asn Leu Asn Glu Phe Thr Thr Tyr Gly Ser Glu Glu Ser Thr Lys
195 200 205

Pro Ala Ser Val Arg Ala Leu Leu Phe Asp Ile Ser Phe Leu Met Leu
210 215 220

Cys His Val Ala Gln Thr Tyr Gly Ser Glu Val Ile Leu Ser Glu Ser
225 230 235 240

Arg Thr Gly Ala Glu Val Pro Phe Phe Glu Thr Trp Met Gln Thr Cys
245 250 255

Met Pro Glu Glu Gly Lys Ile Leu Asn Pro Asp His Pro Cys Phe Arg
260 265 270

Pro Asp Ser Thr Lys Val Glu Ser Leu Val Ala Leu Leu Asn Asn Ser
275 280 285

Ser Glu Met Lys Leu Val Gln Met Lys Trp His Glu Ala Cys Leu Ser
290 295 300

Ile Ser Ala Ala Ile Leu Glu Ile Leu Asn Ala Trp Glu Asn Gly Val
305 310 315 320

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

Val Cys Ser Leu Ala Val Cys Ala Val Ala Trp Leu Val Ala His Val
340 345 350

Arg Met Leu Gly Leu Asp Glu Arg Glu Lys Ser Leu Gln Met Ile Arg
355 360 365

Gln Leu Ala Gly Pro Leu Phe Ser Glu Asn Thr Leu Gln Phe Tyr Asn
370 375 380

Glu Arg Val Val Ile Met Asn Ser Ile Leu Glu Arg Met Cys Ala Asp
385 390 395 400

Val Leu Gln Gln Thr Ala Thr Gln Ile Lys Phe Pro Ser Thr Gly Val
405 410 415

Asp Thr Met Pro Tyr Trp Asn Leu Leu Pro Pro Lys Arg Pro Ile Lys
420 425 430

Glu Val Leu Thr Asp Ile Phe Ala Lys Val Leu Glu Lys Gly Trp Val
435 440 445

Asp Ser Arg Ser Ile His Ile Phe Asp Thr Leu Leu His Met Gly Gly
450 455 460

Val Tyr Trp Phe Cys Asn Asn Leu Ile Lys Glu Leu Leu Lys Glu Thr
465 470 475 480

Arg Lys Glu His Thr Leu Arg Ala Val Glu Leu Leu Tyr Ser Ile Phe
485 490 495

Cys Leu Asp Met Gln Gln Val Thr Leu Val Leu Leu Gly His Ile Leu
500 505 510

Pro Gly Leu Leu Thr Asp Ser Ser Lys Trp His Ser Leu Met Asp Pro
515 520 525

Pro Gly Thr Ala Leu Ala Lys Leu Ala Val Trp Cys Ala Leu Ser Ser
530 535 540

Tyr Ser Ser His Lys Gly Gln Ala Ser Thr Arg Gln Lys Lys Arg His
545 550 555 560

Arg Glu Asp Ile Glu Asp Tyr Ile Ser Leu Phe Pro Leu Asp Asp Val
565 570 575

Gln Pro Ser Lys Leu Met Arg Leu Leu Ser Ser Asn Glu Asp Asp Ala
580 585 590

Asn Ile Leu Ser Ser Pro Thr Asp Arg Ser Met Ser Ser Ser Leu Ser
595 600 605

Ala Ser Gln Leu His Thr Val Asn Met Arg Asp Pro Leu Asn Arg Val
610 615 620

Leu Ala Asn Leu Phe Leu Leu Ile Ser Ser Ile Leu Gly Ser Arg Thr
625 630 635 640

Ala Gly Pro His Thr Gln Phe Val Gln Trp Phe Met Glu Glu Cys Val
645 650 655

Asp Cys Leu Glu Gln Gly Gly Arg Gly Ser Val Leu Gln Phe Met Pro
660 665 670

Phe Thr Thr Val Ser Glu Leu Val Lys Val Ser Ala Met Ser Ser Pro
675 680 685

Lys Val Val Leu Ala Ile Thr Asp Leu Ser Leu Pro Leu Gly Arg Gln
690 695 700

Val Ala Ala Lys Ala Ile Ala Ala Leu
705 710

<210> 142
<211> 576
<212> PRT
<213> Homo sapiens

<400> 142
Met Lys Val Val Asn Leu Lys Gln Ala Ile Leu Gln Ala Trp Lys Glu
1 5 10 15

Arg Trp Ser Asp Tyr Gln Trp Ala Ile Asn Met Lys Lys Phe Phe Pro
20 25 30

Lys Gly Ala Thr Trp Asp Ile Leu Asn Leu Ala Asp Ala Leu Leu Glu
35 40 45

Gln Ala Met Ile Gly Pro Ser Pro Asn Pro Leu Ile Leu Ser Tyr Leu
50 55 60

Lys Tyr Ala Ile Ser Ser Gln Met Val Ser Tyr Ser Ser Val Leu Thr
65 70 75 80

Ala Ile Ser Lys Phe Asp Asp Phe Ser Arg Asp Leu Cys Val Gln Ala
85 90 95

Leu Leu Asp Ile Met Asp Met Phe Cys Asp Arg Leu Ser Cys His Gly
100 105 110

Lys Ala Glu Glu Cys Ile Gly Leu Cys Arg Ala Leu Leu Ser Ala Leu
115 120 125

His Trp Leu Leu Arg Cys Thr Ala Ala Ser Ala Glu Arg Leu Arg Glu
130 135 140

Gly Leu Glu Ala Gly Thr Pro Ala Ala Gly Glu Lys Gln Leu Ala Met
145 150 155 160

Cys Leu Gln Arg Leu Glu Lys Thr Leu Ser Ser Thr Lys Asn Arg Ala
165 170 175

Leu Leu His Ile Ala Lys Leu Glu Glu Ala Ser Ser Trp Thr Ala Ile
180 185 190

Glu His Ser Leu Leu Lys Leu Gly Glu Ile Leu Ala Asn Leu Ser Asn
195 200 205

Pro Gln Leu Arg Ser Gln Ala Glu Gln Cys Gly Thr Leu Ile Arg Ser
210 215 220

Ile Pro Thr Met Leu Ser Val His Ala Glu Gln Met His Lys Thr Gly
225 230 235 240

Phe Pro Thr Val His Ala Val Ile Leu Leu Glu Gly Thr Met Asn Leu
245 250 255

Thr Gly Glu Thr Gln Ser Leu Val Glu Gln Gln Thr Ala Thr Gln Ile
260 265 270

Lys Phe Pro Ser Thr Gly Val Asp Thr Met Pro Tyr Trp Asn Leu Leu
275 280 285

Pro Pro Lys Arg Pro Ile Lys Glu Val Leu Thr Asp Ile Phe Ala Lys
290 295 300

Val Leu Glu Lys Gly Trp Val Asp Ser Arg Ser Ile His Ile Phe Asp
305 310 315 320

Thr Leu Leu His Met Gly Gly Val Tyr Trp Phe Cys Asn Asn Leu Ile
325 330 335

Lys Glu Leu Leu Lys Glu Thr Arg Lys Glu His Thr Leu Arg Ala Val
340 345 350

Glu Leu Leu Tyr Ser Ile Phe Cys Leu Asp Met Gln Gln Val Thr Leu
355 360 365

Val Leu Leu Gly His Ile Leu Pro Gly Leu Leu Thr Asp Ser Ser Lys
370 375 380

Trp His Ser Leu Met Asp Pro Pro Gly Thr Ala Leu Ala Lys Leu Ala
385 390 395 400

Val Trp Cys Ala Leu Ser Ser Tyr Ser Ser His Lys Gly Gln Ala Ser
405 410 415

Thr Arg Gln Lys Lys Arg His Arg Glu Asp Ile Glu Asp Tyr Ile Ser
420 425 430

Leu Phe Pro Leu Asp Asp Val Gln Pro Ser Lys Leu Met Arg Leu Leu
435 440 445

Ser Ser Asn Glu Asp Asp Ala Asn Ile Leu Ser Ser Pro Thr Asp Arg
450 455 460

Ser Met Ser Ser Ser Leu Ser Ala Ser Gln Leu His Thr Val Asn Met
465 470 475 480

Arg Asp Pro Leu Asn Arg Val Leu Ala Asn Leu Phe Leu Leu Ile Ser
485 490 495

Ser Ile Leu Gly Ser Arg Thr Ala Gly Pro His Thr Gln Phe Val Gln
500 505 510

Trp Phe Met Glu Glu Cys Val Asp Cys Leu Glu Gln Gly Gly Arg Gly
515 520 525

Ser Val Leu Gln Phe Met Pro Phe Thr Thr Val Ser Glu Leu Val Lys
530 535 540

Val Ser Ala Met Ser Ser Pro Lys Val Val Leu Ala Ile Thr Asp Leu
545 550 555 560

Ser Leu Pro Leu Gly Arg Gln Val Ala Ala Lys Ala Ile Ala Ala Leu
565 570 575

<210> 143
<211> 837
<212> PRT
<213> Homo sapiens

<400> 143
Met Lys Val Val Asn Leu Lys Gln Ala Ile Leu Gln Ala Trp Lys Glu
1 5 10 15

Arg Trp Ser Asp Tyr Gln Trp Ala Ile Asn Met Lys Lys Phe Phe Pro
20 25 30

Lys Gly Ala Thr Trp Asp Ile Leu Asn Leu Ala Asp Ala Leu Leu Glu
35 40 45

Gln Ala Met Ile Gly Pro Ser Pro Asn Pro Leu Ile Leu Ser Tyr Leu
50 55 60

Lys Tyr Ala Ile Ser Ser Gln Met Val Ser Tyr Ser Ser Val Leu Thr
65 70 75 80

Ala Ile Ser Lys Phe Asp Asp Phe Ser Arg Asp Leu Cys Val Gln Ala
85 90 95

Leu Leu Asp Ile Met Asp Met Phe Cys Asp Arg Leu Ser Cys His Gly
100 105 110

Lys Ala Glu Glu Cys Ile Gly Leu Cys Arg Ala Leu Leu Ser Ala Leu
115 120 125

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His Trp Leu Leu Arg Cys Thr Ala Ala Ser Ala Glu Arg Leu Arg Glu
    130                 135                 140

Gly Leu Glu Ala Gly Thr Pro Ala Ala Gly Glu Lys Gln Leu Ala Met
145                 150                 155                 160

Cys Leu Gln Arg Leu Glu Lys Thr Leu Ser Ser Thr Lys Asn Arg Ala
                165                 170                 175

Leu Leu His Ile Ala Lys Leu Glu Glu Ala Ser Ser Trp Thr Ala Ile
            180                 185                 190

Glu His Ser Leu Leu Lys Leu Gly Glu Ile Leu Ala Asn Leu Ser Asn
        195                 200                 205

Pro Gln Leu Arg Ser Gln Ala Glu Gln Cys Gly Thr Leu Ile Arg Ser
    210                 215                 220

Ile Pro Thr Met Leu Ser Val His Ala Glu Gln Met His Lys Thr Gly
225                 230                 235                 240

Phe Pro Thr Val His Ala Val Ile Leu Leu Glu Gly Thr Met Asn Leu
                245                 250                 255

Thr Gly Glu Thr Gln Ser Leu Val Glu Gln Leu Thr Met Val Lys Arg
            260                 265                 270

Met Gln His Ile Pro Thr Pro Leu Phe Val Leu Glu Ile Trp Lys Ala
        275                 280                 285

Cys Phe Val Gly Leu Ile Glu Ser Pro Glu Gly Thr Glu Glu Leu Lys
    290                 295                 300

Trp Thr Ala Phe Thr Phe Leu Lys Ile Pro Gln Val Leu Val Lys Leu
305                 310                 315                 320

Lys Lys Tyr Ser His Gly Asp Lys Asp Phe Thr Glu Asp Val Asn Cys
                325                 330                 335

Ala Phe Glu Phe Leu Leu Lys Leu Thr Pro Leu Leu Asp Lys Ala Asp
            340                 345                 350

Gln Arg Cys Asn Cys Asp Cys Thr Asn Phe Leu Leu Gln Glu Cys Gly
        355                 360                 365

Lys Gln Gly Leu Leu Ser Glu Ala Ser Val Asn Asn Leu Met Ala Lys
    370                 375                 380

Arg Lys Ala Asp Arg Glu His Ala Pro Gln Gln Lys Ser Gly Glu Asn
385                 390                 395                 400
```

Ala Asn Ile Gln Pro Asn Ile Gln Leu Ile Leu Arg Ala Glu Pro Thr
405 410 415

Val Thr Asn Ile Leu Lys Thr Met Asp Ala Asp His Ser Lys Ser Pro
420 425 430

Glu Gly Leu Leu Gly Val Leu Gly His Met Leu Ser Gly Lys Ser Leu
435 440 445

Asp Leu Leu Leu Ala Ala Ala Ala Ala Thr Gly Lys Leu Lys Ser Phe
450 455 460

Ala Arg Lys Phe Ile Asn Leu Asn Glu Phe Thr Thr Tyr Gly Ser Glu
465 470 475 480

Glu Ser Thr Lys Pro Ala Ser Val Arg Ala Leu Leu Phe Asp Ile Ser
485 490 495

Phe Leu Met Leu Cys His Val Ala Gln Thr Tyr Gly Ser Glu Val Ile
500 505 510

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

Met Gln Thr Cys Met Pro Glu Glu Gly Lys Ile Leu Asn Pro Asp His
530 535 540

Pro Cys Phe Arg Pro Asp Ser Thr Lys Val Glu Ser Leu Val Ala Leu
545 550 555 560

Leu Asn Asn Ser Ser Glu Met Lys Leu Val Gln Met Lys Trp His Glu
565 570 575

Ala Cys Leu Ser Ile Ser Ala Ala Ile Leu Glu Ile Leu Asn Ala Trp
580 585 590

Glu Asn Gly Val Leu Ala Phe Glu Ser Ile Gln Lys Ile Thr Asp Asn
595 600 605

Ile Lys Gly Lys Val Cys Ser Leu Ala Val Cys Ala Val Ala Trp Leu
610 615 620

Val Ala His Val Arg Met Leu Gly Leu Asp Glu Arg Glu Lys Ser Leu
625 630 635 640

Gln Met Ile Arg Gln Leu Ala Gly Pro Leu Phe Ser Glu Asn Thr Leu
645 650 655

Gln Phe Tyr Asn Glu Arg Val Val Ile Met Asn Ser Ile Leu Glu Arg
660 665 670

Met Cys Ala Asp Val Leu Gln Gln Thr Ala Thr Gln Ile Lys Phe Pro

675 680 685

Ser Thr Gly Val Asp Thr Met Pro Tyr Trp Asn Leu Leu Pro Pro Lys
690 695 700

Arg Pro Ile Lys Glu Val Leu Thr Asp Ile Phe Ala Lys Val Leu Glu
705 710 715 720

Lys Gly Trp Val Asp Ser Arg Ser Ile His Ile Phe Asp Thr Leu Leu
725 730 735

His Met Gly Gly Val Tyr Trp Phe Cys Asn Asn Leu Ile Lys Glu Leu
740 745 750

Leu Lys Glu Thr Arg Lys Glu His Thr Leu Arg Ala Val Glu Leu Leu
755 760 765

Tyr Ser Ile Phe Cys Leu Asp Met Gln Gln Val Thr Leu Val Leu Leu
770 775 780

Gly His Ile Leu Pro Gly Leu Leu Thr Asp Ser Ser Lys Trp His Ser
785 790 795 800

Leu Met Asp Pro Pro Gly Thr Ala Leu Ala Lys Leu Ala Val Trp Cys
805 810 815

Ala Leu Ser Ser Tyr Ser Ser His Lys Gly Gln Ala Ser Thr Arg Gln
820 825 830

Lys Lys Arg His Leu
835

<210> 144
<211> 852
<212> PRT
<213> Homo sapiens

<400> 144
Met Lys Val Val Asn Leu Lys Gln Ala Ile Leu Gln Ala Trp Lys Glu
1 5 10 15

Arg Trp Ser Asp Tyr Gln Trp Ala Ile Asn Met Lys Lys Phe Phe Pro
20 25 30

Lys Gly Ala Thr Trp Asp Ile Leu Asn Leu Ala Asp Ala Leu Leu Glu
35 40 45

Gln Ala Met Ile Gly Pro Ser Pro Asn Pro Leu Ile Leu Ser Tyr Leu
50 55 60

Lys Tyr Ala Ile Ser Ser Gln Met Val Ser Tyr Ser Ser Val Leu Thr
65 70 75 80

```
Ala Ile Ser Lys Phe Asp Asp Phe Ser Arg Asp Leu Cys Val Gln Ala
                85                  90                  95

Leu Leu Asp Ile Met Asp Met Phe Cys Asp Arg Leu Ser Cys His Gly
            100                 105                 110

Lys Ala Glu Glu Cys Ile Gly Leu Cys Arg Ala Leu Leu Ser Ala Leu
        115                 120                 125

His Trp Leu Leu Arg Cys Thr Ala Ala Ser Ala Glu Arg Leu Arg Glu
    130                 135                 140

Gly Leu Glu Ala Gly Thr Pro Ala Ala Gly Glu Lys Gln Leu Ala Met
145                 150                 155                 160

Cys Leu Gln Arg Leu Glu Lys Thr Leu Ser Ser Thr Lys Asn Arg Ala
                165                 170                 175

Leu Leu His Ile Ala Lys Leu Glu Glu Ala Ser Ser Trp Thr Ala Ile
            180                 185                 190

Glu His Ser Leu Leu Lys Leu Gly Glu Ile Leu Ala Asn Leu Ser Asn
        195                 200                 205

Pro Gln Leu Arg Ser Gln Ala Glu Gln Cys Gly Thr Leu Ile Arg Ser
    210                 215                 220

Ile Pro Thr Met Leu Ser Val His Ala Glu Gln Met His Lys Thr Gly
225                 230                 235                 240

Phe Pro Thr Val His Ala Val Ile Leu Leu Glu Gly Thr Met Asn Leu
                245                 250                 255

Thr Gly Glu Thr Gln Ser Leu Val Glu Gln Leu Thr Met Val Lys Arg
            260                 265                 270

Met Gln His Ile Pro Thr Pro Leu Phe Val Leu Glu Ile Trp Lys Ala
        275                 280                 285

Cys Phe Val Gly Leu Ile Glu Ser Pro Glu Gly Thr Glu Glu Leu Lys
    290                 295                 300

Trp Thr Ala Phe Thr Phe Leu Lys Ile Pro Gln Val Leu Val Lys Leu
305                 310                 315                 320

Lys Lys Tyr Ser His Gly Asp Lys Asp Phe Thr Glu Asp Val Asn Cys
                325                 330                 335

Ala Phe Glu Phe Leu Leu Lys Leu Thr Pro Leu Leu Asp Lys Ala Asp
            340                 345                 350

Gln Arg Cys Asn Cys Asp Cys Thr Asn Phe Leu Leu Gln Glu Cys Gly
```

355 360 365

Lys Gln Gly Leu Leu Ser Glu Ala Ser Val Asn Asn Leu Met Ala Lys
370 375 380

Arg Lys Ala Asp Arg Glu His Ala Pro Gln Gln Lys Ser Gly Glu Asn
385 390 395 400

Ala Asn Ile Gln Pro Asn Ile Gln Leu Ile Leu Arg Ala Glu Pro Thr
405 410 415

Val Thr Asn Ile Leu Lys Thr Met Asp Ala Asp His Ser Lys Ser Pro
420 425 430

Glu Gly Leu Leu Gly Val Leu Gly His Met Leu Ser Gly Lys Ser Leu
435 440 445

Asp Leu Leu Leu Ala Ala Ala Ala Ala Thr Gly Lys Leu Lys Ser Phe
450 455 460

Ala Arg Lys Phe Ile Asn Leu Asn Glu Phe Thr Thr Tyr Gly Ser Glu
465 470 475 480

Glu Ser Thr Lys Pro Ala Ser Val Arg Ala Leu Leu Phe Asp Ile Ser
485 490 495

Phe Leu Met Leu Cys His Val Ala Gln Thr Tyr Gly Ser Glu Val Ile
500 505 510

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

Met Gln Thr Cys Met Pro Glu Glu Gly Lys Ile Leu Asn Pro Asp His
530 535 540

Pro Cys Phe Arg Pro Asp Ser Thr Lys Val Glu Ser Leu Val Ala Leu
545 550 555 560

Leu Asn Asn Ser Ser Glu Met Lys Leu Val Gln Met Lys Trp His Glu
565 570 575

Ala Cys Leu Ser Ile Ser Ala Ala Ile Leu Glu Ile Leu Asn Ala Trp
580 585 590

Glu Asn Gly Val Leu Ala Phe Glu Ser Ile Gln Lys Ile Thr Asp Asn
595 600 605

Ile Lys Gly Lys Val Cys Ser Leu Ala Val Cys Ala Val Ala Trp Leu
610 615 620

Val Ala His Val Arg Met Leu Gly Leu Asp Glu Arg Glu Lys Ser Leu
625 630 635 640

Gln Met Ile Arg Gln Leu Ala Gly Pro Leu Phe Ser Glu Asn Thr Leu
645 650 655

Gln Phe Tyr Asn Glu Arg Val Val Ile Met Asn Ser Ile Leu Glu Arg
660 665 670

Met Cys Ala Asp Val Leu Gln Gln Thr Ala Thr Gln Ile Lys Phe Pro
675 680 685

Ser Thr Gly Val Asp Thr Met Pro Tyr Trp Asn Leu Leu Pro Pro Lys
690 695 700

Arg Pro Ile Lys Glu Val Leu Thr Asp Ile Phe Ala Lys Val Leu Glu
705 710 715 720

Lys Gly Trp Val Asp Ser Arg Ser Ile His Ile Phe Asp Thr Leu Leu
725 730 735

His Met Gly Gly Val Tyr Trp Phe Cys Asn Asn Leu Ile Lys Glu Leu
740 745 750

Leu Lys Glu Thr Arg Lys Glu His Thr Leu Arg Ala Val Glu Leu Leu
755 760 765

Tyr Ser Ile Phe Cys Leu Asp Met Gln Gln Val Thr Leu Val Leu Leu
770 775 780

Gly His Ile Leu Pro Gly Leu Leu Thr Asp Ser Ser Lys Trp His Ser
785 790 795 800

Leu Met Asp Pro Pro Gly Thr Ala Leu Ala Lys Leu Ala Val Trp Cys
805 810 815

Ala Leu Ser Ser Tyr Ser Ser His Lys Gly Gln Ala Ser Thr Arg Gln
820 825 830

Lys Lys Arg His Arg Glu Asp Ile Glu Asp Tyr Ile Ser Leu Phe Pro
835 840 845

Ala Pro Asp Ser
850

<210> 145
<211> 221
<212> PRT
<213> Homo sapiens

<400> 145
Met Pro Leu Val Pro Arg Trp Cys Pro Thr Leu Leu Ser Ser Gln Pro
1 5 10 15

Ser Ile Pro Gln Val Leu Val Lys Leu Lys Lys Tyr Ser His Gly Asp

20 25 30

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

Leu Thr Pro Leu Leu Asp Lys Ala Asp Gln Arg Cys Asn Cys Asp Cys
50 55 60

Thr Asn Phe Leu Leu Gln Glu Cys Gly Lys Gln Gly Leu Leu Ser Glu
65 70 75 80

Ala Ser Val Asn Asn Leu Met Ala Lys Arg Lys Ala Asp Arg Glu His
85 90 95

Ala Pro Gln Gln Lys Ser Gly Glu Asn Ala Asn Ile Gln Pro Asn Ile
100 105 110

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

Met Asp Ala Asp His Ser Lys Ser Pro Glu Gly Leu Leu Gly Val Leu
130 135 140

Gly His Met Leu Ser Gly Lys Ser Leu Asp Leu Leu Leu Ala Ala Ala
145 150 155 160

Ala Ala Thr Gly Lys Leu Lys Ser Phe Ala Arg Lys Phe Ile Asn Leu
165 170 175

Asn Glu Phe Thr Thr Tyr Gly Ser Glu Glu Ser Thr Lys Pro Ala Ser
180 185 190

Val Arg Ala Leu Leu Phe Asp Ile Ser Phe Leu Met Leu Cys His Val
195 200 205

Ala Gln Thr Tyr Gly Ser Glu Val Ile Leu Ser Glu Ser
210 215 220

<210> 146
<211> 491
<212> PRT
<213> Homo sapiens

<400> 146
Met Leu Cys His Val Ala Gln Thr Tyr Gly Ser Glu Val Ile Leu Ser
1 5 10 15

Glu Ser Arg Thr Gly Ala Glu Val Pro Phe Phe Glu Thr Trp Met Gln
20 25 30

Thr Cys Met Pro Glu Glu Gly Lys Ile Leu Asn Pro Asp His Pro Cys
35 40 45

```
Phe Arg Pro Asp Ser Thr Lys Val Glu Ser Leu Val Ala Leu Leu Asn
    50                  55                  60

Asn Ser Ser Glu Met Lys Leu Val Gln Met Lys Trp His Glu Ala Cys
65                  70                  75                  80

Leu Ser Ile Ser Ala Ala Ile Leu Glu Ile Leu Asn Ala Trp Glu Asn
                85                  90                  95

Gly Val Leu Ala Phe Glu Ser Ile Gln Lys Ile Thr Asp Asn Ile Lys
            100                 105                 110

Gly Lys Val Cys Ser Leu Ala Val Cys Ala Val Ala Trp Leu Val Ala
        115                 120                 125

His Val Arg Met Leu Gly Leu Asp Glu Arg Glu Lys Ser Leu Gln Met
    130                 135                 140

Ile Arg Gln Leu Ala Gly Pro Leu Phe Ser Glu Asn Thr Leu Gln Phe
145                 150                 155                 160

Tyr Asn Glu Arg Val Val Ile Met Asn Ser Ile Leu Glu Arg Met Cys
                165                 170                 175

Ala Asp Val Leu Gln Gln Thr Ala Thr Gln Ile Lys Phe Pro Ser Thr
            180                 185                 190

Gly Val Asp Thr Met Pro Tyr Trp Asn Leu Leu Pro Pro Lys Arg Pro
        195                 200                 205

Ile Lys Glu Val Leu Thr Asp Ile Phe Ala Lys Val Leu Glu Lys Gly
    210                 215                 220

Trp Val Asp Ser Arg Ser Ile His Ile Phe Asp Thr Leu Leu His Met
225                 230                 235                 240

Gly Gly Val Tyr Trp Phe Cys Asn Asn Leu Ile Lys Glu Leu Leu Lys
                245                 250                 255

Glu Thr Arg Lys Glu His Thr Leu Arg Ala Val Glu Leu Leu Tyr Ser
            260                 265                 270

Ile Phe Cys Leu Asp Met Gln Gln Val Thr Leu Val Leu Leu Gly His
        275                 280                 285

Ile Leu Pro Gly Leu Leu Thr Asp Ser Ser Lys Trp His Ser Leu Met
    290                 295                 300

Asp Pro Pro Gly Thr Ala Leu Ala Lys Leu Ala Val Trp Cys Ala Leu
305                 310                 315                 320

Ser Ser Tyr Ser Ser His Lys Gly Gln Ala Ser Thr Arg Gln Lys Lys
```

325 330 335

Arg His Arg Glu Asp Ile Glu Asp Tyr Ile Ser Leu Phe Pro Leu Asp
340 345 350

Asp Val Gln Pro Ser Lys Leu Met Arg Leu Leu Ser Ser Asn Glu Asp
355 360 365

Asp Ala Asn Ile Leu Ser Ser Pro Thr Asp Arg Ser Met Ser Ser Ser
370 375 380

Leu Ser Ala Ser Gln Leu His Thr Val Asn Met Arg Asp Pro Leu Asn
385 390 395 400

Arg Val Leu Ala Asn Leu Phe Leu Leu Ile Ser Ser Ile Leu Gly Ser
405 410 415

Arg Thr Ala Gly Pro His Thr Gln Phe Val Gln Trp Phe Met Glu Glu
420 425 430

Cys Val Asp Cys Leu Glu Gln Gly Gly Arg Gly Ser Val Leu Gln Phe
435 440 445

Met Pro Phe Thr Thr Val Ser Glu Leu Val Lys Val Ser Ala Met Ser
450 455 460

Ser Pro Lys Val Val Leu Ala Ile Thr Asp Leu Ser Leu Pro Leu Gly
465 470 475 480

Arg Gln Val Ala Ala Lys Ala Ile Ala Ala Leu
485 490

<210> 147
<211> 534
<212> PRT
<213> Homo sapiens

<400> 147
Met Val Pro Gly Ser Glu Gly Pro Ala Arg Ala Gly Ser Val Val Ala
1 5 10 15

Asp Val Val Phe Val Ile Glu Gly Thr Ala Asn Leu Gly Pro Tyr Phe
20 25 30

Glu Gly Leu Arg Lys His Tyr Leu Leu Pro Ala Ile Glu Tyr Phe Asn
35 40 45

Gly Gly Pro Pro Ala Glu Thr Asp Phe Gly Gly Asp Val Pro Gly Asn
50 55 60

Leu Ser Ala Ala Gln Val Ala Ala Gln Asn Ala Val Glu Ala Ala Lys
65 70 75 80

Asn Gln Lys Ala Gly Leu Gly Pro Arg Phe Ser Pro Ile Thr Pro Leu
85 90 95

Gln Gln Ala Ala Pro Gly Val Gly Pro Pro Phe Ser Gln Ala Pro Ala
100 105 110

Pro Gln Leu Pro Pro Gly Pro Pro Gly Ala Pro Lys Pro Pro Pro Ala
115 120 125

Ser Gln Pro Ser Leu Val Ser Thr Val Ala Pro Gly Ser Gly Leu Ala
130 135 140

Pro Thr Ala Gln Pro Gly Ala Pro Ser Met Ala Gly Thr Val Ala Pro
145 150 155 160

Gly Gly Val Ser Gly Pro Ser Pro Ala Gln Leu Gly Ala Pro Ala Leu
165 170 175

Gly Gly Gln Gln Ser Val Ser Asn Lys Leu Leu Ala Trp Ser Gly Val
180 185 190

Leu Glu Trp Gln Glu Lys Pro Lys Pro Ala Ser Val Asp Ala Asn Thr
195 200 205

Lys Leu Thr Arg Ser Leu Pro Cys Gln Val Tyr Val Asn His Gly Glu
210 215 220

Asn Leu Lys Thr Glu Gln Trp Pro Gln Lys Leu Ile Met Gln Leu Ile
225 230 235 240

Pro Gln Gln Leu Leu Thr Thr Leu Gly Pro Leu Phe Arg Asn Ser Arg
245 250 255

Met Val Gln Phe His Phe Thr Asn Lys Asp Leu Glu Ser Leu Lys Gly
260 265 270

Leu Tyr Arg Ile Met Gly Asn Gly Phe Ala Gly Cys Val His Phe Pro
275 280 285

His Thr Ala Pro Cys Glu Val Arg Val Leu Met Leu Leu Tyr Ser Ser
290 295 300

Lys Lys Lys Ile Phe Met Gly Leu Ile Pro Tyr Asp Gln Ser Gly Phe
305 310 315 320

Val Asn Gly Ile Arg Gln Val Ile Thr Asn His Lys Gln Val Gln Gln
325 330 335

Gln Lys Leu Glu Gln Gln Gln Arg Gly Met Gly Gly Gln Gln Ala Pro
340 345 350

Pro Gly Leu Gly Pro Ile Leu Glu Asp Gln Ala Arg Pro Ser Gln Asn

355 360 365

Leu Leu Gln Leu Arg Pro Pro Gln Pro Gln Pro Gln Gly Thr Val Gly
370 375 380

Ala Ser Gly Ala Thr Gly Gln Pro Gln Pro Gln Gly Thr Ala Gln Pro
385 390 395 400

Pro Pro Gly Ala Pro Gln Gly Pro Pro Gly Ala Ala Ser Gly Pro Pro
405 410 415

Pro Pro Gly Pro Ile Leu Arg Pro Gln Asn Pro Gly Ala Asn Pro Gln
420 425 430

Leu Arg Ser Leu Leu Leu Asn Pro Pro Pro Pro Gln Thr Gly Val Pro
435 440 445

Pro Pro Gln Ala Ser Leu His His Leu Gln Pro Pro Gly Ala Pro Ala
450 455 460

Leu Leu Pro Pro Pro His Gln Gly Leu Gly Gln Pro Gln Leu Gly Pro
465 470 475 480

Pro Leu Leu His Pro Pro Pro Ala Gln Ser Trp Pro Ala Gln Leu Pro
485 490 495

Pro Arg Ala Pro Leu Pro Gly Gln Met Leu Leu Ser Gly Gly Pro Arg
500 505 510

Gly Pro Val Pro Gln Pro Gly Leu Gln Pro Ser Val Met Glu Asp Asp
515 520 525

Ile Leu Met Asp Leu Ile
530

<210> 148
<211> 131
<212> PRT
<213> Homo sapiens

<400> 148
Met Val Pro Gly Ser Glu Gly Pro Ala Arg Ala Gly Ser Val Val Ala
1 5 10 15

Asp Val Val Phe Val Ile Glu Gly Thr Ala Asn Pro Gln Leu Arg Ser
20 25 30

Leu Leu Leu Asn Pro Pro Pro Pro Gln Thr Gly Val Pro Pro Pro Gln
35 40 45

Ala Ser Leu His His Leu Gln Pro Pro Gly Ala Pro Ala Leu Leu Pro
50 55 60

Pro Pro His Gln Gly Leu Gly Gln Pro Gln Leu Gly Pro Pro Leu Leu
65 70 75 80

His Pro Pro Pro Ala Gln Ser Trp Pro Ala Gln Leu Pro Pro Arg Ala
85 90 95

Pro Leu Pro Gly Gln Met Leu Leu Ser Gly Gly Pro Arg Gly Pro Val
100 105 110

Pro Gln Pro Gly Leu Gln Pro Ser Val Met Glu Asp Asp Ile Leu Met
115 120 125

Asp Leu Ile
130

<210> 149
<211> 168
<212> PRT
<213> Homo sapiens

<400> 149
Met Val Pro Gly Ser Glu Gly Pro Ala Arg Ala Gly Ser Val Val Ala
1 5 10 15

Asp Val Val Phe Val Ile Glu Gly Thr Ala Asn Leu Gly Pro Tyr Phe
20 25 30

Glu Gly Leu Arg Lys His Tyr Leu Leu Pro Ala Ile Glu Tyr Phe Asn
35 40 45

Gly Gly Pro Pro Gly Pro Ile Leu Arg Pro Gln Asn Pro Gly Ala Asn
50 55 60

Pro Gln Leu Arg Ser Leu Leu Leu Asn Pro Pro Pro Pro Gln Thr Gly
65 70 75 80

Val Pro Pro Pro Gln Ala Ser Leu His His Leu Gln Pro Pro Gly Ala
85 90 95

Pro Ala Leu Leu Pro Pro Pro His Gln Gly Leu Gly Gln Pro Gln Leu
100 105 110

Gly Pro Pro Leu Leu His Pro Pro Pro Ala Gln Ser Trp Pro Ala Gln
115 120 125

Leu Pro Pro Arg Ala Pro Leu Pro Gly Gln Met Leu Leu Ser Gly Gly
130 135 140

Pro Arg Gly Pro Val Pro Gln Pro Gly Leu Gln Pro Ser Val Met Glu
145 150 155 160

Asp Asp Ile Leu Met Asp Leu Ile
165

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<210> 150
<211> 92
<212> PRT
<213> Homo sapiens

<400> 150
Met Thr Ala Ala Pro Ala Ser Pro Gln Gln Ile Arg Asp Arg Leu Leu
1 5 10 15

Gln Ala Ile Asp Pro Gln Ser Asn Ile Arg Asn Met Val Ala Val Leu
20 25 30

Glu Val Ile Ser Ser Leu Glu Lys Tyr Pro Ile Thr Lys Glu Ala Leu
35 40 45

Glu Glu Thr Arg Leu Gly Lys Leu Ile Asn Asp Val Arg Lys Lys Thr
50 55 60

Lys Asn Glu Glu Leu Ala Lys Arg Ala Lys Lys Leu Pro Gly Trp Gln
65 70 75 80

Trp Ala Cys Arg Pro Arg Gly Gln Pro Pro Gly Ala
85 90

<210> 151
<211> 514
<212> PRT
<213> Homo sapiens

<400> 151
Met Thr Ala Ala Pro Ala Ser Pro Gln Gln Ile Arg Asp Arg Leu Leu
1 5 10 15

Gln Ala Ile Asp Pro Gln Ser Asn Ile Arg Asn Met Val Ala Val Leu
20 25 30

Glu Val Ile Ser Ser Leu Glu Lys Tyr Pro Ile Thr Lys Glu Ala Leu
35 40 45

Glu Glu Thr Arg Leu Gly Lys Leu Ile Asn Asp Val Arg Lys Arg Arg
50 55 60

Gly Asp Gln Arg Asp Leu Gly His Pro Gly Pro Pro Pro Lys Val Ser
65 70 75 80

Lys Ala Ser His Asp Pro Leu Val Pro Asn Ser Ser Pro Leu Pro Thr
85 90 95

Asn Gly Ile Ser Gly Ser Pro Glu Ser Phe Ala Ser Ser Leu Asp Gly
100 105 110

Ser Gly His Ala Gly Pro Glu Gly Ser Arg Leu Glu Arg Asp Glu Asn
115 120 125

Asp Lys His Ser Gly Lys Ile Pro Val Asn Ala Val Arg Pro His Thr
130 135 140

Ser Ser Pro Gly Leu Gly Lys Pro Pro Gly Pro Cys Leu Gln Pro Lys
145 150 155 160

Ala Ser Val Leu Gln Gln Leu Asp Arg Val Asp Glu Thr Pro Gly Pro
165 170 175

Pro His Pro Lys Gly Pro Pro Arg Cys Ser Phe Ser Pro Arg Asn Ser
180 185 190

Arg His Glu Gly Ser Phe Ala Arg Gln Gln Ser Leu Tyr Ala Pro Lys
195 200 205

Gly Ser Val Pro Ser Pro Ser Pro Arg Pro Gln Ala Leu Asp Ala Thr
210 215 220

Gln Val Pro Ser Pro Leu Pro Leu Ala Gln Pro Ser Thr Pro Pro Val
225 230 235 240

Arg Arg Leu Glu Leu Leu Pro Ser Ala Glu Ser Pro Val Cys Trp Leu
245 250 255

Glu Gln Pro Glu Ser His Gln Arg Leu Ala Gly Pro Gly Cys Lys Ala
260 265 270

Gly Leu Ser Pro Ala Glu Pro Leu Leu Ser Arg Ala Gly Phe Ser Pro
275 280 285

Asp Ser Ser Lys Ala Asp Ser Asp Ala Ala Ser Ser Gly Gly Ser Asp
290 295 300

Ser Lys Lys Lys Lys Arg Tyr Arg Pro Arg Asp Tyr Thr Val Asn Leu
305 310 315 320

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

Arg Lys Leu Thr Phe Asp Pro Met Thr Arg Gln Ile Lys Pro Leu Thr
340 345 350

Gln Lys Glu Pro Val Arg Ala Asp Ser Pro Val His Met Glu Gln Gln
355 360 365

Ser Arg Thr Glu Leu Asp Lys Gln Glu Ala Lys Ala Ser Leu Gln Ser
370 375 380

Pro Phe Glu Gln Thr Asn Trp Lys Glu Leu Ser Arg Asn Glu Ile Ile
385 390 395 400

Gln Ser Tyr Leu Ser Arg Gln Ser Ser Leu Leu Ser Ser Ser Gly Ala

405 410 415

Gln Thr Pro Gly Ala His His Phe Met Ser Glu Tyr Leu Lys Gln Glu
420 425 430

Glu Ser Thr Arg Gln Gly Ala Arg Gln Leu His Val Leu Val Pro Gln
435 440 445

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

Asp Leu Asp Arg Ile Gln Ala Ser Gln Trp Pro Gly Val Asn Gly Cys
465 470 475 480

Gln Asp Thr Gln Gly Asn Trp Tyr Asp Trp Thr Gln Cys Ile Ser Leu
485 490 495

Asp Pro His Gly Asp Asp Gly Arg Leu Asn Ile Leu Pro Tyr Val Cys
500 505 510

Leu Asp

<210> 152
<211> 195
<212> PRT
<213> Homo sapiens

<400> 152
Met Ala Asp Val Ile Asn Val Ser Val Asn Leu Glu Ala Phe Ser Gln
1 5 10 15

Ala Ile Ser Ala Ile Gln Ala Leu Arg Ser Ser Val Ser Arg Val Phe
20 25 30

Asp Cys Leu Lys Asp Gly Met Arg Asn Lys Glu Thr Leu Glu Gly Arg
35 40 45

Glu Lys Ala Phe Ile Ala His Phe Gln Asp Asn Leu His Ser Val Asn
50 55 60

Arg Asp Leu Asn Glu Leu Glu Arg Leu Ser Asn Leu Val Gly Lys Pro
65 70 75 80

Ser Glu Asn His Pro Leu His Asn Ser Gly Leu Leu Ser Leu Asp Pro
85 90 95

Val Gln Asp Lys Thr Pro Leu Tyr Ser Gln Leu Leu Gln Ala Tyr Lys
100 105 110

Trp Ser Asn Lys Leu Gln Tyr His Ala Gly Leu Ala Ser Gly Leu Leu
115 120 125

Asn Gln Gln Ser Leu Lys Arg Ser Ala Asn Gln Met Gly Val Ser Ala
130 135 140

Lys Arg Arg Pro Lys Ala Gln Pro Thr Thr Leu Val Leu Pro Pro Gln
145 150 155 160

Tyr Val Asp Asp Val Ile Ser Arg Ile Asp Arg Met Phe Pro Glu Met
165 170 175

Ser Ile His Leu Ser Arg Pro Asn Gly Thr Ser Ala Met Leu Leu Val
180 185 190

Arg Ser Ala
195

<210> 153
<211> 182
<212> PRT
<213> Homo sapiens

<400> 153
Met Ala Ala Pro Leu Gly Gly Met Phe Ser Gly Gln Pro Pro Gly Pro
1 5 10 15

Pro Gln Ala Pro Pro Gly Leu Pro Gly Gln Ala Ser Leu Leu Gln Ala
20 25 30

Ala Pro Gly Ala Pro Arg Pro Ser Ser Ser Thr Leu Val Asp Glu Leu
35 40 45

Glu Ser Ser Phe Glu Ala Cys Phe Ala Ser Leu Val Ser Gln Asp Tyr
50 55 60

Val Asn Gly Thr Asp Gln Glu Glu Ile Arg Thr Gly Val Asp Gln Cys
65 70 75 80

Ile Gln Lys Phe Leu Asp Ile Ala Arg Gln Thr Glu Cys Phe Phe Leu
85 90 95

Gln Lys Arg Leu Gln Leu Ser Val Gln Lys Pro Glu Gln Val Ile Lys
100 105 110

Glu Asp Val Ser Glu Leu Arg Asn Glu Leu Gln Arg Lys Asp Ala Leu
115 120 125

Val Gln Lys His Leu Thr Lys Leu Arg His Trp Gln Gln Val Leu Glu
130 135 140

Asp Ile Asn Val Gln His Lys Lys Pro Ala Asp Ile Pro Gln Gly Ser
145 150 155 160

Leu Ala Tyr Leu Glu Gln Ala Ser Ala Asn Ile Pro Ala Pro Leu Lys
165 170 175

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Pro Thr His Leu Thr Gly
180

<210> 154
<211> 125
<212> PRT
<213> Homo sapiens

<400> 154
Met Ala Ala Pro Leu Gly Gly Met Phe Ser Gly Gln Pro Pro Gly Pro
1 5 10 15

Pro Gln Ala Pro Pro Gly Leu Pro Gly Gln Ala Ser Leu Leu Gln Ala
20 25 30

Ala Pro Gly Ala Pro Arg Pro Ser Ser Ser Thr Leu Val Asp Glu Leu
35 40 45

Glu Ser Ser Phe Glu Ala Cys Phe Ala Ser Leu Val Ser Gln Asp Tyr
50 55 60

Val Asn Gly Thr Asp Gln Glu Glu Ile Arg Thr Gly Val Asp Gln Cys
65 70 75 80

Ile Gln Lys Phe Leu Asp Ile Ala Arg Gln Thr Glu Cys Phe Phe Leu
85 90 95

Gln Lys Arg Leu Gln Leu Ser Val Gln Lys Pro Glu Gln Val Ile Lys
100 105 110

Glu Val Phe Leu Leu Arg Lys Lys Lys Thr Thr Cys Pro
115 120 125

<210> 155
<211> 141
<212> PRT
<213> Homo sapiens

<400> 155
Met Ser Thr Pro Pro Leu Ala Ala Ser Gly Met Ala Pro Gly Pro Phe
1 5 10 15

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

Leu Cys Arg Ile Gly Gln Glu Thr Val Gln Asp Ile Val Tyr Arg Thr
35 40 45

Met Glu Ile Phe Gln Leu Leu Arg Asn Met Gln Leu Pro Asn Gly Val
50 55 60

Thr Tyr His Thr Gly Thr Tyr Gln Asp Arg Leu Thr Lys Leu Gln Asp
65 70 75 80

Asn Leu Arg Gln Leu Ser Val Leu Phe Arg Lys Leu Arg Leu Val Tyr
85 90 95

Asp Lys Cys Asn Glu Asn Cys Gly Gly Met Asp Pro Ile Pro Val Glu
100 105 110

Val Ile Phe Cys Asp Arg Gly Arg Met Asn Ile Arg Cys Glu Leu Val
115 120 125

Ser Arg Gln Leu Leu Ile Phe Phe Leu Ser Leu Leu Phe
130 135 140

<210> 156
<211> 153
<212> PRT
<213> Homo sapiens

<400> 156
Met Ser Thr Pro Pro Leu Ala Ala Ser Gly Met Ala Pro Gly Pro Phe
1 5 10 15

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

Leu Cys Arg Ile Gly Gln Glu Thr Val Gln Asp Ile Val Tyr Arg Thr
35 40 45

Met Glu Ile Phe Gln Leu Leu Arg Asn Met Gln Leu Pro Asn Gly Val
50 55 60

Thr Tyr His Thr Gly Thr Tyr Gln Asp Arg Leu Thr Lys Leu Gln Asp
65 70 75 80

Asn Leu Arg Gln Leu Ser Val Leu Phe Arg Lys Leu Arg Leu Val Tyr
85 90 95

Asp Lys Cys Asn Glu Asn Cys Gly Gly Met Asp Pro Ile Pro Val Glu
100 105 110

Gln Leu Ile Pro Tyr Val Glu Glu Asp Gly Ser Lys Asn Asp Asp Arg
115 120 125

Ala Gly Pro Pro Arg Phe Ala Ser Glu Glu Arg Arg Glu Ile Ala Glu
130 135 140

Val Asn Lys Val Leu Gly Glu Ala Phe
145 150

<210> 157
<211> 157
<212> PRT
<213> Homo sapiens

<400> 157
Met Ser Thr Pro Pro Leu Ala Ala Ser Gly Met Ala Pro Gly Pro Phe

1 5 10 15

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

Leu Cys Arg Ile Gly Gln Glu Thr Val Gln Asp Ile Val Tyr Arg Thr
35 40 45

Met Glu Ile Phe Gln Leu Leu Arg Asn Met Gln Leu Pro Asn Gly Val
50 55 60

Thr Tyr His Thr Gly Thr Tyr Gln Asp Arg Leu Thr Lys Leu Gln Asp
65 70 75 80

Asn Leu Arg Gln Leu Ser Val Leu Phe Arg Lys Leu Arg Leu Val Tyr
85 90 95

Asp Lys Cys Asn Glu Asn Cys Gly Gly Met Asp Pro Ile Pro Val Glu
100 105 110

Gln Leu Ile Pro Tyr Val Glu Glu Asp Gly Ser Lys Asn Asp Asp Arg
115 120 125

Ala Gly Pro Pro Arg Phe Ala Ser Glu Glu Arg Arg Glu Ile Ala Glu
130 135 140

Val Asn Lys Ala Leu Ser Ser Val Pro Glu Phe Leu Pro
145 150 155

<210> 158
<211> 43
<212> PRT
<213> Homo sapiens

<400> 158
Met Ala Ala Ala Val Ala Met Glu Thr Asp Asp Ala Gly Asn Arg Leu
1 5 10 15

Arg Phe Gln Leu Glu Leu Glu Phe Val Gln Cys Leu Ala Asn Pro Asn
20 25 30

Tyr Leu Asn Cys Thr Leu Ser Val Tyr Thr Cys
35 40

<210> 159
<211> 57
<212> PRT
<213> Homo sapiens

<400> 159
Met Leu Glu Leu Leu Gln Tyr Glu His Phe Arg Lys Glu Leu Val Asn
1 5 10 15

Ala Gln Cys Ala Lys Phe Ile Asp Glu Gln Gln Ile Leu His Trp Gln
20 25 30

His Tyr Ser Arg Lys Arg Met Arg Leu Gln Gln Ala Leu Ala Glu Gln
35 40 45

Gln Gln Gln Asn Asn Thr Ser Gly Lys
50 55

<210> 160
<211> 44
<212> PRT
<213> Homo sapiens

<400> 160
Met Ala Ala Ala Val Ala Met Glu Thr Asp Asp Ala Gly Asn Arg Leu
1 5 10 15

Arg Phe Gln Leu Glu Leu Glu Phe Val Gln Cys Leu Ala Asn Pro Asn
20 25 30

Tyr Leu Asn Cys Lys Leu Leu Ser Thr Ser Leu Asn
35 40

<210> 161
<211> 416
<212> PRT
<213> Homo sapiens

<400> 161
Met Asp Tyr Asp Phe Lys Val Lys Leu Ser Ser Glu Arg Glu Arg Val
1 5 10 15

Glu Asp Leu Phe Glu Tyr Glu Gly Cys Lys Val Gly Arg Gly Thr Tyr
20 25 30

Gly His Val Tyr Lys Ala Lys Arg Lys Asp Gly Lys Asp Asp Lys Asp
35 40 45

Tyr Ala Leu Lys Gln Ile Glu Gly Thr Gly Ile Ser Met Ser Ala Cys
50 55 60

Arg Glu Ile Ala Leu Leu Arg Glu Leu Lys His Pro Asn Val Ile Ser
65 70 75 80

Leu Gln Lys Val Phe Leu Ser His Ala Asp Arg Lys Val Trp Leu Leu
85 90 95

Phe Asp Tyr Ala Glu His Asp Leu Trp His Ile Ile Lys Phe His Arg
100 105 110

Ala Ser Lys Ala Asn Lys Lys Pro Val Gln Leu Pro Arg Gly Met Val
115 120 125

Lys Ser Leu Leu Tyr Gln Ile Leu Asp Gly Ile His Tyr Leu His Ala
130 135 140

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Asn Trp Val Leu His Arg Asp Leu Lys Pro Ala Asn Ile Leu Val Met
145                 150                 155                 160

Gly Glu Gly Pro Glu Arg Gly Arg Val Lys Ile Ala Asp Met Gly Phe
                165                 170                 175

Ala Arg Leu Phe Asn Ser Pro Leu Lys Pro Leu Ala Asp Leu Asp Pro
            180                 185                 190

Val Val Val Thr Phe Trp Tyr Arg Ala Pro Glu Leu Leu Leu Gly Ala
        195                 200                 205

Arg His Tyr Thr Lys Ala Ile Asp Lys Asp Trp Glu Asp Ile Lys Lys
    210                 215                 220

Met Pro Glu His Ser Thr Leu Met Lys Asp Phe Arg Arg Asn Thr Tyr
225                 230                 235                 240

Thr Asn Cys Ser Leu Ile Lys Tyr Met Glu Lys His Lys Val Lys Pro
                245                 250                 255

Asp Ser Lys Ala Phe His Leu Leu Gln Lys Leu Leu Thr Met Asp Pro
            260                 265                 270

Ile Lys Arg Ile Thr Ser Glu Gln Ala Met Gln Asp Pro Tyr Phe Leu
        275                 280                 285

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

Tyr Pro Lys Arg Glu Phe Leu Thr Glu Glu Glu Pro Asp Asp Lys Gly
305                 310                 315                 320

Asp Lys Lys Asn Gln Gln Gln Gln Gln Gly Asn Asn His Thr Asn Gly
                325                 330                 335

Thr Gly His Pro Gly Asn Gln Asp Ser Ser His Thr Gln Gly Pro Pro
            340                 345                 350

Leu Lys Lys Val Arg Val Val Pro Pro Thr Thr Thr Ser Gly Gly Leu
        355                 360                 365

Ile Met Thr Ser Asp Tyr Gln Arg Ser Asn Pro His Ala Ala Tyr Pro
    370                 375                 380

Asn Pro Gly Pro Ser Thr Ser Gln Pro Gln Ser Ser Met Gly Tyr Ser
385                 390                 395                 400

Ala Thr Ser Gln Gln Pro Pro Gln Tyr Ser His Gln Thr His Arg Tyr
                405                 410                 415
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<210> 162
<211> 163
<212> PRT
<213> Homo sapiens

<400> 162
Met Val Ala Pro Arg Pro Leu Arg Arg Val Val Leu Phe Tyr Gln Gly
1 5 10 15

Lys Leu Cys Ser Met Ala Gly Asn Phe Trp Gln Ser Ser His Tyr Leu
20 25 30

Gln Trp Ile Leu Asp Lys Gln Asp Leu Leu Lys Glu Arg Gln Lys Asp
35 40 45

Leu Lys Phe Leu Ser Glu Glu Glu Tyr Trp Lys Leu Gln Ile Phe Phe
50 55 60

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

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

Ser Leu Lys Ser Ile Asp Pro Val Leu Met Ala Pro Thr Cys Val Phe
100 105 110

Leu Ala Ser Lys Val Glu Glu Phe Gly Val Val Ser Asn Thr Arg Leu
115 120 125

Ile Ala Ala Ala Thr Ser Val Cys Lys Cys Lys Lys Tyr Ile Cys Phe
130 135 140

Lys Asp Val Ile Leu Lys Lys Ala Pro Glu Tyr Ile Asp Phe Phe Phe
145 150 155 160

Phe Ser Leu

<210> 163
<211> 50
<212> PRT
<213> Homo sapiens

<400> 163
Met Ala Gly Asn Phe Trp Gln Ser Ser His Tyr Leu Gln Trp Ile Leu
1 5 10 15

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

Ser Glu Glu Glu Tyr Trp Lys Leu Gln Ile Phe Phe Thr Asn Gly Lys
35 40 45

Leu Phe

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50

<210> 164
<211> 302
<212> PRT
<213> Homo sapiens

<400> 164

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Met Val Ala Pro Arg Pro Leu Arg Arg Val Val Leu Phe Tyr Gln Gly
1               5                  10                  15

Lys Leu Cys Ser Met Ala Gly Asn Phe Trp Gln Ser Ser His Tyr Leu
            20                  25                  30

Gln Trp Ile Leu Asp Lys Gln Asp Leu Leu Lys Glu Arg Gln Lys Asp
        35                  40                  45

Leu Lys Phe Leu Ser Glu Glu Glu Tyr Trp Lys Leu Gln Ile Phe Phe
    50                  55                  60

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

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

Ser Leu Lys Ser Ile Asp Pro Val Leu Met Ala Pro Thr Cys Val Phe
            100                 105                 110

Leu Ala Ser Lys Val Glu Glu Phe Gly Val Val Ser Asn Thr Arg Leu
        115                 120                 125

Ile Ala Ala Ala Thr Ser Val Leu Lys Thr Arg Phe Ser Tyr Ala Phe
    130                 135                 140

Pro Lys Glu Phe Pro Tyr Arg Met Asn His Ile Leu Glu Cys Glu Phe
145                 150                 155                 160

Tyr Leu Leu Glu Leu Met Asp Cys Cys Leu Ile Val Tyr His Pro Tyr
                165                 170                 175

Arg Pro Leu Leu Gln Tyr Val Gln Asp Met Gly Gln Glu Asp Met Leu
            180                 185                 190

Leu Pro Leu Ala Trp Arg Ile Val Asn Asp Thr Tyr Arg Thr Asp Leu
        195                 200                 205

Cys Leu Leu Tyr Pro Pro Phe Met Ile Ala Leu Ala Cys Leu His Val
    210                 215                 220

Ala Cys Val Val Gln Gln Lys Asp Ala Arg Gln Trp Phe Ala Glu Leu
225                 230                 235                 240
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Ser Val Asp Met Glu Lys Ile Leu Glu Ile Ile Arg Val Ile Leu Lys
245 250 255

Leu Tyr Glu Gln Trp Lys Asn Phe Asp Glu Arg Lys Glu Met Ala Thr
260 265 270

Ile Leu Ser Lys Met Pro Lys Pro Lys Pro Pro Pro Asn Arg Asn Ser
275 280 285

Leu Ser Asp Ser Pro Leu Val Ala Gly Pro Glu Ala Ala Arg
290 295 300

<210> 165
<211> 964
<212> PRT
<213> Homo sapiens

<400> 165
Met Asp Pro Glu Tyr Glu Glu Lys Met Lys Ala Asp Arg Ala Lys Arg
1 5 10 15

Phe Glu Phe Leu Leu Lys Gln Thr Glu Leu Phe Ala His Phe Ile Gln
20 25 30

Pro Ser Ala Gln Lys Ser Pro Thr Ser Pro Leu Asn Met Lys Leu Gly
35 40 45

Arg Pro Arg Ile Lys Lys Asp Glu Lys Gln Ser Leu Ile Ser Ala Gly
50 55 60

Asp Tyr Arg His Arg Arg Thr Glu Gln Glu Glu Asp Glu Glu Leu Leu
65 70 75 80

Ser Glu Ser Arg Lys Thr Ser Asn Val Cys Ile Arg Phe Glu Val Ser
85 90 95

Pro Ser Tyr Val Lys Gly Gly Pro Leu Arg Asp Tyr Gln Ile Arg Gly
100 105 110

Leu Asn Trp Leu Ile Ser Leu Tyr Glu Asn Gly Val Asn Gly Ile Leu
115 120 125

Ala Asp Glu Met Gly Leu Gly Lys Thr Leu Gln Thr Ile Ala Leu Leu
130 135 140

Gly Tyr Leu Lys His Tyr Arg Asn Ile Pro Gly Pro His Met Val Leu
145 150 155 160

Val Pro Lys Ser Thr Leu His Asn Trp Met Asn Glu Phe Lys Arg Trp
165 170 175

Val Pro Ser Leu Arg Val Ile Cys Phe Val Gly Asp Lys Asp Ala Arg
180 185 190

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Ala Ala Phe Ile Arg Asp Glu Met Met Pro Gly Glu Trp Asp Val Cys
        195                 200                 205

Val Thr Ser Tyr Glu Met Val Ile Lys Glu Lys Ser Val Phe Lys Lys
    210                 215                 220

Phe His Trp Arg Tyr Leu Val Ile Asp Glu Ala His Arg Ile Lys Asn
225                 230                 235                 240

Glu Lys Ser Lys Leu Ser Glu Ile Val Arg Glu Phe Lys Ser Thr Asn
                245                 250                 255

Arg Leu Leu Leu Thr Gly Thr Pro Leu Gln Asn Asn Leu His Glu Leu
            260                 265                 270

Trp Ala Leu Leu Asn Phe Leu Leu Pro Asp Val Phe Asn Ser Ala Asp
        275                 280                 285

Asp Phe Asp Ser Trp Phe Asp Thr Lys Asn Cys Leu Gly Asp Gln Lys
    290                 295                 300

Leu Val Glu Arg Leu His Ala Val Leu Lys Pro Phe Leu Leu Arg Arg
305                 310                 315                 320

Ile Lys Thr Asp Val Glu Lys Ser Leu Pro Pro Lys Lys Glu Ile Lys
                325                 330                 335

Ile Tyr Leu Gly Leu Ser Lys Met Gln Arg Glu Trp Tyr Thr Lys Ile
            340                 345                 350

Leu Met Lys Asp Ile Asp Val Leu Asn Ser Ser Gly Lys Met Asp Lys
        355                 360                 365

Met Arg Leu Leu Asn Ile Leu Met Gln Leu Arg Lys Cys Cys Asn His
    370                 375                 380

Pro Tyr Leu Phe Asp Gly Ala Glu Pro Gly Pro Pro Tyr Thr Thr Asp
385                 390                 395                 400

Glu His Ile Val Ser Asn Ser Gly Lys Met Val Val Leu Asp Lys Leu
                405                 410                 415

Leu Ala Lys Leu Lys Glu Gln Gly Ser Arg Val Leu Ile Phe Ser Gln
            420                 425                 430

Met Thr Arg Leu Leu Asp Ile Leu Glu Asp Tyr Cys Met Trp Arg Gly
        435                 440                 445

Tyr Glu Tyr Cys Arg Leu Asp Gly Gln Thr Pro His Glu Glu Arg Glu
    450                 455                 460
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Glu Ala Ile Glu Ala Phe Asn Ala Pro Asn Ser Ser Lys Phe Ile Phe
465 470 475 480

Met Leu Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala
485 490 495

Asp Val Val Ile Leu Tyr Asp Ser Asp Trp Asn Pro Gln Val Asp Leu
500 505 510

Gln Ala Met Asp Arg Ala His Arg Ile Gly Gln Lys Lys Pro Val Arg
515 520 525

Val Phe Arg Leu Ile Thr Asp Asn Thr Val Glu Glu Arg Ile Val Glu
530 535 540

Arg Ala Glu Ile Lys Leu Arg Leu Asp Ser Ile Val Ile Gln Gln Gly
545 550 555 560

Arg Leu Ile Asp Gln Gln Ser Asn Lys Leu Ala Lys Glu Glu Met Leu
565 570 575

Gln Met Ile Arg His Gly Ala Thr His Val Phe Ala Ser Lys Glu Ser
580 585 590

Glu Leu Thr Asp Glu Asp Ile Thr Thr Ile Leu Glu Arg Gly Glu Lys
595 600 605

Lys Thr Ala Glu Met Asn Glu Arg Leu Gln Lys Met Gly Glu Ser Ser
610 615 620

Leu Arg Asn Phe Arg Met Asp Ile Glu Gln Ser Leu Tyr Lys Phe Glu
625 630 635 640

Gly Glu Asp Tyr Arg Glu Lys Gln Lys Leu Gly Met Val Glu Trp Ile
645 650 655

Glu Pro Pro Lys Arg Glu Arg Lys Ala Asn Tyr Ala Val Asp Ala Tyr
660 665 670

Phe Arg Glu Ala Leu Arg Val Ser Glu Pro Lys Ile Pro Lys Ala Pro
675 680 685

Arg Pro Pro Lys Gln Pro Asn Val Gln Asp Phe Gln Phe Phe Pro Pro
690 695 700

Arg Leu Phe Glu Leu Leu Glu Lys Glu Ile Leu Tyr Tyr Arg Lys Thr
705 710 715 720

Ile Gly Tyr Lys Val Pro Arg Asn Pro Asp Ile Pro Asn Pro Ala Leu
725 730 735

Ala Gln Arg Glu Glu Gln Lys Lys Ile Asp Gly Ala Glu Pro Leu Thr

740 745 750

Pro Glu Glu Thr Glu Glu Lys Glu Lys Leu Leu Thr Gln Gly Phe Thr
755 760 765

Asn Trp Thr Lys Arg Asp Phe Asn Gln Phe Ile Lys Ala Asn Glu Lys
770 775 780

Tyr Gly Arg Asp Asp Ile Asp Asn Ile Ala Arg Glu Val Glu Gly Lys
785 790 795 800

Ser Pro Glu Glu Val Met Glu Tyr Ser Ala Val Phe Trp Glu Arg Cys
805 810 815

Asn Glu Leu Gln Asp Ile Glu Lys Ile Met Ala Gln Ile Glu Arg Gly
820 825 830

Glu Ala Arg Ile Gln Arg Arg Ile Ser Ile Lys Lys Ala Leu Asp Ala
835 840 845

Lys Ile Ala Arg Tyr Lys Ala Pro Phe His Gln Leu Arg Ile Gln Tyr
850 855 860

Gly Thr Ser Lys Gly Lys Asn Tyr Thr Glu Glu Glu Asp Arg Phe Leu
865 870 875 880

Ile Cys Met Leu His Lys Met Gly Phe Asp Arg Glu Asn Val Tyr Glu
885 890 895

Glu Leu Arg Gln Cys Val Arg Asn Ala Pro Gln Phe Arg Phe Asp Trp
900 905 910

Phe Ile Lys Ser Arg Thr Ala Met Glu Phe Gln Arg Arg Cys Asn Thr
915 920 925

Leu Ile Ser Leu Ile Glu Lys Glu Asn Met Glu Ile Glu Glu Arg Glu
930 935 940

Arg Ala Glu Lys Lys Lys Arg Ala Thr Lys Thr Pro Met Val Lys Phe
945 950 955 960

Ser Ala Phe Ser

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<211> 837
<212> PRT
<213> Homo sapiens

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Phe Glu Phe Leu Leu Lys Gln Thr Glu Leu Phe Ala His Phe Ile Gln
20 25 30

Pro Ser Ala Gln Lys Ser Pro Thr Ser Pro Leu Asn Met Lys Leu Gly
35 40 45

Arg Pro Arg Ile Lys Lys Asp Glu Lys Gln Ser Leu Ile Ser Ala Gly
50 55 60

Asp Tyr Arg His Arg Arg Thr Glu Gln Glu Glu Asp Glu Glu Leu Leu
65 70 75 80

Ser Glu Ser Arg Lys Thr Ser Asn Val Cys Ile Arg Phe Glu Val Ser
85 90 95

Pro Ser Tyr Val Lys Gly Gly Pro Leu Arg Asp Tyr Gln Ile Arg Gly
100 105 110

Leu Asn Trp Leu Ile Ser Leu Tyr Glu Asn Gly Val Asn Gly Ile Leu
115 120 125

Ala Asp Glu Met Gly Leu Gly Lys Thr Leu Gln Thr Ile Ala Leu Leu
130 135 140

Gly Tyr Leu Lys His Tyr Arg Asn Ile Pro Gly Pro His Met Val Leu
145 150 155 160

Val Pro Lys Ser Thr Leu His Asn Trp Met Asn Glu Phe Lys Arg Trp
165 170 175

Val Pro Ser Leu Arg Val Ile Cys Phe Val Gly Asp Lys Asp Ala Arg
180 185 190

Ala Ala Phe Ile Arg Asp Glu Met Met Pro Gly Glu Trp Asp Val Cys
195 200 205

Val Thr Ser Tyr Glu Met Val Ile Lys Glu Lys Ser Val Phe Lys Lys
210 215 220

Phe His Trp Arg Tyr Leu Val Ile Asp Glu Ala His Arg Ile Lys Asn
225 230 235 240

Glu Lys Ser Lys Leu Ser Glu Ile Val Arg Glu Phe Lys Ser Thr Asn
245 250 255

Arg Leu Leu Leu Thr Gly Thr Pro Leu Gln Asn Asn Leu His Glu Leu
260 265 270

Trp Ala Leu Leu Asn Phe Leu Leu Pro Asp Val Phe Asn Ser Ala Asp
275 280 285

Asp Phe Asp Ser Trp Phe Asp Thr Lys Asn Cys Leu Gly Asp Gln Lys

290 295 300

Leu Val Glu Arg Leu His Ala Val Leu Lys Pro Phe Leu Leu Arg Arg
305 310 315 320

Ile Lys Thr Asp Val Glu Lys Ser Leu Pro Pro Lys Lys Glu Ile Lys
325 330 335

Ile Tyr Leu Gly Leu Ser Lys Met Gln Arg Glu Trp Tyr Thr Lys Ile
340 345 350

Leu Met Lys Asp Ile Asp Val Leu Asn Ser Ser Gly Lys Met Asp Lys
355 360 365

Met Arg Leu Leu Asn Ile Leu Met Gln Leu Arg Lys Cys Cys Asn His
370 375 380

Pro Tyr Leu Phe Asp Gly Ala Glu Pro Gly Pro Pro Tyr Thr Thr Asp
385 390 395 400

Glu His Ile Val Ser Asn Ser Gly Lys Met Val Val Leu Asp Lys Leu
405 410 415

Leu Ala Lys Leu Lys Glu Gln Gly Ser Arg Val Leu Ile Phe Ser Gln
420 425 430

Met Thr Arg Leu Leu Asp Ile Leu Glu Asp Tyr Cys Met Trp Arg Gly
435 440 445

Tyr Glu Tyr Cys Arg Leu Asp Gly Gln Thr Pro His Glu Glu Arg Glu
450 455 460

Ser Glu Leu Thr Asp Glu Asp Ile Thr Thr Ile Leu Glu Arg Gly Glu
465 470 475 480

Lys Lys Thr Ala Glu Met Asn Glu Arg Leu Gln Lys Met Gly Glu Ser
485 490 495

Ser Leu Arg Asn Phe Arg Met Asp Ile Glu Gln Ser Leu Tyr Lys Phe
500 505 510

Glu Gly Glu Asp Tyr Arg Glu Lys Gln Lys Leu Gly Met Val Glu Trp
515 520 525

Ile Glu Pro Pro Lys Arg Glu Arg Lys Ala Asn Tyr Ala Val Asp Ala
530 535 540

Tyr Phe Arg Glu Ala Leu Arg Val Ser Glu Pro Lys Ile Pro Lys Ala
545 550 555 560

Pro Arg Pro Pro Lys Gln Pro Asn Val Gln Asp Phe Gln Phe Phe Pro
565 570 575

Pro Arg Leu Phe Glu Leu Leu Glu Lys Glu Ile Leu Tyr Tyr Arg Lys
580 585 590

Thr Ile Gly Tyr Lys Val Pro Arg Asn Pro Asp Ile Pro Asn Pro Ala
595 600 605

Leu Ala Gln Arg Glu Glu Gln Lys Lys Ile Asp Gly Ala Glu Pro Leu
610 615 620

Thr Pro Glu Glu Thr Glu Glu Lys Glu Lys Leu Leu Thr Gln Gly Phe
625 630 635 640

Thr Asn Trp Thr Lys Arg Asp Phe Asn Gln Phe Ile Lys Ala Asn Glu
645 650 655

Lys Tyr Gly Arg Asp Asp Ile Asp Asn Ile Ala Arg Glu Val Glu Gly
660 665 670

Lys Ser Pro Glu Glu Val Met Glu Tyr Ser Ala Val Phe Trp Glu Arg
675 680 685

Cys Asn Glu Leu Gln Asp Ile Glu Lys Ile Met Ala Gln Ile Glu Arg
690 695 700

Gly Glu Ala Arg Ile Gln Arg Arg Ile Ser Ile Lys Lys Ala Leu Asp
705 710 715 720

Ala Lys Ile Ala Arg Tyr Lys Ala Pro Phe His Gln Leu Arg Ile Gln
725 730 735

Tyr Gly Thr Ser Lys Gly Lys Asn Tyr Thr Glu Glu Glu Asp Arg Phe
740 745 750

Leu Ile Cys Met Leu His Lys Met Gly Phe Asp Arg Glu Asn Val Tyr
755 760 765

Glu Glu Leu Arg Gln Cys Val Arg Asn Ala Pro Gln Phe Arg Phe Asp
770 775 780

Trp Phe Ile Lys Ser Arg Thr Ala Met Glu Phe Gln Arg Arg Cys Asn
785 790 795 800

Thr Leu Ile Ser Leu Ile Glu Lys Glu Asn Met Glu Ile Glu Glu Arg
805 810 815

Glu Arg Ala Glu Lys Lys Lys Arg Ala Thr Lys Thr Pro Met Val Lys
820 825 830

Phe Ser Ala Phe Ser
835

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<211> 2241
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Met Ser Thr Pro Thr Asp Pro Gly Ala Met Pro His Pro Gly Pro Ser
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Pro Gly Pro Gly Pro Ser Pro Gly Pro Ile Leu Gly Pro Ser Pro Gly
20 25 30

Pro Gly Pro Ser Pro Gly Ser Val His Ser Met Met Gly Pro Ser Pro
35 40 45

Gly Pro Pro Ser Val Ser His Pro Met Pro Thr Met Gly Ser Thr Asp
50 55 60

Phe Pro Gln Glu Gly Met His Gln Met His Lys Pro Ile Asp Gly Ile
65 70 75 80

His Asp Lys Gly Ile Val Glu Asp Ile His Cys Gly Ser Met Lys Gly
85 90 95

Thr Gly Met Arg Pro Pro His Pro Gly Met Gly Pro Pro Gln Ser Pro
100 105 110

Met Asp Gln His Ser Gln Gly Tyr Met Ser Pro His Pro Ser Pro Leu
115 120 125

Gly Ala Pro Glu His Val Ser Ser Pro Met Ser Gly Gly Gly Pro Thr
130 135 140

Pro Pro Gln Met Pro Pro Ser Gln Pro Gly Ala Leu Ile Pro Gly Asp
145 150 155 160

Pro Gln Ala Met Ser Gln Pro Asn Arg Gly Pro Ser Pro Phe Ser Pro
165 170 175

Val Gln Leu His Gln Leu Arg Ala Gln Ile Leu Ala Tyr Lys Met Leu
180 185 190

Ala Arg Gly Gln Pro Leu Pro Glu Thr Leu Gln Leu Ala Val Gln Gly
195 200 205

Lys Arg Thr Leu Pro Gly Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln
210 215 220

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Gln
225 230 235 240

Gln Gln Pro Pro Gln Pro Gln Thr Gln Gln Gln Gln Gln Pro Ala Leu
245 250 255

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Val Asn Tyr Asn Arg Pro Ser Gly Pro Gly Pro Glu Leu Ser Gly Pro
260 265 270

Ser Thr Pro Gln Lys Leu Pro Val Pro Ala Pro Gly Gly Arg Pro Ser
275 280 285

Pro Ala Pro Pro Ala Ala Ala Gln Pro Pro Ala Ala Ala Val Pro Gly
290 295 300

Pro Ser Val Pro Gln Pro Ala Pro Gly Gln Pro Ser Pro Val Leu Gln
305 310 315 320

Leu Gln Gln Lys Gln Ser Arg Ile Ser Pro Ile Gln Lys Pro Gln Gly
325 330 335

Leu Asp Pro Val Glu Ile Leu Gln Glu Arg Glu Tyr Arg Leu Gln Ala
340 345 350

Arg Ile Ala His Arg Ile Gln Glu Leu Glu Asn Leu Pro Gly Ser Leu
355 360 365

Pro Pro Asp Leu Arg Thr Lys Ala Thr Val Glu Leu Lys Ala Leu Arg
370 375 380

Leu Leu Asn Phe Gln Arg Gln Leu Arg Gln Glu Val Val Ala Cys Met
385 390 395 400

Arg Arg Asp Thr Thr Leu Glu Thr Ala Leu Asn Ser Lys Ala Tyr Lys
405 410 415

Arg Ser Lys Arg Gln Thr Leu Arg Glu Ala Arg Met Thr Glu Lys Leu
420 425 430

Glu Lys Gln Gln Lys Ile Glu Gln Glu Arg Lys Arg Arg Gln Lys His
435 440 445

Gln Glu Tyr Leu Asn Ser Ile Leu Gln His Ala Lys Asp Phe Lys Glu
450 455 460

Tyr His Arg Ser Val Ala Gly Lys Ile Gln Lys Leu Ser Lys Ala Val
465 470 475 480

Ala Thr Trp His Ala Asn Thr Glu Arg Glu Gln Lys Lys Glu Thr Glu
485 490 495

Arg Ile Glu Lys Glu Arg Met Arg Arg Leu Met Ala Glu Asp Glu Glu
500 505 510

Gly Tyr Arg Lys Leu Ile Asp Gln Lys Lys Asp Arg Arg Leu Ala Tyr
515 520 525

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Leu Leu Gln Gln Thr Asp Glu Tyr Val Ala Asn Leu Thr Asn Leu Val
    530                 535                 540

Trp Glu His Lys Gln Ala Gln Ala Ala Lys Glu Lys Lys Lys Arg Arg
545                 550                 555                 560

Arg Arg Lys Lys Lys Ala Glu Glu Asn Ala Glu Gly Gly Glu Ser Ala
                565                 570                 575

Leu Gly Pro Asp Gly Glu Pro Ile Asp Glu Ser Ser Gln Met Ser Asp
            580                 585                 590

Leu Pro Val Lys Val Thr His Thr Glu Thr Gly Lys Val Leu Phe Gly
        595                 600                 605

Pro Glu Ala Pro Lys Ala Ser Gln Leu Asp Ala Trp Leu Glu Met Asn
    610                 615                 620

Pro Gly Tyr Glu Val Ala Pro Arg Ser Asp Ser Glu Glu Ser Asp Ser
625                 630                 635                 640

Asp Tyr Glu Glu Glu Asp Glu Glu Glu Glu Ser Ser Arg Gln Glu Thr
                645                 650                 655

Glu Glu Lys Ile Leu Leu Asp Pro Asn Ser Glu Glu Val Ser Glu Lys
            660                 665                 670

Asp Ala Lys Gln Ile Ile Glu Thr Ala Lys Gln Asp Val Asp Asp Glu
        675                 680                 685

Tyr Ser Met Gln Tyr Ser Ala Arg Gly Ser Gln Ser Tyr Tyr Thr Val
    690                 695                 700

Ala His Ala Ile Ser Glu Arg Val Glu Lys Gln Ser Ala Leu Leu Ile
705                 710                 715                 720

Asn Gly Thr Leu Lys His Tyr Gln Leu Gln Gly Leu Glu Trp Met Val
                725                 730                 735

Ser Leu Tyr Asn Asn Asn Leu Asn Gly Ile Leu Ala Asp Glu Met Gly
            740                 745                 750

Leu Gly Lys Thr Ile Gln Thr Ile Ala Leu Ile Thr Tyr Leu Met Glu
        755                 760                 765

His Lys Arg Leu Asn Gly Pro Tyr Leu Ile Ile Val Pro Leu Ser Thr
    770                 775                 780

Leu Ser Asn Trp Thr Tyr Glu Phe Asp Lys Trp Ala Pro Ser Val Val
785                 790                 795                 800
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Lys Ile Ser Tyr Lys Gly Thr Pro Ala Met Arg Arg Ser Leu Val Pro
805 810 815

Gln Leu Arg Ser Gly Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr
820 825 830

Ile Ile Lys Asp Lys His Ile Leu Ala Lys Ile Arg Trp Lys Tyr Met
835 840 845

Ile Val Asp Glu Gly His Arg Met Lys Asn His His Cys Lys Leu Thr
850 855 860

Gln Val Leu Asn Thr His Tyr Val Ala Pro Arg Arg Ile Leu Leu Thr
865 870 875 880

Gly Thr Pro Leu Gln Asn Lys Leu Pro Glu Leu Trp Ala Leu Leu Asn
885 890 895

Phe Leu Leu Pro Thr Ile Phe Lys Ser Cys Ser Thr Phe Glu Gln Trp
900 905 910

Phe Asn Ala Pro Phe Ala Met Thr Gly Glu Arg Val Asp Leu Asn Glu
915 920 925

Glu Glu Thr Ile Leu Ile Ile Arg Arg Leu His Lys Val Leu Arg Pro
930 935 940

Phe Leu Leu Arg Arg Leu Lys Lys Glu Val Glu Ser Gln Leu Pro Glu
945 950 955 960

Lys Val Glu Tyr Val Ile Lys Cys Asp Met Ser Ala Leu Gln Lys Ile
965 970 975

Leu Tyr Arg His Met Gln Ala Lys Gly Ile Leu Leu Thr Asp Gly Ser
980 985 990

Glu Lys Asp Lys Lys Gly Lys Gly Gly Ala Lys Thr Leu Met Asn Thr
995 1000 1005

Ile Met Gln Leu Arg Lys Ile Cys Asn His Pro Tyr Met Phe Gln
1010 1015 1020

His Ile Glu Glu Ser Phe Ala Glu His Leu Gly Tyr Ser Asn Gly
1025 1030 1035

Val Ile Asn Gly Ala Glu Leu Tyr Arg Ala Ser Gly Lys Phe Glu
1040 1045 1050

Leu Leu Asp Arg Ile Leu Pro Lys Leu Arg Ala Thr Asn His Arg
1055 1060 1065

Val Leu Leu Phe Cys Gln Met Thr Ser Leu Met Thr Ile Met Glu

1070 1075 1080

Asp Tyr Phe Ala Phe Arg Asn Phe Leu Tyr Leu Arg Leu Asp Gly
1085 1090 1095

Thr Thr Lys Ser Glu Asp Arg Ala Ala Leu Leu Lys Lys Phe Asn
1100 1105 1110

Glu Pro Gly Ser Gln Tyr Phe Ile Phe Leu Leu Ser Thr Arg Ala
1115 1120 1125

Gly Gly Leu Gly Leu Asn Leu Gln Ala Ala Asp Thr Val Val Ile
1130 1135 1140

Phe Asp Ser Asp Trp Asn Pro His Gln Asp Leu Gln Ala Gln Asp
1145 1150 1155

Arg Ala His Arg Ile Gly Gln Gln Asn Glu Val Arg Val Leu Arg
1160 1165 1170

Leu Cys Thr Val Asn Ser Val Glu Glu Lys Ile Leu Ala Ala Ala
1175 1180 1185

Lys Tyr Lys Leu Asn Val Asp Gln Lys Val Ile Gln Ala Gly Met
1190 1195 1200

Phe Asp Gln Lys Ser Ser Ser His Glu Arg Arg Ala Phe Leu Gln
1205 1210 1215

Ala Ile Leu Glu His Glu Glu Glu Asn Glu Glu Glu Asp Glu Val
1220 1225 1230

Pro Asp Asp Glu Thr Leu Asn Gln Met Ile Ala Arg Arg Glu Glu
1235 1240 1245

Glu Phe Asp Leu Phe Met Arg Met Asp Met Asp Arg Arg Arg Glu
1250 1255 1260

Asp Ala Arg Asn Pro Lys Arg Lys Pro Arg Leu Met Glu Glu Asp
1265 1270 1275

Glu Leu Pro Ser Trp Ile Ile Lys Asp Asp Ala Glu Val Glu Arg
1280 1285 1290

Leu Thr Cys Glu Glu Glu Glu Glu Lys Ile Phe Gly Arg Gly Ser
1295 1300 1305

Arg Gln Arg Arg Asp Val Asp Tyr Ser Asp Ala Leu Thr Glu Lys
1310 1315 1320

Gln Trp Leu Arg Ala Ile Glu Asp Gly Asn Leu Glu Glu Met Glu
1325 1330 1335

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Glu Glu Val Arg Leu Lys Lys Arg Lys Arg Arg Arg Asn Val Asp
1340 1345 1350

Lys Asp Pro Ala Lys Glu Asp Val Glu Lys Ala Lys Lys Arg Arg
1355 1360 1365

Gly Arg Pro Pro Ala Glu Lys Leu Ser Pro Asn Pro Pro Lys Leu
1370 1375 1380

Thr Lys Gln Met Asn Ala Ile Ile Asp Thr Val Ile Asn Tyr Lys
1385 1390 1395

Asp Ser Ser Gly Arg Gln Leu Ser Glu Val Phe Ile Gln Leu Pro
1400 1405 1410

Ser Arg Lys Glu Leu Pro Glu Tyr Tyr Glu Leu Ile Arg Lys Pro
1415 1420 1425

Val Asp Phe Pro Leu Ser Thr Leu Ser Asn Trp Thr Tyr Glu Phe
1430 1435 1440

Asp Lys Trp Ala Pro Ser Val Val Lys Ile Ser Tyr Lys Gly Thr
1445 1450 1455

Pro Ala Met Arg Arg Ser Leu Val Pro Gln Leu Arg Ser Gly Lys
1460 1465 1470

Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Ile Lys Asp Lys
1475 1480 1485

His Ile Leu Ala Lys Ile Arg Trp Lys Tyr Met Ile Val Asp Glu
1490 1495 1500

Gly His Arg Met Lys Asn His His Cys Lys Leu Thr Gln Val Leu
1505 1510 1515

Asn Thr His Tyr Val Ala Pro Arg Arg Ile Leu Leu Thr Gly Thr
1520 1525 1530

Pro Leu Gln Asn Lys Leu Pro Glu Leu Trp Ala Leu Leu Asn Phe
1535 1540 1545

Leu Leu Pro Thr Ile Phe Lys Ser Cys Ser Thr Phe Glu Gln Trp
1550 1555 1560

Phe Asn Ala Pro Phe Ala Met Thr Gly Glu Arg Val Asp Leu Asn
1565 1570 1575

Glu Glu Glu Thr Ile Leu Ile Ile Arg Arg Leu His Lys Val Leu
1580 1585 1590

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Arg Pro Phe Leu Leu Arg Arg Leu Lys Lys Glu Val Glu Ser Gln
1595 1600 1605

Leu Pro Glu Lys Val Glu Tyr Val Ile Lys Cys Asp Met Ser Ala
1610 1615 1620

Leu Gln Lys Ile Leu Tyr Arg His Met Gln Ala Lys Gly Ile Leu
1625 1630 1635

Leu Thr Asp Gly Ser Glu Lys Asp Lys Lys Gly Lys Gly Gly Ala
1640 1645 1650

Lys Thr Leu Met Asn Thr Ile Met Gln Leu Arg Lys Ile Cys Asn
1655 1660 1665

His Pro Tyr Met Phe Gln His Ile Glu Glu Ser Phe Ala Glu His
1670 1675 1680

Leu Gly Tyr Ser Asn Gly Val Ile Asn Gly Ala Glu Leu Tyr Arg
1685 1690 1695

Ala Ser Gly Lys Phe Glu Leu Leu Asp Arg Ile Leu Pro Lys Leu
1700 1705 1710

Arg Ala Thr Asn His Arg Val Leu Leu Phe Cys Gln Met Thr Ser
1715 1720 1725

Leu Met Thr Ile Met Glu Asp Tyr Phe Ala Phe Arg Asn Phe Leu
1730 1735 1740

Tyr Leu Arg Leu Asp Gly Thr Thr Lys Ser Glu Asp Arg Ala Ala
1745 1750 1755

Leu Leu Lys Lys Phe Asn Glu Pro Gly Ser Gln Tyr Phe Ile Phe
1760 1765 1770

Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly Leu Asn Leu Gln Ala
1775 1780 1785

Ala Asp Thr Val Val Ile Phe Asp Ser Asp Trp Asn Pro His Gln
1790 1795 1800

Asp Leu Gln Ala Gln Asp Arg Ala His Arg Ile Gly Gln Gln Asn
1805 1810 1815

Glu Val Arg Val Leu Arg Leu Cys Thr Val Asn Ser Val Glu Glu
1820 1825 1830

Lys Ile Leu Ala Ala Ala Lys Tyr Lys Leu Asn Val Asp Gln Lys
1835 1840 1845

Val Ile Gln Ala Gly Met Phe Asp Gln Lys Ser Ser Ser His Glu
1850 1855 1860

Arg Arg Ala Phe Leu Gln Ala Ile Leu Glu His Glu Glu Glu Asn
1865 1870 1875

Glu Glu Glu Asp Glu Val Pro Asp Asp Glu Thr Leu Asn Gln Met
1880 1885 1890

Ile Ala Arg Arg Glu Glu Glu Phe Asp Leu Phe Met Arg Met Asp
1895 1900 1905

Met Asp Arg Arg Arg Glu Asp Ala Arg Asn Pro Lys Arg Lys Pro
1910 1915 1920

Arg Leu Met Glu Glu Asp Glu Leu Pro Ser Trp Ile Ile Lys Asp
1925 1930 1935

Asp Ala Glu Val Glu Arg Leu Thr Cys Glu Glu Glu Glu Glu Lys
1940 1945 1950

Ile Phe Gly Arg Gly Ser Arg Gln Arg Arg Asp Val Asp Tyr Ser
1955 1960 1965

Asp Ala Leu Thr Glu Lys Gln Trp Leu Arg Ala Ile Glu Asp Gly
1970 1975 1980

Asn Leu Glu Glu Met Glu Glu Glu Val Arg Leu Lys Lys Arg Lys
1985 1990 1995

Arg Arg Arg Asn Val Asp Lys Asp Pro Ala Lys Glu Asp Val Glu
2000 2005 2010

Lys Ala Lys Lys Arg Arg Gly Arg Pro Pro Ala Glu Lys Leu Ser
2015 2020 2025

Pro Asn Pro Pro Lys Leu Thr Lys Gln Met Asn Ala Ile Ile Asp
2030 2035 2040

Thr Val Ile Asn Tyr Lys Asp Arg Cys Asn Val Glu Lys Val Pro
2045 2050 2055

Ser Asn Ser Gln Leu Glu Ile Glu Gly Asn Ser Ser Gly Arg Gln
2060 2065 2070

Leu Ser Glu Val Phe Ile Gln Leu Pro Ser Arg Lys Glu Leu Pro
2075 2080 2085

Glu Tyr Tyr Glu Leu Ile Arg Lys Pro Val Asp Phe Lys Lys Ile
2090 2095 2100

Lys Glu Arg Ile Arg Asn His Lys Tyr Arg Ser Leu Gly Asp Leu

2105 2110 2115

Glu Lys Asp Val Met Leu Leu Cys His Asn Ala Gln Thr Phe Asn
2120 2125 2130

Leu Glu Gly Ser Gln Ile Tyr Glu Asp Ser Ile Val Leu Gln Ser
2135 2140 2145

Val Phe Lys Ser Ala Arg Gln Lys Ile Ala Lys Glu Glu Glu Ser
2150 2155 2160

Glu Asp Glu Ser Asn Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu
2165 2170 2175

Ser Glu Ser Glu Ala Lys Ser Val Lys Val Lys Ile Lys Leu Asn
2180 2185 2190

Lys Lys Asp Asp Lys Gly Arg Asp Lys Gly Lys Gly Lys Lys Arg
2195 2200 2205

Pro Asn Arg Gly Lys Ala Lys Pro Val Val Ser Asp Phe Asp Ser
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Asp Glu Glu Gln Asp Glu Arg Glu Gln Ser Glu Gly Ser Gly Thr
2225 2230 2235

Asp Asp Glu
2240

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<213> Homo sapiens

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Pro Gly Pro Ser Pro Gly Ser Val His Ser Met Met Gly Pro Ser Pro
35 40 45

Gly Pro Pro Ser Val Ser His Pro Met Pro Thr Met Gly Ser Thr Asp
50 55 60

Phe Pro Gln Glu Gly Met His Gln Met His Lys Pro Ile Asp Gly Ile
65 70 75 80

His Asp Lys Gly Ile Val Glu Asp Ile His Cys Gly Ser Met Lys Gly
85 90 95

Thr Gly Met Arg Pro Pro His Pro Gly Met Gly Pro Pro Gln Ser Pro
100 105 110

Met Asp Gln His Ser Gln Gly Tyr Met Ser Pro His Pro Ser Pro Leu
115 120 125

Gly Ala Pro Glu His Val Ser Ser Pro Met Ser Gly Gly Gly Pro Thr
130 135 140

Pro Pro Gln Met Pro Pro Ser Gln Pro Gly Ala Leu Ile Pro Gly Asp
145 150 155 160

Pro Gln Ala Met Ser Gln Pro Asn Arg Gly Pro Ser Pro Phe Ser Pro
165 170 175

Val Gln Leu His Gln Leu Arg Ala Gln Ile Leu Ala Tyr Lys Met Leu
180 185 190

Ala Arg Gly Gln Pro Leu Pro Glu Thr Leu Gln Leu Ala Val Gln Gly
195 200 205

Lys Arg Thr Leu Pro Gly Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln
210 215 220

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro
225 230 235 240

Gln Pro Gln Thr Gln Gln Gln Gln Pro Ala Leu Val Asn Tyr Asn
245 250 255

Arg Pro Ser Gly Pro Gly Pro Glu Leu Ser Gly Pro Ser Thr Pro Gln
260 265 270

Lys Leu Pro Val Pro Ala Pro Gly Gly Arg Pro Ser Pro Ala Pro Pro
275 280 285

Ala Ala Ala Gln Pro Pro Ala Ala Ala Val Pro Gly Pro Ser Val Pro
290 295 300

Gln Pro Ala Pro Gly Gln Pro Ser Pro Val Leu Gln Leu Gln Gln Lys
305 310 315 320

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

Glu Ile Leu Gln Glu Arg Glu Tyr Arg Leu Gln Ala Arg Ile Ala His
340 345 350

Arg Ile Gln Glu Leu Glu Asn Leu Pro Gly Ser Leu Pro Pro Asp Leu
355 360 365

Arg Thr Lys Ala Thr Val Glu Leu Lys Ala Leu Arg Leu Leu Asn Phe

370 375 380

Gln Arg Gln Leu Arg Gln Glu Val Val Ala Cys Met Arg Arg Asp Thr
385 390 395 400

Thr Leu Glu Thr Ala Leu Asn Ser Lys Ala Tyr Lys Arg Ser Lys Arg
405 410 415

Gln Thr Leu Arg Glu Ala Arg Met Thr Glu Lys Leu Glu Lys Gln Gln
420 425 430

Lys Ile Glu Gln Glu Arg Lys Arg Arg Gln Lys His Gln Glu Tyr Leu
435 440 445

Asn Ser Ile Leu Gln His Ala Lys Asp Phe Lys Glu Tyr His Arg Ser
450 455 460

Val Ala Gly Lys Ile Gln Lys Leu Ser Lys Ala Val Ala Thr Trp His
465 470 475 480

Ala Asn Thr Glu Arg Glu Gln Lys Lys Glu Thr Glu Arg Ile Glu Lys
485 490 495

Glu Arg Met Arg Arg Leu Met Ala Glu Asp Glu Glu Gly Tyr Arg Lys
500 505 510

Leu Ile Asp Gln Lys Lys Asp Arg Arg Leu Ala Tyr Leu Leu Gln Gln
515 520 525

Thr Asp Glu Tyr Val Ala Asn Leu Thr Asn Leu Val Trp Glu His Lys
530 535 540

Gln Ala Gln Ala Ala Lys Glu Lys Lys Lys Arg Arg Arg Arg Lys Lys
545 550 555 560

Lys Ala Glu Glu Asn Ala Glu Gly Gly Glu Ser Ala Leu Gly Pro Asp
565 570 575

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

Val Thr His Thr Glu Thr Gly Lys Val Leu Phe Gly Pro Glu Ala Pro
595 600 605

Lys Ala Ser Gln Leu Asp Ala Trp Leu Glu Met Asn Pro Gly Tyr Glu
610 615 620

Val Ala Pro Arg Ser Asp Ser Glu Glu Ser Asp Ser Asp Tyr Glu Glu
625 630 635 640

Glu Asp Glu Glu Glu Glu Ser Ser Arg Gln Glu Thr Glu Glu Lys Ile
645 650 655

Leu Leu Asp Pro Asn Ser Glu Glu Val Ser Glu Lys Asp Ala Lys Gln
660 665 670

Ile Ile Glu Thr Ala Lys Gln Asp Val Asp Asp Glu Tyr Ser Met Gln
675 680 685

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

Ser Glu Trp Val Glu Lys Gln Ser Ala Leu Leu Ile Asn Gly Thr Leu
705 710 715 720

Lys His Tyr Gln Leu Gln Gly Leu Glu Trp Met Val Ser Leu Tyr Asn
725 730 735

Asn Asn Leu Asn Gly Ile Leu Ala Asp Glu Met Gly Leu Gly Lys Thr
740 745 750

Ile Gln Thr Ile Ala Leu Ile Thr Tyr Leu Met Glu His Lys Arg Leu
755 760 765

Asn Gly Pro Tyr Leu Ile Ile Val Pro Leu Ser Thr Leu Ser Asn Trp
770 775 780

Thr Tyr Glu Phe Asp Lys Trp Ala Pro Ser Val Val Lys Ile Ser Tyr
785 790 795 800

Lys Gly Thr Pro Ala Met Arg Arg Ser Leu Val Pro Gln Leu Arg Ser
805 810 815

Gly Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Ile Lys Asp
820 825 830

Lys His Ile Leu Ala Lys Ile Arg Trp Lys Tyr Met Ile Val Asp Glu
835 840 845

Gly His Arg Met Lys Asn His His Cys Lys Leu Thr Gln Val Leu Asn
850 855 860

Thr His Tyr Val Ala Pro Arg Arg Ile Leu Leu Thr Gly Thr Pro Leu
865 870 875 880

Gln Asn Lys Leu Pro Glu Leu Trp Ala Leu Leu Asn Phe Leu Leu Pro
885 890 895

Thr Ile Phe Lys Ser Cys Ser Thr Phe Glu Gln Trp Phe Asn Ala Pro
900 905 910

Phe Ala Met Thr Gly Glu Arg Val Asp Leu Asn Glu Glu Glu Thr Ile
915 920 925

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Leu Ile Ile Arg Arg Leu His Lys Val Leu Arg Pro Phe Leu Leu Arg
    930                 935                 940

Arg Leu Lys Lys Glu Val Glu Ser Gln Leu Pro Glu Lys Val Glu Tyr
945                 950                 955                 960

Val Ile Lys Cys Asp Met Ser Ala Leu Gln Lys Ile Leu Tyr Arg His
                965                 970                 975

Met Gln Ala Lys Gly Ile Leu Leu Thr Asp Gly Ser Glu Lys Asp Lys
            980                 985                 990

Lys Gly Lys Gly Gly Ala Lys Thr  Leu Met Asn Thr Ile  Met Gln Leu
        995                 1000                1005

Arg Lys  Ile Cys Asn His Pro  Tyr Met Phe Gln His  Ile Glu Glu
    1010                1015                1020

Ser Phe  Ala Glu His Leu Gly  Tyr Ser Asn Gly Val  Ile Asn Gly
    1025                1030                1035

Ala Glu  Leu Tyr Arg Ala Ser  Gly Lys Phe Glu Leu  Leu Asp Arg
    1040                1045                1050

Ile Leu  Pro Lys Leu Arg Ala  Thr Asn His Arg Val  Leu Leu Phe
    1055                1060                1065

Cys Gln  Met Thr Ser Leu Met  Thr Ile Met Glu Asp  Tyr Phe Ala
    1070                1075                1080

Phe Arg  Asn Phe Leu Tyr Leu  Arg Leu Asp Gly Thr  Thr Lys Ser
    1085                1090                1095

Glu Asp  Arg Ala Ala Leu Leu  Lys Lys Phe Asn Glu  Pro Gly Ser
    1100                1105                1110

Gln Tyr  Phe Ile Phe Leu Leu  Ser Thr Arg Ala Gly  Gly Leu Gly
    1115                1120                1125

Leu Asn  Leu Gln Ala Ala Asp  Thr Val Val Ile Phe  Asp Ser Asp
    1130                1135                1140

Trp Asn  Pro His Gln Asp Leu  Gln Ala Gln Asp Arg  Ala His Arg
    1145                1150                1155

Ile Gly  Gln Gln Asn Glu Val  Arg Val Leu Arg Leu  Cys Thr Val
    1160                1165                1170

Asn Ser  Val Glu Glu Lys Ile  Leu Ala Ala Ala Lys  Tyr Lys Leu
    1175                1180                1185
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Asn Val Asp Gln Lys Val Ile Gln Ala Gly Met Phe Asp Gln Lys
1190 1195 1200

Ser Ser Ser His Glu Arg Arg Ala Phe Leu Gln Ala Ile Leu Glu
1205 1210 1215

His Glu Glu Glu Asn Glu Glu Glu Asp Glu Val Pro Asp Asp Glu
1220 1225 1230

Thr Leu Asn Gln Met Ile Ala Arg Arg Glu Glu Glu Phe Asp Leu
1235 1240 1245

Phe Met Arg Met Asp Met Asp Arg Arg Arg Glu Asp Ala Arg Asn
1250 1255 1260

Pro Lys Arg Lys Pro Arg Leu Met Glu Glu Asp Glu Leu Pro Ser
1265 1270 1275

Trp Ile Ile Lys Asp Asp Ala Glu Val Glu Arg Leu Thr Cys Glu
1280 1285 1290

Glu Glu Glu Glu Lys Ile Phe Gly Arg Gly Ser Arg Gln Arg Arg
1295 1300 1305

Asp Val Asp Tyr Ser Asp Ala Leu Thr Glu Lys Gln Trp Leu Arg
1310 1315 1320

Ala Ile Glu Asp Gly Asn Leu Glu Glu Met Glu Glu Glu Val Arg
1325 1330 1335

Leu Lys Lys Arg Lys Arg Arg Arg Asn Val Asp Lys Asp Pro Ala
1340 1345 1350

Lys Glu Asp Val Glu Lys Ala Lys Lys Arg Arg Gly Arg Pro Pro
1355 1360 1365

Ala Glu Lys Leu Ser Pro Asn Pro Pro Lys Leu Thr Lys Gln Met
1370 1375 1380

Asn Ala Ile Ile Asp Thr Val Ile Asn Tyr Lys Asp Ser Ser Gly
1385 1390 1395

Arg Gln Leu Ser Glu Val Phe Ile Gln Leu Pro Ser Arg Lys Glu
1400 1405 1410

Leu Pro Glu Tyr Tyr Glu Leu Ile Arg Lys Pro Val Asp Phe Lys
1415 1420 1425

Lys Ile Lys Glu Arg Ile Arg Asn His Lys Tyr Arg Ser Leu Gly
1430 1435 1440

Asp Leu Glu Lys Asp Val Met Leu Leu Cys His Asn Ala Gln Thr

1445 1450 1455

Phe Asn Leu Glu Gly Ser Gln Ile Tyr Glu Asp Ser Ile Val Leu
1460 1465 1470

Gln Ser Val Phe Lys Ser Ala Arg Gln Lys Ile Ala Lys Glu Glu
1475 1480 1485

Glu Ser Glu Asp Glu Ser Asn Glu Glu Glu Glu Glu Glu Asp Glu
1490 1495 1500

Glu Glu Ser Glu Ser Glu Gly Thr Val Arg Arg Lys Trp Asp Gly
1505 1510 1515

<210> 169
<211> 1433
<212> PRT
<213> Homo sapiens

<400> 169
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Pro Gly Pro Gly Pro Ser Pro Gly Pro Ile Leu Gly Pro Ser Pro Gly
20 25 30

Pro Gly Pro Ser Pro Gly Ser Val His Ser Met Met Gly Pro Ser Pro
35 40 45

Gly Pro Pro Ser Val Ser His Pro Met Pro Thr Met Gly Ser Thr Asp
50 55 60

Phe Pro Gln Glu Gly Met His Gln Met His Lys Pro Ile Asp Gly Ile
65 70 75 80

His Asp Lys Gly Ile Val Glu Asp Ile His Cys Gly Ser Met Lys Gly
85 90 95

Thr Gly Met Arg Pro Pro His Pro Gly Met Gly Pro Pro Gln Ser Pro
100 105 110

Met Asp Gln His Ser Gln Gly Tyr Met Ser Pro His Pro Ser Pro Leu
115 120 125

Gly Ala Pro Glu His Val Ser Ser Pro Met Ser Gly Gly Gly Pro Thr
130 135 140

Pro Pro Gln Met Pro Pro Ser Gln Pro Gly Ala Leu Ile Pro Gly Asp
145 150 155 160

Pro Gln Ala Met Ser Gln Pro Asn Arg Gly Pro Ser Pro Phe Ser Pro
165 170 175

Val Gln Leu His Gln Leu Arg Ala Gln Ile Leu Ala Tyr Lys Met Leu
180 185 190

Ala Arg Gly Gln Pro Leu Pro Glu Thr Leu Gln Leu Ala Val Gln Gly
195 200 205

Lys Arg Thr Leu Pro Gly Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln
210 215 220

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Gln
225 230 235 240

Gln Gln Pro Pro Gln Pro Gln Thr Gln Gln Gln Gln Gln Pro Ala Leu
245 250 255

Val Asn Tyr Asn Arg Pro Ser Gly Pro Gly Pro Glu Leu Ser Gly Pro
260 265 270

Ser Thr Pro Gln Lys Leu Pro Val Pro Ala Pro Gly Gly Arg Pro Ser
275 280 285

Pro Ala Pro Pro Ala Ala Ala Gln Pro Pro Ala Ala Ala Val Pro Gly
290 295 300

Pro Ser Val Pro Gln Pro Ala Pro Gly Gln Pro Ser Pro Val Leu Gln
305 310 315 320

Leu Gln Gln Lys Gln Ser Arg Ile Ser Pro Ile Gln Lys Pro Gln Gly
325 330 335

Leu Asp Pro Val Glu Ile Leu Gln Glu Arg Glu Tyr Arg Leu Gln Ala
340 345 350

Arg Ile Ala His Arg Ile Gln Glu Leu Glu Asn Leu Pro Gly Ser Leu
355 360 365

Pro Pro Asp Leu Arg Thr Lys Ala Thr Val Glu Leu Lys Ala Leu Arg
370 375 380

Leu Leu Asn Phe Gln Arg Gln Leu Arg Gln Glu Val Val Ala Cys Met
385 390 395 400

Arg Arg Asp Thr Thr Leu Glu Thr Ala Leu Asn Ser Lys Ala Tyr Lys
405 410 415

Arg Ser Lys Arg Gln Thr Leu Arg Glu Ala Arg Met Thr Glu Lys Leu
420 425 430

Glu Lys Gln Gln Lys Ile Glu Gln Glu Arg Lys Arg Arg Gln Lys His
435 440 445

Gln Glu Tyr Leu Asn Ser Ile Leu Gln His Ala Lys Asp Phe Lys Glu

450 455 460

Tyr His Arg Ser Val Ala Gly Lys Ile Gln Lys Leu Ser Lys Ala Val
465 470 475 480

Ala Thr Trp His Ala Asn Thr Glu Arg Glu Gln Lys Lys Glu Thr Glu
485 490 495

Arg Ile Glu Lys Glu Arg Met Arg Arg Leu Met Ala Glu Asp Glu Glu
500 505 510

Gly Tyr Arg Lys Leu Ile Asp Gln Lys Lys Asp Arg Arg Leu Ala Tyr
515 520 525

Leu Leu Gln Gln Thr Asp Glu Tyr Val Ala Asn Leu Thr Asn Leu Val
530 535 540

Trp Glu His Lys Gln Ala Gln Ala Ala Lys Glu Lys Lys Lys Arg Arg
545 550 555 560

Arg Arg Lys Lys Lys Ala Glu Glu Asn Ala Glu Gly Gly Glu Ser Ala
565 570 575

Leu Gly Pro Asp Gly Glu Pro Ile Asp Glu Ser Ser Gln Met Ser Asp
580 585 590

Leu Pro Val Lys Val Thr His Thr Glu Thr Gly Lys Val Leu Phe Gly
595 600 605

Pro Glu Ala Pro Lys Ala Ser Gln Leu Asp Ala Trp Leu Glu Met Asn
610 615 620

Pro Gly Tyr Glu Val Ala Pro Arg Ser Asp Ser Glu Glu Ser Asp Ser
625 630 635 640

Asp Tyr Glu Glu Glu Asp Glu Glu Glu Glu Ser Ser Arg Gln Glu Thr
645 650 655

Glu Glu Lys Ile Leu Leu Asp Pro Asn Ser Glu Glu Val Ser Glu Lys
660 665 670

Asp Ala Lys Gln Ile Ile Glu Thr Ala Lys Gln Asp Val Asp Asp Glu
675 680 685

Tyr Ser Met Gln Tyr Ser Ala Arg Gly Ser Gln Ser Tyr Tyr Thr Val
690 695 700

Ala His Ala Ile Ser Glu Arg Val Glu Lys Gln Ser Ala Leu Leu Ile
705 710 715 720

Asn Gly Thr Leu Lys His Tyr Gln Leu Gln Gly Leu Glu Trp Met Val
725 730 735

Ser Leu Tyr Asn Asn Asn Leu Asn Gly Ile Leu Ala Asp Glu Met Gly
740 745 750

Leu Gly Lys Thr Ile Gln Thr Ile Ala Leu Ile Thr Tyr Leu Met Glu
755 760 765

His Lys Arg Leu Asn Gly Pro Tyr Leu Ile Ile Val Pro Leu Ser Thr
770 775 780

Leu Ser Asn Trp Thr Tyr Glu Phe Asp Lys Trp Ala Pro Ser Val Val
785 790 795 800

Lys Ile Ser Tyr Lys Gly Thr Pro Ala Met Arg Arg Ser Leu Val Pro
805 810 815

Gln Leu Arg Ser Gly Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr
820 825 830

Ile Ile Lys Asp Lys His Ile Leu Ala Lys Ile Arg Trp Lys Tyr Met
835 840 845

Ile Val Asp Glu Gly His Arg Met Lys Asn His His Cys Lys Leu Thr
850 855 860

Gln Val Leu Asn Thr His Tyr Val Ala Pro Arg Arg Ile Leu Leu Thr
865 870 875 880

Gly Thr Pro Leu Gln Asn Lys Leu Pro Glu Leu Trp Ala Leu Leu Asn
885 890 895

Phe Leu Leu Pro Thr Ile Phe Lys Ser Cys Ser Thr Phe Glu Gln Trp
900 905 910

Phe Asn Ala Pro Phe Ala Met Thr Gly Glu Arg Val Asp Leu Asn Glu
915 920 925

Glu Glu Thr Ile Leu Ile Ile Arg Arg Leu His Lys Val Leu Arg Pro
930 935 940

Phe Leu Leu Arg Arg Leu Lys Lys Glu Val Glu Ser Gln Leu Pro Glu
945 950 955 960

Lys Val Glu Tyr Val Ile Lys Cys Asp Met Ser Ala Leu Gln Lys Ile
965 970 975

Leu Tyr Arg His Met Gln Ala Lys Gly Ile Leu Leu Thr Asp Gly Ser
980 985 990

Glu Lys Asp Lys Lys Gly Lys Gly Gly Ala Lys Thr Leu Met Asn Thr
995 1000 1005

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Ile Met Gln Leu Arg Lys Ile Cys Asn His Pro Tyr Met Phe Gln
1010 1015 1020

His Ile Glu Glu Ser Phe Ala Glu His Leu Gly Tyr Ser Asn Gly
1025 1030 1035

Val Ile Asn Gly Ala Glu Leu Tyr Arg Ala Ser Gly Lys Phe Glu
1040 1045 1050

Leu Leu Asp Arg Ile Leu Pro Lys Leu Arg Ala Thr Asn His Arg
1055 1060 1065

Val Leu Leu Phe Cys Gln Met Thr Ser Leu Met Thr Ile Met Glu
1070 1075 1080

Asp Tyr Phe Ala Phe Arg Asn Phe Leu Tyr Leu Arg Leu Asp Gly
1085 1090 1095

Thr Thr Lys Ser Glu Asp Arg Ala Ala Leu Leu Lys Lys Phe Asn
1100 1105 1110

Glu Pro Gly Ser Gln Tyr Phe Ile Phe Leu Leu Ser Thr Arg Ala
1115 1120 1125

Gly Gly Leu Gly Leu Asn Leu Gln Ala Ala Asp Thr Val Val Ile
1130 1135 1140

Phe Asp Ser Asp Trp Asn Pro His Gln Asp Leu Gln Ala Gln Asp
1145 1150 1155

Arg Ala His Arg Ile Gly Gln Gln Asn Glu Val Arg Val Leu Arg
1160 1165 1170

Leu Cys Thr Val Asn Ser Val Glu Glu Lys Ile Leu Ala Ala Ala
1175 1180 1185

Lys Tyr Lys Leu Asn Val Asp Gln Lys Val Ile Gln Ala Gly Met
1190 1195 1200

Phe Asp Gln Lys Ser Ser Ser His Glu Arg Arg Ala Phe Leu Gln
1205 1210 1215

Ala Ile Leu Glu His Glu Glu Glu Asn Glu Glu Glu Asp Glu Val
1220 1225 1230

Pro Asp Asp Glu Thr Leu Asn Gln Met Ile Ala Arg Arg Glu Glu
1235 1240 1245

Glu Phe Asp Leu Phe Met Arg Met Asp Met Asp Arg Arg Arg Glu
1250 1255 1260

Asp Ala Arg Asn Pro Lys Arg Lys Pro Arg Leu Met Glu Glu Asp
1265 1270 1275

Glu Leu Pro Ser Trp Ile Ile Lys Asp Asp Ala Glu Val Glu Arg
1280 1285 1290

Leu Thr Cys Glu Glu Glu Glu Glu Lys Ile Phe Gly Arg Gly Ser
1295 1300 1305

Arg Gln Arg Arg Asp Val Asp Tyr Ser Asp Ala Leu Thr Glu Lys
1310 1315 1320

Gln Trp Leu Arg Ala Ile Glu Asp Gly Asn Leu Glu Glu Met Glu
1325 1330 1335

Glu Glu Val Arg Leu Lys Lys Arg Lys Arg Arg Arg Asn Val Asp
1340 1345 1350

Lys Asp Pro Ala Lys Glu Asp Val Glu Lys Ala Lys Lys Arg Arg
1355 1360 1365

Gly Arg Pro Pro Ala Glu Lys Leu Ser Pro Asn Pro Pro Lys Leu
1370 1375 1380

Thr Lys Gln Met Asn Ala Ile Ile Asp Thr Val Ile Asn Tyr Lys
1385 1390 1395

Asp Arg Asn Ser Gln Lys Glu Val Gly Arg Met Met Ser Asp Gln
1400 1405 1410

Tyr Gly Pro Phe Ser Leu Val Glu Leu Asn Ser Phe Leu Pro Cys
1415 1420 1425

Leu Ile Ser Thr Gln
1430

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<212> PRT
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<400> 170
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Ser Pro Gly Pro Gly Pro Ser Pro Gly Ala Met Leu Gly Pro Ser Pro
20 25 30

Gly Pro Ser Pro Gly Ser Ala His Ser Met Met Gly Pro Ser Pro Gly
35 40 45

Pro Pro Ser Ala Gly His Pro Ile Pro Thr Gln Gly Pro Gly Gly Tyr
50 55 60

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Pro Gln Asp Asn Met His Gln Met His Lys Pro Met Glu Ser Met His
65 70 75 80

Glu Lys Gly Met Ser Asp Asp Pro Arg Tyr Asn Gln Met Lys Gly Met
85 90 95

Gly Met Arg Ser Gly Gly His Ala Gly Met Gly Pro Pro Pro Ser Pro
100 105 110

Met Asp Gln His Ser Gln Gly Tyr Pro Ser Pro Leu Gly Gly Ser Glu
115 120 125

His Ala Ser Ser Pro Val Pro Ala Ser Gly Pro Ser Ser Gly Pro Gln
130 135 140

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

Ala Leu Gly Gln Gln Asn Arg Gly Pro Thr Pro Phe Asn Gln Asn Gln
165 170 175

Leu His Gln Leu Arg Ala Gln Ile Met Ala Tyr Lys Met Leu Ala Arg
180 185 190

Gly Gln Pro Leu Pro Asp His Leu Gln Met Ala Val Gln Gly Lys Arg
195 200 205

Pro Met Pro Gly Met Gln Gln Gln Met Pro Thr Leu Pro Pro Pro Ser
210 215 220

Val Ser Ala Thr Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro
225 230 235 240

Gly Pro Gly Pro Ala Pro Pro Asn Tyr Ser Arg Pro His Gly Met Gly
245 250 255

Gly Pro Asn Met Pro Pro Pro Gly Pro Ser Gly Val Pro Pro Gly Met
260 265 270

Pro Gly Gln Pro Pro Gly Gly Pro Pro Lys Pro Trp Pro Glu Gly Pro
275 280 285

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

Pro Gln Pro Thr Gly Arg Pro Ser Pro Ala Pro Pro Ala Val Pro Pro
305 310 315 320

Ala Ala Ser Pro Val Met Pro Pro Gln Thr Gln Ser Pro Gly Gln Pro
325 330 335

Ala Gln Pro Ala Pro Met Val Pro Leu His Gln Lys Gln Ser Arg Ile
340 345 350

Thr Pro Ile Gln Lys Pro Arg Gly Leu Asp Pro Val Glu Ile Leu Gln
355 360 365

Glu Arg Glu Tyr Arg Leu Gln Ala Arg Ile Ala His Arg Ile Gln Glu
370 375 380

Leu Glu Asn Leu Pro Gly Ser Leu Ala Gly Asp Leu Arg Thr Lys Ala
385 390 395 400

Thr Ile Glu Leu Lys Ala Leu Arg Leu Leu Asn Phe Gln Arg Gln Leu
405 410 415

Arg Gln Glu Val Val Val Cys Met Arg Arg Asp Thr Ala Leu Glu Thr
420 425 430

Ala Leu Asn Ala Lys Ala Tyr Lys Arg Ser Lys Arg Gln Ser Leu Arg
435 440 445

Glu Ala Arg Ile Thr Glu Lys Leu Glu Lys Gln Gln Lys Ile Glu Gln
450 455 460

Glu Arg Lys Arg Arg Gln Lys His Gln Glu Tyr Leu Asn Ser Ile Leu
465 470 475 480

Gln His Ala Lys Asp Phe Lys Glu Tyr His Arg Ser Val Thr Gly Lys
485 490 495

Ile Gln Lys Leu Thr Lys Ala Val Ala Thr Tyr His Ala Asn Thr Glu
500 505 510

Arg Glu Gln Lys Lys Glu Asn Glu Arg Ile Glu Lys Glu Arg Met Arg
515 520 525

Arg Leu Met Ala Glu Asp Glu Glu Gly Tyr Arg Lys Leu Ile Asp Gln
530 535 540

Lys Lys Asp Lys Arg Leu Ala Tyr Leu Leu Gln Gln Thr Asp Glu Tyr
545 550 555 560

Val Ala Asn Leu Thr Glu Leu Val Arg Gln His Lys Ala Ala Gln Val
565 570 575

Ala Lys Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys Ala Glu Asn Ala
580 585 590

Glu Gly Gln Thr Pro Ala Ile Gly Pro Asp Gly Glu Pro Leu Asp Glu
595 600 605

Thr Ser Gln Met Ser Asp Leu Pro Val Lys Val Ile His Val Glu Ser

610 615 620

Gly Lys Ile Leu Thr Gly Thr Asp Ala Pro Lys Ala Gly Gln Leu Glu
625 630 635 640

Ala Trp Leu Glu Met Asn Pro Gly Tyr Glu Val Ala Pro Arg Ser Asp
645 650 655

Ser Glu Glu Ser Gly Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
660 665 670

Gln Pro Gln Ala Ala Gln Pro Pro Thr Leu Pro Val Glu Glu Lys Lys
675 680 685

Lys Ile Pro Asp Pro Asp Ser Asp Asp Val Ser Glu Val Asp Ala Arg
690 695 700

His Ile Ile Glu Asn Ala Lys Gln Asp Val Asp Asp Glu Tyr Gly Val
705 710 715 720

Ser Gln Ala Leu Ala Arg Gly Leu Gln Ser Tyr Tyr Ala Val Ala His
725 730 735

Ala Val Thr Glu Arg Val Asp Lys Gln Ser Ala Leu Met Val Asn Gly
740 745 750

Val Leu Lys Gln Tyr Gln Ile Lys Gly Leu Glu Trp Leu Val Ser Leu
755 760 765

Tyr Asn Asn Asn Leu Asn Gly Ile Leu Ala Asp Glu Met Gly Leu Gly
770 775 780

Lys Thr Ile Gln Thr Ile Ala Leu Ile Thr Tyr Leu Met Glu His Lys
785 790 795 800

Arg Ile Asn Gly Pro Phe Leu Ile Ile Val Pro Leu Ser Thr Leu Ser
805 810 815

Asn Trp Ala Tyr Glu Phe Asp Lys Trp Ala Pro Ser Val Val Lys Val
820 825 830

Ser Tyr Lys Gly Ser Pro Ala Ala Arg Arg Ala Phe Val Pro Gln Leu
835 840 845

Arg Ser Gly Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Ile
850 855 860

Lys Asp Lys His Ile Leu Ala Lys Ile Arg Trp Lys Tyr Met Ile Val
865 870 875 880

Asp Glu Gly His Arg Met Lys Asn His His Cys Lys Leu Thr Gln Val
885 890 895

Leu Asn Thr His Tyr Val Ala Pro Arg Arg Leu Leu Leu Thr Gly Thr
900 905 910

Pro Leu Gln Asn Lys Leu Pro Glu Leu Trp Ala Leu Leu Asn Phe Leu
915 920 925

Leu Pro Thr Ile Phe Lys Ser Cys Ser Thr Phe Glu Gln Trp Phe Asn
930 935 940

Ala Pro Phe Ala Met Thr Gly Glu Lys Val Asp Leu Asn Glu Glu Glu
945 950 955 960

Thr Ile Leu Ile Ile Arg Arg Leu His Lys Val Leu Arg Pro Phe Leu
965 970 975

Leu Arg Arg Leu Lys Lys Glu Val Glu Ala Gln Leu Pro Glu Lys Val
980 985 990

Glu Tyr Val Ile Lys Cys Asp Met Ser Ala Leu Gln Arg Val Leu Tyr
995 1000 1005

Arg His Met Gln Ala Lys Gly Val Leu Leu Thr Asp Gly Ser Glu
1010 1015 1020

Lys Asp Lys Lys Gly Lys Gly Gly Thr Lys Thr Leu Met Asn Thr
1025 1030 1035

Ile Met Gln Leu Arg Lys Ile Cys Asn His Pro Tyr Met Phe Gln
1040 1045 1050

His Ile Glu Glu Ser Phe Ser Glu His Leu Gly Phe Thr Gly Gly
1055 1060 1065

Ile Val Gln Gly Leu Asp Leu Tyr Arg Ala Ser Gly Lys Phe Glu
1070 1075 1080

Leu Leu Asp Arg Ile Leu Pro Lys Leu Arg Ala Thr Asn His Lys
1085 1090 1095

Val Leu Leu Phe Cys Gln Met Thr Ser Leu Met Thr Ile Met Glu
1100 1105 1110

Asp Tyr Phe Ala Tyr Arg Gly Phe Lys Tyr Leu Arg Leu Asp Gly
1115 1120 1125

Thr Thr Lys Ala Glu Asp Arg Gly Met Leu Leu Lys Thr Phe Asn
1130 1135 1140

Glu Pro Gly Ser Glu Tyr Phe Ile Phe Leu Leu Ser Thr Arg Ala
1145 1150 1155

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Gly Gly Leu Gly Leu Asn Leu Gln Ser Ala Asp Thr Val Ile Ile
1160 1165 1170

Phe Asp Ser Asp Trp Asn Pro His Gln Asp Leu Gln Ala Gln Asp
1175 1180 1185

Arg Ala His Arg Ile Gly Gln Gln Asn Glu Val Arg Val Leu Arg
1190 1195 1200

Leu Cys Thr Val Asn Ser Val Glu Glu Lys Ile Leu Ala Ala Ala
1205 1210 1215

Lys Tyr Lys Leu Asn Val Asp Gln Lys Val Ile Gln Ala Gly Met
1220 1225 1230

Phe Asp Gln Lys Ser Ser Ser His Glu Arg Arg Ala Phe Leu Gln
1235 1240 1245

Ala Ile Leu Glu His Glu Glu Gln Asp Glu Glu Glu Asp Glu Val
1250 1255 1260

Pro Asp Asp Glu Thr Val Asn Gln Met Ile Ala Arg His Glu Glu
1265 1270 1275

Glu Phe Asp Leu Phe Met Arg Met Asp Leu Asp Arg Arg Arg Glu
1280 1285 1290

Glu Ala Arg Asn Pro Lys Arg Lys Pro Arg Leu Met Glu Glu Asp
1295 1300 1305

Glu Leu Pro Ser Trp Ile Ile Lys Asp Asp Ala Glu Val Glu Arg
1310 1315 1320

Leu Thr Cys Glu Glu Glu Glu Glu Lys Met Phe Gly Arg Gly Ser
1325 1330 1335

Arg His Arg Lys Glu Val Asp Tyr Ser Asp Ser Leu Thr Glu Lys
1340 1345 1350

Gln Trp Leu Lys Ala Ile Glu Glu Gly Thr Leu Glu Glu Ile Glu
1355 1360 1365

Glu Glu Val Arg Gln Lys Lys Ser Ser Arg Lys Arg Lys Arg Asp
1370 1375 1380

Ser Asp Ala Gly Ser Ser Thr Pro Thr Thr Ser Thr Arg Ser Arg
1385 1390 1395

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

Pro Ala Glu Lys Leu Ser Pro Asn Pro Pro Asn Leu Thr Lys Lys
1415 1420 1425

Met Lys Lys Ile Val Asp Ala Val Ile Lys Tyr Lys Asp Ser Ser
1430 1435 1440

Ser Gly Arg Gln Leu Ser Glu Val Phe Ile Gln Leu Pro Ser Arg
1445 1450 1455

Lys Glu Leu Pro Glu Tyr Tyr Glu Leu Ile Arg Lys Pro Val Asp
1460 1465 1470

Phe Lys Lys Ile Lys Glu Arg Ile Arg Asn His Lys Tyr Arg Ser
1475 1480 1485

Leu Asn Asp Leu Glu Lys Asp Val Met Leu Leu Cys Gln Asn Ala
1490 1495 1500

Gln Thr Phe Asn Leu Glu Gly Ser Leu Ile Tyr Glu Asp Ser Ile
1505 1510 1515

Val Leu Gln Ser Val Phe Thr Ser Val Arg Gln Lys Ile Glu Lys
1520 1525 1530

Glu Asp Asp Ser Glu Gly Glu Glu Ser Glu Glu Glu Glu Glu Gly
1535 1540 1545

Glu Glu Glu Gly Ser Glu Ser Glu Ser Arg Ser Val Lys Val Lys
1550 1555 1560

Ile Lys Leu Gly Arg Lys Glu Lys Ala Gln Asp Arg Leu Lys Gly
1565 1570 1575

Gly Arg Arg Arg Pro Ser Arg Gly Ser Arg Ala Lys Pro Val Val
1580 1585 1590

Ser Asp Asp Asp Ser Glu Glu Glu Gln Glu Glu Asp Arg Ser Gly
1595 1600 1605

Ser Gly Ser Glu Glu Asp
1610

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<213> Homo sapiens

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Pro Ser Pro Gly Ser Ala His Ser Met Met Gly Pro Ser Pro Gly Pro
35 40 45

Pro Ser Ala Gly His Pro Ile Pro Thr Gln Gly Pro Gly Gly Tyr Pro
50 55 60

Gln Asp Asn Met His Gln Met His Lys Pro Met Glu Ser Met His Glu
65 70 75 80

Lys Gly Met Ser Asp Pro Arg Tyr Asn Gln Met Lys Gly Met Gly Met
85 90 95

Arg Ser Gly Gly His Ala Gly Met Gly Pro Pro Pro Ser Pro Met Asp
100 105 110

Gln His Ser Gln Gly Tyr Pro Ser Pro Leu Gly Gly Ser Glu His Ala
115 120 125

Ser Ser Pro Val Pro Ala Ser Gly Pro Ser Ser Gly Pro Gln Met Ser
130 135 140

Ser Gly Pro Gly Gly Ala Pro Leu Asp Gly Ala Asp Pro Gln Ala Leu
145 150 155 160

Gly Gln Gln Asn Arg Gly Pro Thr Pro Phe Asn Gln Asn Gln Leu His
165 170 175

Gln Leu Arg Ala Gln Ile Met Ala Tyr Lys Met Leu Ala Arg Gly Gln
180 185 190

Pro Leu Pro Asp His Leu Gln Met Ala Val Gln Gly Lys Arg Pro Met
195 200 205

Pro Gly Met Gln Gln Gln Met Pro Thr Leu Pro Pro Pro Ser Val Ser
210 215 220

Ala Thr Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro
225 230 235 240

Gly Pro Ala Pro Pro Asn Tyr Ser Arg Pro His Gly Met Gly Gly Pro
245 250 255

Asn Met Pro Pro Pro Gly Pro Ser Gly Val Pro Pro Gly Met Pro Gly
260 265 270

Gln Pro Pro Gly Gly Pro Pro Lys Pro Trp Pro Glu Gly Pro Met Ala
275 280 285

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

Pro Thr Gly Arg Pro Ser Pro Ala Pro Pro Ala Val Pro Pro Ala Ala
305 310 315 320

Ser Pro Val Met Pro Pro Gln Thr Gln Ser Pro Gly Gln Pro Ala Gln
325 330 335

Pro Ala Pro Met Val Pro Leu His Gln Lys Gln Ser Arg Ile Thr Pro
340 345 350

Ile Gln Lys Pro Arg Gly Leu Asp Pro Val Glu Ile Leu Gln Glu Arg
355 360 365

Glu Tyr Arg Leu Gln Ala Arg Ile Ala His Arg Ile Gln Glu Leu Glu
370 375 380

Asn Leu Pro Gly Ser Leu Ala Gly Asp Leu Arg Thr Lys Ala Thr Ile
385 390 395 400

Glu Leu Lys Ala Leu Arg Leu Leu Asn Phe Gln Arg Gln Leu Arg Gln
405 410 415

Glu Val Val Val Cys Met Arg Arg Asp Thr Ala Leu Glu Thr Ala Leu
420 425 430

Asn Ala Lys Ala Tyr Lys Arg Ser Lys Arg Gln Ser Leu Arg Glu Ala
435 440 445

Arg Ile Thr Glu Lys Leu Met Glu Lys Gln Gln Lys Ile Glu Gln Glu
450 455 460

Arg Lys Arg Arg Gln Lys His Gln Glu Tyr Leu Asn Ser Ile Leu Gln
465 470 475 480

His Ala Lys Asp Phe Lys Glu Tyr His Arg Ser Val Thr Gly Lys Ile
485 490 495

Gln Lys Leu Thr Lys Ala Val Ala Thr Tyr His Ala Asn Thr Glu Arg
500 505 510

Glu Gln Lys Lys Glu Asn Glu Arg Ile Glu Lys Glu Arg Met Arg Arg
515 520 525

Leu Met Ala Glu Asp Glu Glu Gly Tyr Arg Lys Leu Ile Asp Gln Lys
530 535 540

Lys Asp Lys Arg Leu Ala Tyr Leu Leu Gln Gln Thr Asp Glu Tyr Val
545 550 555 560

Ala Asn Leu Thr Glu Leu Val Arg Gln His Lys Ala Ala Gln Val Ala
565 570 575

Lys Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys Ala Glu Asn Ala Glu

580 585 590

Gly Gln Thr Pro Ala Ile Gly Pro Asp Gly Glu Pro Leu Asp Glu Thr
595 600 605

Ser Gln Met Ser Asp Leu Pro Val Lys Val Ser Tyr Lys Gly Ser Pro
610 615 620

Ala Ala Arg Arg Ala Phe Val Pro Gln Leu Arg Ser Gly Lys Phe Asn
625 630 635 640

Val Leu Leu Thr Thr Tyr Glu Tyr Ile Ile Lys Asp Lys His Ile Leu
645 650 655

Ala Lys Ile Arg Trp Lys Tyr Met Ile Val Asp Glu Gly His Arg Met
660 665 670

Lys Asn His His Cys Lys Leu Thr Gln Val Leu Asn Thr His Tyr Val
675 680 685

Ala Pro Arg Arg Leu Leu Leu Thr Gly Thr Pro Leu Gln Asn Lys Leu
690 695 700

Pro Glu Leu Trp Ala Leu Leu Asn Phe Leu Leu Pro Thr Ile Phe Lys
705 710 715 720

Ser Cys Ser Thr Phe Glu Gln Trp Phe Asn Ala Pro Phe Ala Met Thr
725 730 735

Gly Glu Lys Val Asp Leu Asn Glu Glu Glu Thr Ile Leu Ile Ile Arg
740 745 750

Arg Leu His Lys Val Leu Arg Pro Phe Leu Leu Arg Arg Leu Lys Lys
755 760 765

Glu Val Glu Ala Gln Leu Pro Glu Lys Val Glu Tyr Val Ile Lys Cys
770 775 780

Asp Met Ser Ala Leu Gln Arg Val Leu Tyr Arg His Met Gln Ala Lys
785 790 795 800

Gly Val Leu Leu Thr Asp Gly Ser Glu Lys Asp Lys Lys Gly Lys Gly
805 810 815

Gly Thr Lys Thr Leu Met Asn Thr Ile Met Gln Leu Arg Lys Ile Cys
820 825 830

Asn His Pro Tyr Met Phe Gln His Ile Glu Glu Ser Phe Ser Glu His
835 840 845

Leu Gly Phe Thr Gly Gly Ile Val Gln Gly Leu Asp Leu Tyr Arg Ala
850 855 860

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Ser Gly Lys Phe Glu Leu Leu Asp Arg Ile Leu Pro Lys Leu Arg Ala
865                 870                 875                 880

Thr Asn His Lys Val Leu Leu Phe Cys Gln Met Thr Ser Leu Met Thr
                885                 890                 895

Ile Met Glu Asp Tyr Phe Ala Tyr Arg Gly Phe Lys Tyr Leu Arg Leu
            900                 905                 910

Asp Gly Thr Thr Lys Ala Glu Asp Arg Gly Met Leu Leu Lys Thr Phe
        915                 920                 925

Asn Glu Pro Gly Ser Glu Tyr Phe Ile Phe Leu Leu Ser Thr Arg Ala
    930                 935                 940

Gly Gly Leu Gly Leu Asn Leu Gln Ser Ala Asp Thr Val Ile Ile Phe
945                 950                 955                 960

Asp Ser Asp Trp Asn Pro His Gln Asp Leu Gln Ala Gln Asp Arg Ala
                965                 970                 975

His Arg Ile Gly Gln Gln Asn Glu Val Arg Val Leu Arg Leu Cys Thr
            980                 985                 990

Val Asn Ser Val Glu Glu Lys Ile Leu Ala Ala Ala Lys Tyr Lys Leu
        995                 1000                1005

Asn Val Asp Gln Lys Val Ile Gln Ala Gly Met Phe Asp Gln Lys
    1010                1015                1020

Ser Ser Ser His Glu Arg Arg Ala Phe Leu Gln Ala Ile Leu Glu
    1025                1030                1035

His Glu Glu Gln Asp Glu Ser Arg His Cys Ser Thr Gly Ser Gly
    1040                1045                1050

Ser Ala Ser Phe Ala His Thr Ala Pro Pro Pro Ala Gly Val Asn
    1055                1060                1065

Pro Asp Leu Glu Glu Pro Pro Leu Lys Glu Glu Asp Glu Val Pro
    1070                1075                1080

Asp Asp Glu Thr Val Asn Gln Met Ile Ala Arg His Glu Glu Glu
    1085                1090                1095

Phe Asp Leu Phe Met Arg Met Asp Leu Asp Arg Arg Arg Glu Glu
    1100                1105                1110

Ala Arg Asn Pro Lys Arg Lys Pro Arg Leu Met Glu Glu Asp Glu
    1115                1120                1125
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Leu Pro Ser Trp Ile Ile Lys Asp Asp Ala Glu Val Glu Arg Leu
1130 1135 1140

Thr Cys Glu Glu Glu Glu Glu Lys Met Phe Gly Arg Gly Ser Arg
1145 1150 1155

His Arg Lys Glu Val Asp Tyr Ser Asp Ser Leu Thr Glu Lys Gln
1160 1165 1170

Trp Leu Lys Ala Ile Glu Glu Gly Thr Leu Glu Glu Ile Glu Glu
1175 1180 1185

Glu Val Arg Gln Lys Lys Ser Ser Arg Lys Arg Lys Arg Asp Ser
1190 1195 1200

Asp Ala Gly Ser Ser Thr Pro Thr Thr Ser Thr Arg Ser Arg Asp
1205 1210 1215

Lys Asp Asp Glu Ser Lys Lys Gln Lys Lys Arg Gly Arg Pro Pro
1220 1225 1230

Ala Glu Lys Leu Ser Pro Asn Pro Pro Asn Leu Thr Lys Lys Met
1235 1240 1245

Lys Lys Ile Val Asp Ala Val Ile Lys Tyr Lys Asp Ser Ser Ser
1250 1255 1260

Gly Arg Gln Leu Ser Glu Val Phe Ile Gln Leu Pro Ser Arg Lys
1265 1270 1275

Glu Leu Pro Glu Tyr Tyr Glu Leu Ile Arg Lys Pro Val Asp Phe
1280 1285 1290

Lys Lys Ile Lys Glu Arg Ile Arg Asn His Lys Tyr Arg Ser Leu
1295 1300 1305

Asn Asp Leu Glu Lys Asp Val Met Leu Leu Cys Gln Asn Ala Gln
1310 1315 1320

Thr Phe Asn Leu Glu Gly Ser Leu Ile Tyr Glu Asp Ser Ile Val
1325 1330 1335

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

Asp Asp Ser Glu Gly Glu Glu Ser Glu Glu Glu Glu Glu Gly Glu
1355 1360 1365

Glu Glu Gly Ser Glu Ser Glu Ser Arg Ser Val Lys Val Lys Ile
1370 1375 1380

Lys Leu Gly Arg Lys Glu Lys Ala Gln Asp Arg Leu Lys Gly Gly
1385 1390 1395

Arg Arg Arg Pro Ser Arg Gly Ser Arg Ala Lys Pro Val Val Ser
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Asp Asp Asp Ser Glu Glu Glu Gln Glu Glu Asp Arg Ser Gly Ser
1415 1420 1425

Gly Ser Glu Glu Asp
1430

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Pro Ser Pro Gly Ser Ala His Ser Met Met Gly Pro Ser Pro Gly Pro
35 40 45

Pro Ser Ala Gly His Pro Ile Pro Thr Gln Gly Pro Gly Gly Tyr Pro
50 55 60

Gln Asp Asn Met His Gln Met His Lys Pro Met Glu Ser Met His Glu
65 70 75 80

Lys Gly Met Ser Asp Pro Arg Tyr Asn Gln Met Lys Gly Met Gly Met
85 90 95

Arg Ser Gly Gly His Ala Gly Met Gly Pro Pro Pro Ser Pro Met Asp
100 105 110

Gln His Ser Gln Gly Tyr Pro Ser Pro Leu Gly Gly Ser Glu His Ala
115 120 125

Ser Ser Pro Val Pro Ala Ser Gly Pro Ser Ser Gly Pro Gln Met Ser
130 135 140

Ser Gly Pro Gly Gly Ala Pro Leu Asp Gly Ala Asp Pro Gln Ala Leu
145 150 155 160

Gly Gln Gln Asn Arg Gly Pro Thr Pro Phe Asn Gln Asn Gln Leu His
165 170 175

Gln Leu Arg Ala Gln Ile Met Ala Tyr Lys Met Leu Ala Arg Gly Gln
180 185 190

Pro Leu Pro Asp His Leu Gln Met Ala Val Gln Gly Lys Arg Pro Met
195 200 205

Pro Gly Met Gln Gln Gln Met Pro Thr Leu Pro Pro Pro Ser Val Ser
210 215 220

Ala Thr Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro
225 230 235 240

Gly Pro Ala Pro Pro Asn Tyr Ser Arg Pro His Gly Met Gly Gly Pro
245 250 255

Asn Met Pro Pro Pro Gly Pro Ser Gly Val Pro Pro Gly Met Pro Gly
260 265 270

Gln Pro Pro Gly Gly Pro Pro Lys Pro Trp Pro Glu Gly Pro Met Ala
275 280 285

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

Pro Thr Gly Arg Pro Ser Pro Ala Pro Pro Ala Val Pro Pro Ala Ala
305 310 315 320

Ser Pro Val Met Pro Pro Gln Thr Gln Ser Pro Gly Gln Pro Ala Gln
325 330 335

Pro Ala Pro Met Val Pro Leu His Gln Lys Gln Ser Arg Ile Thr Pro
340 345 350

Ile Gln Lys Pro Arg Gly Leu Asp Pro Val Glu Ile Leu Gln Glu Arg
355 360 365

Glu Tyr Arg Leu Gln Ala Arg Ile Ala His Arg Ile Gln Glu Leu Glu
370 375 380

Asn Leu Pro Gly Ser Leu Ala Gly Asp Leu Arg Thr Lys Ala Thr Ile
385 390 395 400

Glu Leu Lys Ala Leu Arg Leu Leu Asn Phe Gln Arg Gln Leu Arg Gln
405 410 415

Glu Val Val Val Cys Met Arg Arg Asp Thr Ala Leu Glu Thr Ala Leu
420 425 430

Asn Ala Lys Ala Tyr Lys Arg Ser Lys Arg Gln Ser Leu Arg Glu Ala
435 440 445

Arg Ile Thr Glu Lys Leu Glu Lys Gln Gln Lys Ile Glu Gln Glu Arg
450 455 460

Lys Arg Arg Gln Lys His Gln Glu Tyr Leu Asn Ser Ile Leu Gln His
465 470 475 480

Ala Lys Asp Phe Lys Glu Tyr His Arg Ser Val Thr Gly Lys Ile Gln
485 490 495

Lys Leu Thr Lys Ala Val Ala Thr Tyr His Ala Asn Thr Glu Arg Glu
500 505 510

Gln Lys Lys Glu Asn Glu Arg Ile Glu Lys Glu Arg Met Arg Arg Leu
515 520 525

Ile Ile Val Pro Leu Ser Thr Leu Ser Asn Trp Ala Tyr Glu Phe Asp
530 535 540

Lys Trp Ala Pro Ser Val Val Lys Val Ser Tyr Lys Gly Ser Pro Ala
545 550 555 560

Ala Arg Arg Ala Phe Val Pro Gln Leu Arg Ser Gly Lys Phe Asn Val
565 570 575

Leu Leu Thr Thr Tyr Glu Tyr Ile Ile Lys Asp Lys His Ile Leu Ala
580 585 590

Lys Ile Arg Trp Lys Tyr Met Ile Val Asp Glu Gly His Arg Met Lys
595 600 605

Asn His His Cys Lys Leu Thr Gln Val Leu Asn Thr His Tyr Val Ala
610 615 620

Pro Arg Arg Leu Leu Leu Thr Gly Thr Pro Leu Gln Asn Lys Leu Pro
625 630 635 640

Glu Leu Trp Ala Leu Leu Asn Phe Leu Leu Pro Thr Ile Phe Lys Ser
645 650 655

Cys Ser Thr Phe Glu Gln Trp Phe Asn Ala Pro Phe Ala Met Thr Gly
660 665 670

Glu Lys Val Asp Leu Asn Glu Glu Glu Thr Ile Leu Ile Ile Arg Arg
675 680 685

Leu His Lys Val Leu Arg Pro Phe Leu Leu Arg Arg Leu Lys Lys Glu
690 695 700

Val Glu Ala Gln Leu Pro Glu Lys Val Glu Tyr Val Ile Lys Cys Asp
705 710 715 720

Met Ser Ala Leu Gln Arg Val Leu Tyr Arg His Met Gln Ala Lys Gly
725 730 735

Val Leu Leu Thr Asp Gly Ser Glu Lys Asp Lys Lys Gly Lys Gly Gly

740 745 750

Thr Lys Thr Leu Met Asn Thr Ile Met Gln Leu Arg Lys Ile Cys Asn
755 760 765

His Pro Tyr Met Phe Gln His Ile Glu Glu Ser Phe Ser Glu His Leu
770 775 780

Gly Phe Thr Gly Gly Ile Val Gln Gly Leu Asp Leu Tyr Arg Ala Ser
785 790 795 800

Gly Lys Phe Glu Leu Leu Asp Arg Ile Leu Pro Lys Leu Arg Ala Thr
805 810 815

Asn His Lys Val Leu Leu Phe Cys Gln Met Thr Ser Leu Met Thr Ile
820 825 830

Met Glu Asp Tyr Phe Ala Tyr Arg Gly Phe Lys Tyr Leu Arg Leu Asp
835 840 845

Gly Thr Thr Lys Ala Glu Asp Arg Gly Met Leu Leu Lys Thr Phe Asn
850 855 860

Glu Pro Gly Ser Glu Tyr Phe Ile Phe Leu Leu Ser Thr Arg Ala Gly
865 870 875 880

Gly Leu Gly Leu Asn Leu Gln Ser Ala Asp Thr Val Ile Ile Phe Asp
885 890 895

Ser Asp Trp Asn Pro His Gln Asp Leu Gln Ala Gln Asp Arg Ala His
900 905 910

Arg Ile Gly Gln Gln Asn Glu Val Arg Val Leu Arg Leu Cys Thr Val
915 920 925

Asn Ser Val Glu Glu Lys Ile Leu Ala Ala Ala Lys Tyr Lys Leu Asn
930 935 940

Val Asp Gln Lys Val Ile Gln Ala Gly Met Phe Asp Gln Lys Ser Ser
945 950 955 960

Ser His Glu Arg Arg Ala Phe Leu Gln Ala Ile Leu Glu His Glu Glu
965 970 975

Gln Asp Glu Ser Arg His Cys Ser Thr Gly Ser Gly Ser Ala Ser Phe
980 985 990

Ala His Thr Ala Pro Pro Pro Ala Gly Val Asn Pro Asp Leu Glu Glu
995 1000 1005

Pro Pro Leu Lys Glu Glu Asp Glu Val Pro Asp Asp Glu Thr Val
1010 1015 1020

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Asn Gln Met Ile Ala Arg His Glu Glu Glu Phe Asp Leu Phe Met
1025 1030 1035

Arg Met Asp Leu Asp Arg Arg Arg Glu Glu Ala Arg Asn Pro Lys
1040 1045 1050

Arg Lys Pro Arg Leu Met Glu Glu Asp Glu Leu Pro Ser Trp Ile
1055 1060 1065

Ile Lys Asp Asp Ala Glu Val Glu Arg Leu Thr Cys Glu Glu Glu
1070 1075 1080

Glu Glu Lys Met Phe Gly Arg Gly Ser Arg His Arg Lys Glu Val
1085 1090 1095

Asp Tyr Ser Asp Ser Leu Thr Glu Lys Gln Trp Leu Lys Ala Ile
1100 1105 1110

Glu Glu Gly Thr Leu Glu Glu Ile Glu Glu Glu Val Arg Gln Lys
1115 1120 1125

Lys Ser Ser Arg Lys Arg Lys Arg Asp Ser Asp Ala Gly Ser Ser
1130 1135 1140

Thr Pro Thr Thr Ser Thr Arg Ser Arg Asp Lys Asp Asp Glu Ser
1145 1150 1155

Lys Lys Gln Lys Lys Arg Gly Arg Pro Pro Ala Glu Lys Leu Ser
1160 1165 1170

Pro Asn Pro Pro Asn Leu Thr Lys Lys Met Lys Lys Ile Val Asp
1175 1180 1185

Ala Val Ile Lys Tyr Lys Asp Ser Ser Ser Gly Arg Gln Leu Ser
1190 1195 1200

Glu Val Phe Ile Gln Leu Pro Ser Arg Lys Glu Leu Pro Glu Tyr
1205 1210 1215

Tyr Glu Leu Ile Arg Lys Pro Val Asp Phe Lys Lys Ile Lys Glu
1220 1225 1230

Arg Ile Arg Asn His Lys Tyr Arg Ser Leu Asn Asp Leu Glu Lys
1235 1240 1245

Asp Val Met Leu Leu Cys Gln Asn Ala Gln Thr Phe Asn Leu Glu
1250 1255 1260

Gly Ser Leu Ile Tyr Glu Asp Ser Ile Val Leu Gln Ser Val Phe
1265 1270 1275

Thr Ser Val Arg Gln Lys Ile Glu Lys Glu Asp Asp Ser Glu Gly
1280 1285 1290

Glu Glu Ser Glu Glu Glu Glu Glu Gly Glu Glu Glu Gly Ser Glu
1295 1300 1305

Ser Glu Ser Arg Ser Val Lys Val Lys Ile Lys Leu Gly Arg Lys
1310 1315 1320

Glu Lys Ala Gln Asp Arg Leu Lys Gly Gly Arg Arg Arg Pro Ser
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Arg Gly Ser Arg Ala Lys Pro Val Val Ser Asp Asp Asp Ser Glu
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35 40 45

Pro Ser Ala Gly His Pro Ile Pro Thr Gln Gly Pro Gly Gly Tyr Pro
50 55 60

Gln Asp Asn Met His Gln Met His Lys Pro Met Glu Ser Met His Glu
65 70 75 80

Lys Gly Met Ser Asp Pro Arg Tyr Asn Gln Met Lys Gly Met Gly Met
85 90 95

Arg Ser Gly Gly His Ala Gly Met Gly Pro Pro Pro Ser Pro Met Asp
100 105 110

Gln His Ser Gln Gly Tyr Pro Ser Pro Leu Gly Gly Ser Glu His Ala
115 120 125

Ser Ser Pro Val Pro Ala Ser Gly Pro Ser Ser Gly Pro Gln Met Ser
130 135 140

Ser Gly Pro Gly Gly Ala Pro Leu Asp Gly Ala Asp Pro Gln Ala Leu
145 150 155 160

Gly Gln Gln Asn Arg Gly Pro Thr Pro Phe Asn Gln Asn Gln Leu His
165 170 175

Gln Leu Arg Ala Gln Ile Met Ala Tyr Lys Met Leu Ala Arg Gly Gln
180 185 190

Pro Leu Pro Asp His Leu Gln Met Ala Val Gln Gly Lys Arg Pro Met
195 200 205

Pro Gly Met Gln Gln Gln Met Pro Thr Leu Pro Pro Pro Ser Val Ser
210 215 220

Ala Thr Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro
225 230 235 240

Gly Pro Ala Pro Pro Asn Tyr Ser Arg Pro His Gly Met Gly Gly Pro
245 250 255

Asn Met Pro Pro Pro Gly Pro Ser Gly Val Pro Pro Gly Met Pro Gly
260 265 270

Gln Pro Pro Gly Gly Pro Pro Lys Pro Trp Pro Glu Gly Pro Met Ala
275 280 285

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

Pro Thr Gly Arg Pro Ser Pro Ala Pro Pro Ala Val Pro Pro Ala Ala
305 310 315 320

Ser Pro Val Met Pro Pro Gln Thr Gln Ser Pro Gly Gln Pro Ala Gln
325 330 335

Pro Ala Pro Met Val Pro Leu His Gln Lys Gln Ser Arg Ile Thr Pro
340 345 350

Ile Gln Lys Pro Arg Gly Leu Asp Pro Val Glu Ile Leu Gln Glu Arg
355 360 365

Glu Tyr Arg Leu Gln Ala Arg Ile Ala His Arg Ile Gln Glu Leu Glu
370 375 380

Asn Leu Pro Gly Ser Leu Ala Gly Asp Leu Arg Thr Lys Ala Thr Ile
385 390 395 400

Glu Leu Lys Ala Leu Arg Leu Leu Asn Phe Gln Arg Gln Leu Arg Gln
405 410 415

Glu Val Val Val Cys Met Arg Arg Asp Thr Ala Leu Glu Thr Ala Leu
420 425 430

Asn Ala Lys Ala Tyr Lys Arg Ser Lys Arg Gln Ser Leu Arg Glu Ala
435 440 445

Arg Ile Thr Glu Lys Leu Glu Lys Gln Gln Lys Ile Glu Gln Glu Arg
450 455 460

Lys Arg Arg Gln Lys His Gln Glu Tyr Leu Asn Ser Ile Leu Gln His
465 470 475 480

Ala Lys Asp Phe Lys Glu Tyr His Arg Ser Val Thr Gly Lys Ile Gln
485 490 495

Lys Leu Thr Lys Ala Val Ala Thr Tyr His Ala Asn Thr Glu Arg Glu
500 505 510

Gln Lys Lys Glu Asn Glu Arg Ile Glu Lys Glu Arg Met Arg Arg Leu
515 520 525

Met Ala Glu Asp Glu Glu Gly Tyr Arg Lys Leu Ile Asp Gln Lys Lys
530 535 540

Asp Lys Arg Leu Ala Tyr Leu Leu Gln Gln Thr Asp Glu Tyr Val Ala
545 550 555 560

Asn Leu Thr Glu Leu Val Pro Gln His Lys Ala Ala Gln Val Ala Lys
565 570 575

Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys Ala Glu Asn Ala Glu Gly
580 585 590

Gln Thr Pro Ala Ile Gly Pro Asp Gly Glu Pro Leu Asp Glu Thr Ser
595 600 605

Gln Met Ser Asp Leu Pro Val Lys Val Ile His Val Glu Ser Gly Lys
610 615 620

Ile Leu Thr Gly Thr Asp Ala Pro Lys Ala Gly Gln Leu Glu Ala Trp
625 630 635 640

Leu Glu Met Asn Pro Gly Tyr Glu Val Ala Pro Arg Ser Asp Ser Glu
645 650 655

Glu Ser Gly Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gln Pro
660 665 670

Gln Ala Ala Gln Pro Pro Thr Leu Pro Val Glu Glu Lys Lys Lys Ile
675 680 685

Pro Asp Pro Asp Ser Asp Asp Val Ser Glu Val Asp Ala Arg His Ile
690 695 700

Ile Glu Asn Ala Lys Gln Asp Val Asp Asp Glu Tyr Gly Val Ser Gln
705 710 715 720

Ala Leu Ala Arg Gly Leu Gln Ser Tyr Tyr Ala Val Ala His Ala Val
725 730 735

Thr Glu Arg Val Asp Lys Gln Ser Ala Leu Met Val Asn Gly Val Leu
740 745 750

Lys Gln Tyr Gln Ile Lys Gly Leu Glu Trp Leu Val Ser Leu Tyr Asn
755 760 765

Asn Asn Leu Asn Gly Ile Leu Ala Asp Glu Met Gly Leu Gly Lys Thr
770 775 780

Ile Gln Thr Ile Ala Leu Ile Thr Tyr Leu Met Glu His Lys Arg Ile
785 790 795 800

Asn Gly Pro Phe Leu Ile Ile Val Pro Leu Ser Thr Leu Ser Asn Trp
805 810 815

Ala Tyr Glu Phe Asp Lys Trp Ala Pro Ser Val Val Lys Val Ser Tyr
820 825 830

Lys Gly Ser Pro Ala Ala Arg Arg Ala Phe Val Pro Gln Leu Arg Ser
835 840 845

Gly Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Ile Lys Asp
850 855 860

Lys His Ile Leu Ala Lys Ile Arg Trp Lys Tyr Met Ile Val Asp Glu
865 870 875 880

Gly His Arg Met Lys Asn His His Cys Lys Leu Thr Gln Val Leu Asn
885 890 895

Thr His Tyr Val Ala Pro Arg Arg Leu Leu Leu Thr Gly Thr Pro Leu
900 905 910

Gln Asn Lys Leu Pro Glu Leu Trp Ala Leu Leu Asn Phe Leu Leu Pro
915 920 925

Thr Ile Phe Lys Ser Cys Ser Thr Phe Glu Gln Trp Phe Asn Ala Pro
930 935 940

Phe Ala Met Thr Gly Glu Lys Val Asp Leu Asn Glu Glu Glu Thr Ile
945 950 955 960

Leu Ile Ile Arg Arg Leu His Lys Val Leu Arg Pro Phe Leu Leu Arg
965 970 975

Arg Leu Lys Lys Glu Val Glu Ala Gln Leu Pro Glu Lys Val Glu Tyr

980 985 990

Val Ile Lys Cys Asp Met Ser Ala Leu Gln Arg Val Leu Tyr Arg His
995 1000 1005

Met Gln Ala Lys Gly Val Leu Leu Thr Asp Gly Ser Glu Lys Asp
1010 1015 1020

Lys Lys Gly Lys Gly Gly Thr Lys Thr Leu Met Asn Thr Ile Met
1025 1030 1035

Gln Leu Arg Lys Ile Cys Asn His Pro Tyr Met Phe Gln His Ile
1040 1045 1050

Glu Glu Ser Phe Ser Glu His Leu Gly Phe Thr Gly Gly Ile Val
1055 1060 1065

Gln Gly Leu Asp Leu Tyr Arg Ala Ser Gly Lys Phe Glu Leu Leu
1070 1075 1080

Asp Arg Ile Leu Pro Lys Leu Arg Ala Thr Asn His Lys Val Leu
1085 1090 1095

Leu Phe Cys Gln Met Thr Ser Leu Met Thr Ile Met Glu Asp Tyr
1100 1105 1110

Phe Ala Tyr Arg Gly Phe Lys Tyr Leu Arg Leu Asp Gly Thr Thr
1115 1120 1125

Ser Thr Arg Ser Arg Asp Lys Asp Asp Glu Ser Lys Lys Gln Lys
1130 1135 1140

Lys Arg Gly Arg Pro Pro Ala Glu Lys Leu Ser Pro Asn Pro Pro
1145 1150 1155

Asn Leu Thr Lys Lys Met Lys Lys Ile Val Asp Ala Val Ile Lys
1160 1165 1170

Tyr Lys Asp Ser Ser Ser Gly Arg Gln Leu Ser Glu Val Phe Ile
1175 1180 1185

Gln Leu Pro Ser Arg Lys Glu Leu Pro Glu Tyr Tyr Glu Leu Ile
1190 1195 1200

Arg Lys Pro Val Asp Phe Lys Lys Ile Lys Glu Arg Ile Arg Asn
1205 1210 1215

His Lys Tyr Arg Ser Leu Asn Asp Leu Glu Lys Asp Val Met Leu
1220 1225 1230

Leu Cys Gln Asn Ala Gln Thr Phe Asn Leu Glu Gly Ser Leu Ile
1235 1240 1245

Tyr Glu Asp Ser Ile Val Leu Gln Ser Val Phe Thr Ser Val Arg
1250 1255 1260

Gln Lys Ile Glu Lys Glu Asp Asp Ser Glu Gly Glu Glu Ser Glu
1265 1270 1275

Glu Glu Glu Glu Gly Glu Glu Glu Gly Ser Glu Ser Glu Ser Arg
1280 1285 1290

Ser Val Lys Val Lys Ile Lys Leu Gly Arg Lys Glu Lys Ala Gln
1295 1300 1305

Asp Arg Leu Lys Gly Gly Arg Arg Arg Pro Ser Arg Gly Ser Arg
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35 40 45

Pro Ser Ala Gly His Pro Ile Pro Thr Gln Gly Pro Gly Gly Tyr Pro
50 55 60

Gln Asp Asn Met His Gln Met His Lys Pro Met Glu Ser Met His Glu
65 70 75 80

Lys Gly Met Ser Asp Pro Arg Tyr Asn Gln Met Lys Gly Met Gly Met
85 90 95

Arg Ser Gly Gly His Ala Gly Met Gly Pro Pro Pro Ser Pro Met Asp
100 105 110

Gln His Ser Gln Gly Tyr Pro Ser Pro Leu Gly Gly Ser Glu His Ala
115 120 125

Ser Ser Pro Val Pro Ala Ser Gly Pro Ser Ser Gly Pro Gln Met Ser

130 135 140

Ser Gly Pro Gly Gly Ala Pro Leu Asp Gly Ala Asp Pro Gln Ala Leu
145 150 155 160

Gly Gln Gln Asn Arg Gly Pro Thr Pro Phe Asn Gln Asn Gln Leu His
165 170 175

Gln Leu Arg Ala Gln Ile Met Ala Tyr Lys Met Leu Ala Arg Gly Gln
180 185 190

Pro Leu Pro Asp His Leu Leu Asn Phe Gln Arg Gln Leu Arg Gln Glu
195 200 205

Val Val Val Cys Met Arg Arg Asp Thr Ala Leu Glu Thr Ala Leu Asn
210 215 220

Ala Lys Ala Tyr Lys Arg Ser Lys Arg Gln Ser Leu Arg Glu Ala Arg
225 230 235 240

Ile Thr Glu Lys Leu Glu Lys Gln Gln Lys Ile Glu Gln Glu Arg Lys
245 250 255

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

Lys Asp Phe Lys Glu Tyr His Arg Ser Val Thr Gly Lys Ile Gln Lys
275 280 285

Leu Thr Lys Ala Val Ala Thr Tyr His Ala Asn Thr Glu Arg Glu Gln
290 295 300

Lys Lys Glu Asn Glu Arg Ile Glu Lys Glu Arg Met Arg Arg Leu Met
305 310 315 320

Ala Glu Asp Glu Glu Gly Tyr Arg Lys Leu Ile Asp Gln Lys Lys Asp
325 330 335

Lys Arg Leu Ala Tyr Leu Leu Gln Gln Thr Asp Glu Tyr Val Ala Asn
340 345 350

Leu Thr Glu Leu Val Pro Gln His Lys Ala Ala Gln Val Ala Lys Glu
355 360 365

Lys Lys Lys Lys Lys Lys Lys Lys Lys Ala Glu Asn Ala Glu Gly Gln
370 375 380

Thr Pro Ala Ile Gly Pro Asp Gly Glu Pro Leu Asp Glu Thr Ser Gln
385 390 395 400

Met Ser Asp Leu Pro Val Lys Val Ile His Val Glu Ser Gly Lys Ile
405 410 415

Leu Thr Gly Thr Asp Ala Pro Lys Ala Gly Gln Leu Glu Ala Trp Leu
420 425 430

Glu Met Asn Pro Gly Tyr Glu Val Ala Pro Arg Ser Asp Ser Glu Glu
435 440 445

Ser Gly Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gln Pro Gln
450 455 460

Ala Ala Gln Pro Pro Thr Leu Pro Val Glu Glu Lys Lys Lys Ile Pro
465 470 475 480

Asp Pro Asp Ser Asp Asp Val Ser Glu Val Asp Ala Arg His Ile Ile
485 490 495

Glu Asn Ala Lys Gln Asp Val Asp Asp Glu Tyr Gly Val Ser Gln Ala
500 505 510

Leu Ala Arg Gly Leu Gln Ser Tyr Tyr Ala Val Ala His Ala Val Thr
515 520 525

Glu Arg Val Asp Lys Gln Ser Ala Leu Met Val Asn Gly Val Leu Lys
530 535 540

Gln Tyr Gln Ile Lys Gly Leu Glu Trp Leu Val Ser Leu Tyr Asn Asn
545 550 555 560

Asn Leu Asn Gly Ile Leu Ala Asp Glu Met Gly Leu Gly Lys Thr Ile
565 570 575

Gln Thr Ile Ala Leu Ile Thr Tyr Leu Met Glu His Lys Arg Ile Asn
580 585 590

Gly Pro Phe Leu Ile Ile Val Pro Leu Ser Thr Leu Ser Asn Trp Ala
595 600 605

Tyr Glu Phe Asp Lys Trp Ala Pro Ser Val Val Lys Val Ser Tyr Lys
610 615 620

Gly Ser Pro Ala Ala Arg Arg Ala Phe Val Pro Gln Leu Arg Ser Gly
625 630 635 640

Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Ile Lys Asp Lys
645 650 655

His Ile Leu Ala Lys Ile Arg Trp Lys Tyr Met Ile Val Asp Glu Gly
660 665 670

His Arg Met Lys Asn His His Cys Lys Leu Thr Gln Val Leu Asn Thr
675 680 685

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His Tyr Val Ala Pro Arg Arg Leu Leu Leu Thr Gly Thr Pro Leu Gln
690 695 700

Asn Lys Leu Pro Glu Leu Trp Ala Leu Leu Asn Phe Leu Leu Pro Thr
705 710 715 720

Ile Phe Lys Ser Cys Ser Thr Phe Glu Gln Trp Phe Asn Ala Pro Phe
725 730 735

Ala Met Thr Gly Glu Lys Val Asp Leu Asn Glu Glu Glu Thr Ile Leu
740 745 750

Ile Ile Arg Arg Leu His Lys Val Leu Arg Pro Phe Leu Leu Arg Arg
755 760 765

Leu Lys Lys Glu Val Glu Ala Gln Leu Pro Glu Lys Val Glu Tyr Val
770 775 780

Ile Lys Cys Asp Met Ser Ala Leu Gln Arg Val Leu Tyr Arg His Met
785 790 795 800

Gln Ala Lys Gly Val Leu Leu Thr Asp Gly Ser Glu Lys Asp Lys Lys
805 810 815

Gly Lys Gly Gly Thr Lys Thr Leu Met Asn Thr Ile Met Gln Leu Arg
820 825 830

Lys Ile Cys Asn His Pro Tyr Met Phe Gln His Ile Glu Glu Ser Phe
835 840 845

Ser Glu His Leu Gly Phe Thr Gly Gly Ile Val Gln Gly Leu Asp Leu
850 855 860

Tyr Arg Ala Ser Gly Lys Phe Glu Leu Leu Asp Arg Ile Leu Pro Lys
865 870 875 880

Leu Arg Ala Thr Asn His Lys Val Leu Leu Phe Cys Gln Met Thr Ser
885 890 895

Leu Met Thr Ile Met Glu Asp Tyr Phe Ala Tyr Arg Gly Phe Lys Tyr
900 905 910

Leu Arg Leu Asp Gly Thr Thr Lys Ala Glu Asp Arg Gly Met Leu Leu
915 920 925

Lys Thr Phe Asn Glu Pro Gly Ser Glu Tyr Phe Ile Phe Leu Leu Ser
930 935 940

Thr Arg Ala Gly Gly Leu Gly Leu Asn Leu Gln Ser Ala Asp Thr Val
945 950 955 960

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Ile Ile Phe Asp Ser Asp Trp Asn Pro His Gln Asp Leu Gln Ala Gln
965 970 975

Asp Arg Ala His Arg Ile Gly Gln Gln Asn Glu Val Arg Val Leu Arg
980 985 990

Leu Cys Thr Val Asn Ser Val Glu Glu Lys Ile Leu Ala Ala Ala Lys
995 1000 1005

Tyr Lys Leu Asn Val Asp Gln Lys Val Ile Gln Ala Gly Met Phe
1010 1015 1020

Asp Gln Lys Ser Ser Ser His Glu Arg Arg Ala Phe Leu Gln Ala
1025 1030 1035

Ile Leu Glu His Glu Glu Gln Asp Glu Ser Arg His Cys Ser Thr
1040 1045 1050

Gly Ser Gly Ser Ala Ser Phe Ala His Thr Ala Pro Pro Pro Ala
1055 1060 1065

Gly Val Asn Pro Asp Leu Glu Glu Pro Pro Leu Lys Glu Glu Asp
1070 1075 1080

Glu Val Pro Asp Asp Glu Thr Val Asn Gln Met Ile Ala Arg His
1085 1090 1095

Glu Glu Glu Phe Asp Leu Phe Met Arg Met Asp Leu Asp Arg Arg
1100 1105 1110

Arg Glu Glu Ala Arg Asn Pro Lys Arg Lys Pro Arg Leu Met Glu
1115 1120 1125

Glu Asp Glu Leu Pro Ser Trp Ile Ile Lys Asp Asp Ala Glu Val
1130 1135 1140

Glu Arg Leu Thr Cys Glu Glu Glu Glu Glu Lys Met Phe Gly Arg
1145 1150 1155

Gly Ser Arg His Arg Lys Glu Val Asp Tyr Ser Asp Ser Leu Thr
1160 1165 1170

Glu Lys Gln Trp Leu Lys Ala Ile Glu Glu Gly Thr Leu Glu Glu
1175 1180 1185

Ile Glu Glu Glu Val Arg Gln Lys Lys Ser Ser Arg Lys Arg Lys
1190 1195 1200

Arg Asp Ser Asp Ala Gly Ser Ser Thr Pro Thr Thr Ser Thr Arg
1205 1210 1215

Ser Arg Asp Lys Asp Asp Glu Ser Lys Lys Gln Lys Lys Arg Gly

1220 1225 1230

Arg Pro Pro Ala Glu Lys Leu Ser Pro Asn Pro Pro Asn Leu Thr
1235 1240 1245

Lys Lys Met Lys Lys Ile Val Asp Ala Val Ile Lys Tyr Lys Asp
1250 1255 1260

Ser Ser Ser Gly Arg Gln Leu Ser Glu Val Phe Ile Gln Leu Pro
1265 1270 1275

Ser Arg Lys Glu Leu Pro Glu Tyr Tyr Glu Leu Ile Arg Lys Pro
1280 1285 1290

Val Asp Phe Lys Lys Ile Lys Glu Arg Ile Arg Asn His Lys Tyr
1295 1300 1305

Arg Ser Leu Asn Asp Leu Glu Lys Asp Val Met Leu Leu Cys Gln
1310 1315 1320

Asn Ala Gln Thr Phe Asn Leu Glu Gly Ser Leu Ile Tyr Glu Asp
1325 1330 1335

Ser Ile Val Leu Gln Ser Val Phe Thr Ser Val Arg Gln Lys Ile
1340 1345 1350

Glu Lys Glu Asp Asp Ser Glu Gly Glu Glu Ser Glu Glu Glu Glu
1355 1360 1365

Glu Gly Glu Glu Glu Gly Ser Glu Ser Glu Ser Arg Ser Val Lys
1370 1375 1380

Val Lys Ile Lys Leu Gly Arg Lys Glu Lys Ala Gln Asp Arg Leu
1385 1390 1395

Lys Gly Gly Arg Arg Arg Pro Ser Arg Gly Ser Arg Ala Lys Pro
1400 1405 1410

Val Val Ser Asp Asp Asp Ser Glu Glu Glu Gln Glu Glu Asp Arg
1415 1420 1425

Ser Gly Ser Gly Ser Glu Glu Asp
1430 1435

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<400> 175
Met Ser Thr Pro Asp Pro Pro Leu Gly Thr Pro Arg Pro Gly Pro Ser
1 5 10 15

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Pro Gly Pro Gly Pro Ser Pro Gly Ala Met Leu Gly Pro Ser Pro Gly
            20                  25                  30

Pro Ser Pro Gly Ser Ala His Ser Met Met Gly Pro Ser Pro Gly Pro
        35                  40                  45

Pro Ser Ala Gly His Pro Ile Pro Thr Gln Gly Pro Gly Gly Tyr Pro
    50                  55                  60

Gln Asp Asn Met His Gln Met His Lys Pro Met Glu Ser Met His Glu
65                  70                  75                  80

Lys Gly Met Ser Asp Pro Arg Tyr Asn Gln Met Lys Gly Met Gly Met
                85                  90                  95

Arg Ser Gly Gly His Ala Gly Met Gly Pro Pro Pro Ser Pro Met Asp
            100                 105                 110

Gln His Ser Gln Gly Tyr Pro Ser Pro Leu Gly Gly Ser Glu His Ala
        115                 120                 125

Ser Ser Pro Val Pro Ala Ser Gly Pro Ser Ser Gly Pro Gln Met Ser
    130                 135                 140

Ser Gly Pro Gly Gly Ala Pro Leu Asp Gly Ala Asp Pro Gln Ala Leu
145                 150                 155                 160

Gly Gln Gln Asn Arg Gly Pro Thr Pro Phe Asn Gln Asn Gln Leu His
                165                 170                 175

Gln Leu Arg Ala Gln Ile Met Ala Tyr Lys Met Leu Ala Arg Gly Gln
            180                 185                 190

Pro Leu Pro Asp His Leu Gln Met Ala Val Gln Glu Arg Lys Arg Arg
        195                 200                 205

Gln Lys His Gln Glu Tyr Leu Asn Ser Ile Leu Gln His Ala Lys Asp
    210                 215                 220

Phe Lys Glu Tyr His Arg Ser Val Thr Gly Lys Ile Gln Lys Leu Thr
225                 230                 235                 240

Lys Ala Val Ala Thr Tyr His Ala Asn Thr Glu Arg Glu Gln Lys Lys
                245                 250                 255

Glu Asn Glu Arg Ile Glu Lys Glu Arg Met Arg Arg Leu Met Ala Glu
            260                 265                 270

Asp Glu Glu Gly Tyr Arg Lys Leu Ile Asp Gln Lys Lys Asp Lys Arg
        275                 280                 285

Leu Ala Tyr Leu Leu Gln Gln Thr Asp Glu Tyr Val Ala Asn Leu Thr
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290 295 300

Glu Leu Val Pro Gln His Lys Ala Ala Gln Val Ala Lys Glu Lys Lys
305 310 315 320

Lys Lys Lys Lys Lys Lys Lys Ala Glu Asn Ala Glu Gly Gln Thr Pro
325 330 335

Ala Ile Gly Pro Asp Gly Glu Pro Leu Asp Glu Thr Ser Gln Met Ser
340 345 350

Asp Leu Pro Val Lys Val Ile His Val Glu Ser Gly Lys Ile Leu Thr
355 360 365

Gly Thr Asp Ala Pro Lys Ala Gly Gln Leu Glu Ala Trp Leu Glu Met
370 375 380

Asn Pro Gly Tyr Glu Val Ala Pro Arg Ser Asp Ser Glu Glu Ser Gly
385 390 395 400

Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gln Pro Gln Ala Ala
405 410 415

Gln Pro Pro Thr Leu Pro Val Glu Glu Lys Lys Lys Ile Pro Asp Pro
420 425 430

Asp Ser Asp Asp Val Ser Glu Val Asp Ala Arg His Ile Ile Glu Asn
435 440 445

Ala Lys Gln Asp Val Asp Asp Glu Tyr Gly Val Ser Gln Ala Leu Ala
450 455 460

Arg Gly Leu Gln Ser Tyr Tyr Ala Val Ala His Ala Val Thr Glu Arg
465 470 475 480

Val Asp Lys Gln Ser Ala Leu Met Val Asn Gly Val Leu Lys Gln Tyr
485 490 495

Gln Ile Lys Gly Leu Glu Trp Leu Val Ser Leu Tyr Asn Asn Asn Leu
500 505 510

Asn Gly Ile Leu Ala Asp Glu Met Gly Leu Gly Lys Thr Ile Gln Thr
515 520 525

Ile Ala Leu Ile Thr Tyr Leu Met Glu His Lys Arg Ile Asn Gly Pro
530 535 540

Phe Leu Ile Ile Val Pro Leu Ser Thr Leu Ser Asn Trp Ala Tyr Glu
545 550 555 560

Phe Asp Lys Trp Ala Pro Ser Val Val Lys Val Ser Tyr Lys Gly Ser
565 570 575

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Pro Ala Ala Arg Arg Ala Phe Val Pro Gln Leu Arg Ser Gly Lys Phe
580 585 590

Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Ile Lys Asp Lys His Ile
595 600 605

Leu Ala Lys Ile Arg Trp Lys Tyr Met Ile Val Asp Glu Gly His Arg
610 615 620

Met Lys Asn His His Cys Lys Leu Thr Gln Val Leu Asn Thr His Tyr
625 630 635 640

Val Ala Pro Arg Arg Leu Leu Leu Thr Gly Thr Pro Leu Gln Asn Lys
645 650 655

Leu Pro Glu Leu Trp Ala Leu Leu Asn Phe Leu Leu Pro Thr Ile Phe
660 665 670

Lys Ser Cys Ser Thr Phe Glu Gln Trp Phe Asn Ala Pro Phe Ala Met
675 680 685

Thr Gly Glu Lys Val Asp Leu Asn Glu Glu Glu Thr Ile Leu Ile Ile
690 695 700

Arg Arg Leu His Lys Val Leu Arg Pro Phe Leu Leu Arg Arg Leu Lys
705 710 715 720

Lys Glu Val Glu Ala Gln Leu Pro Glu Lys Val Glu Tyr Val Ile Lys
725 730 735

Cys Asp Met Ser Ala Leu Gln Arg Val Leu Tyr Arg His Met Gln Ala
740 745 750

Lys Gly Val Leu Leu Thr Asp Gly Ser Glu Lys Asp Lys Lys Gly Lys
755 760 765

Gly Gly Thr Lys Thr Leu Met Asn Thr Ile Met Gln Leu Arg Lys Ile
770 775 780

Cys Asn His Pro Tyr Met Phe Gln His Ile Glu Glu Ser Phe Ser Glu
785 790 795 800

His Leu Gly Phe Thr Gly Gly Ile Val Gln Gly Leu Asp Leu Tyr Arg
805 810 815

Ala Ser Gly Lys Phe Glu Leu Leu Asp Arg Ile Leu Pro Lys Leu Arg
820 825 830

Ala Thr Asn His Lys Val Leu Leu Phe Cys Gln Met Thr Ser Leu Met
835 840 845

```
Thr Ile Met Glu Asp Tyr Phe Ala Tyr Arg Gly Phe Lys Tyr Leu Arg
    850                 855                 860

Leu Asp Gly Thr Thr Lys Ala Glu Asp Arg Gly Met Leu Leu Lys Thr
865                 870                 875                 880

Phe Asn Glu Pro Gly Ser Glu Tyr Phe Ile Phe Leu Leu Ser Thr Arg
                885                 890                 895

Ala Gly Gly Leu Gly Leu Asn Leu Gln Ser Ala Asp Thr Val Ile Ile
            900                 905                 910

Phe Asp Ser Asp Trp Asn Pro His Gln Asp Leu Gln Ala Gln Asp Arg
        915                 920                 925

Ala His Arg Ile Gly Gln Gln Asn Glu Val Arg Val Leu Arg Leu Cys
    930                 935                 940

Thr Val Asn Ser Val Glu Glu Lys Ile Leu Ala Ala Ala Lys Tyr Lys
945                 950                 955                 960

Leu Asn Val Asp Gln Lys Val Ile Gln Ala Gly Met Phe Asp Gln Lys
                965                 970                 975

Ser Ser Ser His Glu Arg Arg Ala Phe Leu Gln Ala Ile Leu Glu His
            980                 985                 990

Glu Glu Gln Asp Glu Ser Arg His  Cys Ser Thr Gly Ser  Gly Ser Ala
        995                 1000                1005

Ser Phe  Ala His Thr Ala Pro  Pro Pro Ala Gly Val  Asn Pro Asp
    1010                1015                1020

Leu Glu  Glu Pro Pro Leu Lys  Glu Glu Asp Glu Val  Pro Asp Asp
    1025                1030                1035

Glu Thr  Val Asn Gln Met Ile  Ala Arg His Glu Glu  Glu Phe Asp
    1040                1045                1050

Leu Phe  Met Arg Met Asp Leu  Asp Arg Arg Arg Glu  Glu Ala Arg
    1055                1060                1065

Asn Pro  Lys Arg Lys Pro Arg  Leu Met Glu Glu Asp  Glu Leu Pro
    1070                1075                1080

Ser Trp  Ile Ile Lys Asp Asp  Ala Glu Val Glu Arg  Leu Thr Cys
    1085                1090                1095

Glu Glu  Glu Glu Glu Lys Met  Phe Gly Arg Gly Ser  Arg His Arg
    1100                1105                1110
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Lys Glu Val Asp Tyr Ser Asp Ser Leu Thr Glu Lys Gln Trp Leu
1115 1120 1125

Lys Ala Ile Glu Glu Gly Thr Leu Glu Glu Ile Glu Glu Glu Val
1130 1135 1140

Arg Gln Lys Lys Ser Ser Arg Lys Arg Lys Arg Asp Ser Asp Ala
1145 1150 1155

Gly Ser Ser Thr Pro Thr Thr Ser Thr Arg Ser Arg Asp Lys Asp
1160 1165 1170

Asp Glu Ser Lys Lys Gln Lys Lys Arg Gly Arg Pro Pro Ala Glu
1175 1180 1185

Lys Leu Ser Pro Asn Pro Pro Asn Leu Thr Lys Lys Met Lys Lys
1190 1195 1200

Ile Val Asp Ala Val Ile Lys Tyr Lys Asp Ser Ser Ser Gly Arg
1205 1210 1215

Gln Leu Ser Glu Val Phe Ile Gln Leu Pro Ser Arg Lys Glu Leu
1220 1225 1230

Pro Glu Tyr Tyr Glu Leu Ile Arg Lys Pro Val Asp Phe Lys Lys
1235 1240 1245

Ile Lys Glu Arg Ile Arg Asn His Lys Tyr Arg Ser Leu Asn Asp
1250 1255 1260

Leu Glu Lys Asp Val Met Leu Leu Cys Gln Asn Ala Gln Thr Phe
1265 1270 1275

Asn Leu Glu Gly Ser Leu Ile Tyr Glu Asp Ser Ile Val Leu Gln
1280 1285 1290

Ser Val Phe Thr Ser Val Arg Gln Lys Ile Glu Lys Glu Asp Asp
1295 1300 1305

Ser Glu Gly Glu Glu Ser Glu Glu Glu Glu Glu Gly Glu Glu Glu
1310 1315 1320

Gly Ser Glu Ser Glu Ser Arg Ser Val Lys Val Lys Ile Lys Leu
1325 1330 1335

Gly Arg Lys Glu Lys Ala Gln Asp Arg Leu Lys Gly Gly Arg Arg
1340 1345 1350

Arg Pro Ser Arg Gly Ser Arg Ala Lys Pro Val Val Ser Asp Asp
1355 1360 1365

Asp Ser Glu Glu Glu Gln Glu Glu Asp Arg Ser Gly Ser Gly Ser

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1370 1375 1380

Glu Glu Asp
1385

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<400> 176

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

Ala Thr Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro
225 230 235 240

Gly Pro Ala Pro Pro Asn Tyr Ser Arg Pro His Gly Met Gly Gly Pro
245 250 255

Asn Met Pro Pro Pro Gly Pro Ser Gly Val Pro Pro Gly Met Pro Gly
260 265 270

Gln Pro Pro Gly Gly Pro Pro Lys Pro Trp Pro Glu Gly Pro Met Ala
275 280 285

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

Pro Thr Gly Arg Pro Ser Pro Ala Pro Pro Ala Val Pro Pro Ala Ala
305 310 315 320

Ser Pro Val Met Pro Pro Gln Thr Gln Ser Pro Gly Gln Pro Ala Gln
325 330 335

Pro Ala Pro Met Val Pro Leu His Gln Lys Gln Ser Arg Ile Thr Pro
340 345 350

Ile Gln Lys Pro Arg Gly Leu Asp Pro Val Glu Ile Leu Gln Glu Arg
355 360 365

Glu Tyr Arg Leu Gln Ala Arg Ile Ala His Arg Ile Gln Glu Leu Glu
370 375 380

Asn Leu Pro Gly Ser Leu Ala Gly Asp Leu Arg Thr Lys Ala Thr Ile
385 390 395 400

Glu Leu Lys Ala Leu Arg Leu Leu Asn Phe Gln Arg Gln Leu Arg Gln
405 410 415

Glu Val Val Val Cys Met Arg Arg Asp Thr Ala Leu Glu Thr Ala Leu
420 425 430

Asn Ala Lys Ala Tyr Lys Arg Ser Lys Arg Gln Ser Leu Arg Glu Ala
435 440 445

Arg Ile Thr Glu Lys Leu Glu Lys Gln Gln Lys Ile Glu Gln Glu Arg
450 455 460

Lys Arg Arg Gln Lys His Gln Glu Tyr Leu Asn Ser Ile Leu Gln His
465 470 475 480

Ala Lys Asp Phe Lys Glu Tyr His Arg Ser Val Thr Gly Lys Ile Gln
485 490 495

Lys Leu Thr Lys Ala Val Ala Thr Tyr His Ala Asn Thr Glu Arg Glu

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            500                 505                 510

Gln Lys Lys Glu Asn Glu Arg Ile Glu Lys Glu Arg Met Arg Arg Leu
        515                 520                 525

Met Ala Glu Asp Glu Glu Gly Tyr Arg Lys Leu Ile Asp Gln Lys Lys
    530                 535                 540

Asp Lys Arg Leu Ala Tyr Leu Leu Gln Gln Thr Asp Glu Tyr Val Ala
545                 550                 555                 560

Asn Leu Thr Glu Leu Val Pro Gln His Lys Ala Ala Gln Val Ala Lys
                565                 570                 575

Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys Ala Glu Asn Ala Glu Gly
            580                 585                 590

Gln Thr Pro Ala Ile Gly Pro Asp Gly Glu Pro Leu Asp Glu Thr Ser
        595                 600                 605

Gln Met Ser Asp Leu Pro Val Lys Val Ile His Val Glu Ser Gly Lys
    610                 615                 620

Ile Leu Thr Gly Thr Asp Ala Pro Lys Ala Gly Gln Leu Glu Ala Trp
625                 630                 635                 640

Leu Glu Met Asn Pro Gly Tyr Glu Val Ala Pro Arg Ser Asp Ser Glu
                645                 650                 655

Glu Ser Gly Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gln Pro
            660                 665                 670

Gln Ala Ala Gln Pro Pro Thr Leu Pro Val Glu Glu Lys Lys Lys Ile
        675                 680                 685

Pro Asp Pro Asp Ser Asp Asp Val Ser Glu Val Asp Ala Arg His Ile
    690                 695                 700

Ile Glu Asn Ala Lys Gln Asp Val Asp Asp Glu Tyr Gly Val Ser Gln
705                 710                 715                 720

Ala Leu Ala Arg Gly Leu Gln Ser Tyr Tyr Ala Val Ala His Ala Val
                725                 730                 735

Thr Glu Arg Val Asp Lys Gln Ser Ala Leu Met Val Asn Gly Val Leu
            740                 745                 750

Lys Gln Tyr Gln Ile Lys Gly Leu Glu Trp Leu Val Ser Leu Tyr Asn
        755                 760                 765

Asn Asn Leu Asn Gly Ile Leu Ala Asp Glu Met Gly Leu Gly Lys Thr
    770                 775                 780
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Ile Gln Thr Ile Ala Leu Ile Thr Tyr Leu Met Glu His Lys Arg Ile
785 790 795 800

Asn Gly Pro Phe Leu Ile Ile Val Pro Leu Ser Thr Leu Ser Asn Trp
805 810 815

Ala Tyr Glu Phe Asp Lys Trp Ala Pro Ser Val Val Lys Val Ser Tyr
820 825 830

Lys Gly Ser Pro Ala Ala Arg Arg Ala Phe Val Pro Gln Leu Arg Ser
835 840 845

Gly Lys Phe Asn Val Leu Leu Thr Thr Tyr Glu Tyr Ile Ile Lys Asp
850 855 860

Lys His Ile Leu Ala Lys Ile Arg Trp Lys Tyr Met Ile Val Asp Glu
865 870 875 880

Gly His Arg Met Lys Asn His His Cys Lys Leu Thr Gln Val Leu Asn
885 890 895

Thr His Tyr Val Ala Pro Arg Arg Leu Leu Leu Thr Gly Thr Pro Leu
900 905 910

Gln Asn Lys Leu Pro Glu Leu Trp Ala Leu Leu Asn Phe Leu Leu Pro
915 920 925

Thr Ile Phe Lys Ser Cys Ser Thr Phe Glu Gln Trp Phe Asn Ala Pro
930 935 940

Phe Ala Met Thr Gly Glu Lys Val Asp Leu Asn Glu Glu Glu Thr Ile
945 950 955 960

Leu Ile Ile Arg Arg Leu His Lys Val Leu Arg Pro Phe Leu Leu Arg
965 970 975

Arg Leu Lys Lys Glu Val Glu Ala Gln Leu Pro Glu Lys Val Glu Tyr
980 985 990

Val Ile Lys Cys Asp Met Ser Ala Leu Gln Arg Val Leu Tyr Arg His
995 1000 1005

Met Gln Ala Lys Gly Val Leu Leu Thr Asp Gly Ser Glu Lys Asp
1010 1015 1020

Lys Lys Gly Lys Gly Gly Thr Lys Thr Leu Met Asn Thr Ile Met
1025 1030 1035

Gln Leu Arg Lys Ile Cys Asn His Pro Tyr Met Phe Gln His Ile
1040 1045 1050

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Glu Glu Ser Phe Ser Glu His Leu Gly Phe Thr Gly Gly Ile Val
1055 1060 1065

Gln Gly Leu Asp Leu Tyr Arg Ala Ser Gly Lys Phe Glu Leu Leu
1070 1075 1080

Asp Arg Ile Leu Pro Lys Leu Arg Ala Thr Asn His Lys Val Leu
1085 1090 1095

Leu Phe Cys Gln Met Thr Ser Leu Met Thr Ile Met Glu Asp Tyr
1100 1105 1110

Phe Ala Tyr Arg Gly Phe Lys Tyr Leu Arg Leu Asp Gly Thr Thr
1115 1120 1125

Lys Ala Glu Asp Arg Gly Met Leu Leu Lys Thr Phe Asn Glu Pro
1130 1135 1140

Gly Ser Glu Tyr Phe Ile Phe Leu Leu Ser Thr Arg Ala Gly Gly
1145 1150 1155

Leu Gly Leu Asn Leu Gln Ser Ala Asp Thr Val Ile Ile Phe Asp
1160 1165 1170

Ser Asp Trp Asn Pro His Gln Val Lys Ala Gly Arg Ala Pro Gly
1175 1180 1185

Arg Gly Glu Gly Arg Gly Cys Leu Gln Asn Leu Glu Glu Thr Ala
1190 1195 1200

Leu Ala
1205

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Ala Ala Asp Thr Val Thr Gln Phe Asp Asn Val Arg Leu Trp Leu Gly
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Lys Asn Tyr Lys Lys Tyr Ile Gln Ala Asp Thr Pro Ser Gly Leu Val
35 40 45

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

Leu Asn Phe Pro Asp Lys Gly Lys Glu Lys Pro Thr Asp Met Gln Asn
65 70 75 80

Phe Gly Leu Arg Thr Asp Met Tyr Thr Lys Lys Asn Val Pro Ser Lys
85 90 95

Ser Lys Ala Ala Ala Ser Ala Thr Arg Glu Trp Thr Glu Gln Glu Thr
100 105 110

Leu Leu Leu Leu Glu Ala Leu Glu Met Tyr Lys Asp Asp Trp Asn Lys
115 120 125

Val Ser Glu His Val Gly Ser Arg Thr Gln Asp Glu Cys Ile Leu His
130 135 140

Phe Leu Arg Leu Pro Ile Glu Asp Pro Tyr Leu Glu Asp Ser Glu Ala
145 150 155 160

Ser Leu Gly Pro Leu Ala Tyr Gln Pro Ile Pro Phe Ser Gln Ser Gly
165 170 175

Asn Pro Val Met Ser Thr Val Ala Phe Leu Ala Ser Val Val Asp Pro
180 185 190

Arg Val Ala Ser Ala Ala Ala Lys Ser Ala Leu Glu Glu Phe Ser Lys
195 200 205

Met Lys Glu Glu Val Pro Thr Ala Leu Val Glu Ala His Val Arg Lys
210 215 220

Val Glu Glu Ala Ala Lys Val Thr Gly Lys Ala Asp Pro Ala Phe Gly
225 230 235 240

Leu Glu Ser Ser Gly Ile Ala Gly Thr Thr Ser Asp Glu Pro Glu Arg
245 250 255

Ile Glu Glu Ser Gly Asn Asp Glu Ala Arg Val Glu Gly Gln Ala Thr
260 265 270

Asp Glu Lys Lys Glu Pro Lys Glu Pro Arg Glu Gly Gly Gly Ala Ile
275 280 285

Glu Glu Glu Ala Lys Glu Lys Thr Ser Glu Ala Pro Lys Lys Asp Glu
290 295 300

Glu Lys Gly Lys Glu Gly Asp Ser Glu Lys Glu Ser Glu Lys Ser Asp
305 310 315 320

Gly Asp Pro Ile Val Asp Pro Glu Lys Glu Lys Glu Pro Lys Glu Gly
325 330 335

Gln Glu Glu Val Leu Lys Glu Val Val Glu Ser Glu Gly Glu Arg Lys
340 345 350

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Thr Lys Val Glu Arg Asp Ile Gly Glu Gly Asn Leu Ser Thr Ala Ala
355 360 365

Ala Ala Ala Leu Ala Ala Ala Ala Val Lys Ala Lys His Leu Ala Ala
370 375 380

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

Gln Met Lys Lys Leu Glu Ile Lys Leu Arg His Phe Glu Glu Leu Glu
405 410 415

Thr Ile Met Asp Arg Glu Arg Glu Ala Leu Glu Tyr Gln Arg Gln Gln
420 425 430

Leu Leu Ala Asp Arg Gln Ala Phe His Met Glu Gln Leu Lys Tyr Ala
435 440 445

Glu Met Arg Ala Arg Gln Gln His Phe Gln Gln Met His Gln Gln Gln
450 455 460

Gln Gln Pro Pro Pro Ala Leu Pro Pro Gly Ser Gln Pro Ile Pro Pro
465 470 475 480

Thr Gly Ala Ala Gly Pro Pro Ala Val His Gly Leu Ala Val Ala Pro
485 490 495

Ala Ser Val Val Pro Ala Pro Ala Gly Ser Gly Ala Pro Pro Gly Ser
500 505 510

Leu Gly Pro Ser Glu Gln Ile Gly Gln Ala Gly Ser Thr Ala Gly Pro
515 520 525

Gln Gln Gln Gln Pro Ala Gly Ala Pro Gln Pro Gly Ala Val Pro Pro
530 535 540

Gly Val Pro Pro Pro Gly Pro His Gly Pro Ser Pro Phe Pro Asn Gln
545 550 555 560

Gln Thr Pro Pro Ser Met Met Pro Gly Ala Val Pro Gly Ser Gly His
565 570 575

Pro Gly Val Ala Gly Asn Ala Pro Leu Gly Leu Pro Phe Gly Met Pro
580 585 590

Pro Pro Pro Pro Pro Pro Ala Pro Ser Ile Ile Pro Phe Gly Ser Leu
595 600 605

Ala Asp Ser Ile Ser Ile Asn Leu Pro Ala Pro Pro Asn Leu His Gly
610 615 620

His His His His Leu Pro Phe Ala Pro Gly Thr Leu Pro Pro Pro Asn
625 630 635 640

Leu Pro Val Ser Met Ala Asn Pro Leu His Pro Asn Leu Pro Ala Thr
645 650 655

Thr Thr Met Pro Ser Ser Leu Pro Leu Gly Pro Gly Leu Gly Ser Ala
660 665 670

Ala Ala Gln Ser Pro Ala Ile Val Ala Ala Val Gln Gly Asn Leu Leu
675 680 685

Pro Ser Ala Ser Pro Leu Pro Asp Pro Gly Thr Pro Leu Pro Pro Asp
690 695 700

Pro Thr Ala Pro Ser Pro Gly Thr Val Thr Pro Val Pro Pro Pro Gln
705 710 715 720

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<400> 178
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Ala Ala Asp Thr Val Thr Gln Phe Asp Asn Val Arg Leu Trp Leu Gly
20 25 30

Lys Asn Tyr Lys Lys Tyr Ile Gln Ala Glu Pro Pro Thr Asn Lys Ser
35 40 45

Leu Ser Ser Leu Val Val Gln Leu Leu Gln Phe Gln Glu Glu Val Phe
50 55 60

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

Phe Leu Asp Phe Lys Ala Gly Gly Ser Leu Cys His Ile Leu Ala Ala
85 90 95

Ala Tyr Lys Phe Lys Ser Asp Gln Val Asp Ala Asp Thr Lys Ala Gly
100 105 110

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

Lys Pro Glu Leu Gln Thr Ser Ala Ser Gln Gln Met Leu Asn Phe Pro
130 135 140

Asp Lys Gly Lys Glu Lys Pro Thr Asp Met Gln Asn Phe Gly Leu Arg
145 150 155 160

Thr Asp Met Tyr Thr Lys Lys Asn Val Pro Ser Lys Ser Lys Ala Ala
165 170 175

Ala Ser Ala Thr Arg Glu Trp Thr Glu Gln Glu Thr Leu Leu Leu Leu
180 185 190

Glu Ala Leu Glu Met Tyr Lys Asp Asp Trp Asn Lys Val Ser Glu His
195 200 205

Val Gly Ser Arg Thr Gln Asp Glu Cys Ile Leu His Phe Leu Arg Leu
210 215 220

Pro Ile Glu Asp Pro Tyr Leu Glu Asp Ser Glu Ala Ser Leu Gly Pro
225 230 235 240

Leu Ala Tyr Gln Pro Ile Pro Phe Ser Gln Ser Gly Asn Pro Val Met
245 250 255

Ser Thr Val Ala Phe Leu Ala Ser Val Val Asp Pro Arg Val Ala Ser
260 265 270

Ala Ala Ala Lys Ser Ala Leu Glu Glu Phe Ser Lys Met Lys Glu Glu
275 280 285

Val Pro Thr Ala Leu Val Glu Ala His Val Arg Lys Val Glu Glu Ala
290 295 300

Ala Lys Val Thr Gly Lys Ala Asp Pro Ala Phe Gly Leu Glu Ser Ser
305 310 315 320

Gly Ile Ala Gly Thr Thr Ser Asp Glu Pro Glu Arg Ile Glu Glu Ser
325 330 335

Gly Asn Asp Glu Ala Arg Val Glu Gly Gln Ala Thr Asp Glu Lys Lys
340 345 350

Glu Pro Lys Glu Pro Arg Glu Gly Gly Gly Ala Ile Glu Glu Glu Ala
355 360 365

Lys Glu Lys Thr Ser Glu Ala Pro Lys Lys Asp Glu Glu Lys Gly Lys
370 375 380

Glu Gly Asp Ser Glu Lys Glu Ser Glu Lys Ser Asp Gly Asp Pro Ile
385 390 395 400

Val Asp Pro Glu Lys Glu Lys Glu Pro Lys Glu Gly Gln Glu Glu Val
405 410 415

Leu Lys Glu Val Val Glu Ser Glu Gly Glu Arg Lys Thr Lys Val Glu
420 425 430

Arg Asp Ile Gly Glu Gly Asn Leu Ser Thr Ala Ala Ala Ala Ala Leu
435 440 445

Ala Ala Ala Ala Val Lys Ala Lys His Leu Ala Ala Val Glu Glu Arg
450 455 460

Lys Ile Lys Ser Leu Val Ala Leu Leu Val Glu Thr Gln Met Lys Lys
465 470 475 480

Leu Glu Ile Lys Leu Arg His Phe Glu Glu Leu Glu Thr Ile Met Asp
485 490 495

Arg Glu Arg Glu Ala Leu Glu Tyr Gln Arg Gln Gln Leu Leu Ala Asp
500 505 510

Arg Gln Ala Phe His Met Glu Gln Leu Lys Tyr Ala Glu Met Arg Ala
515 520 525

Arg Gln Gln His Phe Gln Gln Met His Gln Gln Gln Gln Gln Pro Pro
530 535 540

Pro Ala Leu Pro Pro Gly Ser Gln Pro Ile Pro Pro Thr Gly Ala Ala
545 550 555 560

Gly Pro Pro Ala Val His Gly Leu Ala Val Ala Pro Ala Ser Val Val
565 570 575

Pro Ala Pro Ala Gly Ser Gly Ala Pro Pro Gly Ser Leu Gly Pro Ser
580 585 590

Glu Gln Ile Gly Gln Ala Gly Ser Thr Ala Gly Pro Gln Gln Gln Gln
595 600 605

Pro Ala Gly Ala Pro Gln Pro Gly Ala Val Pro Pro Gly Val Pro Pro
610 615 620

Pro Gly Pro His Gly Pro Ser Pro Phe Pro Asn Gln Gln Thr Pro Pro
625 630 635 640

Ser Met Met Pro Gly Ala Val Pro Gly Ser Gly His Pro Gly Val Ala
645 650 655

Gly Asn Ala Pro Leu Gly Leu Pro Phe Gly Met Pro Pro Pro Pro Pro
660 665 670

Pro Pro Ala Pro Ser Ile Ile Pro Phe Gly Ser Leu Ala Asp Ser Ile
675 680 685

Ser Ile Asn Leu Pro Ala Pro Pro Asn Leu His Gly His His His His
690 695 700

Leu Pro Phe Ala Pro Gly Thr Leu Pro Pro Pro Asn Leu Pro Val Ser

705 710 715 720

Met Ala Asn Pro Leu His Pro Asn Leu Pro Ala Thr Thr Thr Met Pro
725 730 735

Ser Ser Leu Pro Leu Gly Pro Gly Leu Gly Ser Ala Ala Ala Gln Ser
740 745 750

Pro Ala Ile Val Ala Ala Val Gln Gly Asn Leu Leu Pro Ser Ala Ser
755 760 765

Pro Leu Pro Asp Pro Gly Thr Pro Leu Pro Pro Asp Pro Thr Ala Pro
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Ser Pro Gly Thr Val Thr Pro Val Pro Pro Pro Gln
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Lys Asn Tyr Lys Lys Tyr Ile Gln Ala Glu Pro Pro Thr Asn Lys Ser
35 40 45

Leu Ser Ser Leu Val Val Gln Leu Leu Gln Phe Gln Glu Glu Val Phe
50 55 60

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

Phe Leu Asp Phe Lys Ala Gly Gly Ser Leu Cys His Ile Leu Ala Ala
85 90 95

Ala Tyr Lys Phe Lys Ser Asp Gln Gly Trp Arg Arg Tyr Asp Phe Gln
100 105 110

Asn Pro Ser Arg Met Asp Arg Asn Val Glu Met Phe Met Thr Ile Glu
115 120 125

Lys Ser Leu Val Gln Asn Asn Cys Leu Ser Arg Pro Asn Ile Phe Leu
130 135 140

Cys Pro Glu Ile Glu Pro Lys Leu Leu Gly Lys Leu Lys Asp Ile Ile
145 150 155 160

Lys Arg His Gln Gly Thr Val Thr Glu Asp Lys Asn Asn Ala Ser His
165 170 175

Val Val Tyr Pro Val Pro Gly Asn Leu Glu Glu Glu Glu Trp Val Arg
180 185 190

Pro Val Met Lys Arg Asp Lys Gln Val Leu Leu His Trp Gly Tyr Tyr
195 200 205

Pro Asp Ser Tyr Asp Thr Trp Ile Pro Ala Ser Glu Ile Glu Ala Ser
210 215 220

Val Glu Asp Ala Pro Thr Pro Glu Lys Pro Arg Lys Val His Ala Lys
225 230 235 240

Trp Ile Leu Asp Thr Asp Thr Phe Asn Glu Trp Met Asn Glu Glu Asp
245 250 255

Tyr Glu Val Asn Asp Asp Lys Asn Pro Val Ser Arg Arg Lys Lys Ile
260 265 270

Ser Ala Lys Thr Leu Thr Asp Glu Val Asn Ser Pro Asp Ser Asp Arg
275 280 285

Arg Asp Lys Lys Gly Gly Asn Tyr Lys Lys Arg Lys Arg Ser Pro Ser
290 295 300

Pro Ser Pro Thr Pro Glu Ala Lys Lys Lys Asn Ala Lys Lys Gly Pro
305 310 315 320

Ser Thr Pro Tyr Thr Lys Ser Lys Arg Gly His Arg Glu Glu Glu Gln
325 330 335

Glu Asp Leu Thr Lys Asp Met Asp Glu Pro Ser Pro Val Pro Asn Val
340 345 350

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

Ser Ala Pro Val Lys Gly Gly Thr Met Thr Asp Leu Asp Glu Gln Glu
370 375 380

Asp Glu Ser Met Glu Thr Thr Gly Lys Asp Glu Asp Glu Asn Ser Thr
385 390 395 400

Gly Asn Lys Gly Glu Gln Thr Lys Asn Pro Asp Leu His Glu Asp Asn
405 410 415

Val Thr Glu Gln Thr His His Ile Ile Ile Pro Ser Tyr Ala Ala Trp
420 425 430

Phe Asp Tyr Asn Ser Val His Ala Ile Glu Arg Arg Ala Leu Pro Glu

435 440 445

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

Tyr Arg Asn Phe Met Ile Asp Thr Tyr Arg Leu Asn Pro Gln Glu Tyr
465 470 475 480

Leu Thr Ser Thr Ala Cys Arg Arg Asn Leu Ala Gly Asp Val Cys Ala
485 490 495

Ile Met Arg Val His Ala Phe Leu Glu Gln Trp Gly Leu Ile Asn Tyr
500 505 510

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

Ser His Phe His Val Leu Ala Asp Thr Pro Ser Gly Leu Val Pro Leu
530 535 540

Gln Pro Lys Thr Pro Gln Gln Thr Ser Ala Ser Gln Gln Met Leu Asn
545 550 555 560

Phe Pro Asp Lys Gly Lys Glu Lys Pro Thr Asp Met Gln Asn Phe Gly
565 570 575

Leu Arg Thr Asp Met Tyr Thr Lys Lys Asn Val Pro Ser Lys Ser Lys
580 585 590

Ala Ala Ala Ser Ala Thr Arg Glu Trp Thr Glu Gln Glu Thr Leu Leu
595 600 605

Leu Leu Glu Ala Leu Glu Met Tyr Lys Asp Asp Trp Asn Lys Val Ser
610 615 620

Glu His Val Gly Ser Arg Thr Gln Asp Glu Cys Ile Leu His Phe Leu
625 630 635 640

Arg Leu Pro Ile Glu Asp Pro Tyr Leu Glu Asp Ser Glu Ala Ser Leu
645 650 655

Gly Pro Leu Ala Tyr Gln Pro Ile Pro Phe Ser Gln Ser Gly Asn Pro
660 665 670

Val Met Ser Thr Val Ala Phe Leu Ala Ser Val Val Asp Pro Arg Val
675 680 685

Ala Ser Ala Ala Ala Lys Ser Ala Leu Glu Glu Phe Ser Lys Met Lys
690 695 700

Glu Glu Val Pro Thr Ala Leu Val Glu Ala His Val Arg Lys Val Glu
705 710 715 720

Glu Ala Ala Lys Val Thr Gly Lys Ala Asp Pro Ala Phe Gly Leu Glu
725 730 735

Ser Ser Gly Ile Ala Gly Thr Thr Ser Asp Glu Pro Glu Arg Ile Glu
740 745 750

Glu Ser Gly Asn Asp Glu Ala Arg Val Glu Gly Gln Ala Thr Asp Glu
755 760 765

Lys Lys Glu Pro Lys Glu Pro Arg Glu Gly Gly Gly Ala Ile Glu Glu
770 775 780

Glu Ala Lys Glu Lys Thr Ser Glu Ala Pro Lys Lys Asp Glu Glu Lys
785 790 795 800

Gly Lys Glu Gly Asp Ser Glu Lys Glu Ser Glu Lys Ser Asp Gly Asp
805 810 815

Pro Ile Val Asp Pro Glu Lys Glu Lys Glu Pro Lys Glu Gly Gln Glu
820 825 830

Glu Val Leu Lys Glu Val Val Glu Ser Glu Gly Glu Arg Lys Thr Lys
835 840 845

Val Glu Arg Asp Ile Gly Glu Gly Asn Leu Ser Thr Ala Ala Ala Ala
850 855 860

Ala Leu Ala Ala Ala Ala Val Lys Ala Lys His Leu Ala Ala Val Glu
865 870 875 880

Glu Arg Lys Ile Lys Ser Leu Val Ala Leu Leu Val Glu Thr Gln Met
885 890 895

Lys Lys Leu Glu Ile Lys Leu Arg His Phe Glu Glu Leu Glu Thr Ile
900 905 910

Met Asp Arg Glu Arg Glu Ala Leu Glu Tyr Gln Arg Gln Gln Leu Leu
915 920 925

Ala Asp Arg Gln Ala Phe His Met Glu Gln Leu Lys Tyr Ala Glu Met
930 935 940

Arg Ala Arg Gln Gln His Phe Gln Gln Met His Gln Gln Gln Gln Gln
945 950 955 960

Pro Pro Pro Ala Leu Pro Pro Gly Ser Gln Pro Ile Pro Pro Thr Gly
965 970 975

Ala Ala Gly Pro Pro Ala Val His Gly Leu Ala Val Ala Pro Ala Ser
980 985 990

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Val Val Pro Ala Pro Ala Gly Ser Gly Ala Pro Pro Gly Ser Leu Gly
995 1000 1005

Pro Ser Glu Gln Ile Gly Gln Ala Gly Ser Thr Ala Gly Pro Gln
1010 1015 1020

Gln Gln Gln Pro Ala Gly Ala Pro Gln Pro Gly Ala Val Pro Pro
1025 1030 1035

Gly Val Pro Pro Pro Gly Pro His Gly Pro Ser Pro Phe Pro Asn
1040 1045 1050

Gln Gln Thr Pro Pro Ser Met Met Pro Gly Ala Val Pro Gly Ser
1055 1060 1065

Gly His Pro Gly Val Ala Gly Asn Ala Pro Leu Gly Leu Pro Phe
1070 1075 1080

Gly Met Pro Pro Pro Pro Pro Pro Pro Ala Pro Ser Ile Ile Pro
1085 1090 1095

Phe Gly Ser Leu Ala Asp Ser Ile Ser Ile Asn Leu Pro Ala Pro
1100 1105 1110

Pro Asn Leu His Gly His His His His Leu Pro Phe Ala Pro Gly
1115 1120 1125

Thr Leu Pro Pro Pro Asn Leu Pro Val Ser Met Ala Asn Pro Leu
1130 1135 1140

His Pro Asn Leu Pro Ala Thr Thr Thr Met Pro Ser Ser Leu Pro
1145 1150 1155

Leu Gly Pro Gly Leu Gly Ser Ala Ala Ala Gln Ser Pro Ala Ile
1160 1165 1170

Val Ala Ala Val Gln Gly Asn Leu Leu Pro Ser Ala Ser Pro Leu
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Pro Asp Pro Gly Thr Pro Leu Pro Pro Asp Pro Thr Ala Pro Ser
1190 1195 1200

Pro Gly Thr Val Thr Pro Val Pro Pro Pro Gln
1205 1210

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<400> 180
Met Ala Val Arg Lys Lys Asp Gly Gly Pro Asn Val Lys Tyr Tyr Glu
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Ala Ala Asp Thr Val Thr Gln Phe Asp Asn Val Arg Leu Trp Leu Gly
            20                  25                  30

Lys Asn Tyr Lys Lys Tyr Ile Gln Ala Glu Pro Pro Thr Asn Lys Ser
        35                  40                  45

Leu Ser Ser Leu Val Val Gln Leu Leu Gln Phe Gln Glu Glu Val Phe
    50                  55                  60

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

Phe Leu Asp Phe Lys Ala Gly Gly Ser Leu Cys His Ile Leu Ala Ala
                85                  90                  95

Ala Tyr Lys Phe Lys Ser Asp Gln Gly Trp Arg Arg Tyr Asp Phe Gln
            100                 105                 110

Asn Pro Ser Arg Met Asp Arg Asn Val Glu Met Phe Met Thr Ile Glu
        115                 120                 125

Lys Ser Leu Val Gln Asn Asn Cys Leu Ser Arg Pro Asn Ile Phe Leu
    130                 135                 140

Cys Pro Glu Ile Glu Pro Lys Leu Leu Gly Lys Leu Lys Asp Ile Ile
145                 150                 155                 160

Lys Arg His Gln Gly Thr Val Thr Glu Asp Lys Asn Asn Ala Ser His
                165                 170                 175

Val Val Tyr Pro Val Pro Gly Asn Leu Glu Glu Glu Glu Trp Val Arg
            180                 185                 190

Pro Val Met Lys Arg Asp Lys Gln Val Leu Leu His Trp Gly Tyr Tyr
        195                 200                 205

Pro Asp Ser Tyr Asp Thr Trp Ile Pro Ala Ser Glu Ile Glu Ala Ser
    210                 215                 220

Val Glu Asp Ala Pro Thr Pro Glu Lys Pro Arg Lys Val His Ala Lys
225                 230                 235                 240

Trp Ile Leu Asp Thr Asp Thr Phe Asn Glu Trp Met Asn Glu Glu Asp
                245                 250                 255

Tyr Glu Val Asn Asp Asp Lys Asn Pro Val Ser Arg Arg Lys Lys Ile
            260                 265                 270

Ser Ala Lys Thr Leu Thr Asp Glu Val Asn Ser Pro Asp Ser Asp Arg
        275                 280                 285
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Arg Asp Lys Lys Gly Gly Asn Tyr Lys Lys Arg Lys Arg Ser Pro Ser
    290                 295                 300

Pro Ser Pro Thr Pro Glu Ala Lys Lys Lys Asn Ala Lys Lys Gly Pro
305                 310                 315                 320

Ser Thr Pro Tyr Thr Lys Ser Lys Arg Gly His Arg Glu Glu Glu Gln
                325                 330                 335

Glu Asp Leu Thr Lys Asp Met Asp Glu Pro Ser Pro Val Pro Asn Val
            340                 345                 350

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

Ser Ala Pro Val Lys Gly Gly Thr Met Thr Asp Leu Asp Glu Gln Glu
    370                 375                 380

Asp Glu Ser Met Glu Thr Thr Gly Lys Asp Glu Asp Glu Asn Ser Thr
385                 390                 395                 400

Gly Asn Lys Gly Glu Gln Thr Lys Asn Pro Asp Leu His Glu Asp Asn
                405                 410                 415

Val Thr Glu Gln Thr His His Ile Ile Ile Pro Ser Tyr Ala Ala Trp
            420                 425                 430

Phe Asp Tyr Asn Ser Val His Ala Ile Glu Arg Arg Ala Leu Pro Glu
        435                 440                 445

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

Tyr Arg Asn Phe Met Ile Asp Thr Tyr Arg Leu Asn Pro Gln Glu Tyr
465                 470                 475                 480

Leu Thr Ser Thr Ala Cys Arg Arg Asn Leu Ala Gly Asp Val Cys Ala
                485                 490                 495

Ile Met Arg Val His Ala Phe Leu Glu Gln Trp Gly Leu Ile Asn Tyr
            500                 505                 510

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

Ser His Phe His Val Leu Ala Asp Thr Pro Ser Gly Leu Val Pro Leu
    530                 535                 540

Gln Pro Lys Thr Pro Gln Gln Thr Ser Ala Ser Gln Gln Met Leu Asn
545                 550                 555                 560
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Phe Pro Asp Lys Gly Lys Glu Lys Pro Thr Asp Met Gln Asn Phe Gly
565 570 575

Leu Arg Thr Asp Met Tyr Thr Lys Lys Asn Val Pro Ser Lys Ser Lys
580 585 590

Ala Ala Ala Ser Ala Thr Arg Glu Trp Thr Glu Gln Glu Thr Leu Leu
595 600 605

Leu Leu Glu Ala Leu Glu Met Tyr Lys Asp Asp Trp Asn Lys Val Ser
610 615 620

Glu His Val Gly Ser Arg Thr Gln Asp Glu Cys Ile Leu His Phe Leu
625 630 635 640

Arg Leu Pro Ile Glu Asp Pro Tyr Leu Glu Asp Ser Glu Ala Ser Leu
645 650 655

Gly Pro Leu Ala Tyr Gln Pro Ile Pro Phe Ser Gln Ser Gly Asn Pro
660 665 670

Val Met Ser Thr Val Ala Phe Leu Ala Ser Val Val Asp Pro Arg Val
675 680 685

Ala Ser Ala Ala Ala Lys Ser Ala Leu Glu Glu Phe Ser Lys Met Lys
690 695 700

Glu Glu Val Pro Thr Ala Leu Val Glu Ala His Val Arg Lys Val Glu
705 710 715 720

Glu Ala Ala Lys Val Thr Gly Lys Ala Asp Pro Ala Phe Gly Leu Glu
725 730 735

Ser Ser Gly Ile Ala Gly Thr Thr Ser Asp Glu Pro Glu Arg Ile Glu
740 745 750

Glu Ser Gly Asn Asp Glu Ala Arg Val Glu Gly Gln Ala Thr Asp Glu
755 760 765

Lys Lys Glu Pro Lys Glu Pro Arg Glu Gly Gly Gly Ala Ile Glu Glu
770 775 780

Glu Ala Lys Glu Lys Thr Ser Glu Ala Pro Lys Lys Asp Glu Glu Lys
785 790 795 800

Gly Lys Glu Gly Asp Ser Glu Lys Glu Ser Glu Lys Ser Asp Gly Asp
805 810 815

Pro Ile Val Asp Pro Glu Lys Glu Lys Glu Pro Lys Glu Gly Gln Glu
820 825 830

Glu Val Leu Lys Glu Val Val Glu Ser Glu Gly Glu Arg Lys Thr Lys

835 840 845

Val Glu Arg Asp Ile Gly Glu Gly Asn Leu Ser Thr Ala Ala Ala Ala
850 855 860

Ala Leu Ala Ala Ala Ala Val Lys Ala Lys His Leu Ala Ala Val Glu
865 870 875 880

Glu Arg Lys Ile Lys Ser Leu Val Ala Leu Leu Val Glu Thr Gln Met
885 890 895

Lys Lys Leu Glu Ile Lys Leu Arg His Phe Glu Glu Leu Glu Thr Ile
900 905 910

Met Asp Arg Glu Arg Glu Ala Leu Glu Tyr Gln Arg Gln Gln Leu Leu
915 920 925

Ala Asp Arg Gln Ala Phe His Met Glu Gln Leu Lys Tyr Ala Glu Met
930 935 940

Arg Ala Arg Gln Gln His Phe Gln Gln Met His Gln Gln Gln Gln Gln
945 950 955 960

Pro Pro Pro Ala Leu Pro Pro Gly Ser Gln Pro Ile Pro Pro Thr Gly
965 970 975

Ala Ala Gly Pro Pro Ala Val His Gly Leu Ala Val Ala Pro Ala Ser
980 985 990

Val Val Pro Ala Pro Ala Gly Ser Gly Ala Pro Pro Gly Ser Leu Gly
995 1000 1005

Pro Ser Glu Gln Ile Gly Gln Ala Gly Ser Thr Ala Gly Pro Gln
1010 1015 1020

Gln Gln Gln Pro Ala Gly Ala Pro Gln Pro Gly Ala Val Pro Pro
1025 1030 1035

Gly Val Pro Pro Pro Gly Pro His Gly Pro Ser Pro Phe Pro Asn
1040 1045 1050

Gln Gln Thr Pro Pro Pro Ala Pro Ser Ile Ile Pro Phe Gly Ser
1055 1060 1065

Leu Ala Asp Ser Ile Ser Ile Asn Leu Pro Ala Pro Pro Asn Leu
1070 1075 1080

His Gly His His His His Leu Pro Phe Ala Pro Gly Thr Leu Pro
1085 1090 1095

Pro Pro Asn Leu Pro Val Ser Met Ala Asn Pro Leu His Pro Asn
1100 1105 1110

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Leu Pro Ala Thr Thr Thr Met Pro Ser Ser Leu Pro Leu Gly Pro
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Gly Leu Gly Ser Ala Ala Ala Gln Ser Pro Ala Ile Val Ala Ala
1130 1135 1140

Val Gln Gly Asn Leu Leu Pro Ser Ala Ser Pro Leu Pro Asp Pro
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Val Thr Pro Val Pro Pro Pro Gln
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Ala Ala Asp Thr Val Thr Gln Phe Asp Asn Val Arg Leu Trp Leu Gly
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Lys Asn Tyr Lys Lys Tyr Ile Gln Ala Glu Pro Pro Thr Asn Lys Ser
35 40 45

Leu Ser Ser Leu Val Val Gln Leu Leu Gln Phe Gln Glu Glu Val Phe
50 55 60

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

Phe Leu Asp Phe Lys Ala Gly Gly Ser Leu Cys His Ile Leu Ala Ala
85 90 95

Ala Tyr Lys Phe Lys Ser Asp Gln Gly Trp Arg Arg Tyr Asp Phe Gln
100 105 110

Asn Pro Ser Arg Met Asp Arg Asn Val Glu Met Phe Met Thr Ile Glu
115 120 125

Lys Ser Leu Val Gln Asn Asn Cys Leu Ser Arg Pro Asn Ile Phe Leu
130 135 140

Cys Pro Glu Ile Glu Pro Lys Leu Leu Gly Lys Leu Lys Asp Ile Ile
145 150 155 160

Lys Arg His Gln Gly Thr Val Thr Glu Asp Lys Asn Asn Ala Ser His

165 170 175

Val Val Tyr Pro Val Pro Gly Asn Leu Glu Glu Glu Glu Trp Val Arg
180 185 190

Pro Val Met Lys Arg Asp Lys Gln Val Leu Leu His Trp Gly Tyr Tyr
195 200 205

Pro Asp Ser Tyr Asp Thr Trp Ile Pro Ala Ser Glu Ile Glu Ala Ser
210 215 220

Val Glu Asp Ala Pro Thr Pro Glu Lys Pro Arg Lys Val His Ala Lys
225 230 235 240

Trp Ile Leu Asp Thr Asp Thr Phe Asn Glu Trp Met Asn Glu Glu Asp
245 250 255

Tyr Glu Val Asn Asp Asp Lys Asn Pro Val Ser Arg Arg Lys Lys Ile
260 265 270

Ser Ala Lys Thr Leu Thr Asp Glu Val Asn Ser Pro Asp Ser Asp Arg
275 280 285

Arg Asp Lys Lys Gly Gly Asn Tyr Lys Lys Arg Lys Arg Ser Pro Ser
290 295 300

Pro Ser Pro Thr Pro Glu Ala Lys Lys Lys Asn Ala Lys Lys Gly Pro
305 310 315 320

Ser Thr Pro Tyr Thr Lys Ser Lys Arg Gly His Arg Glu Glu Glu Gln
325 330 335

Glu Asp Leu Thr Lys Asp Met Asp Glu Pro Ser Pro Val Pro Asn Val
340 345 350

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

Ser Ala Pro Val Lys Gly Gly Thr Met Thr Asp Leu Asp Glu Gln Glu
370 375 380

Asp Glu Ser Met Glu Thr Thr Gly Lys Asp Glu Asp Glu Asn Ser Thr
385 390 395 400

Gly Asn Lys Gly Glu Gln Thr Lys Asn Pro Asp Leu His Glu Asp Asn
405 410 415

Val Thr Glu Gln Thr His His Ile Ile Ile Pro Ser Tyr Ala Ala Trp
420 425 430

Phe Asp Tyr Asn Ser Val His Ala Ile Glu Arg Arg Ala Leu Pro Glu
435 440 445

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

Tyr Arg Asn Phe Met Ile Asp Thr Tyr Arg Leu Asn Pro Gln Glu Tyr
465 470 475 480

Leu Thr Ser Thr Ala Cys Arg Arg Asn Leu Ala Gly Asp Val Cys Ala
485 490 495

Ile Met Arg Val His Ala Phe Leu Glu Gln Trp Gly Leu Ile Asn Tyr
500 505 510

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

Ser His Phe His Val Leu Ala Asp Thr Pro Ser Gly Leu Val Pro Leu
530 535 540

Gln Pro Lys Thr Pro Gln Gln Thr Ser Ala Ser Gln Gln Met Leu Asn
545 550 555 560

Phe Pro Asp Lys Gly Lys Glu Lys Pro Thr Asp Met Gln Asn Phe Gly
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Leu Arg Thr Asp Met Tyr Thr Lys Lys Asn Val Pro Ser Lys Leu Leu
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His Phe Leu Trp Ile Lys Lys Lys Lys Lys Lys
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Lys Asn Tyr Lys Lys Tyr Ile Gln Ala Glu Pro Pro Thr Asn Lys Ser
35 40 45

Leu Ser Ser Leu Val Val Gln Leu Leu Gln Phe Gln Glu Glu Val Phe
50 55 60

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

Phe Leu Asp Phe Lys Ala Gly Gly Ser Leu Cys His Ile Leu Ala Ala

85 90 95

Ala Tyr Lys Phe Lys Ser Asp Gln Gly Trp Arg Arg Tyr Asp Phe Gln
100 105 110

Asn Pro Ser Arg Met Asp Arg Asn Val Glu Met Phe Met Thr Ile Glu
115 120 125

Lys Ser Leu Val Gln Asn Asn Cys Leu Ser Arg Pro Asn Ile Phe Leu
130 135 140

Cys Pro Glu Ile Glu Pro Lys Leu Leu Gly Lys Leu Lys Asp Ile Ile
145 150 155 160

Lys Arg His Gln Gly Thr Val Thr Glu Asp Lys Asn Asn Ala Ser His
165 170 175

Val Val Tyr Pro Val Pro Gly Asn Leu Glu Glu Glu Glu Trp Val Arg
180 185 190

Pro Val Met Lys Arg Asp Lys Gln Val Leu Leu His Trp Gly Tyr Tyr
195 200 205

Pro Asp Ser Tyr Asp Thr Trp Ile Pro Ala Ser Glu Ile Glu Ala Ser
210 215 220

Val Glu Asp Ala Pro Thr Pro Glu Lys Pro Arg Lys Val His Ala Lys
225 230 235 240

Trp Ile Leu Asp Thr Asp Thr Phe Asn Glu Trp Met Asn Glu Glu Asp
245 250 255

Tyr Glu Val Asn Asp Asp Lys Asn Pro Val Ser Arg Arg Lys Lys Ile
260 265 270

Ser Ala Lys Thr Leu Thr Asp Glu Val Asn Ser Pro Asp Ser Asp Arg
275 280 285

Arg Asp Lys Lys Gly Gly Asn Tyr Lys Lys Arg Lys Arg Ser Pro Ser
290 295 300

Pro Ser Pro Thr Pro Glu Ala Lys Lys Lys Asn Ala Lys Lys Gly Pro
305 310 315 320

Ser Thr Pro Tyr Thr Lys Ser Lys Arg Gly His Arg Glu Glu Glu Gln
325 330 335

Glu Asp Leu Thr Lys Asp Met Asp Glu Pro Ser Pro Val Pro Asn Val
340 345 350

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

Ser Ala Pro Val Lys Gly Gly Thr Met Thr Asp Leu Asp Glu Gln Glu
370 375 380

Asp Glu Ser Met Glu Thr Thr Gly Lys Asp Glu Asp Glu Asn Ser Thr
385 390 395 400

Gly Asn Lys Gly Glu Gln Thr Lys Asn Pro Asp Leu His Glu Asp Asn
405 410 415

Val Thr Glu Gln Thr His His Ile Ile Ile Pro Ser Tyr Ala Ala Trp
420 425 430

Phe Asp Tyr Asn Ser Val His Ala Ile Glu Arg Arg Ala Leu Pro Glu
435 440 445

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

Tyr Arg Asn Phe Met Ile Asp Thr Tyr Arg Leu Asn Pro Gln Glu Tyr
465 470 475 480

Leu Thr Ser Thr Ala Cys Arg Arg Asn Leu Ala Gly Asp Val Cys Ala
485 490 495

Ile Met Arg Val His Ala Phe Leu Glu Gln Trp Gly Leu Ile Asn Tyr
500 505 510

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

Ser His Phe His Val Leu Ala Asp Thr Pro Ser Gly Leu Val Pro Leu
530 535 540

Gln Pro Lys Thr Pro Gln Gln Thr Ser Ala Ser Gln Gln Met Leu Asn
545 550 555 560

Phe Pro Asp Lys Gly Lys Glu Lys Pro Thr Asp Met Gln Asn Phe Gly
565 570 575

Leu Arg Thr Asp Met Tyr Thr Lys Lys Asn Val Pro Ser Lys Ser Lys
580 585 590

Ala Ala Ala Ser Ala Thr Arg Glu Trp Thr Glu Gln Glu Thr Leu Leu
595 600 605

Leu Leu Glu Ala Leu Glu Met Tyr Lys Asp Asp Trp Asn Lys Val Ser
610 615 620

Glu His Val Gly Ser Arg Thr Gln Asp Glu Cys Ile Leu His Phe Leu
625 630 635 640

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Arg Leu Pro Ile Glu Asp Pro Tyr Leu Glu Asp Ser Glu Ala Ser Leu
645 650 655

Gly Pro Leu Ala Tyr Gln Pro Ile Pro Phe Ser Gln Ser Gly Asn Pro
660 665 670

Val Met Ser Thr Val Ala Phe Leu Ala Ser Val Val Asp Pro Arg Val
675 680 685

Ala Ser Ala Ala Ala Lys Ser Ala Leu Glu Glu Phe Ser Lys Met Lys
690 695 700

Glu Glu Val Pro Thr Ala Leu Val Glu Ala His Val Arg Lys Val Glu
705 710 715 720

Glu Ala Ala Lys Val Thr Gly Lys Ala Asp Pro Ala Phe Gly Leu Glu
725 730 735

Ser Ser Gly Ile Ala Gly Thr Thr Ser Asp Glu Pro Glu Arg Ile Glu
740 745 750

Glu Ser Gly Asn Asp Glu Ala Arg Val Glu Gly Gln Ala Thr Asp Glu
755 760 765

Lys Lys Glu Pro Lys Glu Pro Arg Glu Gly Gly Gly Ala Ile Glu Glu
770 775 780

Glu Ala Lys Glu Lys Thr Ser Glu Ala Pro Lys Lys Asp Glu Glu Lys
785 790 795 800

Gly Lys Glu Gly Asp Ser Glu Lys Glu Ser Glu Lys Ser Asp Gly Asp
805 810 815

Pro Ile Val Asp Pro Glu Lys Glu Lys Glu Pro Lys Glu Gly Gln Glu
820 825 830

Glu Val Leu Lys Glu Val Val Glu Ser Glu Gly Glu Arg Lys Thr Lys
835 840 845

Val Glu Arg Asp Ile Gly Glu Gly Asn Leu Ser Thr Ala Ala Ala Ala
850 855 860

Ala Leu Ala Ala Ala Ala Val Lys Ala Lys His Leu Ala Ala Val Glu
865 870 875 880

Glu Arg Lys Ile Lys Ser Leu Val Ala Leu Leu Val Glu Thr Gln Met
885 890 895

Lys Lys Leu Glu Ile Lys Leu Arg His Phe Glu Glu Leu Glu Thr Ile
900 905 910

Met Asp Arg Glu Arg Glu Ala Leu Glu Tyr Gln Arg Gln Gln Leu Leu
915 920 925

Ala Asp Arg Gln Ala Phe His Met Glu Gln Leu Lys Tyr Ala Glu Met
930 935 940

Arg Ala Arg Gln Gln His Phe Gln Gln Met His Gln Gln Gln Gln Gln
945 950 955 960

Pro Pro Pro Ala Leu Pro Pro Gly Ser Gln Pro Ile Pro Pro Thr Gly
965 970 975

Ala Ala Gly Pro Pro Ala Val His Gly Leu Ala Val Ala Pro Ala Ser
980 985 990

Val Val Pro Ala Pro Ala Gly Ser Gly Ala Pro Pro Gly Ser Leu Gly
995 1000 1005

Pro Ser Glu Gln Ile Gly Gln Ala Gly Ser Thr Ala Gly Pro Gln
1010 1015 1020

Gln Gln Gln Pro Ala Gly Ala Pro Gln Pro Gly Ala Val Pro Pro
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Gly Val Pro Pro Pro Gly Pro His Gly Pro Ser Pro Phe Pro Asn
1040 1045 1050

Gln Gln Thr Pro Pro Ser Met Met Pro Gly Ala Val Pro Gly Ser
1055 1060 1065

Gly His Pro Gly Val Ala Gly Asn Ala Pro Leu Gly Leu Pro Phe
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Gly Met Pro Pro Pro Pro Pro Pro Pro Asp Pro Thr Ala Pro Ser
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Pro Gly Thr Val Thr Pro Val Pro Pro Pro Gln
1100 1105

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Ala Ala Asp Thr Val Thr Gln Phe Asp Asn Val Arg Leu Trp Leu Gly
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Lys Asn Tyr Lys Lys Tyr Ile Gln Ala Glu Pro Pro Thr Asn Lys Ser
35 40 45

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Leu Ser Ser Leu Val Val Gln Leu Leu Gln Phe Gln Glu Glu Val Phe
    50                  55                  60

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

Phe Leu Asp Phe Lys Ala Gly Gly Ser Leu Cys His Ile Leu Ala Ala
                85                  90                  95

Ala Tyr Lys Phe Lys Ser Asp Gln Gly Trp Arg Arg Tyr Asp Phe Gln
            100                 105                 110

Asn Pro Ser Arg Met Asp Arg Asn Val Glu Met Phe Met Thr Ile Glu
        115                 120                 125

Lys Ser Leu Val Gln Asn Asn Cys Leu Ser Arg Pro Asn Ile Phe Leu
    130                 135                 140

Cys Pro Glu Ile Glu Pro Lys Leu Leu Gly Lys Leu Lys Asp Ile Ile
145                 150                 155                 160

Lys Arg His Gln Gly Thr Val Thr Glu Asp Lys Asn Asn Ala Ser His
                165                 170                 175

Val Val Tyr Pro Val Pro Gly Asn Leu Glu Glu Glu Glu Trp Val Arg
            180                 185                 190

Pro Val Met Lys Arg Asp Lys Gln Val Leu Leu His Trp Gly Tyr Tyr
        195                 200                 205

Pro Asp Ser Tyr Asp Thr Trp Ile Pro Ala Ser Glu Ile Glu Ala Ser
    210                 215                 220

Val Glu Asp Ala Pro Thr Pro Glu Lys Pro Arg Lys Val His Ala Lys
225                 230                 235                 240

Trp Ile Leu Asp Thr Asp Thr Phe Asn Glu Trp Met Asn Glu Glu Asp
                245                 250                 255

Tyr Glu Val Asn Asp Asp Lys Asn Pro Val Ser Arg Arg Lys Lys Ile
            260                 265                 270

Ser Ala Lys Thr Leu Thr Asp Glu Val Asn Ser Pro Asp Ser Asp Arg
        275                 280                 285

Arg Asp Lys Lys Gly Gly Asn Tyr Lys Lys Arg Lys Arg Ser Pro Ser
    290                 295                 300

Pro Ser Pro Thr Pro Glu Ala Lys Lys Lys Asn Ala Lys Lys Gly Pro
305                 310                 315                 320
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Ser Thr Pro Tyr Thr Lys Ser Lys Arg Gly His Arg Glu Glu Glu Gln
325 330 335

Glu Asp Leu Thr Lys Asp Met Asp Glu Pro Ser Pro Val Pro Asn Val
340 345 350

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

Ser Ala Pro Val Lys Gly Gly Thr Met Thr Asp Leu Asp Glu Gln Glu
370 375 380

Asp Glu Ser Met Glu Thr Thr Gly Lys Asp Glu Asp Glu Asn Ser Thr
385 390 395 400

Gly Asn Lys Gly Glu Gln Thr Lys Asn Pro Asp Leu His Glu Asp Asn
405 410 415

Val Thr Glu Gln Thr His His Ile Ile Ile Pro Ser Tyr Ala Ala Trp
420 425 430

Phe Asp Tyr Asn Ser Val His Ala Ile Glu Arg Arg Ala Leu Pro Glu
435 440 445

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

Tyr Arg Asn Phe Met Ile Asp Thr Tyr Arg Leu Asn Pro Gln Glu Tyr
465 470 475 480

Leu Thr Ser Thr Ala Cys Arg Arg Asn Leu Ala Gly Asp Val Cys Ala
485 490 495

Ile Met Arg Val His Ala Phe Leu Glu Gln Trp Gly Leu Ile Asn Tyr
500 505 510

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

Ser His Phe His Val Leu Ala Asp Thr Pro Ser Gly Leu Val Pro Leu
530 535 540

Gln Pro Lys Thr Pro Gln Gln Thr Ser Ala Ser Gln Gln Met Leu Asn
545 550 555 560

Phe Pro Asp Lys Gly Lys Glu Lys Pro Thr Asp Met Gln Asn Phe Gly
565 570 575

Leu Arg Thr Asp Met Tyr Thr Lys Lys Asn Val Pro Ser Lys Ser Lys
580 585 590

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

595 600 605

Leu Leu Glu Ala Leu Glu Met Tyr Lys Asp Asp Trp Asn Lys Val Ser
610 615 620

Glu His Val Gly Ser Arg Thr Gln Asp Glu Cys Ile Leu His Phe Leu
625 630 635 640

Arg Leu Pro Ile Glu Asp Pro Tyr Leu Glu Asp Ser Glu Ala Ser Leu
645 650 655

Gly Pro Leu Ala Tyr Gln Pro Ile Pro Phe Ser Gln Ser Gly Asn Pro
660 665 670

Val Met Ser Thr Val Ala Phe Leu Ala Ser Val Val Asp Pro Arg Val
675 680 685

Ala Ser Ala Ala Ala Lys Ser Ala Leu Glu Glu Phe Ser Lys Met Lys
690 695 700

Glu Glu Val Pro Thr Ala Leu Val Glu Ala His Val Arg Lys Val Glu
705 710 715 720

Glu Ala Ala Lys Val Thr Gly Lys Ala Asp Pro Ala Phe Gly Leu Glu
725 730 735

Ser Ser Gly Ile Ala Gly Thr Thr Ser Asp Glu Pro Glu Arg Ile Glu
740 745 750

Glu Ser Gly Asn Asp Glu Ala Arg Val Glu Gly Gln Ala Thr Asp Glu
755 760 765

Lys Lys Glu Pro Lys Glu Pro Arg Glu Gly Gly Gly Ala Ile Glu Glu
770 775 780

Glu Ala Lys Glu Lys Thr Ser Glu Ala Pro Lys Lys Asp Glu Glu Lys
785 790 795 800

Gly Lys Glu Gly Asp Ser Glu Lys Glu Ser Glu Lys Ser Asp Gly Asp
805 810 815

Pro Ile Val Asp Pro Glu Lys Glu Lys Glu Pro Lys Glu Gly Gln Glu
820 825 830

Glu Val Leu Lys Glu Val Val Glu Ser Glu Gly Glu Arg Lys Thr Lys
835 840 845

Val Glu Arg Asp Ile Gly Glu Gly Asn Leu Ser Thr Ala Ala Ala Ala
850 855 860

Ala Leu Ala Ala Ala Ala Val Lys Ala Lys His Leu Ala Ala Val Glu
865 870 875 880

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Glu Arg Lys Ile Lys Ser Leu Val Ala Leu Leu Val Glu Thr Gln Met
885 890 895

Lys Lys Leu Glu Ile Lys Leu Arg His Phe Glu Glu Leu Glu Thr Ile
900 905 910

Met Asp Arg Glu Arg Glu Ala Leu Glu Tyr Gln Arg Gln Gln Leu Leu
915 920 925

Ala Asp Arg Gln Ala Phe His Met Glu Gln Leu Lys Tyr Ala Glu Met
930 935 940

Arg Ala Arg Gln Gln His Phe Gln Gln Met His Gln Gln Gln Gln Gln
945 950 955 960

Pro Pro Pro Ala Leu Pro Pro Gly Ser Gln Pro Ile Pro Pro Thr Gly
965 970 975

Ala Ala Gly Pro Pro Ala Val His Gly Leu Ala Val Ala Pro Ala Ser
980 985 990

Val Val Pro Ala Pro Ala Gly Ser Gly Ala Pro Pro Gly Ser Leu Gly
995 1000 1005

Pro Ser Glu Gln Ile Gly Gln Ala Gly Ser Thr Ala Gly Pro Gln
1010 1015 1020

Gln Gln Gln Pro Ala Gly Ala Pro Gln Pro Gly Ala Val Pro Pro
1025 1030 1035

Gly Val Pro Pro Pro Gly Pro His Gly Pro Ser Pro Phe Pro Asn
1040 1045 1050

Gln Gln Thr Pro Pro Ser Met Met Pro Gly Ala Val Pro Gly Ser
1055 1060 1065

Gly His Pro Gly Val Ala Gly Asn Ala Pro Leu Gly Leu Pro Phe
1070 1075 1080

Gly Met Pro Pro Pro Pro Asn Leu His Gly His His His His Leu
1085 1090 1095

Pro Phe Ala Pro Gly Thr Leu Pro Pro Pro Asn Leu Pro Val Ser
1100 1105 1110

Met Ala Asn Pro Leu His Pro Asn Leu Pro Ala Thr Thr Thr Met
1115 1120 1125

Pro Ser Ser Leu Pro Leu Gly Pro Gly Leu Gly Ser Ala Ala Ala
1130 1135 1140

Gln Ser Pro Ala Ile Val Ala Ala Val Gln Gly Asn Leu Leu Pro
1145 1150 1155

Ser Ala Ser Pro Leu Pro Asp Pro Gly Thr Pro Leu Pro Pro Asp
1160 1165 1170

Pro Thr Ala Pro Ser Pro Gly Thr Val Thr Pro Val Pro Pro Pro
1175 1180 1185

Gln

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<211> 1214
<212> PRT
<213> Homo sapiens

<400> 184
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Ala Ala Asp Thr Val Thr Gln Phe Asp Asn Val Arg Leu Trp Leu Gly
20 25 30

Lys Asn Tyr Lys Lys Tyr Ile Gln Ala Glu Pro Pro Thr Asn Lys Ser
35 40 45

Leu Ser Ser Leu Val Val Gln Leu Leu Gln Phe Gln Glu Glu Val Phe
50 55 60

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

Phe Leu Asp Phe Lys Ala Gly Gly Ser Leu Cys His Ile Leu Ala Ala
85 90 95

Ala Tyr Lys Phe Lys Ser Asp Gln Gly Trp Arg Arg Tyr Asp Phe Gln
100 105 110

Asn Pro Ser Arg Met Asp Arg Asn Val Glu Met Phe Met Thr Ile Glu
115 120 125

Lys Ser Leu Val Gln Asn Asn Cys Leu Ser Arg Pro Asn Ile Phe Leu
130 135 140

Cys Pro Glu Ile Glu Pro Lys Leu Leu Gly Lys Leu Lys Asp Ile Ile
145 150 155 160

Lys Arg His Gln Gly Thr Val Thr Glu Asp Lys Asn Asn Ala Ser His
165 170 175

Val Val Tyr Pro Val Pro Gly Asn Leu Glu Glu Glu Glu Trp Val Arg
180 185 190

Pro Val Met Lys Arg Asp Lys Gln Val Leu Leu His Trp Gly Tyr Tyr
195 200 205

Pro Asp Ser Tyr Asp Thr Trp Ile Pro Ala Ser Glu Ile Glu Ala Ser
210 215 220

Val Glu Asp Ala Pro Thr Pro Glu Lys Pro Arg Lys Val His Ala Lys
225 230 235 240

Trp Ile Leu Asp Thr Asp Thr Phe Asn Glu Trp Met Asn Glu Glu Asp
245 250 255

Tyr Glu Val Asn Asp Asp Lys Asn Pro Val Ser Arg Arg Lys Lys Ile
260 265 270

Ser Ala Lys Thr Leu Thr Asp Glu Val Asn Ser Pro Asp Ser Asp Arg
275 280 285

Arg Asp Lys Lys Gly Gly Asn Tyr Lys Lys Arg Lys Arg Ser Pro Ser
290 295 300

Pro Ser Pro Thr Pro Glu Ala Lys Lys Lys Asn Ala Lys Lys Gly Pro
305 310 315 320

Ser Thr Pro Tyr Thr Lys Ser Lys Arg Gly His Arg Glu Glu Glu Gln
325 330 335

Glu Asp Leu Thr Lys Asp Met Asp Glu Pro Ser Pro Val Pro Asn Val
340 345 350

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

Ser Ala Pro Val Lys Gly Gly Thr Met Thr Asp Leu Asp Glu Gln Glu
370 375 380

Asp Glu Ser Met Glu Thr Thr Gly Lys Asp Glu Asp Glu Asn Ser Thr
385 390 395 400

Gly Asn Lys Gly Glu Gln Thr Lys Asn Pro Asp Leu His Glu Asp Asn
405 410 415

Val Thr Glu Gln Thr His His Ile Ile Ile Pro Ser Tyr Ala Ala Trp
420 425 430

Phe Asp Tyr Asn Ser Val His Ala Ile Glu Arg Arg Ala Leu Pro Glu
435 440 445

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

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Tyr Arg Asn Phe Met Ile Asp Thr Tyr Arg Leu Asn Pro Gln Glu Tyr
465 470 475 480

Leu Thr Ser Thr Ala Cys Arg Arg Asn Leu Ala Gly Asp Val Cys Ala
485 490 495

Ile Met Arg Val His Ala Phe Leu Glu Gln Trp Gly Leu Ile Asn Tyr
500 505 510

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

Ser His Phe His Val Leu Ala Asp Thr Pro Ser Gly Leu Val Pro Leu
530 535 540

Gln Pro Lys Thr Pro Gln Gln Thr Ser Ala Ser Gln Gln Met Leu Asn
545 550 555 560

Phe Pro Asp Lys Gly Lys Glu Lys Pro Thr Asp Met Gln Asn Phe Gly
565 570 575

Leu Arg Thr Asp Met Tyr Thr Lys Lys Asn Val Pro Ser Lys Ser Lys
580 585 590

Ala Ala Ala Ser Ala Thr Arg Glu Trp Thr Glu Gln Glu Thr Leu Leu
595 600 605

Leu Leu Glu Ala Leu Glu Met Tyr Lys Asp Asp Trp Asn Lys Val Ser
610 615 620

Glu His Val Gly Ser Arg Thr Gln Asp Glu Cys Ile Leu His Phe Leu
625 630 635 640

Arg Leu Pro Ile Glu Asp Pro Tyr Leu Glu Asp Ser Glu Ala Ser Leu
645 650 655

Gly Pro Leu Ala Tyr Gln Pro Ile Pro Phe Ser Gln Ser Gly Asn Pro
660 665 670

Val Met Ser Thr Val Ala Phe Leu Ala Ser Val Val Asp Pro Arg Val
675 680 685

Ala Ser Ala Ala Ala Lys Ser Ala Leu Glu Glu Phe Ser Lys Met Lys
690 695 700

Glu Glu Val Pro Thr Ala Leu Val Glu Ala His Val Arg Lys Val Glu
705 710 715 720

Glu Ala Ala Lys Val Thr Gly Lys Ala Asp Pro Ala Phe Gly Leu Glu
725 730 735

Ser Ser Gly Ile Ala Gly Thr Thr Ser Asp Glu Pro Glu Arg Ile Glu
740 745 750

Glu Ser Gly Asn Asp Glu Ala Arg Val Glu Gly Gln Ala Thr Asp Glu
755 760 765

Lys Lys Glu Pro Lys Glu Pro Arg Glu Gly Gly Gly Ala Ile Glu Glu
770 775 780

Glu Ala Lys Glu Lys Thr Ser Glu Ala Pro Lys Lys Asp Glu Glu Lys
785 790 795 800

Gly Lys Glu Gly Asp Ser Glu Lys Glu Ser Glu Lys Ser Asp Gly Asp
805 810 815

Pro Ile Val Asp Pro Glu Lys Glu Lys Glu Pro Lys Glu Gly Gln Glu
820 825 830

Glu Val Leu Lys Glu Val Val Glu Ser Glu Gly Glu Arg Lys Thr Lys
835 840 845

Val Glu Arg Asp Ile Gly Glu Gly Asn Leu Ser Thr Ala Ala Ala Ala
850 855 860

Ala Leu Ala Ala Ala Ala Val Lys Ala Lys His Leu Ala Ala Val Glu
865 870 875 880

Glu Arg Lys Ile Lys Ser Leu Val Ala Leu Leu Val Glu Thr Gln Met
885 890 895

Lys Lys Leu Glu Ile Lys Leu Arg His Phe Glu Glu Leu Glu Thr Ile
900 905 910

Met Asp Arg Glu Arg Glu Ala Leu Glu Tyr Gln Arg Gln Gln Leu Leu
915 920 925

Ala Asp Arg Gln Ala Phe His Met Glu Gln Leu Lys Tyr Ala Glu Met
930 935 940

Arg Ala Arg Gln Gln His Phe Gln Gln Met His Gln Gln Gln Gln Gln
945 950 955 960

Pro Pro Pro Ala Leu Pro Pro Gly Ser Gln Pro Ile Pro Pro Thr Gly
965 970 975

Ala Ala Gly Pro Pro Ala Val His Gly Leu Ala Val Ala Pro Ala Ser
980 985 990

Val Val Pro Ala Pro Ala Gly Ser Gly Ala Pro Pro Gly Ser Leu Gly
995 1000 1005

Pro Ser Glu Gln Ile Gly Gln Ala Gly Ser Thr Ala Gly Pro Gln

1010 1015 1020

Gln Gln Gln Pro Ala Gly Ala Pro Gln Pro Gly Ala Val Pro Pro
1025 1030 1035

Gly Val Pro Pro Pro Gly Pro His Gly Pro Ser Pro Phe Pro Asn
1040 1045 1050

Gln Gln Thr Pro Pro Ser Met Met Pro Gly Ala Val Pro Gly Ser
1055 1060 1065

Gly His Pro Gly Val Ala Gly Asn Ala Pro Leu Gly Leu Pro Phe
1070 1075 1080

Gly Met Pro Pro Pro Pro Pro Pro Pro Ala Pro Ser Ile Ile Pro
1085 1090 1095

Phe Gly Ser Leu Ala Asp Ser Ile Ser Ile Asn Leu Pro Ala Pro
1100 1105 1110

Pro Asn Leu His Gly His His His His Leu Pro Phe Ala Pro Gly
1115 1120 1125

Thr Leu Pro Pro Pro Asn Leu Pro Val Ser Met Ala Asn Pro Leu
1130 1135 1140

His Pro Asn Leu Pro Ala Thr Thr Thr Met Pro Ser Ser Leu Pro
1145 1150 1155

Leu Gly Pro Gly Leu Gly Ser Ala Ala Ala Gln Ser Pro Ala Ile
1160 1165 1170

Val Ala Ala Val Gln Gly Asn Leu Leu Pro Ser Ala Ser Pro Leu
1175 1180 1185

Pro Asp Pro Gly Thr Pro Leu Pro Pro Asp Pro Thr Ala Pro Ser
1190 1195 1200

Pro Gly Thr Val Thr Pro Val Pro Pro Pro Gln
1205 1210

<210> 185
<211> 453
<212> PRT
<213> Homo sapiens

<400> 185
Met Leu Pro Gly Ser Arg Met Thr Pro Gln Gly Pro Ser Met Gly Pro
1 5 10 15

Pro Gly Tyr Gly Gly Asn Pro Ser Val Arg Pro Gly Leu Ala Gln Ser
20 25 30

Gly Met Asp Gln Ser Arg Lys Arg Pro Ala Pro Gln Gln Ile Gln Gln
35 40 45

Val Gln Gln Gln Ala Val Gln Asn Arg Asn His Asn Ala Lys Lys Lys
50 55 60

Lys Met Ala Asp Lys Ile Leu Pro Gln Arg Ile Arg Glu Leu Val Pro
65 70 75 80

Glu Ser Gln Ala Tyr Met Asp Leu Leu Ala Phe Glu Arg Lys Leu Asp
85 90 95

Gln Thr Ile Met Arg Lys Arg Leu Asp Ile Gln Glu Ala Leu Lys Arg
100 105 110

Pro Ile Lys Gln Lys Arg Lys Leu Arg Ile Phe Ile Ser Asn Thr Phe
115 120 125

Asn Pro Ala Lys Ser Asp Ala Glu Asp Gly Glu Gly Thr Val Ala Ser
130 135 140

Trp Glu Leu Arg Val Glu Gly Arg Leu Leu Glu Asp Ser Ala Leu Ser
145 150 155 160

Lys Tyr Asp Ala Thr Lys Gln Lys Arg Lys Phe Ser Ser Phe Phe Lys
165 170 175

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

Leu Val Glu Trp His Arg Thr Ala Thr Thr Gln Glu Thr Asp Gly Phe
195 200 205

Gln Val Lys Arg Pro Gly Asp Val Asn Val Arg Cys Thr Val Leu Leu
210 215 220

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

Arg Leu Leu Gly Ile His Thr Gln Thr Arg Pro Val Ile Ile Gln Ala
245 250 255

Leu Trp Gln Tyr Ile Lys Thr His Lys Leu Gln Asp Pro His Glu Arg
260 265 270

Glu Phe Val Ile Cys Asp Lys Tyr Leu Gln Gln Ile Phe Glu Ser Gln
275 280 285

Arg Met Lys Phe Ser Glu Ile Pro Gln Arg Leu His Ala Leu Leu Met
290 295 300

Pro Pro Glu Pro Ile Ile Ile Asn His Val Ile Ser Val Asp Pro Asn

305 310 315 320

Asp Gln Lys Lys Thr Ala Cys Tyr Asp Ile Asp Val Glu Val Asp Asp
325 330 335

Thr Leu Lys Thr Gln Met Asn Ser Phe Leu Leu Ser Thr Ala Ser Gln
340 345 350

Gln Glu Ile Ala Thr Leu Asp Asn Lys Ile His Glu Thr Ile Glu Thr
355 360 365

Ile Asn Gln Leu Lys Thr Gln Arg Glu Phe Met Leu Ser Phe Ala Arg
370 375 380

Asp Pro Gln Gly Phe Ile Asn Asp Trp Leu Gln Ser Gln Cys Arg Asp
385 390 395 400

Leu Lys Thr Met Thr Asp Val Val Gly Asn Pro Glu Glu Glu Arg Arg
405 410 415

Ala Glu Phe Tyr Phe Gln Pro Trp Ala Gln Glu Ala Val Cys Arg Tyr
420 425 430

Phe Tyr Ser Lys Val Gln Gln Arg Arg Gln Glu Leu Glu Gln Ala Leu
435 440 445

Gly Ile Arg Asn Thr
450

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<211> 435
<212> PRT
<213> Homo sapiens

<400> 186
Met Ala Ala Arg Ala Gly Phe Gln Ser Val Ala Pro Ser Gly Gly Ala
1 5 10 15

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

Thr Pro Gly Pro Pro Val Arg Met Gly Pro Ala Pro Gly Gln Gly Leu
35 40 45

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

Pro Gly Ser Arg Met Thr Pro Gln Gly Pro Ser Met Gly Pro Pro Gly
65 70 75 80

Tyr Gly Gly Asn Pro Ser Val Arg Pro Gly Leu Ala Gln Ser Gly Met
85 90 95

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Asp Gln Ser Arg Lys Arg Pro Ala Pro Gln Gln Ile Gln Gln Val Gln
            100                 105                 110

Gln Gln Ala Val Gln Asn Arg Asn His Asn Ala Lys Lys Lys Lys Met
        115                 120                 125

Ala Asp Lys Ile Leu Pro Gln Arg Ile Arg Glu Leu Val Pro Glu Ser
    130                 135                 140

Gln Ala Tyr Met Asp Leu Leu Ala Phe Glu Arg Lys Leu Asp Gln Thr
145                 150                 155                 160

Ile Met Arg Lys Arg Leu Asp Ile Gln Glu Ala Leu Lys Arg Pro Ile
                165                 170                 175

Lys Trp His Arg Thr Ala Thr Thr Gln Glu Thr Asp Gly Phe Gln Val
            180                 185                 190

Lys Arg Pro Gly Asp Val Asn Val Arg Cys Thr Val Leu Leu Met Leu
        195                 200                 205

Asp Tyr Gln Pro Pro Gln Phe Lys Leu Asp Pro Arg Leu Ala Arg Leu
    210                 215                 220

Leu Gly Ile His Thr Gln Thr Arg Pro Val Ile Ile Gln Ala Leu Trp
225                 230                 235                 240

Gln Tyr Ile Lys Thr His Lys Leu Gln Asp Pro His Glu Arg Glu Phe
                245                 250                 255

Val Ile Cys Asp Lys Tyr Leu Gln Gln Ile Phe Glu Ser Gln Arg Met
            260                 265                 270

Lys Phe Ser Glu Ile Pro Gln Arg Leu His Ala Leu Leu Met Pro Pro
        275                 280                 285

Glu Pro Ile Ile Ile Asn His Val Ile Ser Val Asp Pro Asn Asp Gln
    290                 295                 300

Lys Lys Thr Ala Cys Tyr Asp Ile Asp Val Glu Val Asp Asp Thr Leu
305                 310                 315                 320

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

Ile Ala Thr Leu Asp Asn Lys Ile His Glu Thr Ile Glu Thr Ile Asn
            340                 345                 350

Gln Leu Lys Thr Gln Arg Glu Phe Met Leu Ser Phe Ala Arg Asp Pro
        355                 360                 365

Gln Gly Phe Ile Asn Asp Trp Leu Gln Ser Gln Cys Arg Asp Leu Lys
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370 375 380

Thr Met Thr Asp Val Val Gly Asn Pro Glu Glu Glu Arg Arg Ala Glu
385 390 395 400

Phe Tyr Phe Gln Pro Trp Ala Gln Glu Ala Val Cys Arg Tyr Phe Tyr
405 410 415

Ser Lys Val Gln Gln Arg Arg Gln Glu Leu Glu Gln Ala Leu Gly Ile
420 425 430

Arg Asn Thr
435

<210> 187
<211> 474
<212> PRT
<213> Homo sapiens

<400> 187
Met Ala Ala Arg Ala Gly Phe Gln Ser Val Ala Pro Ser Gly Gly Ala
1 5 10 15

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

Thr Pro Gly Pro Pro Val Arg Met Gly Pro Ala Pro Gly Gln Gly Leu
35 40 45

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

Pro Gly Ser Arg Met Thr Pro Gln Gly Pro Ser Met Gly Pro Pro Gly
65 70 75 80

Tyr Gly Gly Asn Pro Ser Val Arg Pro Gly Leu Ala Gln Ser Gly Met
85 90 95

Asp Gln Ser Arg Lys Arg Pro Ala Pro Gln Gln Ile Gln Gln Val Gln
100 105 110

Gln Gln Ala Val Gln Asn Arg Asn His Asn Ala Lys Lys Lys Lys Met
115 120 125

Ala Asp Lys Ile Leu Pro Gln Arg Ile Arg Glu Leu Val Pro Glu Ser
130 135 140

Gln Ala Tyr Met Asp Leu Leu Ala Phe Glu Arg Lys Leu Asp Gln Thr
145 150 155 160

Ile Met Arg Lys Arg Leu Asp Ile Gln Glu Ala Leu Lys Arg Pro Ile
165 170 175

Lys Ser Ala Leu Ser Lys Tyr Asp Ala Thr Lys Gln Lys Arg Lys Phe
180 185 190

Ser Ser Phe Phe Lys Ser Leu Val Ile Glu Leu Asp Lys Asp Leu Tyr
195 200 205

Gly Pro Asp Asn His Leu Val Glu Trp His Arg Thr Ala Thr Thr Gln
210 215 220

Glu Thr Asp Gly Phe Gln Val Lys Arg Pro Gly Asp Val Asn Val Arg
225 230 235 240

Cys Thr Val Leu Leu Met Leu Asp Tyr Gln Pro Pro Gln Phe Lys Leu
245 250 255

Asp Pro Arg Leu Ala Arg Leu Leu Gly Ile His Thr Gln Thr Arg Pro
260 265 270

Val Ile Ile Gln Ala Leu Trp Gln Tyr Ile Lys Thr His Lys Leu Gln
275 280 285

Asp Pro His Glu Arg Glu Phe Val Ile Cys Asp Lys Tyr Leu Gln Gln
290 295 300

Ile Phe Glu Ser Gln Arg Met Lys Phe Ser Glu Ile Pro Gln Arg Leu
305 310 315 320

His Ala Leu Leu Met Pro Pro Glu Pro Ile Ile Ile Asn His Val Ile
325 330 335

Ser Val Asp Pro Asn Asp Gln Lys Lys Thr Ala Cys Tyr Asp Ile Asp
340 345 350

Val Glu Val Asp Asp Thr Leu Lys Thr Gln Met Asn Ser Phe Leu Leu
355 360 365

Ser Thr Ala Ser Gln Gln Glu Ile Ala Thr Leu Asp Asn Lys Ile His
370 375 380

Glu Thr Ile Glu Thr Ile Asn Gln Leu Lys Thr Gln Arg Glu Phe Met
385 390 395 400

Leu Ser Phe Ala Arg Asp Pro Gln Gly Phe Ile Asn Asp Trp Leu Gln
405 410 415

Ser Gln Cys Arg Asp Leu Lys Thr Met Thr Asp Val Val Gly Asn Pro
420 425 430

Glu Glu Glu Arg Arg Ala Glu Phe Tyr Phe Gln Pro Trp Ala Gln Glu
435 440 445

Ala Val Cys Arg Tyr Phe Tyr Ser Lys Val Gln Gln Arg Arg Gln Glu

450 455 460

Leu Glu Gln Ala Leu Gly Ile Arg Asn Thr
465 470

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

<400> 188
Met Ser Pro Gly Asn Arg Met Pro Met Ala Arg Leu Ala Gly Gly Thr
1 5 10 15

Pro Cys Trp Leu Pro Ile Trp Cys Ser Ser Ser Ala Ser Thr Trp His
20 25 30

Pro Thr His His Asp Gly Ser Ile Pro Lys Thr Pro Ala Cys Ala Pro
35 40 45

Ala Gln Pro Pro Met Pro Ala Gln Arg Arg Gly Leu Lys Arg Arg Lys
50 55 60

Met Ala Asp Lys Val Leu Pro Gln Arg Ile Arg Glu Leu Val Pro Glu
65 70 75 80

Ser Gln Ala Tyr Met Asp Leu Leu Ala Phe Glu Arg Lys Leu Asp Gln
85 90 95

Thr Ile Ala Arg Lys Arg Met Glu Ile Gln Glu Ala Ile Lys Lys Pro
100 105 110

Leu Thr Gln Lys Arg Lys Leu Arg Ile Tyr Ile Ser Asn Thr Phe Ser
115 120 125

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

Gly Thr Pro Ala Gly Asp Lys Val Ala Ser Trp Glu Leu Arg Val Glu
145 150 155 160

Gly Lys Leu Leu Asp Asp Pro Ser Lys Gln Lys Arg Lys Phe Ser Ser
165 170 175

Phe Phe Ser Phe Leu Asn Leu Cys Lys Arg Leu Trp Pro Pro Ser Ser
180 185 190

Pro Gly Met Pro Glu Gly Cys Leu Ser Ser Gly Leu Gly Arg Gly Gly
195 200 205

Asp Thr Pro Val Leu
210

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<210> 189
<211> 261
<212> PRT
<213> Homo sapiens

<400> 189

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

Pro Cys Trp Leu Pro Ile Trp Cys Ser Ser Ser Ala Ser Thr Trp His
            20                  25                  30

Pro Thr His His Asp Gly Ser Ile Pro Lys Thr Pro Ala Cys Ala Pro
        35                  40                  45

Ala Gln Pro Pro Met Pro Ala Gln Arg Arg Gly Leu Lys Arg Arg Lys
    50                  55                  60

Met Ala Asp Lys Val Leu Pro Gln Arg Ile Arg Glu Leu Val Pro Glu
65                  70                  75                  80

Ser Gln Ala Tyr Met Asp Leu Leu Ala Phe Glu Arg Lys Leu Asp Gln
                85                  90                  95

Thr Ile Ala Arg Lys Arg Met Glu Ile Gln Glu Ala Ile Lys Lys Pro
            100                 105                 110

Leu Thr Gln Lys Arg Lys Leu Arg Ile Tyr Ile Ser Asn Thr Phe Ser
        115                 120                 125

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

Gly Thr Pro Ala Gly Asp Lys Val Ala Ser Trp Glu Leu Arg Val Glu
145                 150                 155                 160

Gly Lys Leu Leu Asp Asp Pro Ser Leu Ser Lys Pro Lys Phe Phe Ala
                165                 170                 175

Ile Pro Thr Ser Pro Ala Leu Leu Leu Val Phe Ser Phe Pro Leu Gly
            180                 185                 190

Ile Cys Thr Ile Leu Gly Ala Ser Phe Leu Cys Gly Ser His Phe Phe
        195                 200                 205

Cys Thr Gly Val Ser Trp Gly Phe Ser Gly Ser Leu Leu Gly Ala Ser
    210                 215                 220

Phe Phe Ser Phe Leu Asn Leu Cys Lys Arg Leu Trp Pro Pro Ser Ser
225                 230                 235                 240

Pro Gly Met Pro Glu Gly Cys Leu Ser Ser Gly Leu Gly Arg Gly Gly
                245                 250                 255
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Asp Thr Pro Val Leu
260

<210> 190
<211> 153
<212> PRT
<213> Homo sapiens

<400> 190
Met Ser Pro Gly Asn Arg Met Pro Met Ala Arg Leu Ala Gly Gly Thr
1 5 10 15

Pro Cys Trp Leu Pro Ile Trp Cys Ser Ser Ser Ala Ser Thr Trp His
20 25 30

Pro Thr His His Asp Gly Ser Ile Pro Lys Thr Pro Ala Cys Ala Pro
35 40 45

Ala Gln Pro Pro Met Pro Ala Gln Arg Arg Gly Leu Lys Arg Arg Lys
50 55 60

Met Ala Asp Lys Val Leu Pro Gln Arg Ile Arg Glu Leu Val Pro Glu
65 70 75 80

Ser Gln Ala Tyr Met Asp Leu Leu Ala Phe Glu Arg Lys Leu Asp Gln
85 90 95

Thr Ile Ala Arg Lys Arg Met Glu Ile Gln Glu Ala Ile Lys Lys Pro
100 105 110

Leu Thr Gln Lys Arg Lys Leu Arg Ile Tyr Ile Ser Asn Thr Phe Ser
115 120 125

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

Gly Thr His Val Glu Ala Arg Val Arg
145 150

<210> 191
<211> 207
<212> PRT
<213> Homo sapiens

<400> 191
Met Ser Pro Gly Asn Arg Met Pro Met Ala Arg Leu Ala Gly Gly Thr
1 5 10 15

Pro Cys Trp Leu Pro Ile Trp Cys Ser Ser Ser Ala Ser Thr Trp His
20 25 30

Pro Thr His His Asp Gly Ser Ile Pro Lys Thr Pro Ala Cys Ala Pro
35 40 45

Ala Gln Pro Pro Met Pro Ala Gln Arg Arg Gly Leu Lys Arg Arg Lys
50 55 60

Met Ala Asp Lys Val Leu Pro Gln Arg Ile Arg Glu Leu Val Pro Glu
65 70 75 80

Ser Gln Ala Tyr Met Asp Leu Leu Ala Phe Glu Arg Lys Leu Asp Gln
85 90 95

Thr Ile Ala Arg Lys Arg Met Glu Ile Gln Glu Ala Ile Lys Lys Pro
100 105 110

Leu Thr Gln Lys Arg Lys Leu Arg Ile Tyr Ile Ser Asn Thr Phe Ser
115 120 125

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

Gly Thr Pro Ala Gly Glu Pro Val Arg Cys Leu Leu Leu Phe Phe Pro
145 150 155 160

Gln Ser Met Gln Ala Ala Leu Ala Ala Ile Ile Ser Trp Asp Ala Arg
165 170 175

Gly Leu Pro Leu Gln Arg Leu Gly Pro Gly Arg Gly His Ser Ser Ser
180 185 190

Leu Ala Trp Pro Glu Val Trp Gly Met Cys Met Trp Arg Pro Gly
195 200 205

<210> 192
<211> 147
<212> PRT
<213> Homo sapiens

<400> 192
Met Leu Pro Gly Pro Ala Leu Arg Gly Pro Gly Pro Ala Gln Tyr Gln
1 5 10 15

Arg Pro Gly Met Ser Pro Gly Asn Arg Met Pro Met Ala Arg Leu Ala
20 25 30

Gly Gly Thr Pro Cys Trp Leu Pro Ile Trp Cys Ser Ser Ser Ala Ser
35 40 45

Thr Trp His Pro Thr His His Asp Gly Ser Ile Pro Lys Thr Pro Ala
50 55 60

Cys Ala Pro Ala Gln Pro Pro Met Pro Ala Gln Arg Arg Gly Leu Lys
65 70 75 80

Arg Arg Lys Met Ala Asp Lys Val Leu Pro Gln Arg Arg Asp Leu Lys
85 90 95

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Ile Ile Thr Asp Val Ile Gly Asn Pro Glu Glu Glu Arg Arg Ala Ala
100 105 110

Phe Tyr His Gln Pro Trp Ala Gln Glu Ala Val Gly Arg His Ile Phe
115 120 125

Ala Lys Val Gln Gln Arg Arg Gln Glu Leu Glu Gln Val Leu Gly Ile
130 135 140

Arg Leu Thr
145

<210> 193
<211> 148
<212> PRT
<213> Homo sapiens

<400> 193
Met Leu Pro Gly Pro Ala Leu Arg Gly Pro Gly Pro Ala Gln Tyr Gln
1 5 10 15

Arg Pro Gly Met Ser Pro Gly Asn Arg Met Pro Met Ala Arg Leu Ala
20 25 30

Gly Gly Thr Pro Cys Trp Leu Pro Ile Trp Cys Ser Ser Ser Ala Ser
35 40 45

Thr Trp His Pro Thr His His Asp Gly Ser Ile Pro Lys Thr Pro Ala
50 55 60

Cys Ala Pro Ala Gln Pro Pro Met Pro Ala Gln Arg Arg Gly Leu Lys
65 70 75 80

Arg Arg Lys Met Ala Asp Lys Val Phe Arg Glu Pro Val Arg Cys Leu
85 90 95

Leu Leu Phe Phe Pro Gln Ser Met Gln Ala Ala Leu Ala Ala Ile Ile
100 105 110

Ser Trp Asp Ala Arg Gly Leu Pro Leu Gln Arg Leu Gly Pro Gly Arg
115 120 125

Gly His Ser Ser Ser Leu Ala Trp Pro Glu Val Trp Gly Met Cys Met
130 135 140

Trp Arg Pro Gly
145

<210> 194
<211> 426
<212> PRT
<213> Homo sapiens

<400> 194

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Met Ala Ala Asp Glu Val Ala Gly Gly Ala Arg Lys Ala Thr Lys Ser
1               5                  10                  15

Lys Leu Phe Glu Phe Leu Val His Gly Val Arg Pro Gly Met Pro Ser
            20                  25                  30

Gly Ala Arg Met Pro His Gln Gly Ala Pro Met Gly Pro Pro Gly Ser
        35                  40                  45

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

Met Glu Pro Ala Arg Lys Arg Ala Ala Pro Pro Pro Gly Gln Ser Gln
65                  70                  75                  80

Ala Gln Ser Gln Gly Gln Pro Val Pro Thr Ala Pro Ala Arg Ser Arg
                85                  90                  95

Ser Ala Lys Arg Arg Lys Met Ala Asp Lys Ile Leu Pro Gln Arg Ile
            100                 105                 110

Arg Glu Leu Val Pro Glu Ser Gln Ala Tyr Met Asp Leu Leu Ala Phe
        115                 120                 125

Glu Arg Lys Leu Asp Gln Thr Ile Met Arg Lys Arg Val Asp Ile Gln
    130                 135                 140

Glu Ala Leu Lys Arg Pro Met Lys Gln Lys Arg Lys Leu Arg Leu Tyr
145                 150                 155                 160

Ile Ser Asn Thr Phe Asn Pro Ala Lys Pro Asp Ala Glu Asp Ser Asp
                165                 170                 175

Gly Ser Ile Ala Ser Trp Glu Leu Arg Val Glu Gly Lys Leu Leu Asp
            180                 185                 190

Asp Pro Ser Lys Gln Lys Arg Lys Phe Ser Ser Phe Phe Lys Ser Leu
        195                 200                 205

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

Glu Trp His Arg Thr Pro Thr Thr Gln Glu Thr Asp Gly Phe Gln Val
225                 230                 235                 240

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

Asp Tyr Gln Pro Pro Gln Phe Lys Leu Asp Pro Arg Leu Ala Arg Leu
            260                 265                 270

Leu Gly Leu His Thr Gln Ser Arg Ser Ala Ile Val Gln Ala Leu Trp
```

275 280 285

Gln Tyr Val Lys Thr Asn Arg Leu Gln Asp Ser His Asp Lys Glu Tyr
290 295 300

Ile Asn Gly Asp Lys Tyr Phe Gln Gln Ile Phe Asp Cys Pro Arg Leu
305 310 315 320

Lys Phe Ser Glu Ile Pro Gln Arg Leu Thr Ala Leu Leu Leu Pro Pro
325 330 335

Asp Pro Ile Val Ile Asn His Val Ile Ser Val Asp Pro Ser Asp Gln
340 345 350

Lys Lys Thr Ala Cys Tyr Asp Ile Asp Val Glu Val Glu Glu Pro Leu
355 360 365

Lys Gly Gln Met Ser Ser Phe Leu Leu Ser Thr Ala Asn Gln Gln Glu
370 375 380

Ile Ser Ala Leu Asp Ser Lys Ile His Glu Thr Ile Glu Ser Ile Asn
385 390 395 400

Gln Leu Lys Ile Gln Arg Asp Phe Met Leu Ser Phe Ser Ser Ile Thr
405 410 415

Pro Leu Pro Pro Trp Gly Val Gly Leu Asp
420 425

<210> 195
<211> 451
<212> PRT
<213> Homo sapiens

<400> 195
Met Ala Ala Asp Glu Val Ala Gly Gly Ala Arg Lys Ala Thr Lys Ser
1 5 10 15

Lys Leu Phe Glu Phe Leu Val His Gly Val Arg Pro Gly Met Pro Ser
20 25 30

Gly Ala Arg Met Pro His Gln Gly Ala Pro Met Gly Pro Pro Gly Ser
35 40 45

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

Met Glu Pro Ala Arg Lys Arg Ala Ala Pro Pro Pro Gly Gln Ser Gln
65 70 75 80

Ala Gln Ser Gln Gly Gln Pro Val Pro Thr Ala Pro Ala Arg Ser Arg
85 90 95

Ser Ala Lys Arg Arg Lys Met Ala Asp Lys Ile Leu Pro Gln Arg Ile
100 105 110

Arg Glu Leu Val Pro Glu Ser Gln Ala Tyr Met Asp Leu Leu Ala Phe
115 120 125

Glu Arg Lys Leu Asp Gln Thr Ile Met Arg Arg Val Asp Ile Gln Glu
130 135 140

Ala Leu Lys Arg Pro Met Lys Gln Lys Arg Lys Leu Arg Leu Tyr Ile
145 150 155 160

Ser Asn Thr Phe Asn Pro Ala Lys Pro Asp Ala Glu Asp Ser Asp Gly
165 170 175

Ser Ile Ala Ser Trp Glu Leu Arg Val Glu Gly Lys Leu Leu Asp Asp
180 185 190

Pro Ser Lys Gln Lys Arg Lys Phe Ser Ser Phe Phe Lys Ser Leu Val
195 200 205

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

Trp His Arg Thr Pro Thr Thr Gln Glu Thr Asp Gly Phe Gln Val Lys
225 230 235 240

Arg Pro Gly Asp Leu Ser Val Arg Cys Thr Leu Leu Leu Met Leu Asp
245 250 255

Tyr Gln Pro Pro Gln Phe Lys Leu Asp Pro Arg Leu Ala Arg Leu Leu
260 265 270

Gly Leu His Thr Gln Ser Arg Ser Ala Ile Val Gln Ala Leu Trp Gln
275 280 285

Tyr Val Lys Thr Asn Arg Leu Gln Asp Ser His Asp Lys Glu Tyr Ile
290 295 300

Asn Gly Asp Lys Tyr Phe Gln Gln Ile Phe Asp Cys Pro Arg Leu Lys
305 310 315 320

Phe Ser Glu Ile Pro Gln Arg Leu Thr Ala Leu Leu Leu Pro Pro Asp
325 330 335

Pro Ile Val Ile Asn His Val Ile Ser Val Asp Pro Ser Asp Gln Lys
340 345 350

Lys Thr Ala Cys Tyr Asp Ile Asp Val Glu Val Glu Glu Pro Leu Lys
355 360 365

Gly Gln Met Ser Ser Phe Leu Leu Ser Thr Ala Asn Gln Gln Glu Ile

370 375 380

Ser Ala Leu Asp Ser Lys Ile His Glu Thr Ile Glu Ser Ile Asn Gln
385 390 395 400

Leu Lys Ile Gln Arg Asp Phe Met Leu Ser Phe Ser Arg Asp Pro Lys
405 410 415

Gly Tyr Val Gln Asp Leu Leu Arg Ser Gln Ser Arg Asp Leu Lys Val
420 425 430

Lys Arg Glu Thr Gln Gly Val Gln Asn Thr Asp Thr Cys Ser Cys Ser
435 440 445

His Phe Leu
450

<210> 196
<211> 77
<212> PRT
<213> Homo sapiens

<400> 196
Met Ser Lys Arg Pro Ser Tyr Ala Pro Pro Pro Thr Pro Ala Pro Ala
1 5 10 15

Thr Gln Met Pro Ser Thr Pro Gly Phe Val Gly Tyr Asn Pro Tyr Ser
20 25 30

His Leu Ala Tyr Asn Asn Tyr Arg Leu Gly Gly Asn Pro Gly Thr Asn
35 40 45

Ser Arg Val Thr Val Gly Glu Ser Thr Ile Thr Ala Ser Gly Lys Gln
50 55 60

Leu Glu Leu Thr Arg Asn Ala Phe Arg Ile Arg Ser Phe
65 70 75

<210> 197
<211> 376
<212> PRT
<213> Homo sapiens

<400> 197
Met Ser Lys Arg Pro Ser Tyr Ala Pro Pro Pro Thr Pro Ala Pro Ala
1 5 10 15

Thr Ala Ser Ser Gly Ile Thr Ile Pro Lys Pro Pro Lys Pro Pro Asp
20 25 30

Lys Pro Leu Met Pro Tyr Met Arg Tyr Ser Arg Lys Val Trp Asp Gln
35 40 45

Val Lys Ala Ser Asn Pro Asp Leu Lys Leu Trp Glu Ile Gly Lys Ile
50 55 60

```
Ile Gly Gly Met Trp Arg Asp Leu Thr Asp Glu Glu Lys Gln Glu Tyr
65                  70                  75                  80

Leu Asn Glu Tyr Glu Ala Glu Lys Ile Glu Tyr Asn Glu Ser Met Lys
                85                  90                  95

Ala Tyr His Asn Ser Pro Ala Tyr Leu Ala Tyr Ile Asn Ala Lys Ser
            100                 105                 110

Arg Ala Glu Ala Ala Leu Glu Glu Glu Ser Arg Gln Arg Gln Ser Arg
        115                 120                 125

Met Glu Lys Gly Glu Pro Tyr Met Ser Ile Gln Pro Ala Glu Asp Pro
    130                 135                 140

Asp Asp Tyr Asp Asp Gly Phe Ser Met Lys His Thr Ala Thr Ala Arg
145                 150                 155                 160

Phe Gln Arg Asn His Arg Leu Ile Ser Glu Ile Leu Ser Glu Ser Val
                165                 170                 175

Val Pro Asp Val Arg Ser Val Val Thr Thr Ala Arg Met Gln Val Leu
            180                 185                 190

Lys Arg Gln Val Gln Ser Leu Met Val His Gln Arg Lys Leu Glu Ala
        195                 200                 205

Glu Leu Leu Gln Ile Glu Glu Arg His Gln Glu Lys Lys Arg Lys Phe
    210                 215                 220

Leu Glu Ser Thr Asp Ser Phe Asn Asn Glu Leu Lys Arg Leu Cys Gly
225                 230                 235                 240

Leu Lys Val Glu Val Asp Met Glu Lys Ile Ala Ala Glu Ile Ala Gln
                245                 250                 255

Ala Glu Glu Gln Ala Arg Lys Arg Gln Glu Glu Arg Glu Lys Glu Ala
            260                 265                 270

Ala Glu Gln Ala Glu Arg Ser Gln Ser Ser Ile Val Pro Glu Glu Glu
        275                 280                 285

Gln Ala Ala Asn Lys Gly Glu Glu Lys Lys Asp Asp Glu Asn Ile Pro
    290                 295                 300

Met Glu Thr Glu Glu Thr His Leu Glu Glu Thr Thr Glu Ser Gln Gln
305                 310                 315                 320

Asn Gly Glu Glu Gly Thr Ser Thr Pro Glu Asp Lys Glu Ser Gly Gln
                325                 330                 335
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Glu Gly Val Asp Ser Met Ala Glu Glu Gly Thr Ser Asp Ser Asn Thr
340 345 350

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

Ile Pro Glu Asp Glu Lys Lys Glu
370 375

<210> 198
<211> 341
<212> PRT
<213> Homo sapiens

<400> 198
Met Pro Tyr Met Arg Tyr Ser Arg Lys Val Trp Asp Gln Val Lys Ala
1 5 10 15

Ser Asn Pro Asp Leu Lys Leu Trp Glu Ile Gly Lys Ile Ile Gly Gly
20 25 30

Met Trp Arg Asp Leu Thr Asp Glu Glu Lys Gln Glu Tyr Leu Asn Glu
35 40 45

Tyr Glu Ala Glu Lys Ile Glu Tyr Asn Glu Ser Met Lys Ala Tyr His
50 55 60

Asn Ser Pro Ala Tyr Leu Ala Tyr Ile Asn Ala Lys Ser Arg Ala Glu
65 70 75 80

Ala Ala Leu Glu Glu Glu Ser Arg Gln Arg Gln Ser Arg Met Glu Lys
85 90 95

Gly Glu Pro Tyr Met Ser Ile Gln Pro Ala Glu Asp Pro Asp Asp Tyr
100 105 110

Asp Asp Gly Phe Ser Met Lys His Thr Ala Thr Ala Arg Phe Gln Arg
115 120 125

Asn His Arg Leu Ile Ser Glu Ile Leu Ser Glu Ser Val Val Pro Asp
130 135 140

Val Arg Ser Val Val Thr Thr Ala Arg Met Gln Val Leu Lys Arg Gln
145 150 155 160

Val Gln Ser Leu Met Val His Gln Arg Lys Leu Glu Ala Glu Leu Leu
165 170 175

Gln Ile Glu Glu Arg His Gln Glu Lys Lys Arg Lys Phe Leu Glu Ser
180 185 190

Thr Asp Ser Phe Asn Asn Glu Leu Lys Arg Leu Cys Gly Leu Lys Val
195 200 205

Glu Val Asp Met Glu Lys Ile Ala Ala Glu Ile Ala Gln Ala Glu Glu
210 215 220

Gln Ala Arg Lys Arg Gln Glu Glu Arg Glu Lys Glu Ala Ala Glu Gln
225 230 235 240

Ala Glu Arg Ser Gln Ser Ser Ile Val Pro Glu Glu Glu Gln Ala Ala
245 250 255

Asn Lys Gly Glu Glu Lys Lys Asp Asp Glu Asn Ile Pro Met Glu Thr
260 265 270

Glu Glu Thr His Leu Glu Glu Thr Thr Glu Ser Gln Gln Asn Gly Glu
275 280 285

Glu Gly Thr Ser Thr Pro Glu Asp Lys Glu Ser Gly Gln Glu Gly Val
290 295 300

Asp Ser Met Ala Glu Glu Gly Thr Ser Asp Ser Asn Thr Gly Ser Glu
305 310 315 320

Ser Asn Ser Ala Thr Val Glu Glu Pro Pro Thr Asp Pro Ile Pro Glu
325 330 335

Asp Glu Lys Lys Glu
340

<210> 199
<211> 218
<212> PRT
<213> Homo sapiens

<400> 199
Met Ser Lys Arg Pro Ser Tyr Ala Pro Pro Pro Thr Pro Ala Pro Ala
1 5 10 15

Thr Gln Met Pro Ser Thr Pro Gly Phe Val Gly Tyr Asn Pro Tyr Ser
20 25 30

His Leu Ala Tyr Asn Asn Tyr Arg Leu Gly Gly Asn Pro Gly Thr Asn
35 40 45

Ser Arg Val Thr Ala Ser Ser Gly Ile Thr Ile Pro Lys Pro Pro Lys
50 55 60

Pro Pro Asp Lys Pro Leu Met Pro Tyr Met Arg Tyr Ser Arg Lys Val
65 70 75 80

Trp Asp Gln Val Lys Ala Ser Asn Pro Asp Leu Lys Leu Trp Glu Ile
85 90 95

Gly Lys Ile Ile Gly Gly Met Trp Arg Asp Leu Thr Asp Glu Glu Lys

100 105 110

Gln Glu Tyr Leu Asn Glu Tyr Glu Ala Glu Lys Ile Glu Tyr Asn Glu
115 120 125

Ser Met Lys Ala Tyr His Asn Ser Pro Ala Tyr Leu Ala Tyr Ile Asn
130 135 140

Ala Lys Ser Arg Ala Glu Ala Ala Leu Glu Glu Glu Ser Arg Gln Arg
145 150 155 160

Gln Ser Arg Met Glu Lys Gly Glu Pro Tyr Met Ser Ile Gln Pro Ala
165 170 175

Glu Asp Pro Asp Gly Lys Arg Lys Lys Val Gly Phe Cys Leu Cys Phe
180 185 190

Leu Cys Glu Leu Arg Tyr Glu Lys Ser Leu Lys Tyr Lys Phe Leu Phe
195 200 205

Leu Ile Leu Asn Gly Lys Glu Ser Ile Ile
210 215

<210> 200
<211> 393
<212> PRT
<213> Homo sapiens

<400> 200
Met Pro Ser Thr Pro Gly Phe Val Gly Tyr Asn Pro Tyr Ser His Leu
1 5 10 15

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

Val Thr Ala Ser Ser Gly Ile Thr Ile Pro Lys Pro Pro Lys Pro Pro
35 40 45

Asp Lys Pro Leu Met Pro Tyr Met Arg Tyr Ser Arg Lys Val Trp Asp
50 55 60

Gln Val Lys Ala Ser Asn Pro Asp Leu Lys Leu Trp Glu Ile Gly Lys
65 70 75 80

Ile Ile Gly Gly Met Trp Arg Asp Leu Thr Asp Glu Glu Lys Gln Glu
85 90 95

Tyr Leu Asn Glu Tyr Glu Ala Glu Lys Ile Glu Tyr Asn Glu Ser Met
100 105 110

Lys Ala Tyr His Asn Ser Pro Ala Tyr Leu Ala Tyr Ile Asn Ala Lys
115 120 125

Ser Arg Ala Glu Ala Ala Leu Glu Glu Glu Ser Arg Gln Arg Gln Ser
130 135 140

Arg Met Glu Lys Gly Glu Pro Tyr Met Ser Ile Gln Pro Ala Glu Asp
145 150 155 160

Pro Asp Asp Tyr Asp Asp Gly Phe Ser Met Lys His Thr Ala Thr Ala
165 170 175

Arg Phe Gln Arg Asn His Arg Leu Ile Ser Glu Ile Leu Ser Glu Ser
180 185 190

Val Val Pro Asp Val Arg Ser Val Val Thr Thr Ala Arg Met Gln Val
195 200 205

Leu Lys Arg Gln Val Gln Ser Leu Met Val His Gln Arg Lys Leu Glu
210 215 220

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

Phe Leu Glu Ser Thr Asp Ser Phe Asn Asn Glu Leu Lys Arg Leu Cys
245 250 255

Gly Leu Lys Val Glu Val Asp Met Glu Lys Ile Ala Ala Glu Ile Ala
260 265 270

Gln Ala Glu Glu Gln Ala Arg Lys Arg Gln Glu Glu Arg Glu Lys Glu
275 280 285

Ala Ala Glu Gln Ala Glu Arg Ser Gln Ser Ser Ile Val Pro Glu Glu
290 295 300

Glu Gln Ala Ala Asn Lys Gly Glu Glu Lys Lys Asp Asp Glu Asn Ile
305 310 315 320

Pro Met Glu Thr Glu Glu Thr His Leu Glu Glu Thr Thr Glu Ser Gln
325 330 335

Gln Asn Gly Glu Glu Gly Thr Ser Thr Pro Glu Asp Lys Glu Ser Gly
340 345 350

Gln Glu Gly Val Asp Ser Met Ala Glu Glu Gly Thr Ser Asp Ser Asn
355 360 365

Thr Gly Ser Glu Ser Asn Ser Ala Thr Val Glu Glu Pro Pro Thr Asp
370 375 380

Pro Ile Pro Glu Asp Glu Lys Lys Glu
385 390

<210> 201

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<211> 2229
<212> PRT
<213> Homo sapiens

<400> 201

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

Pro Pro Pro Pro Pro Ser Glu Leu Lys Lys Ala Glu Gln Gln Gln Arg
            20                  25                  30

Glu Glu Ala Gly Gly Glu Ala Ala Ala Ala Ala Ala Ala Glu Arg Gly
        35                  40                  45

Glu Met Lys Ala Ala Ala Gly Gln Glu Ser Glu Gly Pro Ala Val Gly
    50                  55                  60

Pro Pro Gln Pro Leu Gly Lys Glu Leu Gln Asp Gly Ala Glu Ser Asn
65                  70                  75                  80

Gly Gly Gly Gly Gly Gly Gly Ala Gly Ser Gly Gly Gly Pro Gly Ala
                85                  90                  95

Glu Pro Asp Leu Lys Asn Ser Asn Gly Asn Ala Gly Pro Arg Pro Ala
            100                 105                 110

Leu Asn Asn Asn Leu Thr Glu Pro Pro Gly Gly Gly Gly Gly Gly Ser
        115                 120                 125

Ser Asp Gly Val Gly Ala Pro Pro His Ser Ala Ala Ala Ala Leu Pro
    130                 135                 140

Pro Pro Ala Tyr Gly Phe Gly Gln Pro Tyr Gly Arg Ser Pro Ser Ala
145                 150                 155                 160

Val Ala Ala Ala Ala Ala Ala Val Phe His Gln Gln His Gly Gly Gln
                165                 170                 175

Gln Ser Pro Gly Leu Ala Ala Leu Gln Ser Gly Gly Gly Gly Gly Leu
            180                 185                 190

Glu Pro Tyr Ala Gly Pro Gln Gln Asn Ser His Asp His Gly Phe Pro
        195                 200                 205

Asn His Gln Tyr Asn Ser Tyr Tyr Pro Asn Arg Ser Ala Tyr Pro Pro
    210                 215                 220

Pro Ala Pro Ala Tyr Ala Leu Ser Ser Pro Arg Gly Gly Thr Pro Gly
225                 230                 235                 240

Ser Gly Ala Ala Ala Ala Ala Gly Ser Lys Pro Pro Pro Ser Ser Ser
                245                 250                 255
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Ala Ser Ala Ser Ser Ser Ser Ser Phe Ala Gln Gln Arg Phe Gly
260 265 270

Ala Met Gly Gly Gly Gly Pro Ser Ala Ala Gly Gly Gly Thr Pro Gln
275 280 285

Pro Thr Ala Thr Pro Thr Leu Asn Gln Leu Leu Thr Ser Pro Ser Ser
290 295 300

Ala Arg Gly Tyr Gln Gly Tyr Pro Gly Gly Asp Tyr Ser Gly Gly Pro
305 310 315 320

Gln Asp Gly Gly Ala Gly Lys Gly Pro Ala Asp Met Ala Ser Gln Cys
325 330 335

Trp Gly Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ser Gly Gly
340 345 350

Ala Gln Gln Arg Ser His His Ala Pro Met Ser Pro Gly Ser Ser Gly
355 360 365

Gly Gly Gly Gln Pro Leu Ala Arg Thr Pro Gln Pro Ser Ser Pro Met
370 375 380

Asp Gln Met Gly Lys Met Arg Pro Gln Pro Tyr Gly Gly Thr Asn Pro
385 390 395 400

Tyr Ser Gln Gln Gln Gly Pro Pro Ser Gly Pro Gln Gln Gly His Gly
405 410 415

Tyr Pro Gly Gln Pro Tyr Gly Ser Gln Thr Pro Gln Arg Tyr Pro Met
420 425 430

Thr Met Gln Gly Arg Ala Gln Ser Ala Met Gly Gly Leu Ser Tyr Thr
435 440 445

Gln Gln Ile Pro Pro Tyr Gly Gln Gln Gly Pro Ser Gly Tyr Gly Gln
450 455 460

Gln Gly Gln Thr Pro Tyr Tyr Asn Gln Gln Ser Pro His Pro Gln Gln
465 470 475 480

Gln Gln Pro Pro Tyr Ser Gln Gln Pro Pro Ser Gln Thr Pro His Ala
485 490 495

Gln Pro Ser Tyr Gln Gln Gln Pro Gln Ser Gln Pro Pro Gln Leu Gln
500 505 510

Ser Ser Gln Pro Pro Tyr Ser Gln Gln Pro Ser Gln Pro Pro His Gln
515 520 525

Gln Ser Pro Ala Pro Tyr Pro Ser Gln Gln Ser Thr Thr Gln Gln His

530 535 540

Pro Gln Ser Gln Pro Pro Tyr Ser Gln Pro Gln Ala Gln Ser Pro Tyr
545 550 555 560

Gln Gln Gln Gln Pro Gln Gln Pro Ala Pro Ser Thr Leu Ser Gln Gln
565 570 575

Ala Ala Tyr Pro Gln Pro Gln Ser Gln Gln Ser Gln Gln Thr Ala Tyr
580 585 590

Ser Gln Gln Arg Phe Pro Pro Pro Gln Glu Leu Ser Gln Asp Ser Phe
595 600 605

Gly Ser Gln Ala Ser Ser Ala Pro Ser Met Thr Ser Ser Lys Gly Gly
610 615 620

Gln Glu Asp Met Asn Leu Ser Leu Gln Ser Arg Pro Ser Ser Leu Pro
625 630 635 640

Asp Leu Ser Gly Ser Ile Asp Asp Leu Pro Met Gly Thr Glu Gly Ala
645 650 655

Leu Ser Pro Gly Val Ser Thr Ser Gly Ile Ser Ser Ser Gln Gly Glu
660 665 670

Gln Ser Asn Pro Ala Gln Ser Pro Phe Ser Pro His Thr Ser Pro His
675 680 685

Leu Pro Gly Ile Arg Gly Pro Ser Pro Ser Pro Val Gly Ser Pro Ala
690 695 700

Ser Val Ala Gln Ser Arg Ser Gly Pro Leu Ser Pro Ala Ala Val Pro
705 710 715 720

Gly Asn Gln Met Pro Pro Arg Pro Pro Ser Gly Gln Ser Asp Ser Ile
725 730 735

Met His Pro Ser Met Asn Gln Ser Ser Ile Ala Gln Asp Arg Gly Gly
740 745 750

Tyr Pro Arg Gln Pro Asn Tyr Asn Ala Leu Pro Asn Ala Asn Tyr Pro
755 760 765

Ser Ala Gly Met Ala Gly Gly Ile Asn Pro Met Gly Ala Gly Gly Gln
770 775 780

Met His Gly Gln Pro Gly Ile Pro Pro Tyr Gly Thr Leu Pro Pro Gly
785 790 795 800

Arg Met Ser His Ala Ser Met Gly Asn Arg Pro Tyr Gly Pro Asn Met
805 810 815

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Ala Asn Met Pro Pro Gln Val Gly Ser Gly Met Cys Pro Pro Pro Gly
820 825 830

Gly Met Asn Arg Lys Thr Gln Glu Thr Ala Val Ala Met His Val Ala
835 840 845

Ala Asn Ser Ile Gln Asn Arg Pro Pro Gly Tyr Pro Asn Met Asn Gln
850 855 860

Gly Gly Met Met Gly Thr Gly Pro Pro Tyr Gly Gln Gly Ile Asn Ser
865 870 875 880

Met Ala Gly Met Ile Asn Pro Gln Gly Pro Pro Tyr Ser Met Gly Gly
885 890 895

Thr Met Ala Asn Asn Ser Ala Gly Met Ala Ala Ser Pro Glu Met Met
900 905 910

Gly Leu Gly Asp Val Lys Leu Thr Pro Ala Thr Lys Met Asn Asn Lys
915 920 925

Ala Asp Gly Thr Pro Lys Thr Glu Ser Lys Ser Lys Lys Ser Ser Ser
930 935 940

Ser Thr Thr Thr Asn Glu Lys Ile Thr Lys Leu Tyr Glu Leu Gly Gly
945 950 955 960

Glu Pro Glu Arg Lys Met Trp Val Asp Arg Tyr Leu Ala Phe Thr Glu
965 970 975

Glu Lys Ala Met Gly Met Thr Asn Leu Pro Ala Val Gly Arg Lys Pro
980 985 990

Leu Asp Leu Tyr Arg Leu Tyr Val Ser Val Lys Glu Ile Gly Gly Leu
995 1000 1005

Thr Gln Val Asn Lys Asn Lys Lys Trp Arg Glu Leu Ala Thr Asn
1010 1015 1020

Leu Asn Val Gly Thr Ser Ser Ser Ala Ala Ser Ser Leu Lys Lys
1025 1030 1035

Gln Tyr Ile Gln Cys Leu Tyr Ala Phe Glu Cys Lys Ile Glu Arg
1040 1045 1050

Gly Glu Asp Pro Pro Pro Asp Ile Phe Ala Ala Ala Asp Ser Lys
1055 1060 1065

Lys Ser Gln Pro Lys Ile Gln Pro Pro Ser Pro Ala Gly Ser Gly
1070 1075 1080

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Ser Met Gln Gly Pro Gln Thr Pro Gln Ser Thr Ser Ser Ser Met
1085 1090 1095

Ala Glu Gly Gly Asp Leu Lys Pro Pro Thr Pro Ala Ser Thr Pro
1100 1105 1110

His Ser Gln Ile Pro Pro Leu Pro Gly Met Ser Arg Ser Asn Ser
1115 1120 1125

Val Gly Ile Gln Asp Ala Phe Asn Asp Gly Ser Asp Ser Thr Phe
1130 1135 1140

Gln Lys Arg Asn Ser Met Thr Pro Asn Pro Gly Tyr Gln Pro Ser
1145 1150 1155

Met Asn Thr Ser Asp Met Met Gly Arg Met Ser Tyr Glu Pro Asn
1160 1165 1170

Lys Asp Pro Tyr Gly Ser Met Arg Lys Ala Pro Gly Ser Asp Pro
1175 1180 1185

Phe Met Ser Ser Gly Gln Gly Pro Asn Gly Gly Met Gly Asp Pro
1190 1195 1200

Tyr Ser Arg Ala Ala Gly Pro Gly Leu Gly Asn Val Ala Met Gly
1205 1210 1215

Pro Arg Gln His Tyr Pro Tyr Gly Gly Pro Tyr Asp Arg Val Arg
1220 1225 1230

Thr Glu Pro Gly Ile Gly Pro Glu Gly Asn Met Ser Thr Gly Ala
1235 1240 1245

Pro Gln Pro Asn Leu Met Pro Ser Asn Pro Asp Ser Gly Met Tyr
1250 1255 1260

Ser Pro Ser Arg Tyr Pro Pro Gln Gln Gln Gln Gln Gln Gln Gln
1265 1270 1275

Arg His Asp Ser Tyr Gly Asn Gln Phe Ser Thr Gln Gly Thr Pro
1280 1285 1290

Ser Gly Ser Pro Phe Pro Ser Gln Gln Thr Thr Met Tyr Gln Gln
1295 1300 1305

Gln Gln Gln Asn Tyr Lys Arg Pro Met Asp Gly Thr Tyr Gly Pro
1310 1315 1320

Pro Ala Lys Arg His Glu Gly Glu Met Tyr Ser Val Pro Tyr Ser
1325 1330 1335

Thr Gly Gln Gly Gln Pro Gln Gln Gln Leu Pro Pro Ala Gln
1340 1345 1350

Pro Gln Pro Ala Ser Gln Gln Gln Ala Ala Gln Pro Ser Pro Gln
1355 1360 1365

Gln Asp Val Tyr Asn Gln Tyr Gly Asn Ala Tyr Pro Ala Thr Ala
1370 1375 1380

Thr Ala Ala Thr Glu Arg Arg Pro Ala Gly Gly Pro Gln Asn Gln
1385 1390 1395

Phe Pro Phe Gln Phe Gly Arg Asp Arg Val Ser Ala Pro Pro Gly
1400 1405 1410

Thr Asn Ala Gln Gln Asn Met Pro Pro Gln Met Met Gly Gly Pro
1415 1420 1425

Ile Gln Ala Ser Ala Glu Val Ala Gln Gln Gly Thr Met Trp Gln
1430 1435 1440

Gly Arg Asn Asp Met Thr Tyr Asn Tyr Ala Asn Arg Gln Ser Thr
1445 1450 1455

Gly Ser Ala Pro Gln Gly Pro Ala Tyr His Gly Val Asn Arg Thr
1460 1465 1470

Asp Glu Met Leu His Thr Asp Gln Arg Ala Asn His Glu Gly Ser
1475 1480 1485

Trp Pro Ser His Gly Thr Arg Gln Pro Pro Tyr Gly Pro Ser Ala
1490 1495 1500

Pro Val Pro Pro Met Thr Arg Pro Pro Pro Ser Asn Tyr Gln Pro
1505 1510 1515

Pro Pro Ser Met Gln Asn His Ile Pro Gln Val Ser Ser Pro Ala
1520 1525 1530

Pro Leu Pro Arg Pro Met Glu Asn Arg Thr Ser Pro Ser Lys Ser
1535 1540 1545

Pro Phe Leu His Ser Gly Met Lys Met Gln Lys Ala Gly Pro Pro
1550 1555 1560

Val Pro Ala Ser His Ile Ala Pro Ala Pro Val Gln Pro Pro Met
1565 1570 1575

Ile Arg Arg Asp Ile Thr Phe Pro Pro Gly Ser Val Glu Ala Thr
1580 1585 1590

Gln Pro Val Leu Lys Gln Arg Arg Arg Leu Thr Met Lys Asp Ile

1595 1600 1605

Gly Thr Pro Glu Ala Trp Arg Val Met Met Ser Leu Lys Ser Gly
1610 1615 1620

Leu Leu Ala Glu Ser Thr Trp Ala Leu Asp Thr Ile Asn Ile Leu
1625 1630 1635

Leu Tyr Asp Asp Asn Ser Ile Met Thr Phe Asn Leu Ser Gln Leu
1640 1645 1650

Pro Gly Leu Leu Glu Leu Leu Val Glu Tyr Phe Arg Arg Cys Leu
1655 1660 1665

Ile Glu Ile Phe Gly Ile Leu Lys Glu Tyr Glu Val Gly Asp Pro
1670 1675 1680

Gly Gln Arg Thr Leu Leu Asp Pro Gly Arg Phe Ser Lys Val Ser
1685 1690 1695

Ser Pro Ala Pro Met Glu Gly Gly Glu Glu Glu Glu Glu Leu Leu
1700 1705 1710

Gly Pro Lys Leu Glu Glu Glu Glu Glu Glu Glu Val Val Glu Asn
1715 1720 1725

Asp Glu Glu Ile Ala Phe Ser Gly Lys Asp Lys Pro Ala Ser Glu
1730 1735 1740

Asn Ser Glu Glu Lys Leu Ile Ser Lys Phe Asp Lys Leu Pro Val
1745 1750 1755

Lys Ile Val Gln Lys Asn Asp Pro Phe Val Val Asp Cys Ser Asp
1760 1765 1770

Lys Leu Gly Arg Val Gln Glu Phe Asp Ser Gly Leu Leu His Trp
1775 1780 1785

Arg Ile Gly Gly Gly Asp Thr Thr Glu His Ile Gln Thr His Phe
1790 1795 1800

Glu Ser Lys Thr Glu Leu Leu Pro Ser Arg Pro His Ala Pro Cys
1805 1810 1815

Pro Pro Ala Pro Arg Lys His Val Thr Thr Ala Glu Gly Thr Pro
1820 1825 1830

Gly Thr Thr Asp Gln Glu Gly Pro Pro Pro Asp Gly Pro Pro Glu
1835 1840 1845

Lys Arg Ile Thr Ala Thr Met Asp Asp Met Leu Ser Thr Arg Ser
1850 1855 1860

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Ser Thr Leu Thr Glu Asp Gly Ala Lys Ser Ser Glu Ala Ile Lys
1865 1870 1875

Glu Ser Ser Lys Phe Pro Phe Gly Ile Ser Pro Ala Gln Ser His
1880 1885 1890

Arg Asn Ile Lys Ile Leu Glu Asp Glu Pro His Ser Lys Asp Glu
1895 1900 1905

Thr Pro Leu Cys Thr Leu Leu Asp Trp Gln Asp Ser Leu Ala Lys
1910 1915 1920

Arg Cys Val Cys Val Ser Asn Thr Ile Arg Ser Leu Ser Phe Val
1925 1930 1935

Pro Gly Asn Asp Phe Glu Met Ser Lys His Pro Gly Leu Leu Leu
1940 1945 1950

Ile Leu Gly Lys Leu Ile Leu Leu His His Lys His Pro Glu Arg
1955 1960 1965

Lys Gln Ala Pro Leu Thr Tyr Glu Lys Glu Glu Glu Gln Asp Gln
1970 1975 1980

Gly Val Ser Cys Asn Lys Val Glu Trp Trp Trp Asp Cys Leu Glu
1985 1990 1995

Met Leu Arg Glu Asn Thr Leu Val Thr Leu Ala Asn Ile Ser Gly
2000 2005 2010

Gln Leu Asp Leu Ser Pro Tyr Pro Glu Ser Ile Cys Leu Pro Val
2015 2020 2025

Leu Asp Gly Leu Leu His Trp Ala Val Cys Pro Ser Ala Glu Ala
2030 2035 2040

Gln Asp Pro Phe Ser Thr Leu Gly Pro Asn Ala Val Leu Ser Pro
2045 2050 2055

Gln Arg Leu Val Leu Glu Thr Leu Ser Lys Leu Ser Ile Gln Asp
2060 2065 2070

Asn Asn Val Asp Leu Ile Leu Ala Thr Pro Pro Phe Ser Arg Leu
2075 2080 2085

Glu Lys Leu Tyr Ser Thr Met Val Arg Phe Leu Ser Asp Arg Lys
2090 2095 2100

Asn Pro Val Cys Arg Glu Met Ala Val Val Leu Leu Ala Asn Leu
2105 2110 2115

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Ala Gln Gly Asp Ser Leu Ala Ala Arg Ala Ile Ala Val Gln Lys
2120 2125 2130

Gly Ser Ile Gly Asn Leu Leu Gly Phe Leu Glu Asp Ser Leu Ala
2135 2140 2145

Ala Thr Gln Phe Gln Gln Ser Gln Ala Ser Leu Leu His Met Gln
2150 2155 2160

Asn Pro Pro Phe Glu Pro Thr Ser Val Asp Met Met Arg Arg Ala
2165 2170 2175

Ala Arg Ala Leu Leu Ala Leu Ala Lys Val Asp Glu Asn His Ser
2180 2185 2190

Glu Phe Thr Leu Tyr Glu Ser Arg Leu Leu Asp Ile Ser Val Ser
2195 2200 2205

Pro Leu Met Asn Ser Leu Val Ser Gln Val Ile Cys Asp Val Leu
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Phe Leu Ile Gly Gln Ser
2225

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Cys Ser Ser Thr Met Glu Asp Ser Glu Met Asp Phe Asp Ser Gly Leu
20 25 30

Glu Asp Asp Asp Thr Lys Ser Asp Ser Ile Leu Glu Asp Ser Thr Ile
35 40 45

Phe Val Ala Phe Lys Gly Asn Ile Asp Asp Lys Asp Phe Lys Trp Lys
50 55 60

Leu Asp Ala Ile Leu Lys Asn Val Pro Asn Leu Leu His Met Glu Ser
65 70 75 80

Ser Lys Leu Lys Val Gln Lys Val Glu Pro Trp Asn Ser Val Arg Val
85 90 95

Thr Phe Asn Ile Pro Arg Glu Ala Ala Glu Arg Leu Arg Ile Leu Ala
100 105 110

Gln Ser Asn Asn Gln Gln Leu Arg Asp Leu Gly Ile Leu Ser Val Gln
115 120 125

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

Gln Asp Val Arg Met Asn Gly Pro Met Gly Ala Gly Asn Ser Val Arg
145 150 155 160

Met Glu Ala Gly Phe Pro Met Ala Ser Gly Pro Gly Ile Ile Arg Met
165 170 175

Asn Asn Pro Ala Thr Val Met Ile Pro Pro Gly Gly Asn Val Ser Ser
180 185 190

Ser Met Met Ala Pro Gly Pro Asn Pro Glu Leu Gln Pro Arg Thr Pro
195 200 205

Arg Pro Ala Ser Gln Ser Asp Ala Met Asp Pro Leu Leu Ser Gly Leu
210 215 220

His Ile Gln Gln Gln Ser His Pro Ser Gly Ser Leu Ala Pro Pro His
225 230 235 240

His Pro Met Gln Pro Val Ser Val Asn Arg Gln Met Asn Pro Ala Asn
245 250 255

Phe Pro Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
260 265 270

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Ala
275 280 285

Arg Pro Pro Gln Gln His Gln Gln Gln Gln Pro Gln Gly Ile Arg Pro
290 295 300

Gln Phe Thr Ala Pro Thr Gln Val Pro Val Pro Pro Gly Trp Asn Gln
305 310 315 320

Leu Pro Ser Gly Ala Leu Gln Pro Pro Pro Ala Gln Gly Ser Leu Gly
325 330 335

Thr Met Thr Ala Asn Gln Gly Trp Lys Lys Ala Pro Leu Pro Gly Pro
340 345 350

Met Gln Gln Gln Leu Gln Ala Arg Pro Ser Leu Ala Thr Val Gln Thr
355 360 365

Pro Ser His Pro Pro Pro Pro Tyr Pro Phe Gly Ser Gln Gln Ala Ser
370 375 380

Gln Ala His Thr Asn Phe Pro Gln Met Ser Asn Pro Gly Gln Phe Thr
385 390 395 400

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Ala Pro Gln Met Lys Ser Leu Gln Gly Gly Pro Ser Arg Val Pro Thr
405 410 415

Pro Leu Gln Gln Pro His Leu Thr Asn Lys Ser Pro Ala Ser Ser Pro
420 425 430

Ser Ser Phe Gln Gln Gly Ser Pro Ala Ser Ser Pro Thr Val Asn Gln
435 440 445

Thr Gln Gln Gln Met Gly Pro Arg Pro Pro Gln Asn Asn Pro Leu Pro
450 455 460

Gln Gly Phe Gln Gln Pro Val Ser Ser Pro Gly Arg Asn Pro Met Val
465 470 475 480

Gln Gln Gly Asn Val Pro Pro Asn Phe Met Val Met Gln Gln Gln Pro
485 490 495

Pro Asn Gln Gly Pro Gln Ser Leu His Pro Gly Leu Gly Gly Met Pro
500 505 510

Lys Arg Leu Pro Pro Gly Phe Ser Ala Gly Gln Ala Asn Pro Asn Phe
515 520 525

Met Gln Gly Gln Val Pro Ser Thr Thr Ala Thr Thr Pro Gly Asn Ser
530 535 540

Gly Ala Pro Gln Leu Gln Ala Asn Gln Asn Val Gln His Ala Gly Gly
545 550 555 560

Gln Gly Ala Gly Pro Pro Gln Asn Gln Met Gln Val Ser His Gly Pro
565 570 575

Pro Asn Met Met Gln Pro Ser Leu Met Gly Ile His Gly Asn Met Asn
580 585 590

Asn Gln Gln Ala Gly Thr Ser Gly Val Pro Gln Val Asn Leu Ser Asn
595 600 605

Met Gln Gly Gln Pro Gln Gln Gly Pro Pro Ser Gln Leu Met Gly Met
610 615 620

His Gln Gln Ile Val Pro Ser Gln Gly Gln Met Val Gln Gln Gln Gly
625 630 635 640

Thr Leu Asn Pro Gln Asn Pro Met Ile Leu Ser Arg Ala Gln Leu Met
645 650 655

Pro Gln Gly Gln Met Met Val Asn Pro Pro Ser Gln Asn Leu Gly Pro
660 665 670

Ser Pro Gln Arg Met Thr Pro Pro Lys Gln Met Leu Ser Gln Gln Gly
675 680 685

Pro Gln Met Met Ala Pro His Asn Gln Met Met Gly Pro Gln Gly Gln
690 695 700

Val Leu Leu Gln Gln Asn Pro Met Ile Glu Gln Ile Met Thr Asn Gln
705 710 715 720

Met Gln Gly Asn Lys Gln Gln Phe Asn Thr Gln Asn Gln Ser Asn Val
725 730 735

Met Pro Gly Pro Ala Gln Ile Met Arg Gly Pro Thr Pro Asn Met Gln
740 745 750

Gly Asn Met Val Gln Phe Thr Gly Gln Met Ser Gly Gln Met Leu Pro
755 760 765

Gln Gln Gly Pro Val Asn Asn Ser Pro Ser Gln Val Met Gly Ile Gln
770 775 780

Gly Gln Val Leu Arg Pro Pro Gly Pro Ser Pro His Met Ala Gln Gln
785 790 795 800

His Gly Asp Pro Ala Thr Thr Ala Asn Asn Asp Val Ser Leu Ser Gln
805 810 815

Met Met Pro Asp Val Ser Ile Gln Gln Thr Asn Met Val Pro Pro His
820 825 830

Val Gln Ala Met Gln Gly Asn Ser Ala Ser Gly Asn His Phe Ser Gly
835 840 845

His Gly Met Ser Phe Asn Ala Pro Phe Ser Gly Ala Pro Asn Gly Asn
850 855 860

Gln Met Ser Cys Gly Gln Asn Pro Gly Phe Pro Val Asn Lys Asp Val
865 870 875 880

Thr Leu Thr Ser Pro Leu Leu Val Asn Leu Leu Gln Ser Asp Ile Ser
885 890 895

Ala Gly His Phe Gly Val Asn Asn Lys Gln Asn Asn Thr Asn Ala Asn
900 905 910

Lys Pro Lys Lys Lys Lys Pro Pro Arg Lys Lys Lys Asn Ser Gln Gln
915 920 925

Asp Leu Asn Thr Pro Asp Thr Arg Pro Ala Gly Leu Glu Glu Ala Asp
930 935 940

Gln Pro Pro Leu Pro Gly Glu Gln Gly Ile Asn Leu Asp Asn Ser Gly

945 950 955 960

Pro Lys Leu Pro Glu Phe Ser Asn Arg Pro Pro Ala Pro Ser Gln Asn
965 970 975

Leu Val Ser Lys Glu Thr Ser Thr Thr Ala Leu Gln Ala Ser Val Ala
980 985 990

Arg Pro Glu Leu Glu Val Asn Ala Ala Ile Val Ser Gly Gln Ser Ser
995 1000 1005

Glu Pro Lys Glu Ile Val Glu Lys Ser Lys Ile Pro Gly Arg Arg
1010 1015 1020

Asn Ser Arg Thr Glu Glu Pro Thr Val Ala Ser Glu Ser Val Glu
1025 1030 1035

Asn Gly His Arg Lys Arg Ser Ser Arg Pro Ala Ser Ala Ser Ser
1040 1045 1050

Ser Thr Lys Asp Ile Thr Ser Ala Val Gln Ser Lys Arg Arg Lys
1055 1060 1065

Ser Lys
1070

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Gln Ser Arg Tyr Pro Pro His Ser Val Gln Tyr Thr Phe Pro Asn Thr
20 25 30

Arg His Gln Gln Glu Phe Ala Val Pro Asp Tyr Arg Ser Ser His Leu
35 40 45

Glu Val Ser Gln Ala Ser Gln Leu Leu Gln Gln Gln Gln Gln Gln Gln
50 55 60

Leu Arg Arg Arg Pro Ser Leu Leu Ser Glu Phe His Pro Gly Ser Asp
65 70 75 80

Arg Pro Gln Glu Arg Arg Thr Ser Tyr Glu Pro Phe His Pro Gly Pro
85 90 95

Ser Pro Val Asp His Asp Ser Leu Glu Ser Lys Arg Pro Arg Leu Glu
100 105 110

Gln Val Ser Asp Ser His Phe Gln Arg Val Ser Ala Ala Val Leu Pro
115 120 125

Leu Val His Pro Leu Pro Glu Gly Leu Arg Ala Ser Ala Asp Ala Lys
130 135 140

Lys Asp Pro Ala Phe Gly Gly Lys His Glu Ala Pro Ser Ser Pro Ile
145 150 155 160

Ser Gly Gln Pro Cys Gly Asp Asp Gln Asn Ala Ser Pro Ser Lys Leu
165 170 175

Ser Lys Glu Glu Leu Ile Gln Ser Met Asp Arg Val Asp Arg Glu Ile
180 185 190

Ala Lys Val Glu Gln Gln Ile Leu Lys Leu Lys Lys Lys Gln Gln Gln
195 200 205

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

Pro Pro Pro Val Glu Gln Lys His Arg Ser Ile Val Gln Ile Ile Tyr
225 230 235 240

Asp Glu Asn Arg Lys Lys Ala Glu Glu Ala His Lys Ile Phe Glu Gly
245 250 255

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

Lys Val Tyr His Glu Asn Ile Lys Thr Asn Gln Val Met Arg Lys Lys
275 280 285

Leu Ile Leu Phe Phe Lys Arg Arg Asn His Ala Arg Lys Gln Arg Glu
290 295 300

Gln Lys Ile Cys Gln Arg Tyr Asp Gln Leu Met Glu Ala Trp Glu Lys
305 310 315 320

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

Lys Thr Arg Glu Tyr Tyr Glu Lys Gln Phe Pro Glu Ile Arg Lys Gln
340 345 350

Arg Glu Gln Gln Glu Arg Phe Gln Arg Val Gly Gln Arg Gly Ala Gly
355 360 365

Leu Ser Ala Thr Ile Ala Arg Ser Glu His Glu Ile Ser Glu Ile Ile
370 375 380

Asp Gly Leu Ser Glu Gln Glu Asn Asn Glu Lys Gln Met Arg Gln Leu

385 390 395 400

Ser Val Ile Pro Pro Met Met Phe Asp Ala Glu Gln Arg Arg Val Lys
405 410 415

Phe Ile Asn Met Asn Gly Leu Met Glu Asp Pro Met Lys Val Tyr Lys
420 425 430

Asp Arg Gln Phe Met Asn Val Trp Thr Asp His Glu Lys Glu Ile Phe
435 440 445

Lys Asp Lys Phe Ile Gln His Pro Lys Asn Phe Gly Leu Ile Ala Ser
450 455 460

Tyr Leu Glu Arg Lys Ser Val Pro Asp Cys Val Leu Tyr Tyr Tyr Leu
465 470 475 480

Thr Lys Lys Asn Glu Asn Tyr Lys Ala Leu Val Arg Arg Asn Tyr Gly
485 490 495

Lys Arg Arg Gly Arg Asn Gln Gln Ile Ala Arg Pro Ser Gln Glu Glu
500 505 510

Lys Val Glu Glu Lys Glu Glu Asp Lys Ala Glu Lys Thr Glu Lys Lys
515 520 525

Glu Glu Glu Lys Lys Asp Glu Glu Glu Lys Asp Glu Lys Glu Asp Ser
530 535 540

Lys Glu Asn Thr Lys Glu Lys Asp Lys Ile Asp Gly Thr Ala Glu Glu
545 550 555 560

Thr Glu Glu Arg Glu Gln Ala Thr Pro Arg Gly Arg Lys Thr Ala Asn
565 570 575

Ser Gln Gly Arg Arg Lys Gly Arg Ile Thr Arg Ser Met Thr Asn Glu
580 585 590

Ala Ala Ala Ala Ser Ala Ala Ala Ala Ala Ala Thr Glu Glu Pro Pro
595 600 605

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

Thr Ser Arg Trp Thr Glu Glu Glu Met Glu Val Ala Lys Lys Gly Leu
625 630 635 640

Val Glu His Gly Arg Asn Trp Ala Ala Ile Ala Lys Met Val Gly Thr
645 650 655

Lys Ser Glu Ala Gln Cys Lys Asn Phe Tyr Phe Asn Tyr Lys Arg Arg
660 665 670

His Asn Leu Asp Asn Leu Leu Gln Gln His Lys Gln Lys Thr Ser Arg
675 680 685

Lys Pro Arg Glu Glu Arg Asp Val Ser Gln Cys Glu Ser Val Ala Ser
690 695 700

Thr Val Ser Ala Gln Glu Asp Glu Asp Ile Glu Ala Ser Asn Glu Glu
705 710 715 720

Glu Asn Pro Glu Asp Ser Glu Val Glu Ala Val Lys Pro Ser Glu Asp
725 730 735

Ser Pro Glu Asn Ala Thr Ser Arg Gly Asn Thr Glu Pro Ala Val Glu
740 745 750

Leu Glu Pro Thr Thr Glu Thr Ala Pro Ser Thr Ser Pro Ser Leu Ala
755 760 765

Val Pro Ser Thr Lys Pro Ala Glu Asp Glu Ser Val Glu Thr Gln Val
770 775 780

Asn Asp Ser Ile Ser Ala Glu Thr Ala Glu Gln Met Asp Val Asp Gln
785 790 795 800

Gln Glu His Ser Ala Glu Glu Gly Ser Val Cys Asp Pro Pro Pro Ala
805 810 815

Thr Lys Ala Asp Ser Val Asp Val Glu Val Arg Val Pro Glu Asn His
820 825 830

Ala Ser Lys Val Glu Gly Asp Asn Thr Lys Glu Arg Asp Leu Asp Arg
835 840 845

Ala Ser Glu Lys Val Glu Pro Arg Asp Glu Asp Leu Val Val Ala Gln
850 855 860

Gln Ile Asn Ala Gln Arg Pro Glu Pro Gln Ser Asp Asn Asp Ser Ser
865 870 875 880

Ala Thr Cys Ser Ala Asp Glu Asp Val Asp Gly Glu Pro Glu Arg Gln
885 890 895

Arg Met Phe Pro Met Asp Ser Lys Pro Ser Leu Leu Asn Pro Thr Gly
900 905 910

Ser Ile Leu Val Ser Ser Pro Leu Lys Pro Asn Pro Leu Asp Leu Pro
915 920 925

Gln Leu Gln His Arg Ala Ala Val Ile Pro Pro Met Val Ser Cys Thr
930 935 940

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Pro Cys Asn Ile Pro Ile Gly Thr Pro Val Ser Gly Tyr Ala Leu Tyr
945                 950                 955                 960

Gln Arg His Ile Lys Ala Met His Glu Ser Ala Leu Leu Glu Glu Gln
                965                 970                 975

Arg Gln Arg Gln Glu Gln Ile Asp Leu Glu Cys Arg Ser Ser Thr Ser
            980                 985                 990

Pro Cys Gly Thr Ser Lys Ser Pro  Asn Arg Glu Trp Glu  Val Leu Gln
        995                 1000                1005

Pro Ala  Pro His Gln Val Ile  Thr Asn Leu Pro Glu  Gly Val Arg
    1010                1015                1020

Leu Pro  Thr Thr Arg Pro Thr  Arg Pro Pro Pro Pro  Leu Ile Pro
    1025                1030                1035

Ser Ser  Lys Thr Thr Val Ala  Ser Glu Lys Pro Ser  Phe Ile Met
    1040                1045                1050

Gly Gly  Ser Ile Ser Gln Gly  Thr Pro Gly Thr Tyr  Leu Thr Ser
    1055                1060                1065

His Asn  Gln Ala Ser Tyr Thr  Gln Glu Thr Pro Lys  Pro Ser Val
    1070                1075                1080

Gly Ser  Ile Ser Leu Gly Leu  Pro Arg Gln Gln Glu  Ser Ala Lys
    1085                1090                1095

Ser Ala  Thr Leu Pro Tyr Ile  Lys Gln Glu Glu Phe  Ser Pro Arg
    1100                1105                1110

Ser Gln  Asn Ser Gln Pro Glu  Gly Leu Leu Val Arg  Ala Gln His
    1115                1120                1125

Glu Gly  Val Val Arg Gly Thr  Ala Gly Ala Ile Gln  Glu Gly Ser
    1130                1135                1140

Ile Thr  Arg Gly Thr Pro Thr  Ser Lys Ile Ser Val  Glu Ser Ile
    1145                1150                1155

Pro Ser  Leu Arg Gly Ser Ile  Thr Gln Gly Thr Pro  Ala Leu Pro
    1160                1165                1170

Gln Thr  Gly Ile Pro Thr Glu  Ala Leu Val Lys Gly  Ser Ile Ser
    1175                1180                1185

Arg Met  Pro Ile Glu Asp Ser  Ser Pro Glu Lys Gly  Arg Glu Glu
    1190                1195                1200
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Ala Ala Ser Lys Gly His Val Ile Tyr Glu Gly Lys Ser Gly His
1205 1210 1215

Ile Leu Ser Tyr Asp Asn Ile Lys Asn Ala Arg Glu Gly Thr Arg
1220 1225 1230

Ser Pro Arg Thr Ala His Glu Ile Ser Leu Lys Arg Ser Tyr Glu
1235 1240 1245

Ser Val Glu Gly Asn Ile Lys Gln Gly Met Ser Met Arg Glu Ser
1250 1255 1260

Pro Val Ser Ala Pro Leu Glu Gly Leu Ile Cys Arg Ala Leu Pro
1265 1270 1275

Arg Gly Ser Pro His Ser Asp Leu Lys Glu Arg Thr Val Leu Ser
1280 1285 1290

Gly Ser Ile Met Gln Gly Thr Pro Arg Ala Thr Thr Glu Ser Phe
1295 1300 1305

Glu Asp Gly Leu Lys Tyr Pro Lys Gln Ile Lys Arg Glu Ser Pro
1310 1315 1320

Pro Ile Arg Ala Phe Glu Gly Ala Ile Thr Lys Gly Lys Pro Tyr
1325 1330 1335

Asp Gly Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu
1340 1345 1350

Ile Pro Arg Gln Asp Ile Leu Thr Gln Glu Ser Arg Lys Thr Pro
1355 1360 1365

Glu Val Val Gln Ser Thr Arg Pro Ile Ile Glu Gly Ser Ile Ser
1370 1375 1380

Gln Gly Thr Pro Ile Lys Phe Asp Asn Asn Ser Gly Gln Ser Ala
1385 1390 1395

Ile Lys His Asn Val Lys Ser Leu Ile Thr Gly Pro Ser Lys Leu
1400 1405 1410

Ser Arg Gly Met Pro Pro Leu Glu Ile Val Pro Glu Asn Ile Lys
1415 1420 1425

Val Val Glu Arg Gly Lys Tyr Glu Asp Val Lys Ala Gly Glu Thr
1430 1435 1440

Val Arg Ser Arg His Thr Ser Val Val Ser Ser Gly Pro Ser Val
1445 1450 1455

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

1460 1465 1470

Gly Ile Tyr Asp Asp Thr Ser Ala Arg Arg Thr Pro Val Ser Tyr
1475 1480 1485

Gln Asn Thr Met Ser Arg Gly Ser Pro Met Met Asn Arg Thr Ser
1490 1495 1500

Asp Val Thr Ile Ser Ser Asn Lys Ser Thr Asn His Glu Arg Lys
1505 1510 1515

Ser Thr Leu Thr Pro Thr Gln Arg Glu Ser Ile Pro Ala Lys Ser
1520 1525 1530

Pro Val Pro Gly Val Asp Pro Val Val Ser His Ser Pro Phe Asp
1535 1540 1545

Pro His His Arg Gly Ser Thr Ala Gly Glu Val Tyr Arg Ser His
1550 1555 1560

Leu Pro Thr His Leu Asp Pro Ala Met Pro Phe His Arg Ala Leu
1565 1570 1575

Asp Pro Ala Ala Ala Ala Tyr Leu Phe Gln Arg Gln Leu Ser Pro
1580 1585 1590

Thr Pro Gly Tyr Pro Ser Gln Tyr Gln Leu Tyr Ala Met Glu Asn
1595 1600 1605

Thr Arg Gln Thr Ile Leu Asn Asp Tyr Ile Thr Ser Gln Gln Met
1610 1615 1620

Gln Val Asn Leu Arg Pro Asp Val Ala Arg Gly Leu Ser Pro Arg
1625 1630 1635

Glu Gln Pro Leu Gly Leu Pro Tyr Pro Ala Thr Arg Gly Ile Ile
1640 1645 1650

Asp Leu Thr Asn Met Pro Pro Thr Ile Leu Val Pro His Pro Gly
1655 1660 1665

Gly Thr Ser Thr Pro Pro Met Asp Arg Ile Thr Tyr Ile Pro Gly
1670 1675 1680

Thr Gln Ile Thr Phe Pro Pro Arg Pro Tyr Asn Ser Ala Ser Met
1685 1690 1695

Ser Pro Gly His Pro Thr His Leu Ala Ala Ala Ala Ser Ala Glu
1700 1705 1710

Arg Glu Arg Glu Arg Glu Arg Glu Lys Glu Arg Glu Arg Glu Arg
1715 1720 1725

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Ile Ala Ala Ala Ser Ser Asp Leu Tyr Leu Arg Pro Gly Ser Glu
1730 1735 1740

Gln Pro Gly Arg Pro Gly Ser His Gly Tyr Val Arg Ser Pro Ser
1745 1750 1755

Pro Ser Val Arg Thr Gln Glu Thr Met Leu Gln Gln Arg Pro Ser
1760 1765 1770

Val Phe Gln Gly Thr Asn Gly Thr Ser Val Ile Thr Pro Leu Asp
1775 1780 1785

Pro Thr Ala Gln Leu Arg Ile Met Pro Leu Pro Ala Gly Gly Pro
1790 1795 1800

Ser Ile Ser Gln Gly Leu Pro Ala Ser Arg Tyr Asn Thr Ala Ala
1805 1810 1815

Asp Ala Leu Ala Ala Leu Val Asp Ala Ala Ala Ser Ala Pro Gln
1820 1825 1830

Met Asp Val Ser Lys Thr Lys Glu Ile Ser Ser His Arg Tyr Glu
1835 1840 1845

Thr Pro Ser Asp Ala Ile Glu Val Ile Ser Pro Ala Ser Ser Pro
1850 1855 1860

Ala Pro Pro Gln Glu Lys Leu Gln Thr Tyr Gln Pro Glu Val Val
1865 1870 1875

Lys Ala Asn Gln Ala Glu Asn Asp Pro Thr Arg Gln Tyr Glu Gly
1880 1885 1890

Pro Leu His His Tyr Arg Pro Gln Gln Glu Ser Pro Ser Pro Gln
1895 1900 1905

Gln Gln Leu Pro Pro Ser Ser Gln Ala Glu Gly Met Gly Gln Val
1910 1915 1920

Pro Arg Thr His Arg Leu Ile Thr Leu Ala Asp His Ile Cys Gln
1925 1930 1935

Ile Ile Thr Gln Asp Phe Ala Arg Asn Gln Val Ser Ser Gln Thr
1940 1945 1950

Pro Gln Gln Pro Pro Thr Ser Thr Phe Gln Asn Ser Pro Ser Ala
1955 1960 1965

Leu Val Ser Thr Pro Val Arg Thr Lys Thr Ser Asn Arg Tyr Ser
1970 1975 1980

Pro Glu Ser Gln Ala Gln Ser Val His His Gln Arg Pro Gly Ser
1985 1990 1995

Arg Val Ser Pro Glu Asn Leu Val Asp Lys Ser Arg Gly Ser Arg
2000 2005 2010

Pro Gly Lys Ser Pro Glu Arg Ser His Val Ser Ser Glu Pro Tyr
2015 2020 2025

Glu Pro Ile Ser Pro Pro Gln Val Pro Val Val His Glu Lys Gln
2030 2035 2040

Asp Ser Leu Leu Leu Leu Ser Gln Arg Gly Ala Glu Pro Ala Glu
2045 2050 2055

Gln Arg Asn Asp Ala Arg Ser Pro Gly Ser Ile Ser Tyr Leu Pro
2060 2065 2070

Ser Phe Phe Thr Lys Leu Glu Asn Thr Ser Pro Met Val Lys Ser
2075 2080 2085

Lys Lys Gln Glu Ile Phe Arg Lys Leu Asn Ser Ser Gly Gly Gly
2090 2095 2100

Asp Ser Asp Met Ala Ala Ala Gln Pro Gly Thr Glu Ile Phe Asn
2105 2110 2115

Leu Pro Ala Val Thr Thr Ser Gly Ser Val Ser Ser Arg Gly His
2120 2125 2130

Ser Phe Ala Asp Pro Ala Ser Asn Leu Gly Leu Glu Asp Ile Ile
2135 2140 2145

Arg Lys Ala Leu Met Gly Ser Phe Asp Asp Lys Val Glu Asp His
2150 2155 2160

Gly Val Val Met Ser Gln Pro Met Gly Val Val Pro Gly Thr Ala
2165 2170 2175

Asn Thr Ser Val Val Thr Ser Gly Glu Thr Arg Arg Glu Glu Gly
2180 2185 2190

Asp Pro Ser Pro His Ser Gly Gly Val Cys Lys Pro Lys Leu Ile
2195 2200 2205

Ser Lys Ser Asn Ser Arg Lys Ser Lys Ser Pro Ile Pro Gly Gln
2210 2215 2220

Gly Tyr Leu Gly Thr Glu Arg Pro Ser Ser Val Ser Ser Val His
2225 2230 2235

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Ser Glu Gly Asp Tyr His Arg Gln Thr Pro Gly Trp Ala Trp Glu
2240 2245 2250

Asp Arg Pro Ser Ser Thr Gly Ser Thr Gln Phe Pro Tyr Asn Pro
2255 2260 2265

Leu Thr Met Arg Met Leu Ser Ser Thr Pro Pro Thr Pro Ile Ala
2270 2275 2280

Cys Ala Pro Ser Ala Val Asn Gln Ala Ala Pro His Gln Gln Asn
2285 2290 2295

Arg Ile Trp Glu Arg Glu Pro Ala Pro Leu Leu Ser Ala Gln Tyr
2300 2305 2310

Glu Thr Leu Ser Asp Ser Asp Asp
2315 2320

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Pro Arg Tyr Pro Pro His Ser Leu Ser Tyr Pro Val Gln Ile Ala Arg
20 25 30

Thr His Thr Asp Val Gly Leu Leu Glu Tyr Gln His His Ser Arg Asp
35 40 45

Tyr Ala Ser His Leu Ser Pro Gly Ser Ile Ile Gln Pro Gln Arg Arg
50 55 60

Arg Pro Ser Leu Leu Ser Glu Phe Gln Pro Gly Asn Glu Arg Ser Gln
65 70 75 80

Glu Leu His Leu Arg Pro Glu Ser His Ser Tyr Leu Pro Glu Leu Gly
85 90 95

Lys Ser Glu Met Glu Phe Ile Glu Ser Lys Arg Pro Arg Leu Glu Leu
100 105 110

Leu Pro Asp Pro Leu Leu Arg Pro Ser Pro Leu Leu Ala Thr Gly Gln
115 120 125

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

Leu Glu Pro Val Ser Pro Pro Ser Pro Pro His Thr Asp Pro Glu Leu
145 150 155 160

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Glu Leu Val Pro Pro Arg Leu Ser Lys Glu Glu Leu Ile Gln Asn Met
                165                 170                 175

Asp Arg Val Asp Arg Glu Ile Thr Met Val Glu Gln Gln Ile Ser Lys
            180                 185                 190

Leu Lys Lys Lys Gln Gln Gln Leu Glu Glu Glu Ala Ala Lys Pro Pro
        195                 200                 205

Glu Pro Glu Lys Pro Val Ser Pro Pro Pro Ile Glu Ser Lys His Arg
    210                 215                 220

Ser Leu Val Gln Ile Ile Tyr Asp Glu Asn Arg Lys Lys Ala Glu Ala
225                 230                 235                 240

Ala His Arg Ile Leu Glu Gly Leu Gly Pro Gln Val Glu Leu Pro Leu
                245                 250                 255

Tyr Asn Gln Pro Ser Asp Thr Arg Gln Tyr His Glu Asn Ile Lys Ile
            260                 265                 270

Asn Gln Ala Met Arg Lys Lys Leu Ile Leu Tyr Phe Lys Arg Arg Asn
        275                 280                 285

His Ala Arg Lys Gln Trp Lys Gln Lys Phe Cys Gln Arg Tyr Asp Gln
    290                 295                 300

Leu Met Glu Ala Leu Glu Lys Lys Val Glu Arg Ile Glu Asn Asn Pro
305                 310                 315                 320

Arg Arg Arg Ala Lys Glu Ser Lys Val Arg Glu Tyr Tyr Glu Lys Gln
                325                 330                 335

Phe Pro Glu Ile Arg Lys Gln Arg Glu Leu Gln Glu Arg Met Gln Ser
            340                 345                 350

Arg Val Gly Gln Arg Gly Ser Gly Leu Ser Met Ser Ala Ala Arg Ser
        355                 360                 365

Glu His Glu Val Ser Glu Ile Ile Asp Gly Leu Ser Glu Gln Glu Asn
    370                 375                 380

Leu Glu Lys Gln Met Arg Gln Leu Ala Val Ile Pro Pro Met Leu Tyr
385                 390                 395                 400

Asp Ala Asp Gln Gln Arg Ile Lys Phe Ile Asn Met Asn Gly Leu Met
                405                 410                 415

Ala Asp Pro Met Lys Val Tyr Lys Asp Arg Gln Val Met Asn Met Trp
            420                 425                 430
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Ser Glu Gln Glu Lys Glu Thr Phe Arg Glu Lys Phe Met Gln His Pro
435 440 445

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

Glu Cys Val Leu Tyr Tyr Tyr Leu Thr Lys Lys Asn Glu Asn Tyr Lys
465 470 475 480

Ser Leu Val Arg Arg Ser Tyr Arg Arg Arg Gly Lys Ser Gln Gln Gln
485 490 495

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Met
500 505 510

Pro Arg Ser Ser Gln Glu Glu Lys Asp Glu Lys Glu Lys Glu Lys Glu
515 520 525

Ala Glu Lys Glu Glu Glu Lys Pro Glu Val Glu Asn Asp Lys Glu Asp
530 535 540

Leu Leu Lys Glu Lys Thr Asp Asp Thr Ser Gly Glu Asp Asn Asp Glu
545 550 555 560

Lys Glu Ala Val Ala Ser Lys Gly Arg Lys Thr Ala Asn Ser Gln Gly
565 570 575

Arg Arg Lys Gly Arg Ile Thr Arg Ser Met Ala Asn Glu Ala Asn Ser
580 585 590

Glu Glu Ala Ile Thr Pro Gln Gln Ser Ala Glu Leu Ala Ser Met Glu
595 600 605

Leu Asn Glu Ser Ser Arg Trp Thr Glu Glu Glu Met Glu Thr Ala Lys
610 615 620

Lys Gly Leu Leu Glu His Gly Arg Asn Trp Ser Ala Ile Ala Arg Met
625 630 635 640

Val Gly Ser Lys Thr Val Ser Gln Cys Lys Asn Phe Tyr Phe Asn Tyr
645 650 655

Lys Lys Arg Gln Asn Leu Asp Glu Ile Leu Gln Gln His Lys Leu Lys
660 665 670

Met Glu Lys Glu Arg Asn Ala Arg Arg Lys Lys Lys Lys Ala Pro Ala
675 680 685

Ala Ala Ser Glu Glu Ala Ala Phe Pro Pro Val Val Glu Asp Glu Glu
690 695 700

Met Glu Ala Ser Gly Val Ser Gly Asn Glu Glu Glu Met Val Glu Glu

705 710 715 720

Ala Glu Ala Leu His Ala Ser Gly Asn Glu Val Pro Arg Gly Glu Cys
725 730 735

Ser Gly Pro Ala Thr Val Asn Asn Ser Ser Asp Thr Glu Ser Ile Pro
740 745 750

Ser Pro His Thr Glu Ala Ala Lys Asp Thr Gly Gln Asn Gly Pro Lys
755 760 765

Pro Pro Ala Thr Leu Gly Ala Asp Gly Pro Pro Pro Gly Pro Pro Thr
770 775 780

Pro Pro Arg Arg Thr Ser Arg Ala Pro Ile Glu Pro Thr Pro Ala Ser
785 790 795 800

Glu Ala Thr Gly Ala Pro Thr Pro Pro Pro Ala Pro Pro Ser Pro Ser
805 810 815

Ala Pro Pro Pro Val Val Pro Lys Glu Glu Lys Glu Glu Glu Thr Ala
820 825 830

Ala Ala Pro Pro Val Glu Glu Gly Glu Glu Gln Lys Pro Pro Ala Ala
835 840 845

Glu Glu Leu Ala Val Asp Thr Gly Lys Ala Glu Glu Pro Val Lys Ser
850 855 860

Glu Cys Thr Glu Glu Ala Glu Glu Gly Pro Ala Lys Gly Lys Asp Ala
865 870 875 880

Glu Ala Ala Glu Ala Thr Ala Glu Gly Ala Leu Lys Ala Glu Lys Lys
885 890 895

Glu Gly Gly Ser Gly Arg Ala Thr Thr Ala Lys Ser Ser Gly Ala Pro
900 905 910

Gln Asp Ser Asp Ser Ser Ala Thr Cys Ser Ala Asp Glu Val Asp Glu
915 920 925

Ala Glu Gly Gly Asp Lys Asn Arg Leu Leu Ser Pro Arg Pro Ser Leu
930 935 940

Leu Thr Pro Thr Gly Asp Pro Arg Ala Asn Ala Ser Pro Gln Lys Pro
945 950 955 960

Leu Asp Leu Lys Gln Leu Lys Gln Arg Ala Ala Ala Ile Pro Pro Ile
965 970 975

Gln Val Thr Lys Val His Glu Pro Pro Arg Glu Asp Ala Ala Pro Thr
980 985 990

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Lys Pro Ala Pro Pro Ala Pro Pro Pro Pro Gln Asn Leu Gln Pro Glu
995 1000 1005

Ser Asp Ala Pro Gln Gln Pro Gly Ser Ser Pro Arg Gly Lys Ser
1010 1015 1020

Arg Ser Pro Ala Pro Pro Ala Asp Lys Glu Ala Phe Ala Ala Glu
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Ala Gln Lys Leu Pro Gly Asp Pro Pro Cys Trp Thr Ser Gly Leu
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Pro Phe Pro Val Pro Pro Arg Glu Val Ile Lys Ala Ser Pro His
1055 1060 1065

Ala Pro Asp Pro Ser Ala Phe Ser Tyr Ala Pro Pro Gly His Pro
1070 1075 1080

Leu Pro Leu Gly Leu His Asp Thr Ala Arg Pro Val Leu Pro Arg
1085 1090 1095

Pro Pro Thr Ile Ser Asn Pro Pro Pro Leu Ile Ser Ser Ala Lys
1100 1105 1110

His Pro Ser Val Leu Glu Arg Gln Ile Gly Ala Ile Ser Gln Gly
1115 1120 1125

Met Ser Val Gln Leu His Val Pro Tyr Ser Glu His Ala Lys Ala
1130 1135 1140

Pro Val Gly Pro Val Thr Met Gly Leu Pro Leu Pro Met Asp Pro
1145 1150 1155

Lys Lys Leu Ala Pro Phe Ser Gly Val Lys Gln Glu Gln Leu Ser
1160 1165 1170

Pro Arg Gly Gln Ala Gly Pro Pro Glu Ser Leu Gly Val Pro Thr
1175 1180 1185

Ala Gln Glu Ala Ser Val Leu Arg Gly Thr Ala Leu Gly Ser Val
1190 1195 1200

Pro Gly Gly Ser Ile Thr Lys Gly Ile Pro Ser Thr Arg Val Pro
1205 1210 1215

Ser Asp Ser Ala Ile Thr Tyr Arg Gly Ser Ile Thr His Gly Thr
1220 1225 1230

Pro Ala Asp Val Leu Tyr Lys Gly Thr Ile Thr Arg Ile Ile Gly
1235 1240 1245

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Glu Asp Ser Pro Ser Arg Leu Asp Arg Gly Arg Glu Asp Ser Leu
1250 1255 1260

Pro Lys Gly His Val Ile Tyr Glu Gly Lys Lys Gly His Val Leu
1265 1270 1275

Ser Tyr Glu Gly Gly Met Ser Val Thr Gln Cys Ser Lys Glu Asp
1280 1285 1290

Gly Arg Ser Ser Ser Gly Pro Pro His Glu Thr Ala Ala Pro Lys
1295 1300 1305

Arg Thr Tyr Asp Met Met Glu Gly Arg Val Gly Arg Ala Ile Ser
1310 1315 1320

Ser Ala Ser Ile Glu Gly Leu Met Gly Arg Ala Ile Pro Pro Glu
1325 1330 1335

Arg His Ser Pro His His Leu Lys Glu Gln His His Ile Arg Gly
1340 1345 1350

Ser Ile Thr Gln Gly Ile Pro Arg Ser Tyr Val Glu Ala Gln Glu
1355 1360 1365

Asp Tyr Leu Arg Arg Glu Ala Lys Leu Leu Lys Arg Glu Gly Thr
1370 1375 1380

Pro Pro Pro Pro Pro Pro Ser Arg Asp Leu Thr Glu Ala Tyr Lys
1385 1390 1395

Thr Gln Ala Leu Gly Pro Leu Lys Leu Lys Pro Ala His Glu Gly
1400 1405 1410

Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile
1415 1420 1425

Pro Arg Glu Glu Leu Arg His Thr Pro Glu Leu Pro Leu Ala Pro
1430 1435 1440

Arg Pro Leu Lys Glu Gly Ser Ile Thr Gln Gly Thr Pro Leu Lys
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Tyr Asp Thr Gly Ala Ser Thr Thr Gly Ser Lys Lys His Asp Val
1460 1465 1470

Arg Ser Leu Ile Gly Ser Pro Gly Arg Thr Phe Pro Pro Val His
1475 1480 1485

Pro Leu Asp Val Met Ala Asp Ala Arg Ala Leu Glu Arg Ala Cys
1490 1495 1500

Tyr Glu Glu Ser Leu Lys Ser Arg Pro Gly Thr Ala Ser Ser Ser
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Gly Gly Ser Ile Ala Arg Gly Ala Pro Val Ile Val Pro Glu Leu
1520 1525 1530

Gly Lys Pro Arg Gln Ser Pro Leu Thr Tyr Glu Asp His Gly Ala
1535 1540 1545

Pro Phe Ala Gly His Leu Pro Arg Gly Ser Pro Val Thr Met Arg
1550 1555 1560

Glu Pro Thr Pro Arg Leu Gln Glu Gly Ser Leu Ser Ser Ser Lys
1565 1570 1575

Ala Ser Gln Asp Arg Lys Leu Thr Ser Thr Pro Arg Glu Ile Ala
1580 1585 1590

Lys Ser Pro His Ser Thr Val Pro Glu His His Pro His Pro Ile
1595 1600 1605

Ser Pro Tyr Glu His Leu Leu Arg Gly Val Ser Gly Val Asp Leu
1610 1615 1620

Tyr Arg Ser His Ile Pro Leu Ala Phe Asp Pro Thr Ser Ile Pro
1625 1630 1635

Arg Gly Ile Pro Leu Asp Ala Ala Ala Ala Tyr Tyr Leu Pro Arg
1640 1645 1650

His Leu Ala Pro Asn Pro Thr Tyr Pro His Leu Tyr Pro Pro Tyr
1655 1660 1665

Leu Ile Arg Gly Tyr Pro Asp Thr Ala Ala Leu Glu Asn Arg Gln
1670 1675 1680

Thr Ile Ile Asn Asp Tyr Ile Thr Ser Gln Gln Met His His Asn
1685 1690 1695

Thr Ala Thr Ala Met Ala Gln Arg Ala Asp Met Leu Arg Gly Leu
1700 1705 1710

Ser Pro Arg Glu Ser Ser Leu Ala Leu Asn Tyr Ala Ala Gly Pro
1715 1720 1725

Arg Gly Ile Ile Asp Leu Ser Gln Val Pro His Leu Pro Val Leu
1730 1735 1740

Val Pro Pro Thr Pro Gly Thr Pro Ala Thr Ala Met Asp Arg Leu
1745 1750 1755

Ala Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser

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1760 1765 1770

Ser Ser Pro Leu Ser Pro Gly Gly Pro Thr His Leu Thr Lys Pro
1775 1780 1785

Thr Thr Thr Ser Ser Ser Glu Arg Glu Arg Asp Arg Asp Arg Glu
1790 1795 1800

Arg Asp Arg Asp Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr
1805 1810 1815

Thr Thr Val Glu His Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln
1820 1825 1830

Ser Ser Gly Ser Ser Gly Ser Ser Gly Gly Gly Gly Gly Ser Ser
1835 1840 1845

Ser Arg Pro Ala Ser His Ser His Ala His Gln His Ser Pro Ile
1850 1855 1860

Ser Pro Arg Thr Gln Asp Ala Leu Gln Gln Arg Pro Ser Val Leu
1865 1870 1875

His Asn Thr Gly Met Lys Gly Ile Ile Thr Ala Val Glu Pro Ser
1880 1885 1890

Lys Pro Thr Val Leu Arg Ser Thr Ser Thr Ser Ser Pro Val Arg
1895 1900 1905

Pro Ala Ala Thr Phe Pro Pro Ala Thr His Cys Pro Leu Gly Gly
1910 1915 1920

Thr Leu Asp Gly Val Tyr Pro Thr Leu Met Glu Pro Val Leu Leu
1925 1930 1935

Pro Lys Glu Ala Pro Arg Val Ala Arg Pro Glu Arg Pro Arg Ala
1940 1945 1950

Asp Thr Gly His Ala Phe Leu Ala Lys Pro Pro Ala Arg Ser Gly
1955 1960 1965

Leu Glu Pro Ala Ser Ser Pro Ser Lys Gly Ser Glu Pro Arg Pro
1970 1975 1980

Leu Val Pro Pro Val Ser Gly His Ala Thr Ile Ala Arg Thr Pro
1985 1990 1995

Ala Lys Asn Leu Ala Pro His His Ala Ser Pro Asp Pro Pro Ala
2000 2005 2010

Pro Pro Ala Ser Ala Ser Asp Pro His Arg Glu Lys Thr Gln Ser
2015 2020 2025

Lys Pro Phe Ser Ile Gln Glu Leu Glu Leu Arg Ser Leu Gly Tyr
2030 2035 2040

His Gly Ser Ser Tyr Ser Pro Gln Cys Ala Arg Ser Gly Pro His
2045 2050 2055

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

Val Gly Gly Gln Lys Gly Gln Val Arg Pro Gly Gly Asn Gly Cys
2075 2080 2085

Ser Glu Asp Trp Thr Val Phe Phe Thr His Arg Cys Arg Ser Gly
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Gly Lys Glu Arg Gln Met
2105

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20 25 30

Ile Phe Arg His Tyr Asp Asp Phe Phe Glu Arg Thr Ile Leu Cys Asn
35 40 45

Ser Leu Val Trp Ser Cys Ala Val Thr Gly Arg Pro Gly Leu Thr Tyr
50 55 60

Gln Glu Ala Leu Glu Ser Glu Lys Lys Ala Arg Gln Asn Leu Gln Ser
65 70 75 80

Phe Pro Glu Pro Leu Ile Ile Pro Val Leu Tyr Leu Thr Ser Leu Thr
85 90 95

His Arg Ser Arg Leu His Glu Ile Cys Asp Asp Ile Phe Ala Tyr Val
100 105 110

Lys Asp Arg Tyr Phe Val Glu Glu Thr Val Glu Val Ile Arg Asn Asn
115 120 125

Gly Ala Arg Leu Gln Cys Arg Ile Leu Glu Val Leu Pro Pro Ser His
130 135 140

Gln Asn Gly Phe Ala Asn Gly His Val Asn Ser Val Asp Gly Glu Thr

145 150 155 160

Ile Ile Ile Ser Asp Ser Asp Asp Ser Glu Thr Gln Ser Cys Ser Phe
165 170 175

Gln Asn Gly Lys Lys Lys Asp Ala Ile Asp Pro Leu Leu Phe Lys Tyr
180 185 190

Lys Val Gln Pro Thr Lys Lys Glu Leu His Glu Ser Ala Ile Val Lys
195 200 205

Ala Thr Gln Ile Ser Arg Arg Lys His Leu Phe Ser Arg Asp Lys Leu
210 215 220

Lys Leu Phe Leu Lys Gln His Cys Glu Pro Gln Asp Gly Val Ile Lys
225 230 235 240

Ile Lys Ala Ser Ser Leu Ser Thr Tyr Lys Ile Ala Glu Gln Asp Phe
245 250 255

Ser Tyr Phe Phe Pro Asp Asp Pro Pro Thr Phe Ile Phe Ser Pro Ala
260 265 270

Asn Arg Arg Arg Gly Arg Pro Pro Lys Arg Ile His Ile Ser Gln Glu
275 280 285

Asp Asn Val Ala Asn Lys Gln Thr Leu Ala Ser Tyr Arg Ser Lys Ala
290 295 300

Thr Lys Glu Arg Asp Lys Leu Leu Lys Gln Glu Glu Met Lys Ser Leu
305 310 315 320

Ala Phe Glu Lys Ala Lys Leu Lys Arg Glu Lys Ala Asp Ala Leu Glu
325 330 335

Ala Lys Lys Lys Glu Lys Glu Asp Lys Glu Lys Lys Arg Glu Glu Leu
340 345 350

Lys Lys Ile Val Glu Glu Glu Arg Leu Lys Lys Lys Glu Glu Lys Glu
355 360 365

Arg Leu Lys Val Glu Arg Glu Lys Glu Arg Glu Lys Leu Arg Glu Glu
370 375 380

Lys Arg Lys Tyr Val Glu Tyr Leu Lys Gln Trp Ser Lys Pro Arg Glu
385 390 395 400

Asp Met Glu Cys Asp Asp Leu Lys Glu Leu Pro Glu Pro Thr Pro Val
405 410 415

Lys Thr Arg Leu Pro Pro Glu Ile Phe Gly Asp Ala Leu Met Val Leu
420 425 430

Glu Phe Leu Asn Ala Phe Gly Glu Leu Phe Asp Leu Gln Asp Glu Phe
435 440 445

Pro Asp Gly Val Thr Leu Glu Val Leu Glu Glu Ala Leu Val Gly Asn
450 455 460

Asp Ser Glu Gly Pro Leu Cys Glu Leu Leu Phe Phe Phe Leu Thr Ala
465 470 475 480

Ile Phe Gln Ala Ile Ala Glu Glu Glu Glu Glu Val Ala Lys Glu Gln
485 490 495

Leu Thr Asp Ala Asp Thr Lys Gly Cys Ser Leu Lys Ser Leu Asp Leu
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Asp Ser Cys Thr Leu Ser Glu Ile Leu Arg Leu His Ile Leu Ala Ser
515 520 525

Gly Ala Asp Val Thr Ser Ala Asn Ala Lys Tyr Arg Tyr Gln Lys Arg
530 535 540

Gly Gly Phe Asp Ala Thr Asp Asp Ala Cys Met Glu Leu Arg Leu Ser
545 550 555 560

Asn Pro Ser Leu Val Lys Lys Leu Ser Ser Thr Ser Val Tyr Asp Leu
565 570 575

Thr Pro Gly Glu Lys Met Lys Ile Leu His Ala Leu Cys Gly Lys Leu
580 585 590

Leu Thr Leu Val Ser Thr Arg Asp Phe Ile Glu Asp Tyr Val Asp Ile
595 600 605

Leu Arg Gln Ala Lys Gln Glu Phe Arg Glu Leu Lys Ala Glu Gln His
610 615 620

Arg Lys Glu Arg Glu Glu Ala Ala Ala Arg Ile Arg Lys Arg Lys Glu
625 630 635 640

Glu Lys Leu Lys Glu Gln Glu Gln Lys Met Lys Glu Lys Gln Glu Lys
645 650 655

Leu Lys Glu Asp Glu Gln Arg Asn Ser Thr Ala Asp Ile Ser Ile Gly
660 665 670

Glu Glu Glu Arg Glu Asp Phe Asp Thr Ser Ile Glu Ser Lys Asp Thr
675 680 685

Glu Gln Lys Glu Leu Asp Gln Asp Met Val Thr Glu Asp Glu Asp Asp
690 695 700

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Pro Gly Ser His Lys Arg Gly Arg Arg Gly Lys Arg Gly Gln Asn Gly
705                 710                 715                 720

Phe Lys Glu Phe Thr Arg Gln Glu Gln Ile Asn Cys Val Thr Arg Glu
                725                 730                 735

Pro Leu Thr Ala Asp Glu Glu Glu Ala Leu Lys Gln Glu His Gln Arg
            740                 745                 750

Lys Glu Lys Glu Leu Leu Glu Lys Ile Gln Ser Ala Ile Ala Cys Thr
        755                 760                 765

Asn Ile Phe Pro Leu Gly Arg Asp Arg Met Tyr Arg Arg Tyr Trp Ile
    770                 775                 780

Phe Pro Ser Ile Pro Gly Leu Phe Ile Glu Glu Asp Tyr Ser Gly Leu
785                 790                 795                 800

Thr Glu Asp Met Leu Leu Pro Arg Pro Ser Ser Phe Gln Asn Asn Val
                805                 810                 815

Gln Ser Gln Asp Pro Gln Val Ser Thr Lys Thr Gly Glu Pro Leu Met
            820                 825                 830

Ser Glu Ser Thr Ser Asn Ile Asp Gln Gly Pro Arg Asp His Ser Val
        835                 840                 845

Gln Leu Pro Lys Pro Val His Lys Pro Asn Arg Trp Cys Phe Tyr Ser
    850                 855                 860

Ser Cys Glu Gln Leu Asp Gln Leu Ile Glu Ala Leu Asn Ser Arg Gly
865                 870                 875                 880

His Arg Glu Ser Ala Leu Lys Glu Thr Leu Leu Gln Glu Lys Ser Arg
                885                 890                 895

Ile Cys Ala Gln Leu Ala Arg Phe Ser Glu Glu Lys Phe His Phe Ser
            900                 905                 910

Asp Lys Pro Gln Pro Asp Ser Lys Pro Thr Tyr Ser Arg Gly Arg Ser
        915                 920                 925

Ser Asn Ala Tyr Asp Pro Ser Gln Met Cys Ala Glu Lys Gln Leu Glu
    930                 935                 940

Leu Arg Leu Arg Asp Phe Leu Leu Asp Ile Glu Asp Arg Ile Tyr Gln
945                 950                 955                 960

Gly Thr Leu Gly Ala Ile Lys Val Thr Asp Arg His Ile Trp Arg Ser
                965                 970                 975
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Ala Leu Glu Ser Gly Arg Tyr Glu Leu Leu Ser Glu Glu Asn Lys Glu
            980                 985                 990

Asn Gly Ile Ile Lys Thr Val Asn  Glu Asp Val Glu Glu  Met Glu Ile
        995                1000                1005

Asp Glu  Gln Thr Lys Val Ile  Val Lys Asp Arg Leu  Leu Gly Ile
    1010                1015                1020

Lys Thr  Glu Thr Pro Ser Thr  Val Ser Thr Asn Ala  Ser Thr Pro
    1025                1030                1035

Gln Ser  Val Ser Ser Val Val  His Tyr Leu Ala Met  Ala Leu Phe
    1040                1045                1050

Gln Ile  Glu Gln Gly Ile Glu  Arg Arg Phe Leu Lys  Ala Pro Leu
    1055                1060                1065

Asp Ala  Ser Asp Ser Gly Arg  Ser Tyr Lys Thr Val  Leu Asp Arg
    1070                1075                1080

Trp Arg  Glu Ser Leu Leu Ser  Ser Ala Ser Leu Ser  Gln Val Phe
    1085                1090                1095

Leu His  Leu Ser Thr Leu Asp  Arg Ser Val Ile Trp  Ser Lys Ser
    1100                1105                1110

Ile Leu  Asn Ala Arg Cys Lys  Ile Cys Arg Lys Lys  Gly Asp Ala
    1115                1120                1125

Glu Asn  Met Val Leu Cys Asp  Gly Cys Asp Arg Gly  His His Thr
    1130                1135                1140

Tyr Cys  Val Arg Pro Lys Leu  Lys Thr Val Pro Glu  Gly Asp Trp
    1145                1150                1155

Phe Cys  Pro Glu Cys Arg Pro  Lys Gln Arg Ser Arg  Arg Leu Ser
    1160                1165                1170

Ser Arg  Gln Arg Pro Ser Leu  Glu Ser Asp Glu Asp  Val Glu Asp
    1175                1180                1185

Ser Met  Gly Gly Glu Asp Asp  Glu Val Asp Gly Asp  Glu Glu Glu
    1190                1195                1200

Gly Gln  Ser Glu Glu Glu Glu  Tyr Glu Val Glu Gln  Asp Glu Asp
    1205                1210                1215

Asp Ser  Gln Glu Glu Glu Glu  Val Ser Leu Pro Lys  Arg Gly Arg
    1220                1225                1230

Pro Gln  Val Arg Leu Pro Val  Lys Thr Arg Gly Lys  Leu Ser Ser
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Ser Phe Ser Ser Arg Gly Gln Gln Gln Glu Pro Gly Arg Tyr Pro
1250 1255 1260

Ser Arg Ser Gln Gln Ser Thr Pro Lys Thr Thr Val Ser Ser Lys
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Thr Gly Arg Ser Leu Arg Lys Ile Asn Ser Ala Pro Pro Thr Glu
1280 1285 1290

Thr Lys Ser Leu Arg Ile Ala Ser Arg Ser Thr Arg His Ser His
1295 1300 1305

Gly Pro Leu Gln Ala Asp Val Phe Val Glu Leu Leu Ser Pro Arg
1310 1315 1320

Arg Lys Arg Arg Gly Arg Lys Ser Ala Asn Lys Thr Pro Glu Asn
1325 1330 1335

Ser Pro Asn Phe Pro Asn Phe Arg Val Ile Ala Thr Lys Ser Ser
1340 1345 1350

Glu Gln Ser Arg Ser Val Asn Ile Ala Ser Lys Leu Ser Leu Gln
1355 1360 1365

Glu Ser Glu Ser Lys Arg Arg Cys Lys Lys Arg Gln Ser Pro Glu
1370 1375 1380

Pro Ser Pro Val Thr Leu Gly Arg Arg Ser Ser Gly Arg Gln Gly
1385 1390 1395

Gly Val His Glu Leu Ser Ala Phe Glu Gln Leu Val Val Glu Leu
1400 1405 1410

Val Arg His Asp Asp Ser Trp Pro Phe Leu Lys Leu Val Ser Lys
1415 1420 1425

Ile Gln Val Pro Asp Tyr Tyr Asp Ile Ile Lys Lys Pro Ile Ala
1430 1435 1440

Leu Asn Ile Ile Arg Glu Lys Val Asn Lys Cys Glu Tyr Lys Leu
1445 1450 1455

Ala Ser Glu Phe Ile Asp Asp Ile Glu Leu Met Phe Ser Asn Cys
1460 1465 1470

Phe Glu Tyr Asn Pro Arg Asn Thr Ser Glu Ala Lys Ala Gly Thr
1475 1480 1485

Arg Leu Gln Ala Phe Phe His Ile Gln Ala Gln Lys Leu Gly Leu
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His Val Thr Pro Ser Asn Val Asp Gln Val Ser Thr Pro Pro Ala
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Ala Lys Lys Ser Arg Ile
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Ile Phe Arg His Tyr Asp Asp Phe Phe Glu Arg Thr Ile Leu Cys Asn
35 40 45

Ser Leu Val Trp Ser Cys Ala Val Thr Gly Arg Pro Gly Leu Thr Tyr
50 55 60

Gln Glu Ala Leu Glu Ser Glu Lys Lys Ala Arg Gln Asn Leu Gln Ser
65 70 75 80

Phe Pro Glu Pro Leu Ile Ile Pro Val Leu Tyr Leu Thr Ser Leu Thr
85 90 95

His Arg Ser Arg Leu His Glu Ile Cys Asp Asp Ile Phe Ala Tyr Val
100 105 110

Lys Asp Arg Tyr Phe Val Glu Glu Thr Val Glu Val Ile Arg Asn Asn
115 120 125

Gly Ala Arg Leu Gln Cys Arg Ile Leu Glu Val Leu Pro Pro Ser His
130 135 140

Gln Asn Gly Phe Ala Asn Gly His Val Asn Ser Val Asp Gly Glu Thr
145 150 155 160

Ile Ile Ile Ser Asp Ser Asp Asp Ser Glu Thr Gln Ser Cys Ser Phe
165 170 175

Gln Asn Gly Lys Lys Lys Asp Ala Ile Asp Pro Leu Leu Phe Lys Tyr
180 185 190

Lys Val Gln Pro Thr Lys Lys Glu Leu His Glu Ser Ala Ile Val Lys
195 200 205

Ala Thr Gln Ile Ser Arg Arg Lys His Leu Phe Ser Arg Asp Lys Leu

210 215 220

Lys Leu Phe Leu Lys Gln His Cys Glu Pro Gln Asp Gly Val Ile Lys
225 230 235 240

Ile Lys Ala Ser Ser Leu Ser Thr Tyr Lys Ile Ala Glu Gln Asp Phe
245 250 255

Ser Tyr Phe Phe Pro Asp Asp Pro Pro Thr Phe Ile Phe Ser Pro Ala
260 265 270

Asn Arg Arg Arg Gly Arg Pro Pro Lys Arg Ile His Ile Ser Gln Glu
275 280 285

Asp Asn Val Ala Asn Lys Gln Thr Leu Ala Ser Tyr Arg Ser Lys Ala
290 295 300

Thr Lys Glu Arg Asp Lys Leu Leu Lys Gln Glu Glu Met Lys Ser Leu
305 310 315 320

Ala Phe Glu Lys Ala Lys Leu Lys Arg Glu Lys Ala Asp Ala Leu Glu
325 330 335

Ala Lys Lys Lys Glu Lys Glu Asp Lys Glu Lys Lys Arg Glu Glu Leu
340 345 350

Lys Lys Ile Val Glu Glu Glu Arg Leu Lys Lys Lys Glu Glu Lys Glu
355 360 365

Arg Leu Lys Val Glu Arg Glu Lys Glu Arg Glu Lys Leu Arg Glu Glu
370 375 380

Lys Arg Lys Tyr Val Glu Tyr Leu Lys Gln Trp Ser Lys Pro Arg Glu
385 390 395 400

Asp Met Glu Cys Asp Asp Leu Lys Glu Leu Pro Glu Pro Thr Pro Val
405 410 415

Lys Thr Arg Leu Pro Pro Glu Ile Phe Gly Asp Ala Leu Met Val Leu
420 425 430

Glu Phe Leu Asn Ala Phe Gly Glu Leu Phe Asp Leu Gln Asp Glu Phe
435 440 445

Pro Asp Gly Val Thr Leu Glu Val Leu Glu Glu Ala Leu Val Gly Asn
450 455 460

Asp Ser Glu Gly Pro Leu Cys Glu Leu Leu Phe Phe Phe Leu Thr Ala
465 470 475 480

Ile Phe Gln Ala Ile Ala Glu Glu Glu Glu Glu Val Ala Lys Glu Gln
485 490 495

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Leu Thr Asp Ala Asp Thr Lys Gly Lys Arg Gly Gln Asn Gly Phe Lys
500 505 510

Glu Phe Thr Arg Gln Glu Gln Ile Asn Cys Val Thr Arg Glu Pro Leu
515 520 525

Thr Ala Asp Glu Glu Glu Ala Leu Lys Gln Glu His Gln Arg Lys Glu
530 535 540

Lys Glu Leu Leu Glu Lys Ile Gln Ser Ala Ile Ala Cys Thr Asn Ile
545 550 555 560

Phe Pro Leu Gly Arg Asp Arg Met Tyr Arg Arg Tyr Trp Ile Phe Pro
565 570 575

Ser Ile Pro Gly Leu Phe Ile Glu Glu Asp Tyr Ser Gly Leu Thr Glu
580 585 590

Asp Met Leu Leu Pro Arg Pro Ser Ser Phe Gln Asn Asn Val Gln Ser
595 600 605

Gln Asp Pro Gln Val Ser Thr Lys Thr Gly Glu Pro Leu Met Ser Glu
610 615 620

Ser Thr Ser Asn Ile Asp Gln Gly Pro Arg Asp His Ser Val Gln Leu
625 630 635 640

Pro Lys Pro Val His Lys Pro Asn Arg Trp Cys Phe Tyr Ser Ser Cys
645 650 655

Glu Gln Leu Asp Gln Leu Ile Glu Ala Leu Asn Ser Arg Gly His Arg
660 665 670

Glu Ser Ala Leu Lys Glu Thr Leu Leu Gln Glu Lys Ser Arg Ile Cys
675 680 685

Ala Gln Leu Ala Arg Phe Ser Glu Glu Lys Phe His Phe Ser Asp Lys
690 695 700

Pro Gln Pro Asp Ser Lys Pro Thr Tyr Ser Arg Gly Arg Ser Ser Asn
705 710 715 720

Ala Tyr Asp Pro Ser Gln Met Cys Ala Glu Lys Gln Leu Glu Leu Arg
725 730 735

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

Leu Gly Ala Ile Lys Val Thr Asp Arg His Ile Trp Arg Ser Ala Leu
755 760 765

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Glu Ser Gly Arg Tyr Glu Leu Ser Glu Glu Asn Lys Glu Asn Gly
770 775 780

Ile Ile Lys Thr Val Asn Glu Asp Val Glu Glu Met Glu Ile Asp Glu
785 790 795 800

Gln Thr Lys Val Ile Val Lys Asp Arg Leu Leu Gly Ile Lys Thr Glu
805 810 815

Thr Pro Ser Thr Val Ser Thr Asn Ala Ser Thr Pro Gln Ser Val Ser
820 825 830

Ser Val Val His Tyr Leu Ala Met Ala Leu Phe Gln Ile Glu Gln Gly
835 840 845

Ile Glu Arg Arg Phe Leu Lys Ala Pro Leu Asp Ala Ser Asp Ser Gly
850 855 860

Arg Ser Tyr Lys Thr Val Leu Asp Arg Trp Arg Glu Ser Leu Leu Ser
865 870 875 880

Ser Ala Ser Leu Ser Gln Val Phe Leu His Leu Ser Thr Leu Asp Arg
885 890 895

Ser Val Ile Trp Ser Lys Ser Ile Leu Asn Ala Arg Cys Lys Ile Cys
900 905 910

Arg Lys Lys Gly Asp Ala Glu Asn Met Val Leu Cys Asp Gly Cys Asp
915 920 925

Arg Gly His His Thr Tyr Cys Val Arg Pro Lys Leu Lys Thr Val Pro
930 935 940

Glu Gly Asp Trp Phe Cys Pro Glu Cys Arg Pro Lys Gln Arg Ser Arg
945 950 955 960

Arg Leu Ser Ser Arg Gln Arg Pro Ser Leu Glu Ser Asp Glu Asp Val
965 970 975

Glu Asp Ser Met Gly Gly Glu Asp Asp Glu Val Asp Gly Asp Glu Glu
980 985 990

Glu Gly Gln Ser Glu Glu Glu Glu Tyr Glu Val Glu Gln Asp Glu Asp
995 1000 1005

Asp Ser Gln Glu Glu Glu Glu Val Ser Leu Pro Lys Arg Gly Arg
1010 1015 1020

Pro Gln Val Arg Leu Pro Val Lys Thr Arg Gly Lys Leu Ser Ser
1025 1030 1035

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Ser Phe Ser Ser Arg Gly Gln Gln Gln Glu Pro Gly Arg Tyr Pro
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Ser Arg Ser Gln Gln Ser Thr Pro Lys Thr Thr Val Ser Ser Lys
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Thr Gly Arg Ser Leu Arg Lys Ile Asn Ser Ala Pro Pro Thr Glu
1070 1075 1080

Thr Lys Ser Leu Arg Ile Ala Ser Arg Ser Thr Arg His Ser His
1085 1090 1095

Gly Pro Leu Gln Ala Asp Val Phe Val Glu Leu Leu Ser Pro Arg
1100 1105 1110

Arg Lys Arg Arg Gly Arg Lys Ser Ala Asn Lys Thr Pro Glu Asn
1115 1120 1125

Ser Pro Asn Phe Pro Asn Phe Arg Val Ile Ala Thr Lys Ser Ser
1130 1135 1140

Glu Gln Ser Arg Ser Val Asn Ile Ala Ser Lys Leu Ser Leu Gln
1145 1150 1155

Glu Ser Glu Ser Lys Arg Arg Cys Lys Lys Arg Gln Ser Pro Glu
1160 1165 1170

Pro Ser Pro Val Thr Leu Gly Arg Arg Ser Ser Gly Arg Gln Gly
1175 1180 1185

Gly Val His Glu Leu Ser Ala Phe Glu Gln Leu Val Val Glu Leu
1190 1195 1200

Val Arg His Asp Asp Ser Trp Pro Phe Leu Lys Leu Val Ser Lys
1205 1210 1215

Ile Gln Val Pro Asp Tyr Tyr Asp Ile Ile Lys Lys Pro Ile Ala
1220 1225 1230

Leu Asn Ile Ile Arg Glu Lys Val Asn Lys Cys Glu Tyr Lys Leu
1235 1240 1245

Ala Ser Glu Phe Ile Asp Asp Ile Glu Leu Met Phe Ser Asn Cys
1250 1255 1260

Phe Glu Tyr Asn Pro Arg Asn Thr Ser Glu Ala Lys Ala Gly Thr
1265 1270 1275

Arg Leu Gln Ala Phe Phe His Ile Gln Ala Gln Lys Leu Gly Leu
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His Val Thr Pro Ser Asn Val Asp Gln Val Ser Thr Pro Pro Ala

1295 1300 1305

Ala Lys Lys Ser Arg Ile
1310

<210> 207
<211> 1463
<212> PRT
<213> Homo sapiens

<400> 207
Met Pro Leu Leu His Arg Lys Pro Phe Val Arg Gln Lys Pro Pro Ala
1 5 10 15

Asp Leu Arg Pro Asp Glu Glu Val Phe Tyr Cys Lys Val Thr Asn Glu
20 25 30

Ile Phe Arg His Tyr Glu Leu Gln Cys Arg Ile Leu Glu Val Leu Pro
35 40 45

Pro Ser His Gln Asn Gly Phe Ala Asn Gly His Val Asn Ser Val Asp
50 55 60

Gly Glu Thr Ile Ile Ile Ser Asp Ser Asp Asp Ser Glu Thr Gln Ser
65 70 75 80

Cys Ser Phe Gln Asn Gly Lys Lys Lys Asp Ala Ile Asp Pro Leu Leu
85 90 95

Phe Lys Tyr Lys Val Gln Pro Thr Lys Lys Glu Leu His Glu Ser Ala
100 105 110

Ile Val Lys Ala Thr Gln Ile Ser Arg Arg Lys His Leu Phe Ser Arg
115 120 125

Asp Lys Leu Lys Leu Phe Leu Lys Gln His Cys Glu Pro Gln Asp Gly
130 135 140

Val Ile Lys Ile Lys Ala Ser Ser Leu Ser Thr Tyr Lys Ile Ala Glu
145 150 155 160

Gln Asp Phe Ser Tyr Phe Phe Pro Asp Asp Pro Pro Thr Phe Ile Phe
165 170 175

Ser Pro Ala Asn Arg Arg Arg Gly Arg Pro Pro Lys Arg Ile His Ile
180 185 190

Ser Gln Glu Asp Asn Val Ala Asn Lys Gln Thr Leu Ala Ser Tyr Arg
195 200 205

Ser Lys Ala Thr Lys Glu Arg Asp Lys Leu Leu Lys Gln Glu Glu Met
210 215 220

Lys Ser Leu Ala Phe Glu Lys Ala Lys Leu Lys Arg Glu Lys Ala Asp
225 230 235 240

Ala Leu Glu Ala Lys Lys Lys Glu Lys Glu Asp Lys Glu Lys Lys Arg
245 250 255

Glu Glu Leu Lys Lys Ile Val Glu Glu Glu Arg Leu Lys Lys Lys Glu
260 265 270

Glu Lys Glu Arg Leu Lys Val Glu Arg Glu Lys Glu Arg Glu Lys Leu
275 280 285

Arg Glu Glu Lys Arg Lys Tyr Val Glu Tyr Leu Lys Gln Trp Ser Lys
290 295 300

Pro Arg Glu Asp Met Glu Cys Asp Asp Leu Lys Glu Leu Pro Glu Pro
305 310 315 320

Thr Pro Val Lys Thr Arg Leu Pro Pro Glu Ile Phe Gly Asp Ala Leu
325 330 335

Met Val Leu Glu Phe Leu Asn Ala Phe Gly Glu Leu Phe Asp Leu Gln
340 345 350

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

Val Gly Asn Asp Ser Glu Gly Pro Leu Cys Glu Leu Leu Phe Phe Phe
370 375 380

Leu Thr Ala Ile Phe Gln Ala Ile Ala Glu Glu Glu Glu Glu Val Ala
385 390 395 400

Lys Glu Gln Leu Thr Asp Ala Asp Thr Lys Asp Leu Thr Glu Ala Leu
405 410 415

Asp Glu Asp Ala Asp Pro Thr Lys Ser Ala Leu Ser Ala Val Ala Ser
420 425 430

Leu Ala Ala Ala Trp Pro Gln Leu His Gln Gly Cys Ser Leu Lys Ser
435 440 445

Leu Asp Leu Asp Ser Cys Thr Leu Ser Asp Ile Leu Arg Leu His Ile
450 455 460

Leu Ala Ser Gly Ala Asp Val Thr Ser Ala Asn Ala Lys Tyr Arg Tyr
465 470 475 480

Gln Lys Arg Gly Gly Phe Asp Ala Thr Asp Asp Ala Cys Met Glu Leu
485 490 495

Arg Leu Ser Asn Pro Ser Leu Val Lys Lys Leu Ser Ser Thr Ser Val

500 505 510

Tyr Asp Leu Thr Pro Gly Glu Lys Met Lys Ile Leu His Ala Leu Cys
515 520 525

Gly Lys Leu Leu Thr Leu Val Ser Thr Arg Asp Phe Ile Glu Asp Tyr
530 535 540

Val Asp Ile Leu Arg Gln Ala Lys Gln Glu Phe Arg Glu Leu Lys Ala
545 550 555 560

Glu Gln His Arg Lys Glu Arg Glu Glu Ala Ala Ala Arg Ile Arg Lys
565 570 575

Arg Lys Glu Glu Lys Leu Lys Glu Gln Glu Gln Lys Met Lys Glu Lys
580 585 590

Gln Glu Lys Leu Lys Glu Asp Glu Gln Arg Asn Ser Thr Ala Asp Ile
595 600 605

Ser Ile Gly Glu Glu Glu Arg Glu Asp Phe Asp Thr Ser Ile Glu Ser
610 615 620

Lys Asp Thr Glu Gln Lys Glu Leu Asp Gln Asp Met Val Thr Glu Asp
625 630 635 640

Glu Asp Asp Pro Gly Ser His Lys Arg Gly Arg Arg Gly Lys Arg Gly
645 650 655

Gln Asn Gly Phe Lys Glu Phe Thr Arg Gln Glu Gln Ile Asn Cys Val
660 665 670

Thr Arg Glu Pro Leu Thr Ala Asp Glu Glu Glu Ala Leu Lys Gln Glu
675 680 685

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

Ala Cys Thr Asn Ile Phe Pro Leu Gly Arg Asp Arg Met Tyr Arg Arg
705 710 715 720

Tyr Trp Ile Phe Pro Ser Ile Pro Gly Leu Phe Ile Glu Glu Asp Tyr
725 730 735

Ser Gly Leu Thr Glu Asp Met Leu Leu Pro Arg Pro Ser Ser Phe Gln
740 745 750

Asn Asn Val Gln Ser Gln Asp Pro Gln Val Ser Thr Lys Thr Gly Glu
755 760 765

Pro Leu Met Ser Glu Ser Thr Ser Asn Ile Asp Gln Gly Pro Arg Asp
770 775 780

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His Ser Val Gln Leu Pro Lys Pro Val His Lys Pro Asn Arg Trp Cys
785                 790                 795                 800

Phe Tyr Ser Ser Cys Glu Gln Leu Asp Gln Leu Ile Glu Ala Leu Asn
                805                 810                 815

Ser Arg Gly His Arg Glu Ser Ala Leu Lys Glu Thr Leu Leu Gln Glu
            820                 825                 830

Lys Ser Arg Ile Cys Ala Gln Leu Ala Arg Phe Ser Glu Glu Lys Phe
        835                 840                 845

His Phe Ser Asp Lys Pro Gln Pro Asp Ser Lys Pro Thr Tyr Ser Arg
    850                 855                 860

Gly Arg Ser Ser Asn Ala Tyr Asp Pro Ser Gln Met Cys Ala Glu Lys
865                 870                 875                 880

Gln Leu Glu Leu Arg Leu Arg Asp Phe Leu Leu Asp Ile Glu Asp Arg
                885                 890                 895

Ile Tyr Gln Gly Thr Leu Gly Ala Ile Lys Val Thr Asp Arg His Ile
            900                 905                 910

Trp Arg Ser Ala Leu Glu Ser Gly Arg Tyr Glu Leu Leu Ser Glu Glu
        915                 920                 925

Asn Lys Glu Asn Gly Ile Ile Lys Thr Val Asn Glu Asp Val Glu Glu
    930                 935                 940

Met Glu Ile Asp Glu Gln Thr Lys Val Ile Val Lys Asp Arg Leu Leu
945                 950                 955                 960

Gly Ile Lys Thr Glu Thr Pro Ser Thr Val Ser Thr Asn Ala Ser Thr
                965                 970                 975

Pro Gln Ser Val Ser Ser Val Val His Tyr Leu Ala Met Ala Leu Phe
            980                 985                 990

Gln Ile Glu Gln Gly Ile Glu Arg  Arg Phe Leu Lys Ala  Pro Leu Asp
        995                 1000                1005

Ala Ser  Asp Ser Gly Arg Ser  Tyr Lys Thr Val Leu  Asp Arg Trp
    1010                1015                1020

Arg Glu  Ser Leu Leu Ser Ser  Ala Ser Leu Ser Gln  Val Phe Leu
    1025                1030                1035

His Leu  Ser Thr Leu Asp Arg  Ser Val Ile Trp Ser  Lys Ser Ile
    1040                1045                1050
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Leu Asn Ala Arg Cys Lys Ile Cys Arg Lys Lys Gly Asp Ala Glu
1055 1060 1065

Asn Met Val Leu Cys Asp Gly Cys Asp Arg Gly His His Thr Tyr
1070 1075 1080

Cys Val Arg Pro Lys Leu Lys Thr Val Pro Glu Gly Asp Trp Phe
1085 1090 1095

Cys Pro Glu Cys Arg Pro Lys Gln Arg Ser Arg Arg Leu Ser Ser
1100 1105 1110

Arg Gln Arg Pro Ser Leu Glu Ser Asp Glu Asp Val Glu Asp Ser
1115 1120 1125

Met Gly Gly Glu Asp Asp Glu Val Asp Gly Asp Glu Glu Glu Gly
1130 1135 1140

Gln Ser Glu Glu Glu Glu Tyr Glu Val Glu Gln Asp Glu Asp Asp
1145 1150 1155

Ser Gln Glu Glu Glu Glu Val Ser Leu Pro Lys Arg Gly Arg Pro
1160 1165 1170

Gln Val Arg Leu Pro Val Lys Thr Arg Gly Lys Leu Ser Ser Ser
1175 1180 1185

Phe Ser Ser Arg Gly Gln Gln Gln Glu Pro Gly Arg Tyr Pro Ser
1190 1195 1200

Arg Ser Gln Gln Ser Thr Pro Lys Thr Thr Val Ser Ser Lys Thr
1205 1210 1215

Gly Arg Ser Leu Arg Lys Ile Asn Ser Ala Pro Pro Thr Glu Thr
1220 1225 1230

Lys Ser Leu Arg Ile Ala Ser Arg Ser Thr Arg His Ser His Gly
1235 1240 1245

Pro Leu Gln Ala Asp Val Phe Val Glu Leu Leu Ser Pro Arg Arg
1250 1255 1260

Lys Arg Arg Gly Arg Lys Ser Ala Asn Lys Thr Pro Glu Asn Ser
1265 1270 1275

Pro Asn Phe Pro Asn Phe Arg Val Ile Ala Thr Lys Ser Ser Glu
1280 1285 1290

Gln Ser Arg Ser Val Asn Ile Ala Ser Lys Leu Ser Leu Gln Glu
1295 1300 1305

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Ser Glu Ser Lys Arg Arg Cys Lys Lys Arg Gln Ser Pro Glu Pro
1310 1315 1320

Ser Pro Val Thr Leu Gly Arg Arg Ser Ser Gly Arg Gln Gly Gly
1325 1330 1335

Val His Glu Leu Ser Ala Phe Glu Gln Leu Val Val Glu Leu Val
1340 1345 1350

Arg His Asp Asp Ser Trp Pro Phe Leu Lys Leu Val Ser Lys Ile
1355 1360 1365

Gln Val Pro Asp Tyr Tyr Asp Ile Ile Lys Lys Pro Ile Ala Leu
1370 1375 1380

Asn Ile Ile Arg Glu Lys Val Asn Lys Cys Glu Tyr Lys Leu Ala
1385 1390 1395

Ser Glu Phe Ile Asp Asp Ile Glu Leu Met Phe Ser Asn Cys Phe
1400 1405 1410

Glu Tyr Asn Pro Arg Asn Thr Ser Glu Ala Lys Ala Gly Thr Arg
1415 1420 1425

Leu Gln Ala Phe Phe His Ile Gln Ala Gln Lys Leu Gly Leu His
1430 1435 1440

Val Thr Pro Ser Asn Val Asp Gln Val Ser Thr Pro Pro Ala Ala
1445 1450 1455

Lys Lys Ser Arg Ile
1460